# Text Algorithms

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# 1. Introduction

## 1.1. Texts and their processing

One of the simplest and natural types of information representation is by means of written texts. Data to be processed often does not decompose into independent records. This type of data is characterized by the fact that it can be written down as a long sequence of characters. Such linear sequence is called a *text*. The texts are central in "word processing" systems, which provide facilities for the manipulation of texts. Such systems usually process objects which are quite large. For example, this book contains probably more than a million characters. Text algorithms occur in many areas of science and information processing. Many text editors and programming languages have facilities for processing texts. In biology, text algorithms arise in the study of molecular sequences. The complexity of text algorithms is also one of the central and most studied problems in theoretical computer science. It could be said that it is the domain where the practice and theory are very close together.

The basic textual problem is the problem called *pattern matching*. It is used to access information and probably many computers are solving in this moment this problem as a frequently used operation in some application system. Pattern-matching is comparable in this sense to sorting, or to basic arithmetic operations.

Consider the problem of a reader of the French dictionary "Grand Larousse", who wants all entries related to the word "Marie-Curie-Sklodowska". This is an example of a pattern matching problem, or string-matching. In this case, the word "Marie-Curie-Sklodowska" is the pattern. Generally we may want to find a string called a *pattern* of length $m$ inside a text of length $n$ where $n$ is greater than $m$. The pattern can be described in a more complex way to denote a set of strings and not only a single word. In many cases $m$ is very large. In genetics the pattern can correspond to a genome that can be very long, in image processing the digitized images sent serially take millions of characters each. The string-matching problem is the basic question considered in the book, together with its variations. String-matching is also the basic subproblem in very other algorithmic problems on texts. Below there is a (not exclusive) list of basic groups of problems discussed in the book :

variations on the string-matching problem, problems related to the structure of the segments of a text, data compression, approximation problems, finding regularities, extensions to two-dimensional images, extensions to trees, optimal time-space implementations, optimal parallel implementations.

The formal definition of the string-matching and many other problems is given in the next chapter. We introduce now some of them informally in the context of applications.

## 1.2 Text file facilities

The Unix system uses as a main feature text files for exchanging information. The user can get information from the files and transform them through different existing commands. The tools often behave as filters that read their input once and produce the output simultaneously. These tools can be easily connected with each others, and especially through the pipelining facility. This often reduces the creation of new commands to few lines of already existing commands.

One of these useful commands is *grep*, acronym of "general regular expression print". An example of the format of *grep* is

```
grep  Marie-Curie-Sklodowska  Grand-Larousse
```

provided "Grand-Larousse" is a file on your computer. The output of this command is the list of lines from the file which contain an occurrence of the word "Marie-Curie-Sklodowska".

This is an instance of the **string-matching** problem. Another example with a more complex pattern can be

```
grep  '^Chapter [0-9]'  Book
```

to list the titles of a book assuming titles begin with “Chapter” followed by a number. In this case the pattern denotes a set of strings (even potentially infinite), and not only one string. The notation to specify patterns is known as *regular expressions*. This is an instance of the **regular-expression-matching** problem.

The indispensable complement of *grep* is *sed* (stream editor). It is designed to transform its input. It can replace patterns of the input by specific strings. Regular expressions are also available with *sed*. But the editor contains an even more powerful notation. This allows, for instance, the action on a line of the input text containing twice same word. It can be applied to delete two consecutive occurrences of a same word in a text. This is both an instance of the **repetition-finding** problem, **pattern-matching** problem and, more generally, the problem of finding **regularities in strings**.

The very helpful matching device based on regular expressions is omnipresent in the Unix system. It can be used inside text editors such as *ed* and *vi*, and generally in almost all Unix commands. The above tools, *grep* and *sed*, are based on this mechanism. There is even a programming language based on pattern matching actions. It is the *awk* language, where the name *awk* comes from the initials of the authors, Aho, Weinberger and Kernighan. A simple *awk* program is a sequence of pattern-action statements :

```
pattern1 { action1 }
pattern2 { action2 }
pattern3 { action3 }
```

The basic components of this program are pattern to be find inside the lines of the current file. When a pattern is found, the corresponding action is applied to the line. So, several actions may be applied sequentially to a same line. This is an instance of the **multi-pattern matching** problem. The language *awk* is meant for converting data from one form to another form, counting things, adding up numbers and extracting information for reports. It contains an implicit input loop, and the pattern-action paradigm often eliminate control flow. This also frequently reduces the size of a program to few statements.

For instance, the following *awk* program prints the number of lines of the input that contain the word "abracadabra" :

```
abracadabra     { count++ }
END             { print count }
```

The pattern "END" matches the end of input file, so that the result is printed after the input has been entirely processed. The language contains nice features that strengthen the simplicity of the pattern matching mechanism, such as default initialization for variables, implicit declarations, and associative arrays providing arbitrary kinds of subscripts. All this makes *awk* a convenient tool for rapid prototyping.

The language *awk* can be considered as a generalization of another Unix tool, *lex*, aimed at producing lexical analyzers. The input of a lex program is the specification of a lexical analyzer by means of regular expressions (and few other possibilities). The output is the source in the C programming language of the specified lexical analyzer. A specification in *lex* is mainly a sequence of pattern-action statements as in *awk*. Actions are pieces of C code to be inserted in the lexical analyzer. At run time, these pieces of code execute the action corresponding to the associated pattern, when found.

The following line is a typical statement of a *lex* program :

```
[A-Za-z]+([A-Za-z0-9])*    { yylval = Install(); return(ID); }
```

The pattern specifies identifiers, that is, strings of characters starting with one letter and containing only letters and digits. The action leads the generated lexical analyzer to store the identifier and to return the string type "ID" to the calling parser.

It is another instance of the regular expression matching problem. The question of constructing **pattern-matching automata** is an important component having practical application in the *lex* software.

*Lex* is often combined with *yacc* and *twig* for the development of parsers, translators, compilers, or simply prototypes of these. *Yacc* allows the specification of a parser by grammar rules. It produces the source of the specified parser in C language. *Twig* is a tree-manipulation language that helps to design efficient code generators. It transforms a tree-translation scheme into a code generator based on a fast top-down tree-pattern matching algorithm. The output generator also uses dynamic programming techniques for optimization purposes but the essential feature is the tree-pattern matching action for tree rewriting. It has been shown, by experimental results on few significant applications, that *twig*-generated code generators are often faster than hand-generated compilers even when the latter incorporate some tricky optimizations. One of the basic problems considered for the design of such a tool is the **tree pattern-matching** problem.

Texts such as books or programs are likely to be changed during elaboration. Even after their achievement they often support periodic upgrades. These questions are related to **text comparisons**. Sometimes also we wish to find a string, and we do not completely remember it. The search has to be performed with a non entirely specified pattern. This is an instance of the **approximate pattern matching**.

Keeping track of all consecutive versions of a text sometimes does not help because the text can be very long and changes may be hard to find. The reasonable way to control the process is to have an easy access to differences between the various versions. There is no universal notion on what are the differences, nor conversely what are the similarities between two texts. However, it can be agreed that the intersection of two texts is a longest common subtext of both. This is called in our book the **longest common factor** problem. So that the differences between two texts are the respective complements of the common part. The Unix command *diff* builds on this notion.

Consider the texts A and B as follows (Molière's joke, 1670)

```
Text A : Belle Marquise,
         vos beaux yeux
         me font mourir d'amour
Text B : D'amour mourir me font,
         Belle Marquise,
         vos beaux yeux
```

The command `"diff A B"` produces

```
0a1
> D'amour mourir me font,
3d3
< me font mourir d'amour
```

An option of the command *diff* produces a sequence of *ed* instructions to transform one text into the other text. The similarity of texts can be measured as a minimal number of edit operations to transform one text into the other. The computation of such a measure is an instance of the **edit distance** problem.

## 1.3 Dictionaries

The search for words or patterns in static texts is a quite different question than the previous pattern matching mechanism. Usual dictionaries, for instance, are organized in order to speed up the access to entries. Another example of the same question is given by indexes. Technical books often contain an index of chosen terms that gives pointers to parts of text related to words in index. The algorithms involved in the creation of an index form a specific group.

The use of dictionaries or lexicons is often related to natural language processing. Lexicons of programming languages are small, and their representation is not a hard problem during the development of a compiler. A contrario, English contains approximatively 100,000 words, and even twice more if inflected forms are considered. In French inflected forms produce more than 500,000 words. The representation of lexicons of this size makes the problem a bit harder.

A simple use of dictionaries is made by spelling checkers. The Unix command *spell* reports the words of its input that are not stored in the lexicon. This rough approach does not yield a pertinent checker, but it practically helps to find typing errors. The lexicon used by *spell* contains around 70,000 entries stored within less than 60 kilobytes of random-access memory.

Quick access to lexicons is a necessary condition to produce good parsers. The data structure useful for such accesses is called an index. In our book indexes correspond to data structures representing all factors of a given (presumably long) text. We consider problems of the construction such structures : **suffix trees**, **directed acyclic word graphs**, **factor automata**, **suffix arrays**. The tool *PAT* developed at the NOED Center (Waterloo, Canada) is an implementation of one of these structures tailored to work on large texts. There are several applications that effectively require some understanding of phrases in natural languages, such as data retrieval systems, interactive softwares and character recognition.

An image scanner is a kind of photocopier. It is used to give a digitalised version of an image. When the image is the page of text, the natural output of the scanner must be a digital form available by a text editor. The transformation of a digitalised image of a text into a usual computer representation of the text is realized by an Optical Character Reader (OCR). Scanning a text with an OCR can be 50 times faster than retyping the text on a keyboard. OCR softwares are thus likely to become more common. But they still suffer from a high degree of imprecision. The average rate of errors in the recognition of characters is around one percent. Even if this may happen as rather small, this means that scanning a book produces around one error per line. This is to be compared with the usual very high quality of texts checked by specialized persons. Technical improvements on the hardware can help to eliminate certain kinds of errors occurring on scanned texts in printed forms. But this cannot avoid the problem of recognizing texts written by hand. In this case, isolation of characters is much harder, and ambiguous forms can be encountered at recognition stage. Reduction on the number of errors can thus only be achieved by considering the context of characters, which assumes some understanding of the text. Image processing is related to the problem of **two-dimensional pattern matching**. Another related problem is the data structure for all subimages, this is discussed in the book in the context of the **dictionary of basic factors (subimages)**.

No system is presently able to parse natural languages. Indeed, it is questionable whether such an effective system can exist. Words are certainly units of syntax in languages, but they are not units of meaning. This is both because words can have several meanings, and because they can be parts of compound phrases that carry a meaning only as a whole. It appears that the proportion in the lexicon (of French and several other European languages) of idiomatic sentences, of metaphoric and technical sentences whose meaning cannot be inferred from their elements, is very high. The natural consequence is that compound expressions and the so-called frozen phrases must be included in computerized dictionaries. The data base must also incorporate at least the syntactic properties of the elements. At present, no complete dictionary established according to these principles exists. This certainly represent of huge amount of data to be collected but this seems an indispensable work. Data bases for the European languages, French, English, Italian, and Spanish are presently being built. And studies on Arabic, Chinese, German, Korean and Madagascan have been performed. These question are studied, for instance, at LADL (Paris), and the reader can refer to [Gr 91] for more information on specific aspects of computational linguistics.

The theoretical approach to the representation of lexicons is by means of trees or finite state automata. It appears that both approaches are equally efficient. This shows the practical importance of the **automata theoretic approach** to text problems. We have shown at LITP (Paris) that the use of automata to represent lexicons is particularly efficient. Experiments have been done on a 500,000 word lexicon of LADL (Paris). The representation supports direct access to any word of the lexicon and takes only 300 kbytes of random-access memory.

## 1.4 Data compression

One of the basic problems in keeping a large amount of textual information is the **text compression** problem. Text compression means reducing the representation of a text. It is assumed that the original text can be recovered from its compressed form. No loss of information is allowed. Text compression is related to **Huffman coding problem** and the **factorization problem**. This kind of compression contrasts with other kind of compression technics applied to sounds or images, where approximation is acceptable. Availability of large mass storage does not decrease the interest for compressing data. Indeed, users always use extra available space to store more data or new kind of data. Moreover the question remains important for storing data on secondary storage devices.

Examples of implementations of dictionaries reported above show that **data compression** is important in several domains related to natural language analysis.

Text compression is also useful for telecommunications. It actually reduces the time to transmit documents via telephone networks, for instance. The success of Fax is perhaps to be credited to compression technics.

General compression methods often adapts themselves to the data. This phenomenon is central in getting high compression ratios. But, it appears in practice that methods tailored for specific data lead to the best results. We have experimented this fact on data sent by "géostationnaires" satellites. The data have been compressed to 7% without any loss of information. The compression is very successful if there are redundancies and regularities in the information message. The analysis of data is related to the problem of **detecting regularities in texts**. Efficient algorithms are particularly useful to expertize the data.

## 1.5 Applications of text algorithms in genetics

Molecules of nucleic acids carry a large part of information about the fundamental determinants of life, and in particular about the reproduction of cells. There are two types of nucleic acids known as desoxyrybonucleic acid (DNA) and ribonucleic acid (RNA). DNA is usually found as double-stranded molecules. In vivo, the molecule is folded up like a ball of string. The skeleton of a DNA is a sequence on the four-letter alphabet of nucleotides : adenine (A), guanine (G), cytosine (C), and thymine (T). RNA molecules is usually single-stranded composed of ribonucleotides : A, G, C, and uracil (U). Processes of "transcription" and "translation" lead to the production of proteins, which have also a primary structure as a string composed of 20 amino acids. In a first approach all these molecules can be viewed as texts. The discovery of powerful sequencing techniques fifteen years ago has led to a rapid accumulation of sequence data (more than 10 million nucleotides of sequences). From the collect of sequences up to their analysis a lot of algorithms on texts are implied. Moreover, only fast algorithms are often feasible because of the huge amount of data.

Collecting sequences is made through gel audioradiographs. The automatic transcription of these gels into sequences is a typical **two-dimensional pattern matching** problem in two dimensions. The reconstruction of a whole sequence from small segments is another example of problem that occurs during this step. This problem is called the **shortest common superstring problem** : construction of the shortest text containing several given smaller texts.

Once a new sequence is obtained, the first important question on it is whether it resembles to any other sequence already stored in databanks. Before adding a new molecular sequence into an existing database one needs to know whether the sequence is already present or not. The comparison of several sequences is usually realized by writing one over another. The result is known as an alignment of the set of sequences. This is a common display in molecular biology that can gives an idea on the evolution of the sequences though the mutations, insertions and deletions of nucleotides. Alignment of two sequences is the **edit distance problem** : compute the minimal number of edit operations to transform one string into another. It is realized by algorithms based on dynamic programming techniques similar to the one used by the Unix command *diff*. A tool, called *agrep*, developed at the University of Arizona is devoted to these questions, related to **approximate string-matching**.

Further questions on sequences are related to their analysis. The aim is to discover the functions of all parts of the sequence. For instance, DNA sequences contain important regions (coding sequences) for the production of proteins. But, no good answer is presently known to find all coding sequences of a DNA sequence. Another question on sequences is the reconstruction of their three-dimensional structure. It seems that a part of the information resides in the sequence itself. This is because during the folding process of DNA, for instance, nucleotides match pairwise (A with T, and C with G). This produces approximate palindromic symmetries (as TTAGCGGCTAA). Involved in all these questions are **approximate searches** for specific patterns, for **repetitions**, for **palindromes** or any other **regularities**. The problem of the **longest common subsequence** is a variation of the alignment of sequences.

## 1.6 Structure of the book

The structure of our book reflects both the relationships between applications of text algorithmic techniques and the classification of algorithms according to the measures of complexity considered. The book can be viewed as a "parade" of algorithms in which our main aim is to discuss the foundations of these algorithms and their interconnections.

The book begins with the algorithmic and theoretical foundations: machine models, discussion on algorithmic efficiency, review of basic problems and their interaction, and some combinatorics on words. It is chapter 2.

The topic of Chapters 3 and 4 is STRING-MATCHING. The chapters deal with two famous algorithms, Knuth-Morris-Pratt and Boyer-Moore algorithms respectively. The upmost improvements and results on these algorithms are incorporated. We discuss here those string-matching algorithms which are efficient with respect to only one measure of complexity — sequential time. Hence, the chapter can be treated as a "warm-up" for other chapters devoted to the same topic. We later discuss in Chapter 13 more difficult algorithms — TIME-SPACE OPTIMAL STRING-MATCHING algorithms that work in linear time and simultaneously use only a very small additional memory. The consideration of two complexity measures together usually leads to most complicated algorithms. Chapters 3 and 4 can also be treated as a preparation to Chapters 9 and 14 where are presented advanced PARALLEL STRING-MATCHING algorithms, and to Chapter 12 that deals with two-dimensional pattern matching.

Chapters 5 and 6 are basic chapters of the book. They cover data structures representing succinctly all subwords of a text, namely, SUFFIX TREES and SUBWORD GRAPHS. The considerations are typical from the point of view of data structures manipulations : trees, links, vectors, lists, etc. The prepared data structures are used later in the discussion on other problems; especially in the computation of the longest common factor of texts, factorization problems and finding squares in words. Also it is used to construct in Chapter 7 certain kind of automata related to string-matching.

Chapter 7 gives an automata theoretical approach to string-matching that leads to a natural solution of the MULTI-PATTERN MATCHING problem. It covers Aho-Corasick automata for multi-pattern matching, automata for the set of factors and suffixes of a given text, and application of them.

Chapter 8 considers REGULARITIES IN TEXTS: SYMMETRIES AND REPETITIONS. It covers problems related to symmetries of words as well as problems related to repetitions. Surprisingly it turns out that finding a palindrome in a word in linear time is much easier than finding a square. Generally, problems related to symmetries are easier than that related to repetitions. The basic component of the chapter is a new data structure, called the dictionary of basic factors, that is introduced as a basic technique for the development of efficient, but not necessarily optimal, algorithms.

Chapter 9 deals with PARALLEL ALGORITHMS ON TEXTS. Only one, very general model of parallel computations is considered. The parallel implementation and applications of the dictionary of basic factors, suffix trees and subword graphs are presented. We discuss parallel version of the Karp-Miller-Rosenberg algorithm (Chapter 8) and some computations related to trees.

Chapter 10 is about data compression. It discusses only some of the COMPRESSION TECHNIQUES FOR TEXTS. This area is exceptionally broad as compression of data is the vital part of many real world systems. We focus on few important algorithms. Two of the subjects here are the Ziv-Lempel algorithm, and applications of data structures from Chapters 5 and 6 to the text factorization.

Questions related to algorithms involving the notion of APPROXIMATE PATTERNS are presented in Chapter 11. It starts with algorithms to compute edit distance of sequences (alignment of sequences). Two specific classical notions on approximate patterns are then considered, the first for string-matching with errors, and the second for patterns with “don’t care” symbols.

TWO-DIMENSIONAL PATTERN MATCHING, in Chapter 12, is the problem of identifying a subimage inside a larger one. The notion naturally extends that of pattern matching in texts. Basic techniques on the subject show the importance of algorithms presented in Chapter 7.

Chapter 13 presents three different TIME-SPACE OPTIMAL STRING-MATCHING algorithms. None of them have never appeared in a textbook nor even in a journal, and the third one is presented in a completely new version. This is an advanced material since the algorithms rely heavily on the combinatorics of words, mostly related to periodicities.

The discussion on OPTIMAL PARALLEL ALGORITHM ON TEXTS is the subject of Chapter 14. It includes more technical considerations than Chapter 9. Are presented there the well-known Vishkin's algorithm and a recent optimal parallel algorithm for string-matching, based on suffix versus prefix computations, designed by Kedem, Landau and Palem.

The last chapter considers several miscellaneous problems like tree-pattern matching problem, or the computation shortest common superstrings, maximal suffixes, Lyndon factorizations

One can partition algorithmic problems discussed in this book into practical and theoretical problems. Certainly the string-matching and data compression are in the first class, while most problems related to symmetries and repetitions are in the second. However we believe that all the problems are interesting from an algorithmic point of view and enable the reader to appreciate the importance of combinatorics on words. In most textbooks on algorithms and data structures the presentation of efficient algorithms on words is quite short as compared to issues in graph theory, sorting, searching and some other areas. At the same time, there are many presentations of interesting algorithms on words accessible only in journals and in the form directed mainly to specialists. We hope that this book will cover a gap on algorithms on words in the book literature, and bring together many results presently dispersed in the masses of journal articles.

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# 2. Foundations

The chapter gives algorithmic and theoretical foundations required in further parts of the book. The models of computations are discussed, and basic problems on texts are exposed in a precise way. The chapter ends with combinatorial properties of texts.

## 2.1. Machine models and presentation of algorithms

The model of sequential computations is a Random Access Machine (RAM). Evaluation of the time complexity of algorithms is done according to the uniform cost criterion, i.e. one time unit per basic operation. However, to avoid "abuses" of the model, the sizes of all integers occurring in algorithms will be "reasonable". The integers will be within a polynomial range of input size and can be represented by a *logarithmic numbers* of bits. We refer the reader to *The design and analysis of computer algorithms* by A.V. Aho J.E. Hopcroft and J.D. Ullman for more details on the RAM model.

The sequential algorithms of this book are mainly presented in Pascal programming language. Few more complex algorithms are written in an informal language, in a style and a semantic similar to that of Pascal. Sometimes, the initial algorithm for a given problem is usually more understandable using a kind of a pseudo-language. In this language we can use a terminology appropriate to the natural model for the problem. The flow-of-control constructs can be the same as in Pascal, but with the advantage of having informal names for objects. For example, in algorithms on trees we can use notions such as "next son", or "father of the father", etc. In this situation, an informal algorithm is given to catch the main ideas of the construction. We generally attempt to convert such an informal algorithm into a Pascal program.

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *a* | | *t* | *e* | *x* | *t* | | *a* | *s* | | *a* | *n* | | *a* | *r* | *r* | *a* | *y* | |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 |

**Figure 2.1**. Array representation of a text.

We consider texts as arrays of characters. We stick to the convention that indices of characters of a text run from 1 to the length of the text. The symbols of a text *text* of length *n* are stored in *text*[1], *text*[2], ..., *text*[*n*]. We may assume that location *text*[*n*+1] contains a special character.

Throughout the book, we consider two global variables *pat* and *text* that are declared by

```
var text : text_type; pat : pattern_type;
```

The types can be themselves defined by

```
type text_type = array[1..n] of char ;
     pattern_type = array[1..m] of char,
```

assuming that *n* and *m* are Pascal integer constants declared in a proper way.

We assume a lazy evaluation of boolean expressions. For instance, the expression

```
(i>0) and (t[i]=c)
```

is false when *i*=0, even if *t*[0] does not exists. And the expression

```
(i=0) or (t[i]=c)
```

is true under the same conditions. Replacing all boolean expression to avoid the convention is a straightforward exercise. Doing it in the presentation of algorithms would transform them into an unreadable form.

Pascal functions are presented in the book with the nonstandard (but common) "return" statement. Such instruction exists in almost all modern languages and helps writing more structured programs. The meaning of the statement "**return**(*expression*)" is that the function returns the value of the expression to the calling procedure, and then stops. The following function shows an application of the return statement.

```
function text_inequality(text1, text2: text_type): boolean;
begin
{ left-to-right scan of text1  and text2 }
  m := length(text1); n := length(text2);
  j := 0;
  while j <= min(m, n) do
  { the prefixes of size j are the same }
    if text1[j+1]=text2[j+1] then j := j+1
    else return(true);
  return(false);
end;
```

The "**return**" statement is very useful to shorten the presentation of algorithms. It is also easy to implement. It can be replaced by

```
text_inequality := expression; goto L
```

where L is the label of the last **end** of the function.

The following description of the function *text_inequality* is equivalent to the above text.

```
function text_inequality(text1, text2: text_type): boolean;
label 1992;
begin
{ left-to-right scan of text1  and text2 }
  m := length(text1); n := length(text2);
  j := 0;
  while j <= min(m, n) do
  { the prefixes of size j are the same }
    if text1[j+1]=text2[j+1] then j := j+1
    else begin text_inequality:=true; goto 1992 end;
  text_inequality:= false;
1992: end;
```

Several models of sequential computations more theoretical than the RAM are relevant to text processing : Turing machines, multihead finite automata etc. For example, it is known that string-matching can be done in real time on a Turing machine or even on a multihead finite automaton (without any memory but with constant number of heads). Generally, we do not discuss algorithms on such highly theoretical models; in a few cases we only give some brief remarks related to the computations on these models.

Concerning parallel computations, a very general model is assumed, since we are mainly interested in exposing the parallel nature of some problems without going into the details of the parallel hardware. The parallel random access machine (PRAM), a parallel version of the random accessed machine is used as a standard model for presentation of parallel algorithms.

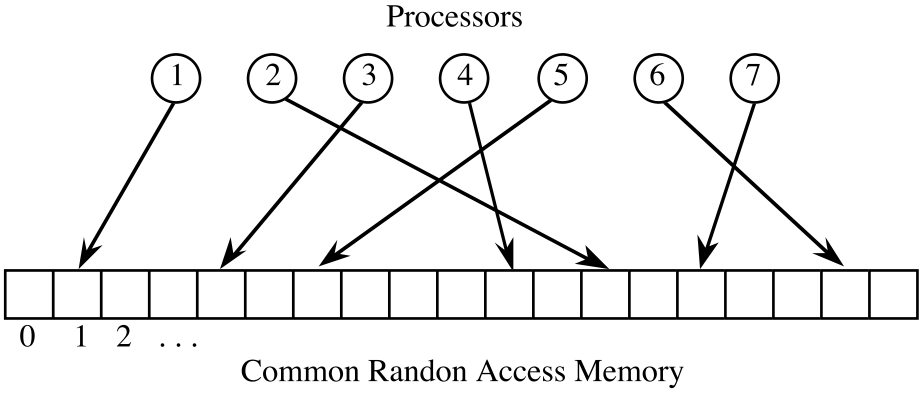

**Figure 2.2**. PRAM machine.

The PRAM consists of a number of processors working synchronously and communicating through a common random access memory. Each processor is a random access machine with the usual operations. The processors are indexed by the consecutive natural numbers, and they synchronously execute the same central program; however, the action of a given processor depends also on its number (known to the processor). In one step, a processor can access one memory location. The models differ with respect to simultaneous access of the same memory location by more than one processor. For the CREW (concurrent read, exclusive write) variety of PRAM machine any number of processors can read from the same memory location simultaneously, but write conflicts are not allowed : no two processors can attempt to write simultaneously into the same location.

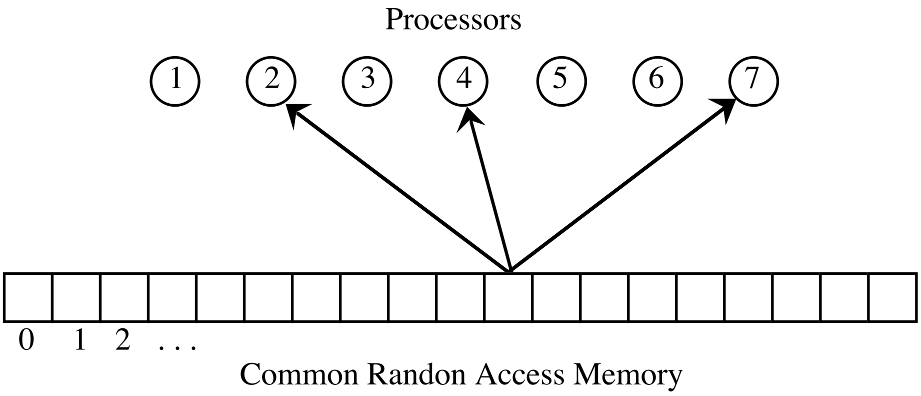

**Figure 2.3**. A Concurrent Read.

We denote by CRCW (concurrent read, concurrent write) the PRAM model in which, in addition to concurrent read, write conflicts are allowed : many processors can attempt to write into the same location simultaneously but only if they all attempt to write the same value.

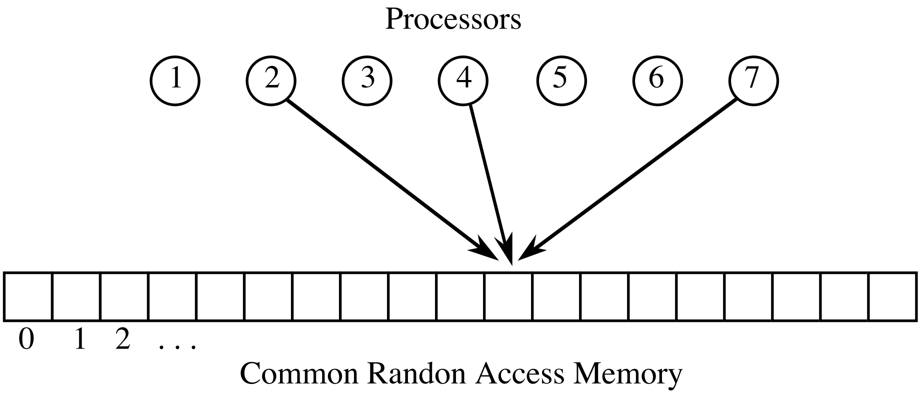

**Figure 2.4**. A Concurrent Write.

Parallel algorithms are presented in a similar way as in *Efficient parallel algorithms* by A. Gibbons and W. Rytter. There is no generally accepted universal language for the presentation of parallel algorithms. The PRAM is a rather idealized model. We have chosen this model as a best suitable for the presentation of algorithms and especially for the presentation of the inherent parallelism of some problems. This would be difficult to nicely present these algorithms with languages oriented towards concrete existing hardware of parallel computer. Moreover, the PRAM model is widely accepted in the literature on parallel computation on texts.

Parallelism will be expressed by the following type of parallel statement :

```
for all i in X in parallel do action(i).
```

Execution of this statement consists of :

— assigning a processor to each element of *X*;

— executing in parallel by assigned processors the operations specified by action(i).

Usually the part "*i* in *X*" looks like "$1 \le i \le n$" if *X* is an interval of integers. We discuss this more deeply in Chapter 7.

## 2.2. Efficiency of algorithms

Efficient algorithms can be classified according to what we mean by efficiency. There are different notions of efficiency depending on the complexity measure involved. Several such measures are discussed in this book : sequential time, memory space, parallel time and number of processors. Our book deals with "feasible" problems. We can define them as problems having efficient algorithms, or as solvable in time bounded by a small-degree polynomial. In the case of sequential computations we are interested to lower down the degree of the polynomial corresponding to time complexity. The most efficient algorithms usually solve a problem in linear time complexity. We are also interested in space complexity. Optimal space complexity often means constant number of (small integer) registers in addition to input data. So, we say that an algorithm is time-space optimal iff it works simultaneously in linear time and constant extra space. These are the most advanced sequential algorithms, and the most interesting also both from practical and theoretical point of view.

In the case of parallel computations we are generally interested in the parallel time $T(n)$ as well as in the number of processors $P(n)$ required for the execution of the parallel algorithm. The total number of elementary operations performed by the parallel algorithm is not greater than the product $T(n)P(n)$. Efficient parallel algorithms are those that operate in no more than polylogarithmic (a polynomial of log's of input size) time with a polynomial number of processors. The class of problems solvable by such algorithms is denoted by NC and we call the related algorithms NC-algorithms. A NC-algorithm is optimal iff the total number of operations $T(n)P(n)$ is linear. Another possible definition is that this number is essentially the same as the time complexity of the best known sequential algorithm solving the given problem. However we adopt here the first option because algorithms on strings usually have a time complexity at least linear.

Evaluating precisely the complexity of an algorithm according to some measure is often difficult, and moreover it is unlikely to be of some use. The “big O” notation makes clear what are the important terms of a complexity expression. It estimates the asymptotic order of the complexity of an algorithm and helps to compare algorithms between each other. Recall that if $f$ and $g$ are two function from and to integers, then we say that $f = O(g)$ if $f(n) \leq C.g(n)$ when $n > N$, for some constants $C$ and $N$.

We write $f = \Theta(g)$ when the functions $f$ and $g$ are of the same order, which means that both equalities $f = O(g)$ and $g = O(f)$ hold.

Comparing functions through their asymptotic orders leads to these kind of inequalities : $O(n^{0.7}) < O(n) < O(n.\log(n))$, or $O(n^{\log(n)}) < O(\log(n)^n) < O(n!)$.

Within sequential models of machine one can distinguish further types of computations : off-line, on-line and real-time. These types are related also to efficiency. It is understood that real-time computations are more efficient than general on-line, and that on-line computations are more efficient than off-line. Each algorithm is an off-line algorithm : "off-line" conceptually means that the whole input data can be put into the memory before the actual computation starts. We are not interested then in the intermediate results computed by the algorithm, but only the final result is sought (though this final result can be a sequence or a vector). The time complexity is measured by the total time from the moment the computation starts (with all input data previously memorized) up to the final termination. In contrast, an on-line algorithm is like a sequential transducer. The portions of the input data are "swallowed" by the algorithm step after step, and after each step an intermediate result is expected (related to the input data read so far). It then reads the next portion of the input, and so on. In on-line algorithms the input can be treated as an infinite stream of data, and so we are not mainly interested in the termination of the algorithm for all such data. The main interest for us is the total time $T(n)$ for which we have to wait to get the $n$-th first outputs. The time $T(n)$ is measured starting at the beginning of the whole computation (activation of the transducer). Suppose that the input data is a sequence and that after reading the $n$-th symbol we want to print "1" if the text read to this moment contains a given pattern as a suffix, otherwise we print "0". Hence we have two streams of data : the stream of input symbols and an output stream of answers "1" or "0". The main feature of the on-line algorithm is that we have to give an output value before reading the next input symbol.

The real time computations are these on-line algorithms which are in a certain sense optimal; the elapsing time between reading two consecutive input symbols (the time spent for computing only the last output value) should be bounded by a constant. Most linear on-line algorithms are in fact real-time.

We are mostly interested in off-line computations whose worst case time is linear, however also on-line and real-time computations as well as average complexities will be sometimes shortly discussed in the book.

## 2.3. Notation and formal definitions of basic problems on texts

Let $A$ be an input *alphabet* — a finite set of symbols. Elements of $A$ are called the *letters*, the *characters*, or the *symbols*. Typical examples of alphabets are : the set of all ordinary letters, or the set of binary digits. The texts (also called words or strings) over $A$ are sequences of elements of $A$. The length (size) of a text is the number of its elements (with repetitions). So, the length of *aba* is 3. The length of a word $x$ is denoted by $|x|$. The input data for our problems will be words and the size $n$ of the input problem will be usually the length of the input word. In some situations, $n$ will denote the maximum length or the total length of several words if the input of the problem consists of several words.
The $i$-th element of the word $x$ is denoted by $x[i]$ and $i$ is its position in $x$. We denote by $x[i\ldots j]$ the subword $x[i]x[i+1]\ldots x[j]$ of $x$. If $i>j$, by convention, the word $x[i\ldots j]$ is the empty word (the sequence of length zero).

We say that the word $x$ of length $n$ is a *factor* (also called a subword) of the word $y$ if $x=y[i+1\ldots i+n]$ for some integer $i$. We also say that $x$ *occurs in* $y$ *at position* $i$ or that the position $i$ is a *match* for $x$ in $y$.

We define also the notion of a *subsequence* (sometimes called a subword). The word $x$ is a subsequence of $y$ if $x$ can be obtained from $y$ by removing zero or more (non necessarily adjacent) letters from it. Equivalently $x$ is a subsequence of $y$ if $x=y[i_1]y[i_2]\ldots y[i_m]$, where $i_1$, $i_2$, …, $i_m$ is an increasing sequence of indices in $y$.

Below we define basic problems and groups of problems covered in the book. We often consider two texts *pat* (the pattern) and *text* of respective lengths $m$ and $n$.

**1. String-matching** (the basic problem)

Given texts *pat* and *text*, verify if *pat* occurs in *text*. Hence it is a decision problem : the output is a boolean value. It is usually assumed that $m\leq n$. So, the size of the problem is $n$.
A slightly advanced version is to search for all occurrences of *pat* in *text*, that is, to compute the set of positions of *pat* in *text*.. Denote by *MATCH*(*pat*, *text*) this set. In most cases an algorithm computing *MATCH*(*pat*, *text*) is a trivial modification of the decision algorithm, hence we sometimes present only the decision algorithm for string-matching.

Instead of one pattern one can consider a finite set of patterns and ask if a given text *text* contains a pattern from this set. The size of the problem is now the total length of all patterns plus the length of *text*.

**2. Construction of string-matching automata**

For a given pattern *pat*, construct the minimal deterministic finite automaton accepting all words containing *pat* as a suffix. Denote such an automaton by *SMA*(*pat*). A more general problem is to construct a similar automaton *SMA*($\prod$) accepting the set of all words containing as a suffix one of the patterns from the set $\prod=\{pat_1, \ldots, pat_k\}$.

## 3. Approximate string-matching

We are given again a pattern *pat* and a text *text*. The problem consists in finding an approximate occurrence of *pat* in *text*, that is, a position *i* such that *dist*(*pat*, *text*[*i*+1…*i*+*m*]) is minimal. Another instance of the problem is to find all positions *i* such that *dist*(*pat*, *text*[*i*+1…*i*+*m*]) is less than a given constant. Here, *dist* is a function defining a distance between two words. There are two standard distances : the Hamming distance (number of positions at which two strings differ) and the edit distance (see Problem 7 below).

## 4. String-matching with don't care symbols

We are given a special universal symbol ø that matches any other symbol (including itself). It is called the “don't care symbol”. In fact, ø can be a common name for several unimportant symbols of the alphabet. For two symbols *a* and *b*, we write *a*≈*b* iff they are equal or at least one of them is a don't care symbol. For two words of the same length we write *x*≈*y* if, for each *i*, *x*[*i*]≈*y*[*i*].

The problem consists in verifying whether *pat*≈*text*[*i*+1…*i*+*m*] for some *i*, or more generally, to compute the set of all such positions *i*.

## 5. Two-dimensional pattern matching

For this problem, the pattern *pat* and the text *text* are two-dimensional arrays (or matrices) whose elements are symbols. We are to answer whether *pat* occurs in *text* as a subarray, or to find all positions of *pat* in *text* . The approximate and don't care versions of the problem can be defined similarly as for the (one-dimensional) string-matching problem.

Instead of arrays one can also consider some other "shapes", e.g. trees.

## 6. Longest common factor

Compute the maximal length of longest common factors of two words *x*, *y* (denoted by *LCF*(*x*, *y*)). One can consider also longest common factors for more than two words.

## 7. Edit distance

Compute the edit distance, *EDIT*(*x*, *y*), between two words. It is the minimal number of edit operations needed to transform one string into the other. Edit operations are : insertion of one character, deletion of one character, and change of one character.

The problem is closely related to the approximate string-matching and to the problem defined below. It is similar to the notion of alignment of DNA sequences in Molecular Biology.

## 8. Longest common subsequence

Compute the maximal length of common subsequences of two words *x*, *y*. The length is denoted by *LCS*(*x*, *y*). Note that several subsequences may have this length and that we may also want to compute one or all this words.

This problem is related to the edit distance problem as follows :
if *l*=*LCS*(*x*, *y*), then one can transform *x* to *y* by first deleting *m-l* symbols of *x* (all but those of a longest common subsequence) and then inserting *n-l* symbols to get *y*. So, the computation of *LCS*'s is a particular case of the computation of edit distances.

### 9. Longest repeated factor

We are to compute a longest factor *x* of the text *text* that occurs at least twice in *text*. Its length is denoted by *LRF*(*text*). Similarly we can consider a longest factor that occurs at least *k* times in *text*. Its length is $LRF_k$(*text*).

### 10. Finding squares and powers

A much harder problem is that of computing the consecutive repetitions of a same factor. A square word (or simply a square) is a nonempty word of the form *xx*. Let us define the predicate *Square-free*(*text*) whose value is 'true' iff *text* does not contain any square word factor. Similarly one can define cubes and the predicate *Cube-free*(*text*). Generally one can define the predicate $Power\text{-}free_k$(*text*) whose value is 'true' iff *text* does not contain any factor of the form $x^k$ (with *x* non-empty).

These problems have seemingly no practical application. However, they are related to the most classical mathematical problems on words (whose investigation started at the beginning of this century).

### 11. Computing symmetries in texts

The word *x* is symmetrical if *x* is equal to its reversed $x^R$. A palindrome is any symmetrical word containing at least two letters (a one-letter word has an uninteresting obvious symmetry!). Even palindromes are palindromes of an even length.
Denote by *Pal* and *P* the set of all palindromes and the set of even length palindromes, respectively.

There are several interesting problems related to symmetries. Compute *PREFPAL*(*text*), the length of the shortest prefix of *text* that is a palindrome. Another interesting problem is to find all factors of the text that are palindromes. Or, compute *MAXPAL*(*text*), the length of a longest symmetrical factor of *text*. .

Another question is to count the number of all palindromes which are factors of *text*. A word is called a *palstar* if it is a composition of palindromes (it is contained in the language $Pal^*$); it is an *even palstar* if it is a composition of even palindromes. Two algorithmic problems related to palstars are : verify if a word is a palstar, or an even palstar.

Instead of asking about the composition of some number of palindromes we can be interested in compositions of a fixed number *k* of palindromes. Let $P_k(text)$ be the predicate whose value is true if *text* is a composition of *k* even palindromes; analogously we can define $Pal_k(text)$ as a predicate related to compositions of any *k* palindromes (odd or even)

**12. Number of all distinct factors**

The problem is to compute the number of all distinct factors of *text*. Observe that there is a quadratic number of factors, while linear time algorithm is possible. Such a linear time counting of a quadratic number of objects is possible due to succinct (linear-sized) representations of the set of all factors of a given text.

**13. Maximal suffix**

Compute the lexicographically maximal suffix of the word *text* (it is denoted by *maxsuf*(*text*) ). Observe that the lexicographically maximal suffix of a text is the same as its lexicographically maximal factor. The lexicographic order is the same order as used, for example, commonly in encyclopaedias or dictionaries (if we omit the question of accents, uppercase letters, hyphens, …).

**14. Cyclic equivalence of words**

Check whether two words *x* and *y* are cyclically equivalent, that is to say, whether *x*=*uv*, *y*=*vu* for some words *u*, *v*. A straightforward linear time algorithm for this problem can be constructed by applying a string-matching procedure to the pattern *pat*=*x* and the text *text*=*yy*. However it is possible to design a much simpler efficient algorithm.

**15. Lyndon factorization**

Compute the decomposition of the text into a non-increasing sequence of Lyndon words Lyndon words are lexicographically (strictly) minimal within the set of all their cyclic shifts. It is known that any word can be uniquely factorized into a sequence of Lyndon words

**16. Compression of texts**

For a given word *text* we would like to have a most succinct representation of *text*. The solution depends on what we mean by a representation. If by representation we mean an encoding of single symbols by binary strings, then, we have the problem of the efficient construction of Huffman codes and Huffman trees. Much more complicated problems arise if some parts of the text *text* are encoded using other parts of the text. This leads to some factorization and textual substitution problems. We spend a whole chapter on this subject.

**17. Unique decipherability problem**

We have a code which is a function *h* assigning to each symbol *a* of the alphabet *K* a word over an alphabet *A*. The function can be in a natural way extended to all words over the alphabet *K* using the equality $h(xy)=h(x)h(y)$. We ask whether the so-extended function is one-to-one (denote by *UD*(*h*) the corresponding predicate). The size *n* of the problem is the total length of all codewords *h*(*a*) over all symbols *a* in *K*.

The next three problems are related to the construction of a succinct (but useful) representation of sets of all factors or all suffixes of a given word *text*. Denote by *Fac*(*text*), *Suf*(*text*) the set of all respectively factors, suffixes of *text*. There can be a quadratic number of elements to be represented but the size of the representation is required to be linear. Moreover, we also require that the construction time is linear in time.

### 18. Suffix trees

The set *Fac*(*text*) is prefix closed. This means that prefixes of words in *Fac*(*text*) are also elements of the set. The natural representation for each prefix closed set *F* of words is a tree *T1* whose edges are labelled with symbols of the alphabet. The set *F* equals the set of labels of all paths from the root down to nodes of the tree. However, such a tree *T1* corresponding to *Fac*(*text*) can be too large. It can have a quadratic number of internal nodes. Fortunately, the number of leaves is always linear and hence the number of internal nodes having at least two sons (out-degree bigger than one) is also linear. Hence, we can construct a tree *T* whose nodes are all "essential" internal nodes and leaves of *T1*. The edges of *T* correspond to maximal paths (chains) in *T1* consisting only of nodes of out-degree one; the label of each such edge is the composite label of all edges of the corresponding chain. Denote the constructed tree *T* by *ST*(*text*). It is called the suffix (or the factor) tree of *text*. The size of the suffix tree is linear and we present also a linear time algorithm to construct it.

The suffix tree is a very useful representation of all factors; the range of applications is essentially the same as of two other data structures considered below : suffix and factor automata.

### 19. Smallest suffix automata and directed acyclic word graphs

Compute the smallest deterministic finite automaton *SA*(*text*) accepting the set *Suf*(*text*) of all suffixes of *text*. The size of the automaton turns out to be linear and we even prove later that its size does not depend on the size of the alphabet (if transitions to dead state are not counted). The automaton *SA*(*text*) is essentially the same data structure as the so-called directed acyclic word graph (dawg, for short). Dawg's are directed graphs whose edges are labelled by symbols, and such a graph represents the set of all words "spelled" by its paths from the root to the sink.

Dawg's are (in a certain sense) more convenient than suffix trees because each edge of the dawg is labelled by a single symbol, while edges of factor trees are labelled by words of varying lengths. It is possible to consider compacted versions of dagw’s though.

## 20. Smallest factor automata

Construct the smallest deterministic automaton *FA*(*text*) accepting the set *Fac*(*text*) of all factors of *text*. This is almost the same problem as the previous one. It will be shown that the size of *FA*(*text*) does not exceed the size of *SA*(*text*). In fact the suffix automaton also accepts (after a minor modification) the set *Fac*(*text*) of all factors. In most applications *SA*(*text*) can be used instead of *FA*(*text*) and the order of magnitude of the complexity does not change very much. However, the factor automaton is the most optimal representation of the set of all subwords.

## 21. Equivalence of two words over a partially commutative alphabet

Let $C$ be a binary relation on the alphabet. This relation represents the commutativity between pair of symbols. The only necessary property of this relation is that it should be symmetric. Two words are equivalent according to $C$ ($x \approx y$) iff one of them can be obtained from the other by commuting certain symbols in the word several times. Formally, $ubav \approx uabv$ if $(a, b) \in C$ (symbols $a$, $b$ commute). The relation $\approx$ is transitive because we can apply operations of commuting two symbols many times. One can reformulate many of the problems defined before in the framework of partially commutative alphabets. Instead of one word, one can also consider the whole equivalence class containing this word (called a *trace*). We can ask if such an equivalence class for a given word contains a square or a palindrome or a given factor (the latter is the string-matching problem for partially commutative alphabets).

However, we consider only the complexity of one basic problem : checking equivalence of two strings. It is one of the simplest problems in this area containing a lot of sophisticated questions.

## 22. Two-dpda's

The acronym “2dpda” is an abbreviation for 'two-way deterministic pushdown automaton'. This is essentially the same device as a pushdown automaton described in many standard textbooks on automata and formal languages; the only difference is its ability to move input heads in two directions. We demonstrate shortly that any language accepted by such an abstract machine has a linear time recognition procedure on a random access machines, which is of algorithmic interest. The notion of 2dpda's is historically interesting. Indeed, one of the first approaches to obtain a linear time algorithm for string-matching used 2dpda's.

The table below shows some relations between chapters and problems. The first introductory chapters are naturally related to all problems.

Chapter 3. Basic string-matching algorithms — 1, 2, 5, 10, 11, 13
Chapter 4. The Boyer-Moore algorithm and its variations — 1, 5
Chapter 5. Suffix trees — 1, 2, 6, 9, 10, 12, 13, 17, 18
Chapter 6. Subword graphs — 1, 2, 6, 9, 10, 12, 13, 17, 19, 20
Chapter 7. Automata-theoretic approach — 1, 2, 3, 5, 6, 9, 10, 12, 13, 19, 20, 22
Chapter 8. Regularities in words : symmetries and repetitions — 9, 10, 11
Chapter 9. Almost optimal parallel algorithms — 1, 2, 9, 10, 11, 15, 18, 19, 20
Chapter 10. Text compression techniques — 10, 16, 19
Chapter 11. Approximate pattern matching — 3, 4, 7, 8, 17
Chapter 12. Two-dimensional pattern matching — 5
Chapter 13. Time-space optimal string-matching — 1, 10, 13
Chapter 14. Time-processor optimal string-matching — 1
Chapter 15. Miscellanies — 1, 5, 13, 14, 15, 17, 19, 21

This book is about efficient algorithms for textual problems. By efficient, we mean algorithms working in polynomial sequential time (usually linear time or $n.\log(n)$ time) or in polylogarithmic parallel time with a polynomial number of processors (usually linear). However, we have to warn the reader that plenty of textual problems have no efficient algorithms (unless one the main question in complexity theory “is P=NP?” holds true, which seems unlikely). We refer the reader to [GJ 79] for the a definition and discussion on NP-completeness. Roughly speaking, an NP-complete problem is a problem that has (with high probability) no efficient exact algorithm.

Below are some examples of NP-complete problems on texts. Usually, NP-complete problems are stated as decision problems, but we present some problems in their more natural version when outputs are not necessarily boolean. Essentially, this does not affect the hardness of the problem.

**Shortest common superstring**

The general problem is to reconstruct a text from a set of its factors. There is of course no unique solution, so the problem is usually constrained to a minimal length condition. Given a finite set *S* of words, find a shortest word *x* that contains all words of *S* as factors, i.e. such that *S* is included in *Fac*(*text*). The length of text is denoted *SCS*(∏).
(see [MS 77]). The size of the problem is the total length of all words in *S*.

**Shortest common supersequence**

Given a finite set *S* of words, find a shortest word *x* such that every word in *S* is a subsequence of *x* (see [Ma 78]). The word *x* is called a supersequence of *S*.

**Longest common subsequence**

Given a finite set $S$ of words, find a longest word $x$ that is a subsequence of every word in $S$ (see [Ma 78]). It is worth observing that the problem is solvable in polynomial time if $|S|$ is a constant. The seemingly similar problem of computing the longest common factor of words of $S$ is also trivially solvable in polynomial time (number of distinct factors in quadratic, as opposed to the exponential number of distinct subsequences).

**String-to-string correction**

Given words $x$ and $y$, and an integer $k$, is it possible to transform $x$ into $y$ by a sequence of at most $k$ operations of single symbol deletion or adjacent-symbol interchange ? (See [Wa 75]). The problem becomes polynomial-time solvable if we allow also operations of changing a single symbol and inserting a symbol (see [WF 74]).

**The rank of a finite set of words**

Given a finite set $X$ of words and an integer $k$, does there exists a set $Y$ of at most $k$ words such that each word in $X$ is a composition of words in $Y$, see [Ne 88]. The smallest $k$ for which $Y$ exists is called the rank of $X$.

There are several other NP-complete textual problems : hitting string [Fa 74], grouping by swapping [Ho 77], and problems concerning data compression [St 77], [SS 78]. We refer the reader to *Computers and Intractability : A Guide to the Theory of NP-Completeness* by M.R. Garey and D.S. Johnson.

## 2.4. Combinatorics of texts

As already seen in the previous section, a text $x$ is simply a sequence of letters. The first natural operation on sequences is concatenation. The concatenation of $x$ and $y$, also called their product, is denoted by a mere juxtaposition : $xy$, or sometimes with an extra dot, $x.y$, to make apparent the decomposition of the resulting word. This is coherent with the notation of sequences as juxtaposition of their elements. The concatenation of $k$ copies of the same word $x$ is denoted by $x^k$.

There is no need to bracket a sequence representing a text because concatenation is associative : $(xy)z = x(yz)$. The empty sequence (of zero length) is denoted by $\varepsilon$. The set of all sequences on the alphabet $A$ is denoted by $A^*$, and the set of non-empty words is denoted by $A^+$. In the algebraic terminology, sequences are called words, and concatenation provides to $A^*$ a structure of monoid (associativity and $\varepsilon$). Moreover this monoid is free, which essentially means that two words are equal iff their letters at same positions coincide.

Consider a word $x$ which decomposes into $uvw$ (for three words $u$, $v$ and $w$). The words $u$, $v$ and $w$ are called *factors* of $x$. Moreover $u$ is called a *prefix* of $x$, and $w$ a *suffix* of $x$. The occurrence of factor $v$ in $x$ can be formally considered as the triplet $(u, v, w)$. The position of this occurrence is the length of $u$ denoted by $|u|$. This notion is intrinsic; it does not depend on the representation of the word $x$. However it coincides with our convention of representing texts by arrays, and with the definition of positions already given in the previous section.

We define the notion of a period of a word, which is central in almost all string-matching algorithms. A *period* of a word $x$ is an integer $p$, $0<p\leq|x|$, such that

$$\forall i \in \{1, \ldots, |x|-p\}\ x[i] = x[i+p].$$

This is the usual definition of a period for a function defined on integers, as $x$ can be viewed. Note that the length of a word is always a period of it, so that any word has at least one period. We denote by *period*($x$) the smallest period of $x$.

**Example**

The periods of *aabaaabaa* (of length 9) are 4, 7, 8 and 9. ♦

**Proposition 2.1**

Let $x$ be a nonempty word and $p$ be an integer such that $0<p\leq|x|$. Then each following condition equivalently defines $p$ as a period of x :

(1) $x$ is a factor of some $y^k$ with $|y| = p$ and $k>0$,

(2) $x$ may be written $(uv)^k u$ with $|uv| = p$, $v$ nonempty and $k>0$,

(3) for some words $y$, $z$ and $w$, $x = yw = wz$ and $|y| = |z| = p$.

**Proof**

Condition 1 is equivalent to say that $p$ is a period of $x$ if one considers $y = x[1\ldots p]$.

1 implies 2 : if $x$ is a factor of $y^k$ it can be written $ry^is$ with $r$ a suffix of $y$ and $s$ a prefix of $y$. Let $t$ be such that $y = tr$. Then $x = r(tr)^is = (rt)^irs$. Since $t$ and $s$ are both prefixes of $y$, one of them is a prefix of the other. If $s$ is a proper prefix of $t$, then $t = sv$ for some nonempty word $v$ and, setting $u = rs$, $x = (rsv)^irs = (uv)^iu$. Furthermore $|uv| = |rsv| = |rt| = |tr| = |y| = p$. Also note that $i>0$ because $|rs|<|y|=p\leq|x|$. In the other situation, $t$ is a prefix of $s$ and the word $u$ such that $s = tu$ is also a prefix of $r$. Then, for some word $w$, $r = uw$ and $x = (uwt)^{i+1}u$ or $x = (uv)^{i+1}u$, if we set $v = wt$. Moreover, $|uv| = |uwt| = |rt| = |tr| = |y| = p$ and $i+1>0$.

2 implies 3 : if $x = (uv)^ku$ with $|uv| = p$, let $y$, $z$ and $w$ be defined by

$$y = uv,\ z = vu,\ w = (uv)^{k-1}u.$$

The definition of $w$ is valid because $k>0$. The conclusion follows : $x = yw = wz$.

3 implies 1 : first note that, if $yw = wz$, we also have $y^iw = wz^i$ for any integer $i$. Since $y$ is nonempty ($|y| = p$ and $p>0$), we can choose an integer $k$ such that $|y^k|>|x|$. The equality $y^kw = wz^k$ shows that $x$ ($=wz$) is a factor and even a prefix of $y^k$ with $|y| = p$.

The proof is complete. ♦

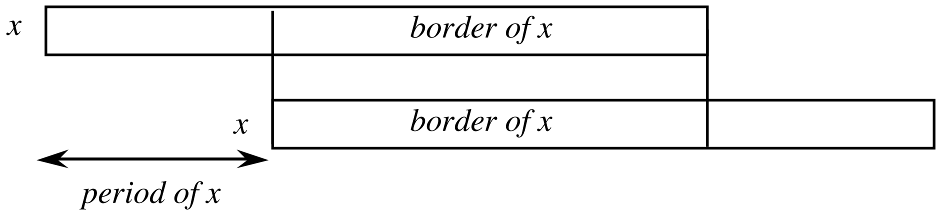

**Figure 2.5**. Duality between periods and borders of texts.

A *border* of a word $x$ is any shorter word that is both a prefix and a suffix of $x$. Borders and periods are dual notions, as shown by condition 3 of the previous proposition. We can state it more precisely, defining *Border*($x$) as the longest proper border of a nonempty word $x$. The border of a word $x$ is the longest (non-trivial) overlap when we try to match $x$ with itself. Since *Border*($x$) is (strictly) shorter than $x$, iterating the function from any non-empty word leads eventually to the empty word. We also say that $x$ is *border-free* if *Border*($x$) is the empty word.

**Example**

The borders of *aabaaabaa* are *aabaa*, *aa*, *a* and ε. ♦

**Proposition 2.2**

Let $x$ be a word and let $k$ ($\geq 0$) be the smallest integer such that $Border^k(x)$ is empty. Then

$$(x, Border(x), Border^2(x), \ldots, Border^k(x))$$

is the sequence of all borders of $x$ in order of decreasing length. Moreover

$$(|x|-|Border(x)|, |x|-|Border^2(x)|, \ldots, |x|-|Border^k(x)|)$$

is the sequence of all periods of $x$ in increasing order.

**Proof**

Both properties hold if $x$ is empty. In this case, the sequence of borders reduces to ($x$) and the sequence of periods is empty since $k = 0$.

Consider a nonempty word $x$ and let $u = Border(x)$. Let $w$ be a border of $x$. Then it is either *Border*($x$) itself or a border of *Border*($x$). By induction it belongs to the sequence

$$(Border(x), Border^2(x), \ldots, Border^k(x))$$

and this proves the first point.

If $p$ is a period of the nonempty word $x$, by condition 3 of Proposition 2.1 we have $x = yw = wz$ with $|y|=p$. Then $w$ is a proper border of $x$ and $p = |x|-|w|$. The conclusion follows from the fact that $(Border(x), Border^2(x), \ldots, Border^k(x))$ is the sequence of proper borders of $x$. ♦

Note that the period *period*($x$) (the smallest period of $x$) corresponds to the longest proper border of $x$ and is precisely $|x|-|Border(x)|$.

The next theorem provides an important property on periods of a word. It is often use in combinatorial proofs on words. We first give a weak version of the theorem often sufficient in applications.

**Lemma 2.3** (Weak Periodicity Lemma)

Let $p$ and $q$ be two periods of a word $x$.

If $p+q \leq |x|$, then gcd($p$, $q$) is also a period of $x$.

**Proof**

The conclusion trivially holds if $p = q$. Assume now that $p > q$. We first show that the condition $p+q \leq |x|$ implies that $p-q$ is a period of $x$. Let $x = x[1]x[2]\ldots x[n]$ ($x[i]$'s are letters). Given $x[i]$ the $i$-th letter of $x$, the condition implies that either $i-q \geq 1$ or $i+p \leq$n. In the first case, $q$ and $p$ being periods of $x$, $x[i] = x[i-q] = x[i-q+p]$. In the second case, for the same reason, $x[i] = x[i+\mathrm{p}] = x[i+p-q]$. Thus $p-q$ is a period of $x$. This situation is shown in the Figure 2.6.

The rest of the proof, left to the reader, is by induction on the integer max($p$, $q$), after noting that gcd($p$, $q$) equals gcd($p-q$, $q$). ♦

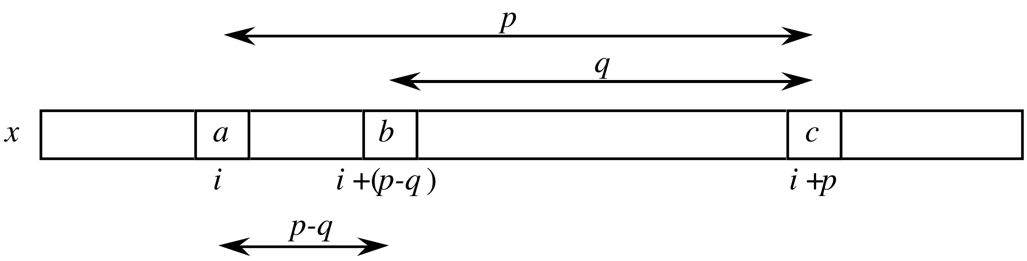

**Figure 2.6**. $p-q$ is also a period : letters $a$ and $b$ are both equal to letter $c$.

**Lemma 2.4** (Periodicity Lemma)

Let $p$ and $q$ be two periods of a word $x$.

If $p+q$-gcd($p$, $q$) $\leq |x|$, then gcd($p$, $q$) is also a period of $x$.

**Proof**

As for the weak periodicity lemma we prove the conclusion by induction on max($p$, $q$). The conclusion trivially holds if $p = q$, so, we assume now that $p > q$ and let $d$ = gcd($p$, $q$). The word $x$ can be written $yv$ with $|y| = p$ and $v$ a border of $x$. It can also be written $zw$ with $|z| = q$ and $w$ a border of $x$.

We first show that $p-q$ is a period of $w$. Since $p > q$, $z$ is a prefix of $y$. Let $z'$ be such that $y = zz'$. From $x = zw = yv$, we get $w = z'v$. But, since $v$ is a border of $x$ shorter than the border $w$, it is also a border of $w$. This proves that $p-q = |z'|$ is a period of $w$, and thus $w$ is a power of $z'$.

To prove that $q$ is a period of $w$, we have only to show that $q \leq |w|$. Indeed, since $d \leq p-q$ (because $p > q$), we have $q \leq p-d = p+q-d-q \leq |x|-q = |w|$.

This also show that $(p-q)+q$-gcd($(p-q)$, $q$) (which is $p-d$) $\leq |w|$. By induction hypothesis, we deduce that $d$ is a period of $w$. Thus $z$ and $z'$, whose lengths are multiple of $d$, are powers of a same word $u$ of length $d$. It is also the case for $w$ (that is a power of $z'$), and then for $x$. Thus, the word $x$ has period $\gcd(p, q)$ as expected. ♦

## Fibonacci words

In some sense, the inequality that appears in the statement of the periodicity lemma is optimal. The aim of the following example is to exhibit a word $x$ having two periods $p$ and $q$ satisfying $p+q-\gcd(p, q) = |x|+1$ and that does not satisfy the conclusion of the lemma.

Fibonacci words are defined on the alphabet $A = \{a, b\}$. Let $Fib_n$ be the $n$-th Fibonacci word ($n \geq 0$). It is defined by

$$Fib_0 = \varepsilon,\ Fib_1 = b,\ Fib_2 = a, \text{ and } Fib_n = Fib_{n-1}Fib_{n-2} \text{ for } n>2.$$

The lengths of Fibonacci words are the well known Fibonacci numbers, $f_0 = 0, f_1 = 1, f_2 = 1$, … The first Fibonacci words of ($Fib_n$, $n>2$) are

| | |
|---|---|
| $Fib_3 = ab$, | $|Fib_3| = 2$, |
| $Fib_4 = aba$, | $|Fib_4| = 3$, |
| $Fib_5 = abaab$, | $|Fib_5| = 5$, |
| $Fib_6 = abaababa$, | $|Fib_6| = 8$, |
| $Fib_7 = abaababaabaab$, | $|Fib_7| = 13$, |
| $Fib_8 = abaababaabaababaababa$, | $|Fib_8| = 21$, |
| $Fib_9 = abaababaabaababaababaabaababaabaab$, | $|Fib_9| = 34$. |

Fibonacci words satisfy a large number of interesting properties related to periods and repetitions. One can note that Fibonacci words (except the two first words of the sequence) are prefixes of their successors. Indeed, there is an even stronger property : the square of any Fibonacci word is a prefix of its succeeding Fibonacci words of high enough rank.

To prove the extreme property of Fibonacci words related to the Periodicity Lemma, we consider, for $n>2$, the prefix of $Fib_n$ of length $|Fib_n|-2$, denoted $g_n$. It can be shown that, for $n>5$, $g_n$ is a prefix of both $Fib_{n-1}{}^2$ and $Fib_{n-2}{}^3$. Then $|Fib_{n-1}|$ and $|Fib_{n-2}|$ are periods of $g_n$. It can also be shown that $\gcd(|Fib_{n-1}|, |Fib_{n-2}|) = 1$, a basic property of Fibonacci numbers. Thus, we get $|Fib_{n-1}|+|Fib_{n-2}|-\gcd(|Fib_{n-1}|, |Fib_{n-2}|) = |Fib_{n-1}|+|Fib_{n-2}|-1 = |Fib_n|-1 = |g_n|+1$. Moreover, the conclusion of the periodicity theorem does not hold on $g_n$ because this would imply that $g_n$ were a power of a single letter which is obviously false.

Among other properties of Fibonacci words, it must be noted that they have no factor of the form $u^4$ ($u$ not empty). So, Fibonacci words contain a large number of periodicities, but none with exponent higher than 3.

Fibonacci words come up in the analysis of some algorithms. A common expression of their length is used there : $|Fib_n|$ is $\Phi^n/\sqrt{5}$ rounded to the nearest integer. It happens then that log's are based Φ, the golden ratio (=(1+√5)/2).

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# 3. Basic string-matching algorithms

The string-matching problem is the most studied problem in algorithmics on words, and there are many algorithms for solving this problem efficiently. Recall that we assumed that the pattern *pat* is of length *m*, and that the text *text* has length *n*. If the only access to text *text* and pattern *pat* is by comparisons of symbols, then the lower bound on the maximum number of comparisons required by a string-matching algorithm is *n-m* . The best algorithms presented in the book will make no more than 2.*n-m* comparisons in the worst case. Recently, the lower bound has been improved, to around 4/3.*n* on a two letter alphabet. However, algorithms become quite sophisticated and are beyond the scope of this book.

We start with a brute-force algorithm that uses quadratic time. Such a naive algorithm is in fact an origin of a series of more and more complicated and more efficient algorithms. The informal scheme of such a naive algorithm is :

```
        for i := 0 to n-m do check if pat=text[i+1…i+m].
```

The actual implementation differs with respect to how we implement the checking operation : scanning the pattern from the left or scanning the pattern from the right. So we get two brute-force algorithms. Both algorithms have quadratic worst-case complexity. We discuss in this chapter the first of them (left-to-right scanning of the pattern).

To shorten the presentation of some algorithms we assume that *pat* and *text* together with their respective lengths, *m* and *n*, are global variables.

```
function brute_force1: boolean;
  var i, j : integer;
begin
  i := 0;
  while i≤n-m do begin
    { left-to-right scan of pat }
    j := 0;
    while j<m and pat[j+1]=text[i+j+1] do j := j+1;
    if j=m then return(true);
    { inv1(i, j) }
    i := i+1; { length of shift = 1 }
  end;
  return(false);
end;
```

If $pat=a^{n/2}b$ and $text=a^{n-1}b$ then a quadratic number of symbol comparisons takes place. However, the average complexity is not so bad. Assume that the alphabet has two symbols and that each symbol appears with the same probability. Then the probability that the test "`pat[j+1]==text[i+j+1]`" is successful is at most 1/2. It is now quite easy to calculate that the average number of such successful tests for a fixed $i$ does not exceed 1. The number of unsuccessful tests does not exceed $n$. Hence, we have the following :

**Fact**

Assume $|A|=2$. The expected number of all symbol comparisons done by algorithm *brute_force1* does not exceed $2.n$.

In the following, we are interested mostly in worst-case time complexity, and especially in linear-time algorithms.

## 3.1. The Knuth-Morris-Pratt algorithm

Our first linear-time algorithm is a natural improved version of the naive algorithm discussed above. We present a constructive proof of the following.

**Theorem 3.1**

The string-matching problem can be solved in $O(|text|+|pat|)$ time using $O(|pat|)$ space. The constants involved in '$O$' notation are independent of the size of the alphabet.

**Remark**

On one point we are disappointed with this theorem. The size of additional memory is rather large though linear in the size of the pattern. In Chapter 13, we show that a constant number of registers suffices to achieve linear time complexity (again the size of the alphabet does not intervene).

Let us look closer at the algorithm *brute_force1* and at its main invariant $inv1(i, j)$ : $pat[1\ldots j]=text[i+1\ldots i+j]$ and $pat[j+1]\neq text[i+j+1]$.In fact, we first use the slightly weaker invariant

$$inv1'(i, j) : pat[1\ldots j]=text[i+1\ldots i+j].$$

The invariant essentially says that the value of $j$ gives a lot of information about the last part of the text scanned so far.

Using the invariant $inv1'(i, j)$, we are able to make longer shifts of the pattern. Present shifts in algorithm *brute_force1* have always length 1. Let $s$ denote (the length of) a "safe" shift, where "safe shift *s*" means that on the basis of the invariant we know that there is no occurrence of the pattern at positions between *i* and *i*+*s*, but possibly at position *i*+*s*.

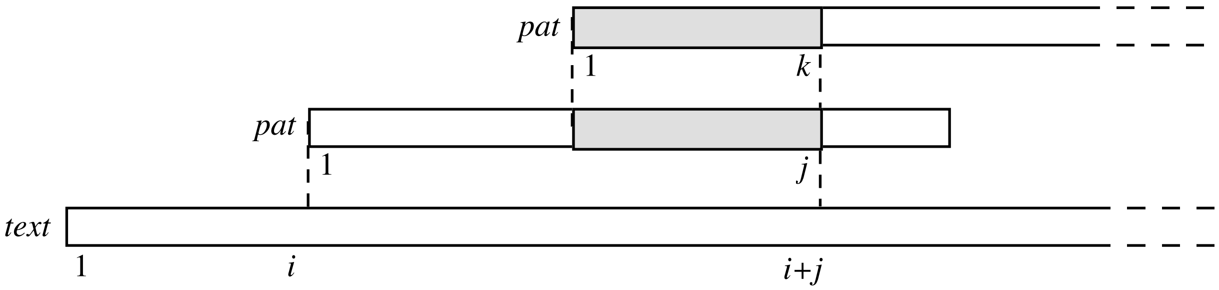


**Figure 3.1**. Shifting the pattern to the next safe position.

Assume *j*>0, let *k*=*j*-*s*, and suppose an occurrence of the pattern starts at position *i*+*s*. Then, *pat*[1…*k*] and *pat*[1…*j*] are suffixes of the same text *text*[1…*i*+*j*] (see Figure 3.1). Hence, the following condition is implied by *inv*1' :

*cond*(*j*, *k*) : *pat*[1…*k*] is a proper suffix of *pat*[1…*j*].

Therefore the shift is safe iff *k* is the smallest number satisfying *cond*(*j*, *k*). Denote this number by *Bord*[*j*]. The function *Bord* is called a failure function, because it helps us in the moment of a failure (mismatch). It is the crucial function. It is stored in a table with the same name. The failure function allows to compute the length of the smallest safe shift, *s*=*j*-*Bord*[*j*]. Note that *Bord*[*j*] is precisely the length of the border of *pat*[1…*j*], and that the length of the smallest safe shift is the smallest period of *pat*[1…*j*] (see Section 2.4). In the case *j*=0, that is, when *pat*[1…*j*].is the empty word, we have a special situation. Since, in this situation, the length of the shift must be 1, we then define *Bord*[0]=-1. Now we have an improved version of algorithm *brute_force1*.

```
function MP : boolean;  { algorithm of Morris and Pratt }
  var i, j : integer;
begin
  i := 0; j := 0;
  while i≤n-m do begin
    while j<m and pat[j+1]=text[i+j+1] do j := j+1;
    if j=m then return(true);
    i := i+j-Bord[j]; j := max(0, Bord[j]);
  end;
  return(false);
end;
```

**Lemma 3.2**

The time complexity of the algorithm MP is linear in the length of the text. The maximal number of character comparisons executed is $2.n\text{-}m$.

**Proof**

Let $T(n)$ be the maximal number of symbol comparisons "$pat[j+1]=text[i+j+1]$ ?" done by the algorithm MP. There are at most $n\text{-}m+1$ unsuccessful comparisons (at most one for a given $i$). Consider the sum $i+j$. Its maximal value is $n$ and minimal 0. Each time a successful comparison is made the value of $i+j$ increases by one unit. This value observed in the moment of comparing symbols never decreases. Hence, there are at most $n$ successful comparisons. Also observe that if the first comparison is successful than we have no unsuccessful comparison for position $i$=0. Finally, we get :

$$T(n) \leq n+n\text{-}m=2.n\text{-}m.$$

For $pat$=$ab$ and $text$=$aaaa…a$ we have $T(n)=2.n\text{-}m$ (in this case $m$=2). ♦

```
procedure compute_borders_1;
{ compute the failure table Bord for pattern pat }
{ a version of algorithm MP with text=pat }
  var i, j : integer;
begin
  i := 1; j := 0;
  while i≤m-1 do begin
    while i+j<m and pat[j+1]=text[i+j+1] do begin
      j := j+1; if Bord[i+j]=-1 then Bord[i+j] := j;
    end;
    i := i+j-Bord[j]; j := max(0, Bord[j]);
  end;
end;
```

There remains the problem of computing the table *Bord*, and the aim is to derive a linear-time algorithm. We present two solutions. The first one is to use algorithm MP itself to compute *Bord*. This, at first glance, can seem contradictory because *Bord* is needed inside the algorithm. However, we compute *Bord* in parts; whenever a value *Bord*[*j*] is needed in the computation of *Bord*[*i*] for $i>j$ then *Bord*[*j*] is already computed. This is a kind of dynamic programming.

Suppose that $text$ =$pat$. We apply algorithm MP starting with $i$=1 (for $i$=0 nothing interesting happens) and continue with $i$=2, 3, …., $m$-1. Then *Bord*[*r*]=$j$>0 whenever $i+j=r$ in a successful comparison for the first time. If *Bord*[*r*]>0 then such a comparison will take place.

Assume that initially $Bord[j]=-1$ for all $j\geq 0$.

Of course, we can delete the statement "**if** *j*=*m* **then return**(true);" because we are not solving now the string-matching problem. In fact, our interest here is only a side effect of the algorithm MP.

The complexity of algorithm *compute_borders_1* is linear. The argument is the same as for algorithm MP. Next, we present another linear-time algorithm computing table *Bord*.

```
procedure compute_borders;
{ compute the failure table Bord for pat, second version }
  var t, j : integer;
begin
  Bord[0] := -1; t := -1;
  for j := 1 to m do begin
    while t≥0 and pat[t+1]≠pat[j] do t := Bord[t];
    t := t+1; Bord[j] := t;
  end;
end;
```

The correctness of the algorithm *compute_borders* essentially follows from Proposition 2.2, or from the fact that if $Bord[j]>0$ then $Bord[j]=t+1$, where $t=Bord^k[j]$ and $k$ is the smallest positive integer such that $pat[Bord^k[j]+1]=pat[j]$.

**Lemma 3.3**

The maximum number of character comparisons executed by algorithm *compute_borders* is $2.m-3$.

**Proof**

The complexity can be analyzed using a so-called 'store principle'. Interpret $t$ as the number of items in a store. Note that when $t<0$, no comparison is done, and $t$ becomes null. So we can consider that initially the store is empty. For each $j$ running from 2 to $m$, we add at most one item (at statement $t := t+1$). However, whenever we execute the statement "`t := Bord[t]`" the value of $t$ strictly decreases, which can be interpreted as deleting a nonzero number of items from the store. The total number of items inserted does not exceed $m$-2. Hence the total number of deletions and executions of statement "`t := Bord[t]`" for unsuccessful comparisons "`pat[t+1]≠pat[j]`" does not exceed $m$-2.

For each $j$ running from 2 to $m$, there is at most one successful comparison. The total number of successful comparisons then does not exceed $m$-1.

Hence, the total number of comparisons does not exceed $2.m-3$. ♦

The notion of failure function can be applied in a different way to the string-matching problem, as follows. Let *w* = *pat*&*text*, where & is a special new symbol. Compute the table *Bord* for this string. Then the pattern *pat* ends in *text* at all positions *j* with *Bord*[*j*]=*m*, where *m* is the size of *pat*. Such an abstract algorithm was given in [FP 74].

We show another application of the failure function computation through algorithm *compute_borders*, the computation of *Maxsuf*(*pat*), lexicographically maximal suffix of *pat*. When computing the value of *Bord*[*j*] we examine consecutive values of the integer variable *t*. These values correspond to all consecutive proper suffixes *pat*[1…*t*] of the word *pat*[1…*j*-1], which are also prefixes of this word. Such examination could be useful in the computation of maximal suffixes because of the following fact :

if *pat*[*q*+1…*j*-1] is the maximal suffix of *pat*[1…*j*-1] and *pat*[*t*+1…*j*] is the maximal suffix of *pat*[1…*j*]  then *pat*[*t*+1…*j*-1] is a prefix and suffix of *pat*[*q*+1…*j*-1]. Hence, to find the next maximum suffix it is enough to examine extensions of suffixes of the last maximal suffix (such suffixes can be given using failure table *Bord*). However, the following unexpected feature of such an approach is that we have to compute borders of *pat*[*q*+1…*j*-1], the current maximal suffix, and simultaneously its failure function. So, we have to compute the table *Bord* for the dynamically changing pattern *pat*[*q*+1…*j*-1]. The trick is that the failure table we need is essentially a prefix of the previous one.

```
function Maxsuf : integer;
{ computes Maxsuf(pat) }
{ application of failure function computation }
  var ms, j, t : integer;
begin
  ms := 0; Bord[0] := -1;
  for j := 1 to m do begin
    t := Bord[j-1];
    while t≥0 and pat[ms+t+1]>pat[j] do begin
      ms = j-1-t; t = Bord[t];
    end;
    while t≥0 and pat[ms+t+1]≠pat[j] do t = Bord[t];
    Bord[j-sm] = t+1;
  end;
  return(ms); { Maxsuf(pat) is pat[ms+1…m] }
end;
}
```

Denote $x(j)=Maxsuf(pat[1...j])$. If we have computed table *Bord* for $x(j-1)$ then $x(j)=x'pat[j]$, where $x'$ is a prefix of $x(j-1)$. Hence, *Bord* is already computed for all positions corresponding to symbols of $x'$; only one entry of *Bord* should be updated (for the last position). We modify the algorithm for the failure function maintaining the following invariant :

$$pat[ms+1...j]=Maxsuf(pat[1...j]),$$

and the values of table *Bord* are correct values of the failure function for the word $pat[ms+1...j]$.

In algorithm *Maxsuf*, parameter $t$ runs through lengths of suffixes of $pat[ms+1...j]$. The algorithm above computes *Maxsuf*(*pat*), as well as the failure function for it, in linear time. Computation also require linear extra space for the table *Bord*. We give in Chapter 11 a linear-time constant-space algorithm for the computation of maximal suffixes. It will be also seen there why maximal suffixes are so interesting.

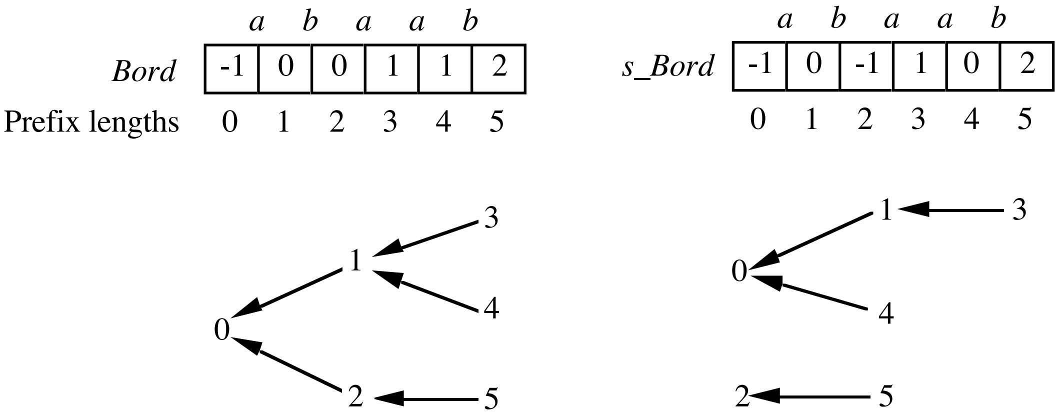
We have not so far taken into account the full invariant *inv*1 of algorithm *brute_force1*, but only its weak version *inv*1'. We have left apart the mismatch property. We develop now a new version of algorithm MP that incorporates the mismatch property. The result algorithm, called KMP, improves on the number of comparisons performed on a given letter of the text.

The clue for improvement is the following : assume that a mismatch in algorithm MP occurs on the letter $pat[j+1]$ of the pattern. The next comparison is between the same letter of the text and $pat[k+1]$ if $k=Bord[j]$. But if $pat[k+1]=pat[j+1]$ the same mismatch recurs. So, we must avoid considering the border of $pat[1...j]$ of length $k$.

For $m>j\geq0$ we consider a condition stronger than $cond(j, k)$ by a "one-comparison" information :

$s\_cond(j, k)$ : ($pat[1...k]$ is a proper suffix of $pat[1...j]$ and $pat[k+1]\neq pat[j+1]$ )

We then define $s\_Bord[j]$ as $k$, when $k$ is the smallest integer satisfying $s\_cond(j, k)$, and as -1 otherwise. Moreover we define $s\_Bord[m]$ as $Bord[m]$. We say that $s\_Bord[j]$ is the length of the longest *strict border* of $pat[1...j]$. This notion of strict-borderness is not intrinsic, but is only defined for prefixes of the pattern.



|  | *a* | *b* | *a* | *a* | *b* |
|---|---|---|---|---|---|
| *Bord* | -1 | 0 | 0 | 1 | 1 | 2 |
| Prefix lengths | 0 | 1 | 2 | 3 | 4 | 5 |

|  | *a* | *b* | *a* | *a* | *b* |
|---|---|---|---|---|---|
| *s_Bord* | -1 | 0 | -1 | 1 | 0 | 2 |
|  | 0 | 1 | 2 | 3 | 4 | 5 |

**Figure 3.2**. Functions *Bord* and *s_Bord* for pattern *abaab*.

The algorithm KMP is the algorithm MP in which table *Bord* is replaced by table *s_Bord*.

```
function KMP: boolean; { algorithm of Knuth, Morris, and Pratt }
{ version of MP with table Bord replaced by s_Bord }
  var i, j : integer;
begin
  i := 0; j := 0;
  while i≤n-m do begin
    while j<m and pat[j+1]=text[i] do j := j+1;
    if j=m then return(true);
    i := i+j-s_Bord[j]; j := max(0, s_Bord[j]);
  end;
  return(false);
end;
```

The table *s_Bord* is more effective in the following on-line version of algorithm KMP. Assume that the text ends with the special end-marker $. At each moment after having processed the current input symbol, we output 1 if the part of the text read up so far ends with the pattern *pat*, and we output 0, otherwise.

```
Algorithm KMP;
{ on-line linear version of KMP search }
  var j : integer; symbol : char;
begin
  read(symbol); j := 0;
  while symbol ≠ end of text do begin
    while j<m and pat[j+1]=symbol do begin
      j := j+1; if j=m then write(1) else write(0);
      read(symbol);
    end;
    if s_Bord[j]=-1 then begin
      write(0); read(symbol); j := 0;
    end else
      j := s_Bord[j];
  end;
end;
```

Computation of strict borders of prefixes of the pattern *pat* relies on the following observation. Let *t*=*Bord*[*j*]. Then, *s_Bord*[*j*]=*t* if *pat*[*t*+1]≠*pat*[*j*+1]. Otherwise, the value of *s_Bord*[*j*] is the same as the value of *s_Bord*[*t*] because *pat*[*t*+1]=*pat*[*j*+1]. The next algorithm applies this fact and is built on algorithm *compute_borders*. Its output is the global table *s_Bord*. Also note that the strict border of *pat* itself is its border, as if *pat* were followed by a marker.

```
procedure compute_s_borders;
{ compute table s_Bord for pattern pat }
  var t, j : integer;
begin
  s_Bord[0] = -1; t = -1;
  for j := 1 to m-1 do begin
    { t equals Bord[j-1] }
    while t≥0 and pat[t+1]≠pat[j] do t = s_Bord[t];
    t := t+1;
    if pat[t+1]≠pat[j+1] then s_Bord[j] = t
    else s_Bord[j] = s_Bord[t];
  end;
  s_Bord[m] = t;
end;
```

Denote by *delay*(*m*) the maximal time (measured as the number of statements "*j* =*s_Bord*[*j*]") done between two consecutive reads, for patterns of length *m*. By *delay_Bord*(*m*) we denote the corresponding time in the situation when *Bord* is used instead of *s_Bord*.

The large gap between *delay*(*m*) and *delay_Bord*(*m*) can be seen on the following example : *pat*=*aaaa*...*a* and *text*=$a^{m-1}ba$. In this case *delay*(*m*)=1 while *delay_Bord*(*m*) is linear in the length of *pat*. The value of *delay*(*m*) is generally small.

**Lemma 3.4**

The time *delay*(*m*) is *O*(log *m*), and the bound is tight.

The proof of Lemma 3.4 is a consequence of the Periodicity Lemma of Section 2.4. The pattern $g_k$ defined in Section 2.4 as a prefix of the *k*-th Fibonacci word (for *k*≥3) yields a sequence of exactly *k*-3 strict borders. The delay is then *k*-3, which is exactly of order log(*m*), if *m*=length($g_k$).

Observe that for texts on binary alphabets *delay*(*m*)≤1. Which means that, in this case, the algorithm is real-time. However, if the patterns are over the alphabet {*a*, *b*} and texts over {*a*, *b*, *c*} then the delays can be logarithmic, as shown by the above example.

It is an interesting exercise in program transformations to modify algorithm KMP to achieve a real-time computation independently of the size of the alphabet. This means that the time between two consecutive reads must be bounded by a constant. The crucial observation is that if we execute "*j* =*s_Bord*[*j*]" then we know that for the next *j*-*s_Bord*[*j*] input symbols the output value will be 0 ("no match"). This allows to disperse output actions between input actions (reading symbol) in such a way that the time between consecutive writes-reads is bounded by a constant. To do so, we can maintain in a table up to $m$ last symbols of the text *text*. We leave details to the reader. It is interesting to observe that real-time condition can be achieved by using any of the tables *Bord*, *s_Bord*.

In this way, we sketched the proof of the following result (which becomes much harder if the model of the computation is a Turing machine).

**Theorem 3.5**

There is a real-time algorithm for string-matching on a random access machine. The algorithm is a version of the KMP algorithm and uses $O(m)$ space. Complexities do not depend on the size of the alphabet.

## 3.2 The Simon algorithm

Algorithm of Simon is a further improvement on algorithm *brute_force1*. The difference with the previous algorithms relies on the way shifts are done. Recall that the main invariant of *brute_force1* is

$$inv1(i, j) : pat[1\ldots j]=text[i+1\ldots i+j] \text{ and } pat[j+1]\neq text[i+j+1],$$

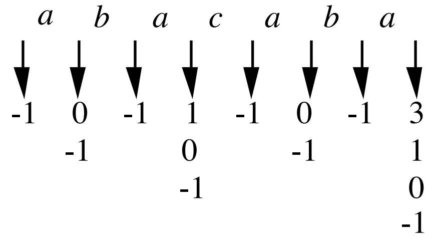
occurring when a shift is to be done. In MP algorithm, the length of the shift is the period of $pat[1\ldots j]$ corresponding to the border of this word. In KMP algorithm, a different notion of period is considered that may be considered as not incompatible with the letter $text[i+j+1]$ that yields the mismatch. This corresponds to the notion of strict borders.

According to the information gathered so far on the text, the best length of the shift would be the period of $pat[1\ldots j]text[i+j+1]$. Pre-computing all periods of $ua$ ($u$ prefix of $pat$, $a$ possible letter of the text) takes time and space $O(|A|.|pat|)$, which depends on the size of the alphabet. This kind of solution is not desirable, especially for short patterns.

This solution amounts to consider the minimal deterministic automaton recognizing the language $A^*x$. Indeed, algorithms MP and KMP implicitly use a representation of this automaton. We, implicitly also, consider here another implementation that leads to a faster algorithm. Relation of all these algorithms to automata is given in Chapter 5.

The idea exploited in Simon algorithm is that we can record only non trivial periods of words $pat[1\ldots j]text[i+j+1]$, namely, those that are less $j+1$. This leads to consider what we call *tagged borders* of prefixes of the pattern *pat*. For each letter $a$ of the alphabet $A$, distinct from letter $pat[j+1]$ if $j<m$, the border of $pat[1\ldots j]$ tagged by $a$ is its largest border $pat[1\ldots k]$ such that $pat[k+1]=a$.

Implementation of Simon algorithm requires lists of tagged borders. They are organized as follows. A table *First* of size *m* gives pointers to another table, *t_Bord* of size 2.*m*, that contains the lengths of tagged borders. Lists of tagged borders end with -1, and are in order of decreasing lengths.



| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| *First* | 0 | 1 | 3 | 4 | 7 | 8 | 10 | 11 |
| | 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 |

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *t_Bord* | -1 | 0 | -1 | -1 | 1 | 0 | -1 | -1 | 0 | -1 | -1 | 3 | 1 | 0 | -1 |
| | 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 |

**Figure 3.3**. Lists of tagged borders for *pat*=*abacaba*, and their implementation.

Algorithm MPS below assumes that the lists associated to all prefixes of the pattern have been pre-computed. Figure 3.4 illustrates the difference between the three algorithms MP, KMP, and MPS.

```
function MPS: boolean;
{ algorithm of Simon, improvement on KMP }
  var i, j, p, k : integer;
begin
  i := 0; j := 0;
  while i≤n-m do begin
    while j<m and pat[j+1]=text[i+j+1] do j := j+1;
    if j=m return(true);
    p := First[j]; k := t_Bord[p];
    while k>-1 and pat[k+1]≠text[i+j+1] do begin
      p := p+1; k := t_Bord[p];
    end;
    i := i+j-k; j := k+1;
  end;
  return(false);
end;
```

```
text      .......abaabac.............
                 abaabaa
                    abaabaa
                      abaabaa
                       abaabaa
                        abaabaa
```

(i) MP. 4 comparisons on letter *c*.

```
text      .......abaabac.............
                 abaabaa
                      abaabaa
                       abaabaa
                        abaabaa
```

(ii) KMP. 3 comparisons on letter *c*.

```
text      .......abaabac.............
                 abaabaa
                      abaabaa
                        abaabaa
```

(iii) MPS. 2 comparisons on letter *c*.

**Figure 3.4**. Behavior of MP, KMP, and MPS.

**Theorem 3.6**

Algorithm MPS works in $O(n)$ time for a text of length $n$. The maximum number of character comparisons it executes is less than $2.n$. The delay between two inspections of a character of the text is $O(|A|)$, where $A$ is the alphabet of the pattern.

**Proof**

It is quite obvious that all comparisons done by algorithm MPS are also done during a run of algorithms KMP or MP. This gives less than $2.n$ comparisons. All extra operations, including the work on lists of tagged borders is proportional to this number. Hence, we get $O(n)$ time. Since the number of tagged borders of a given prefix of *pat* is at most $|A|$, no more than $|A|$ letter comparisons are done on a given symbol of the text. This gives the delay $O(|A|)$. ♦

On a fixed alphabet (of patterns), algorithm MPS runs in real-time. If the alphabet is potentially infinite, the algorithm can be transformed into a real-time algorithm using similar method as for algorithms MP and KMP (see Section 3.1).

Preprocessing the lists of tagged borders can be done with a modified version of algorithm MPS itself. Computation is done in (almost) on-line fashion : tagged borders related to a prefix $u$ of *pat* are computed just after all tagged borders of its prefixes have been computed. We roughly describe how to computed tagged borders for $u$. Assume that $u$=*pat*$[1...j]$ and that *Border*$(u)$=*pat*$[1...k]$ (MPS is used to find it). If $j<m$ and *pat*$[j+1]\neq$*pat*$[k+1]$, *pat*$[1...k]$ is the longest border tagged by *pat*$[k+1]$. Otherwise, *pat*$[1...k]$ is not a tagged border. All other tagged borders are those of *pat*$[1...k]$ which are not tagged by *pat*$[j+1]$. Thus, their computation almost comes down to a copy of list. The details are left to the reader.

The fact that preprocessing of lists can be realized in linear time and space relies on the following property of tagged borders.

**Proposition 3.7**

For a pattern of length $m$, the number of tagged borders of its prefixes is at most $m$. The bound is tight on infinite alphabets.

**Proof**

Let *pat*$[1...k]$ be a border of *pat*$[1...j]$ tagged by $a$. Associate to it the length (shift) $j$-$k$. Then, no other tagged border can be associated to the same value. So, since $0<j\text{-}k\leq m$, the number of tagged borders is at most $m$.

Let $A$ be the infinite alphabet $\{a_1, a_2, ...\}$. Consider the sequence of words defined by $w_1=a_1$ and $w_i=w_{i\text{-}1}a_iw_{i\text{-}1}$, for $i>0$. Then, it is easy to see that $w_i$ has length $2^i$-1, and the same number of tagged borders for all its prefixes. ♦

## 3.3 String-matching by duels

In this section we present a nonclassical string-matching algorithm whose preprocessing phase is closely related to borders, and to KMP algorithm. We also introduce an interesting new operation called the *duel*. A more essential use of this operation will be seen in the chapter on optimal parallel string-matching and two-dimensional pattern matching. Hence, this section can be treated as a preparation for more advanced algorithms presented later.

We assume in this section that the pattern is non-periodic, which means that the smallest period of the pattern *pat* is larger than $|pat|/2$. This assumption implies that two consecutive occurrences of the pattern in the text (if any) are at distance greater than $|pat|/2$. However, it is not clear how to use this property for searching the pattern. We process as follows : after a suitable preprocessing phase, given two close positions in the text, we eliminate one of them as a candidate for a match. This leads to the idea of a duel.

The basic table which enables to search the pattern by a duel-based algorithm can be computed either as a side effect of the Knuth-Morris-Pratt algorithm, or by a use of the table *Bord*. Duels are performed at search phase. We define the following *witness table WIT*: for $0<i<|m|$,

$$WIT[i] = \textbf{any } k \text{ such that } pat[i+k] \neq pat[k],$$

$$WIT[i] = 0, \text{ if there is no such } k.$$

This definition is illustrated in Figure 3.5.

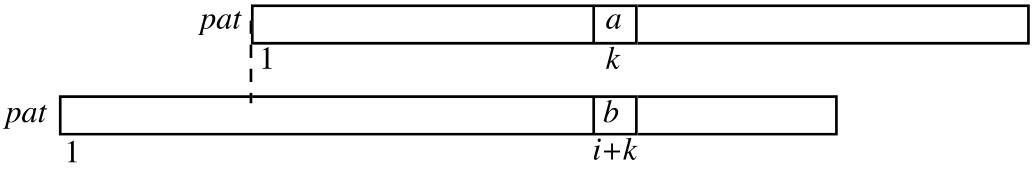


**Fig 3.5**. Witness of mismatch ($a \neq b$), $k = WIT[i]$.

A position *i1* is said to be *in the range of* a position *i2* iff $|i1-i2|<m$. We say that two positions $i1<i2$ in the text are *consistent* iff *i2* is not in the range of *i1*, or if $WIT[i2-i1]=0$. If the positions are not consistent, then, we can remove one of them as a candidate for the starting position of the pattern by just considering position $i2+WIT[i2-i1]$ in the text. This is the operation called a duel (see Figure 3.6). Let $i = i2-i1$, and $k=WIT[i]$. Assume that we have $k>0$, that is, positions *i*1, *i*2 are not consistent. Let $a=pat[k]$ and $b=pat[i+k]$, then $a\neq b$. Let *c* be the symbol in the text at position $i2+k$, which is indicated by '?' in Figure 3.6. We can eliminate at least one of positions *i*1, *i*2 as a candidate for a match by comparing *c* with *a* and *b*. In some situations, even both positions could be eliminated. But, for simplicity, the algorithm below always removes exactly one position. Let us define (recall that $a=pat[WIT[i2-i1]]$):

$$duel(i1, i2) = (\textbf{if } a=c \textbf{ then } i2 \textbf{ else } i1).$$

The position that "survives" is the value of *duel*, the other position is eliminated.

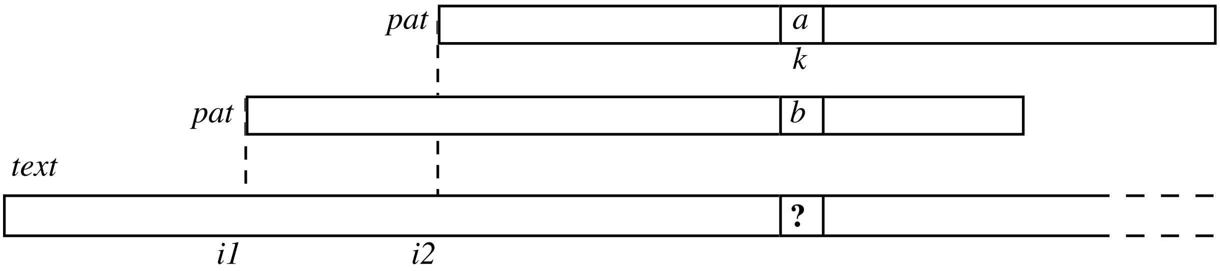


**Fig 3.6**. Duel between two inconsistent positions *i1* and *i2*.
One of them is eliminated by comparing symbol "?" in the text with *a* and *b*.

Assume the witness table is computed. Then, it is possible to reduce the search for *pat* in *text* to the search for pattern 11...111 (repetition of $m$ 1's) in a text of 0's and 1's. This last problem is obviously simpler than the general string-matching problem, and can be solved in linear time (with essentially one counter).

The following property of consistent positions (transitivity) is crucial for the correctness of the algorithm. It is called the *consistency property* : let $i1 < i2 < i3$,

if $i1$, $i2$ are consistent and $i2$,$i3$ are consistent then also $i1$,$i3$ are consistent.

Using this property we are able to eliminate from the text a set of candidate positions in such a way that all remaining positions are pairwise consistent. This can be done using the mechanism of stack (pushdown-store). Assume we have a stack of positions satisfying the property : positions are pairwise consistent, and in increasing order (from the top of the stack). Then if we push on the stack a position both smaller than the top position and consistent with it, then, the stack retains the property.

A set of consistent positions is *complete* if an occurrence of the pattern cannot start at any other position (position not in this set). We say that a position $x$ in the text agrees with a candidate position $y$, iff the symbol at position $x$ agrees with the corresponding symbol of the pattern when it is placed at position $y$ (that is, $text[x]=pat[x-y]$). Assume that $S$ is a complete set of consistent positions, $x$ is any position in the text, and $y$ is any candidate position in S such that $x$ is in the range of $y$ with $x>y$. Then, as a consequence of the consistency property, we have the following :

$x$ agrees with $y$ iff $x$ agrees with all positions in $S$.

Hence, it is enough to check the agreement of each position with any position from a set of consistent positions. In this checking, we flag $x$ with the value 0 or 1 depending on the agreement. Using this feature, the string-matching reduces easily to the matching of unary patterns (patterns consisting entirely of ones).

The duel-based algorithm uses an additional zero-one vector, called *text*1. The value of the vector *text*1 computed by the algorithm satisfies :

pattern $1^m$ occurs at position $i$ in *text*1 iff the original pattern occurs at $i$ in the text.

```
function String_searching_by_duels : boolean;
{ Let S be a stack of positions }
begin
  S := empty stack;
  for i := n downto 1 do begin
    push i on the stack S;
    while $|S|\geq 2$ and
          the two top elements i1, i2 of S are inconsistent do
      replace them in S by the single element duel(i1, i2);
  end;
  mark in the text all position that are in S;
  { all marked positions are pairwise consistent }
  for i := 1 to n do begin
    k := first marked position to the left of i, including  i;
    if k undefined or $pat[i-k+1]\neq text[i]$ then text1[i]:=0
    else text1[i]:=1;
  end;
  if text1 contains the pattern $1^m$ return(true)
  else return(false);
end;
```

The algorithm has obviously the linear time complexity. Moreover, this complexity does not depend on the size of the alphabet. The basic part that remains to be shown is the computation of the witness table *WIT* on the pattern.

We shall see later in the case of parallel computations that the fact that *any* position *k* for a witness is possible has a great importance. It is sufficient, and makes it easier to compute in parallel. However, in the case of sequential computations we can take the smallest such position as a witness. This remains to define *WIT*[*i*]:=*PREF*[*i*], for each position *i.* Section 4.6 contains both the definition of *PREF*, and a linear time algorithm to compute it. The complexity of this latter algorithm is independent of the size of the alphabet.

**Theorem 3.8**

String-matching by duels takes linear time (search phase and preprocessing phase).

We believe that matching by duels is one of the basic algorithms, since the idea of duels is the key to the optimal parallel string-matching of Vishkin presented later in Chapter 14.

However, historically the first optimal (for fixed alphabets) parallel string-matching algorithm uses the idea of a sieve. This algorithm uses implicitly another type of duels which we call *expensive duels*. Its advantage is that no additional table, like the one of witnesses, is needed. Its drawback is that the resulting algorithm is not optimal. We show only the use of expensive duels for a special type of patterns. Assume that the size of the pattern is a power of two. Assume also that *pat*$[1..2^k]$ is non-periodic, for each $k \geq 1$. Such patterns are called here *special*. patterns. An example of a special pattern is "wojtekrytter".

```
function expensive_duel(i, j): integer;
begin
  k := log₂(j-i)+1;
  if text[i..i+2^k]=pat[1..2^k] then kill j else kill i;
  return the survival;
end;
```

The defined function *expensive_duel* is similar to the duel function, however its computation is much more expensive. This is the reason for the name "expensive duel". In the algorithm, we partition the text into disjoint blocks of size $2^k$, we call them *k*-blocks.

```
algorithm String_searching_by_expensive_duels;
{ assume n-m+1 and m are powers of two }
{ assume that the pattern is special }
begin
  initially all positions in [1..n-m] are survivals;
  for k := 1 to logn do begin
    let i and j be the only survivals in the k-blocks;
    make expensive_duel(i, j) a survival;
  end;
  { there are O(n/m) survivals }
  for each survival position i do
    check occurrence of pat at position i naively;
end;
```

Let us observe the very parallel nature of this algorithm: at a given stage *k*, the actions on all *k*-blocks can be performed simultaneously.

**Theorem 3.9**

Assume that all prefixes *pat*$[1..2^k]$ are non-periodic. Then the algorithm *String_searching_by_expensive_duels* takes O($n$ log $m$) time.

**Proof**

At stage $k$ we consider only O($n/2^k$) survivals. Each expensive duel at this stage takes O($2^k$) time. There are $m$/2 stages. This gives together O($n$ log $m$) time. This completes the proof. ♦

The expensive duels are of restricted use. However, historically they appeared before the concept of the duel has appeared. This is the only reason why it is reported here.

## 3.4 String-matching by sampling

Both Knuth-Morris-Pratt algorithm and Boyer-Moore algorithm (in the next chapter) scan symbols at consecutive positions on the pattern. The first one scans a prefix of the pattern, and the second one scans a suffix of the pattern. In this section, we show an algorithm that first scans a sequence of not necessarily consecutive positions on the pattern, and then, in case of success, completes the scan of the pattern. The first scanning sequence is called a ***sample***.

A sample $S$ for the pattern *pat* is a set of positions on *pat*. A sample $S$ occurs at position $i$ in the text iff *pat*[$j$]=*text*[$i$+$j$] for each $j$ in $S$ (see Figure 3.7).

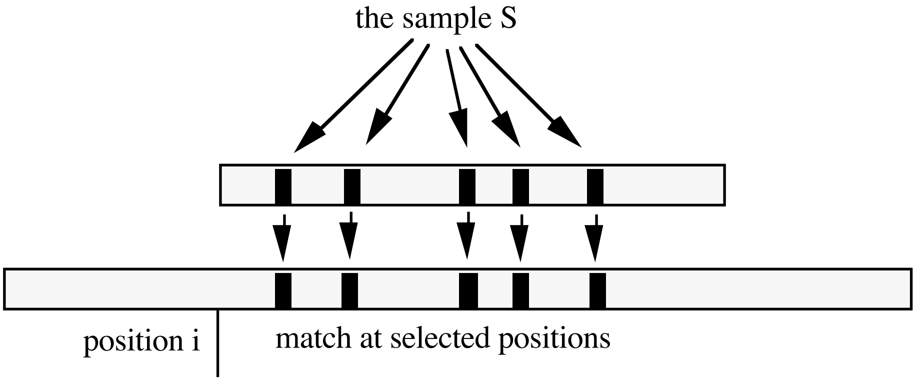


**Figure 3.7.** An occurrence of the sample S in the text.

A sample $S$ is called a **good sample** iff it satisfies the two conditions (see Figure 3.8):

(1) $S$ is small : $|S| = O(\log m)$;

(2) there is an integer $k$ such that if $S$ occurs at position $i$ in the text then no occurrence of the pattern starts in the segment [$i$-$k$..$i$+$m$/2-$k$] (this segment is called the *desert*.), except maybe at $i$.

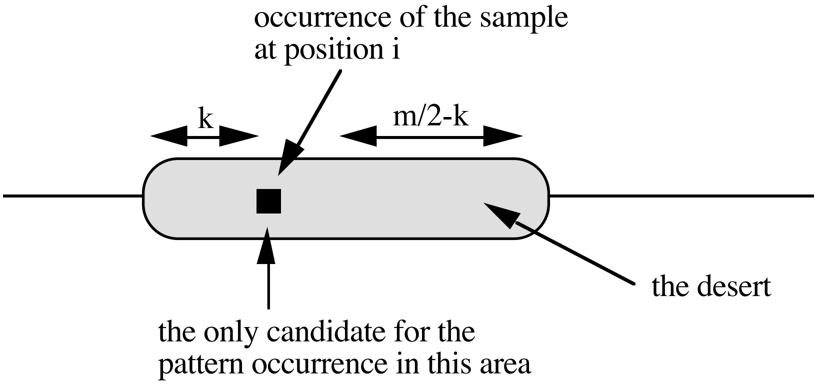

occurrence of the sample at position i
k
m/2-k
the desert
the only candidate for the pattern occurrence in this area

**Figure 3.8.** An occurrence of the sample, and the desert area.

If the pattern has period $p$, then $pat[1..k]$ is called the non-periodic part of the pattern, where $k$=min($m$, 2.$p$-1).

**Theorem 3.10**

Assume we are given the period of the pattern *pat*, and a good sample of its non-periodic part, then, the search for *pat* can be done in $O(n \log n)$ time with only $O(\log n)$ additional memory space.

**Proof**

Assume for a moment that the pattern itself is non-periodic. Let us partition the input text into *windows* of size $m/2$. We consider each window separately, and find the first and the last occurrences of the sample in the window (if there are at least two occurrences). Only these occurrences are possible candidates for an occurrence of the pattern. Each of these occurrences is checked in a naive way (constant size additional memory is enough for that). This proves that non-periodic part of the pattern can be found in the text with the required complexity. The general case of periodic patterns is left as an exercise. One has to find sufficiently many consecutive occurrences of the non-periodic part of the pattern. An additional counter is needed to remember the number of consecutive occurrences. This completes the proof. ♦

**Theorem 3.11**

If the pattern is non-periodic then it has a good sample $S$. The sample can be constructed in linear time.

**Proof**

Assume we have computed the witness table *WIT* (see Section 3.3). Let us consider supposed occurrences of the pattern at positions 1, 2, ..., *m*/2 of some imaginary text. Let us identify these pattern occurrences with numbers 1, 2, ..., *m*/2. The occurrence corresponding to the *i*-th position is called the *i*-th row. If we draw a vertical line at a position *j* then it can intersect a given *i*-th row or not. If it intersects, then there is a symbol at the point of intersection (see the Figure 3.9). Let us denote this symbol by *symbol*(*i*, *j*).

CLAIM 1

Let *i*1, *i*2 be two different elements of [1..*m*/2]. Then, there is an integer *j* such that the *j*-th column intersects both rows *i*1 and *i*2; moreover, *symbol*(*i*1, *j*) ≠ *symbol*(*i*2, *j*). The integer *j* can be found in constant time if the witness table of the pattern is precomputed.

The claim is a reformulation of the property of non-periodicity. Due to non-periodicity, for occurrences of pattern placed at positions *i*1, *i*2 there is a mismatch position *j* given by the *j* = *i*2+*WIT*[*i*2-*i*1]. This means that if we look at the vertical column placed at position *j* then this column intersects occurrences of pattern with different symbols.

CLAIM 2

Let *J* be any set of rows. If a vertical column intersects the first and the last row of *J*, then it intersects all the rows of *J*.

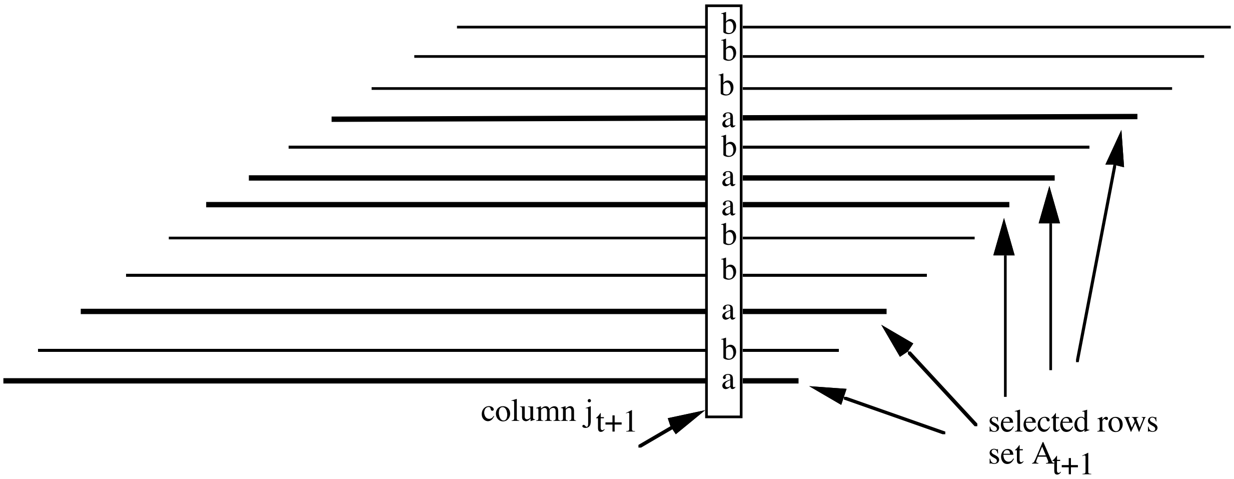


**Fig 3.9.** The set $A_{t+1}$ ={ $i \in A_t$ : *symbol*($i$, $j_{t+1}$)=*a*} is the smaller one.

.

We now prove an equivalent geometrical formulation of the thesis of the theorem.

CLAIM 3

There is a row *i* and a set *J* of *O*(log *m*) vertical columns placed at positions $j_1, j_2, ..., j_k$ such that:

(a) all columns in *J* intersect the row *i*;

(b) if *r* ≠ *i* (*r* in [1..*m*/2]), then there is a column *j* in *J* intersecting rows *i* and *r* and such that *symbol*(*i*, *j*) ≠ *symbol*(*r*, *j*).

PROOF (of the claim)

We construct the set *J* and the row *i* by the algorithm below, which ends the proof of the theorem. ♦

```
Algorithm Find_good_sample;
begin
  $J$ := empty set; $A_0$ := [1..$m$/2]; $t$ := 0;
  while $|A_t|$ > 1 do begin
    find any column $j_{t+1}$ which intersects all rows of $A_t$
    with two different symbols at intersection points;
    { use CLAIM 1 and CLAIM 2 }
    Let $a$, $b$ be the two different symbols at intersections;
    $A_{t+1}$ := smaller of the two sets {$i \in A_t$ / $symbol(i,j_{t+1})=a$}
                                    and {$i \in A_t$ / $symbol(i,j_{t+1})=b$};
    add $j_{t+1}$ to $J$; $t$ := $t$+1;
  end;
  let $i$ be the unique element of $A_t$;
  return($J$, $i$);
end;
```

## Bibliographic notes

The first lower bound on the maximal number of symbol comparisons for string-matching has been given by Rivest [Ri 77]. Recent improvements on this bound are by Colussi, Galil and Giancarlo [CGG 90].

MP algorithm is from Morris and Pratt [MP 70]. The fundamental algorithm considered in this chapter (KMP algorithm) have been designed by Knuth, Morris and Pratt [KMP 77]. Our exposition is slightly different than in this paper.

That the computation of borders is equivalent to string-matching has been noticed in [FP 74]. An application of the notion of failure table to the computation of maximal suffixes can be found in [Bo 80]. A more efficient algorithm computing maximal suffixes based on ideas of Duval is found in Chapter 13 (see also Chapter 15).

Algorithm of Simon is reported from the author. It has recently been proved by Hancart [Ha 93] that Simon's algorithm can be transformed into a searching algorithm reaching the optimal bound of (2-1/*m*).*n* comparisons among algorithms using a 1-letter window on the text.

A criterion that says whether an on-line algorithm can be transformed into a real-time algorithm has been shown by Galil in [Ga 81]. The principle applies to MP, KMP, and MPS algorithms.

The idea of duels can be attributed to Vishkin who applied it for the design of parallel algorithms [Vi 85] (see Chapter 14). Expensive duels are implicitly considered by Galil in [Ga 85]. The notion of sample is from Vishkin [Vi 90].

## Selected references

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# 4. The Boyer-Moore algorithm and its variations

We describe in this chapter another basic approach to string-matching. It is introduced as an improvement on a second version of the naive algorithm of Chapter 3. We can get another naive string-matching algorithm, similar to *brute_force1* of the previous chapter, if the scan of the pattern is done from the right to left. This algorithm has quadratic worst-case behavior, but (similarly to algorithm *brute_force1*) its average time complexity is linear.

In this section we discuss a derivative of this algorithm — the Boyer-Moore string-matching algorithm. The main feature of this algorithm is that it is efficient in the sense of worst-case (for most variants) as well as average-case complexity. For most texts and patterns the algorithm scans only a small part of the text because it performs "jumps" on the text. The algorithm applies to texts and patterns that reside in main memory.

```
function brute_force2 : boolean;
  var i, j : integer;
begin
  i := 0;
  while i≤n-m do begin
    { right-to-left scan of pat }
    j := m;
    while j>0 and pat[j]=text[i+j] do j := j-1;
    if j=0 then return(true);
    { inv2(i, j) }
    i := i+1; { length of shift = 1 }
  end;
  return(false);
end;
```

## 4.1 The Boyer-Moore algorithm

The algorithm BM can be viewed as an improvement on the initial naive algorithm *brute_force2*. We try again, as done in the previous chapter for algorithm *brute_force1*, to analyze this algorithm and look carefully at information the algorithm wastes. This information is related to the invariant in the algorithm *brute_force2*

$$inv2 : pat[j+1\ldots m]=text[i+j+1\ldots i+m] \text{ and } pat[j]\neq text[i+j].$$

Denote by *inv*2' the weaker invariant : $pat[j+1\ldots m]=text[i+j+1\ldots i+m]$.

The information gathered by the algorithm is "stored" in the value of *j*. However, at the next iteration, this information is erased as *j* is set to a fixed value. Suppose that we want to make bigger shifts using the invariant.

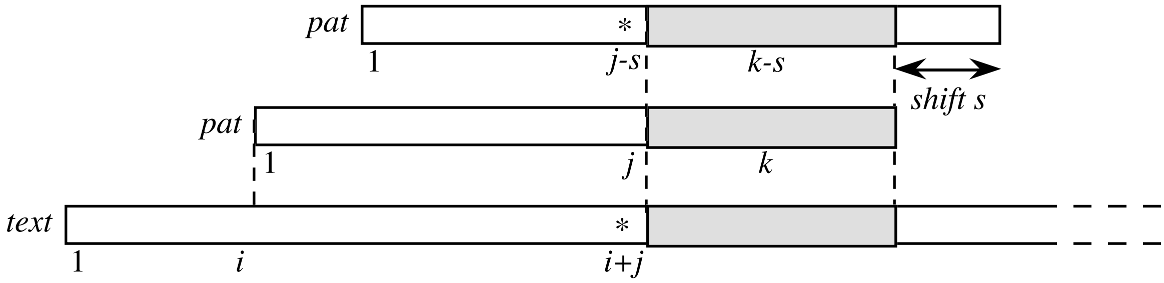


**Figure 4.1**. The case *s*<*j*.

The shift *s* is said to be *safe* iff we are certain that between *i* and *i*+*s* there is no starting position for the pattern in the text. Suppose that the pattern appears at position *i*+*s* (see Figure 4.1, where the case *s*<*j*' is presented). Then, the following conditions hold :

*cond*1(*j*, *s*) : for each *k* s.t. *j*<*k*≤*m*, *s*≥*k* or *pat*[*k*-*s*]=*pat*[*k*],

*cond*2(*j*, *s*) : if *s*<*j* then *pat*[*j*-s]≠*pat*[*j*].

We define two kinds of shifts, each associated with a suffix of the pattern represented by position *j* (<*m*), and defined by its length :

*D*1[*j*] = min {*s*>0 : *cond*1(*j*, *s*) holds},

*D*[*j*] = min {*s*>0 : *cond*1(*j*, *s*) and *cond*2(*j*, *s*) hold}.

We also define *D*1[*m*]=*D*[*m*]=*m*-*Bord*[*m*]. The Boyer-Moore algorithm is a version of *brute_force2* in which, in a mismatch situation, is executed a shift of length *D*[*j*] instead of one position shift.

```
function BM : boolean;
{ improved version of brute_force2 }
begin
  i := 0;
  while i≤n-m do begin
    j := m;
    while j>0 and pat[j]=text[i+j] do j := j-1;
    if j=0 then return(true);
    { inv2(i, j) }
    i := i+D[j];
  end;
  return(false);
end;
```

Let us compare a run of this algorithm with a run of the similar algorithm which uses *D*1 instead of *D*. The history of the computations for *pat*=*cababababa* and *text*=*aaaaaaaaaabababababa* is presented in Figure 4.2.

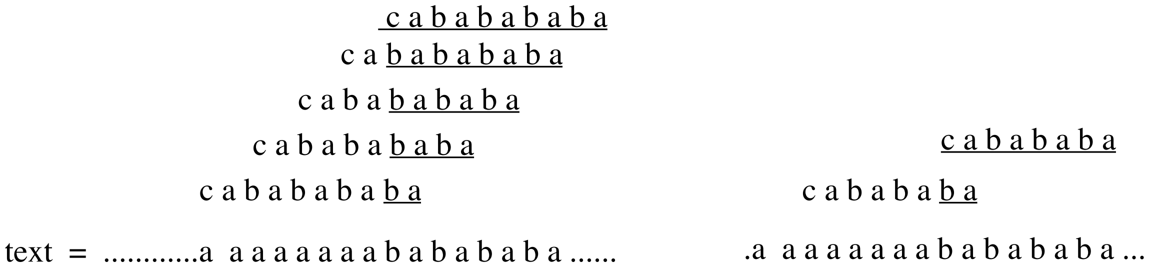
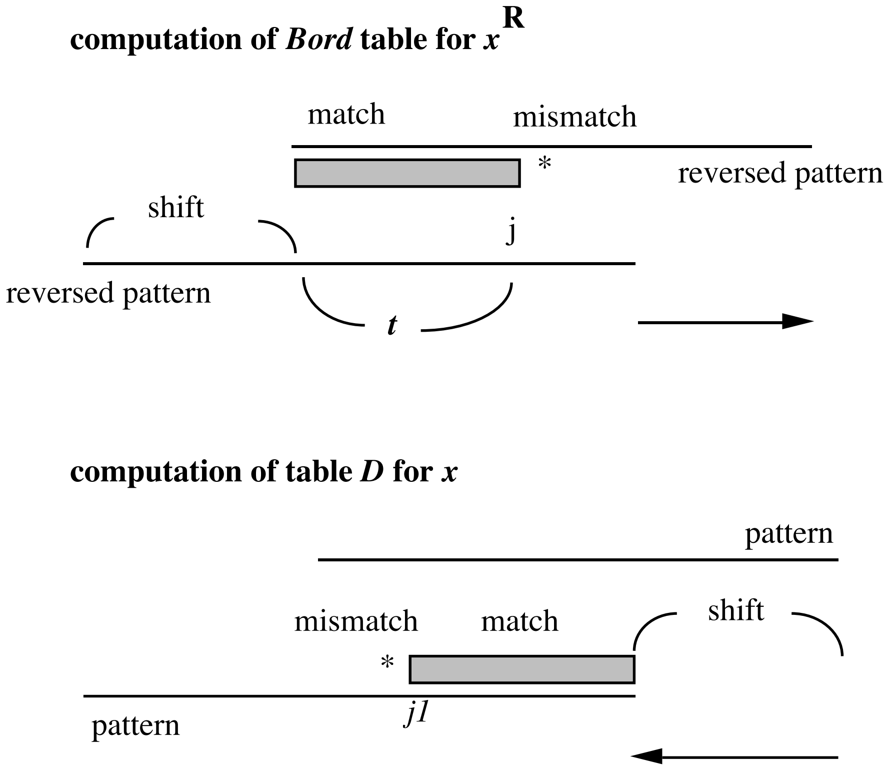


**Figure 4.2**. BM with *D*1-shifts makes 30 comparisons (left)
BM with *D*-shifts makes only 12 comparisons (right).

We show that time complexity of preprocessing the pattern (compute table *D*) is linear. We use a close correspondence between situations in relation with the definition of function *D*; and configurations appearing in the algorithm that computes failure functions, see Figure 4.1 and Figure 4.3.

Let *x*1 be the reverse of *pat*. In the algorithm below, we update values of certain entries of table *D* according to what is shown in Figure 4.3. This figure is related only to the case *D*[*j*1]<*j*1, which is considered during the first stage of the algorithm. We treat separately other entries of the table *D* in the second stage, see Figure 4.4

```
procedure compute_D;
begin
  { m is the maximal possible length of shifts }
  for j1 := 1 to m do D[j1] := m;
  { first stage is a partial computation of table D; }
  { correct values are computed for D[j1]<j1; }
  { we compute table Bord for the reverse of pat; }
  { D is computed as a side-effect }
  Bord[0] := 0; Bord[1] := 0; t := 0;
  for j := 2 to m do begin
    while x1[j]<>x1[t+1] and t>0 do begin { see Figure 4.3 }
      s:=j-t-1; j1:=m-t; D[j1]:=min(D[j1], s ); t:=Bord[t];
    end;
    if x1[t+1]=x[j] then t := t+1
    else { see Figure 4.3 with t=0 } D[m] := min(D[m], j-1);
    Bord[j] := t;
  end;
  { second stage: correct values for D[j1]≥j1, see Figure 4.4 }
  { consider the failure function Bord for the pattern pat }
  { not for the reverse of pat, as before }
  t := Bord[m]; q := 0;
  while t>0 do begin
    s := m-t;
    for j := q to s do D[j] := min(D[j], s);
    q := s+1; t := Bord[t];
  end;
end;
```



**computation of *Bord* table for $x^R$**

**computation of table *D* for *x***

**Figure 4.3**. Situation just before executing $t = Bord[t]$ in the computation of failure function *Bord* for the reverse of pattern. We know that $D[j1] \geq s$, where $s=j-t-1$ and $j1=m-t$.

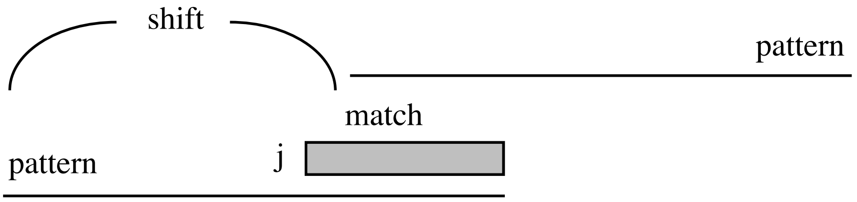


**Figure 4.4**. Case $D[j] \geq j$; $D[j]=s=m-t$, where $t=Bord^k[m]$ for some $k>0$.

Boyer and Moore introduced also another "heuristic" useful in increasing lengths of shifts. Suppose that we have a situation, where $symb=text[i+j]$ (for $j>0$), and *symb* does not occur at all in the pattern. Then, in the mismatch situation, we can make a shift of length $s=j$. For example if $pat=a^{100}$ and $t=(a^{99}b)^{10}$ then we can always shift of 100 positions, and eventually make only 10 symbol comparisons. For the same input words, algorithm BM makes 901 comparisons. But, if we take $pat=ba^{m-1}$ and $text=a^{2.m-1}$, the heuristic used alone (without using table *D*) leads to a quadratic time complexity. Let *last*(*symb*) be the last position of an occurrence of symbol *symb* in *pat*. If there is no occurrence, *last*(*symb*) is set to zero. Then, we can define a new shift, replacing instruction "`i := i+D[j]`" of BM algorithm by "`i := i+max(D[j], j-last(text[i+j])`".

Shift of length *j-last*(*text*[*i*+*j*]) is called an *occurrence shift*. In practice, it may improve the time of the search for some inputs, though theoretically it is not entirely analyzed. If the alphabet is binary, and more generally for small alphabets, the occurrence heuristics have little effect, so, it is almost useless.

## 4.2.* Analysis of Boyer-Moore algorithm

The tight upper bound for the number of comparisons done by BM algorithm is approximately $3.n$. The proof of it is rather difficult but yields a fairly simple proof of a $4.n$ bound. The fact that the bound is linear is completely nontrivial, and even surprising in view of the quadratic behavior of BM algorithm when modified to search for all occurrences of the pattern. The algorithm uses variable *j* to enlarge shifts, but afterwards "forgets" about the checked portion of the text. In fact, the same symbol in *text* can be checked a logarithmic number of times. If we replace *D* by *D*1 then the time complexity becomes quadratic (counterexample is given by text and patterns with the same structure as in the Figure 4.2 : $pat=ca(ba)^k$ and $text=a^{2.k+2}(ba)^k$ ). Hence, one small piece of information (the "one bit" difference between invariants *inv*2, *inv*2') considerably reduces the time complexity in the worst case. This contrasts with improved versions of algorithm *brute_force1*, where *inv*1 and *inv*1' gave similar complexities (see Chapter 3). The difference between the usefulness of information about one mismatched symbol is an evidence of the big importance of a (seemingly) technical difference in scanning the pattern left-to-right versus right-to-left.

Assume that, in a given non-terminating iteration, BM algorithm scans the part $text[i+j-1...i+m]$ of the text and then makes the shift of length $s=D[j]$, where $j>0$ and $s>(m-j)/3$. By *current match* we mean the scanned part of text without the mismatch letter (see Figure 4.5).

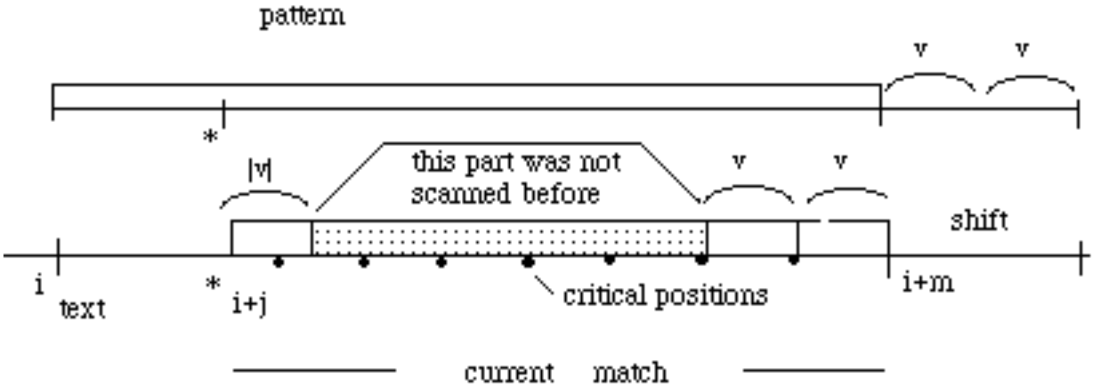


**Fig 4.5**. The part *text*[*i*+*j*-1…*i*+*m*] of the text is the current match; *v* denotes the shortest full period of the suffix of the pattern, *v* is a period of the current match.

**Lemma 4.1**

Let $s$ be the value of the shift made in a given non-terminating iteration of BM algorithm. Then at most $3.s$ positions of the text scanned at this iteration, have been scanned in previous iterations.

**Proof**

It is easier to prove a stronger claim:

/*/ positions in the segment $text[i+j+k \ldots i+m-2.k]$ are scanned in this iteration for the first time, where $k$ is the size of the shortest full period $v$ of $pat[m-s \ldots m]$.

In other words:

only the first $k$ and the last $2.k$ positions of the current match could have been read before.

Denote by $v$ the shortest full period $v$ of $pat[m-s+1 \ldots m]$. The following property of the current match follows directly from the definition of the shift:

**(Basic property)** $v$ is a period of the current match, and $v$ is a suffix of the pattern.

We introduce the notion of ***critical position*** in the current match. These are internal positions in this match whose distance from the right end of the match is a nonzero multiple of $k$, (see Figure 4.5) and distance from the left is at least $k$. We say that a previous match ends at a position $q$ in the text, if, in some previous iteration, the end of the pattern was positioned at $q$.

**Claim 1:**

No previous match ends at a critical position of the current match.

**Proof** (of the claim)

The position $i+m$ is the end position of the current match. It is easy to see that, if a critical point of the current match is the end of the match in a previous iteration $i$, then in the iteration immediate after $i$ the end of the pattern is at position $i+m+shift$. Hence the current match under consideration would not exist, a contradiction. This proves the claim. ‡

**Claim 2**

The length of the overlap of the current match and the previous match is smaller than $k$.

**Proof** (of the claim)

Recall that by a match we mean a scanned part of the text without the mismatch position. The period $v$ is a suffix of the pattern. We already know, from Claim 1, that the end of the previous match cannot end at a critical position. Hence if the overlap is at least $k$ long, then $v$ occurs inside the current match with the end-position not placed at a critical position. Then, the primitive word $v$ properly overlaps itself in a text whose periodicity is $v$. But, this is impossible for primitive words (due to periodicity lemma). This proves the claim. ‡

**Claim 3**

Assume that a previous match ends at position $q$ inside a forbidden one, and is completely contained in the current match. Then there is no critical point (in the current match) to the right of $q$.

**Proof** (of the claim)

Suppose there is a critical position $r$ to the right of $q$. Then it is easy to see that $r$-$q$ is a good candidate for the shift in the BM algorithm. The algorithm takes as an actual shift the smallest such candidate. If the shift is smaller than $r$-$q$, we have a new position $q1<r$. Then, we will have a sequence of previous matches with end-positions $q1$, $q2$, $q3$,... . This sequence terminates in $r$, otherwise we would have an infinite increasing sequence of natural numbers smaller than $r$, which is impossible. This contradicts Claim 1, since we have a previous match ending at a critical position in the current match. This completes the proof of the claim. ‡

**Proof of lemma**

Now, we are ready to show that /*/ holds. The proof is by contradiction. Assume that in some earlier iteration we scan the "forbidden" part of the text (shadowed in Figure 4.5. Let $q$ be the end-position of the match in this iteration. Then, $q$ is not a critical position and this match is contained completely in the current match (its overlap with the current match is shorter than $k$ and $q$ lies too far from the beginning of the current match). By the same argument the rightmost critical position in the current match is to the right of $q$. Hence, we have found a previous match which is completely contained in the current match and whose end-position lies to the left of some critical position. however this is impossible, due to Claim 3. This completes the proof of the lemma. ‡

**Theorem 4.2**

The Boyer-Moore algorithm makes at most $4n$ symbol comparisons to find the first occurrence of the pattern (or to report no matches). The linear time complexity of the algorithm does not depend on the size of the alphabet.

**Proof**

The cost of each non-terminating iteration can be split into two parts:

(1) the cost of scanning some positions of the text for the first time,

(2) three times the length of the shift.

The total cost of all non-terminating iterations can be estimated by summing separately all costs of type (1), this gives at most $n$, and all costs of type (2), which gives at most $3.(n\text{-}m)$.

The cost of a terminating iteration is at most $m$. Hence, the total cost of all iterations is upper bounded by:

$$n + 3(n\text{-}m) + m \leq 4.n.$$

This completes the proof. ‡

## 4.3 Galil's improvement

If we want to find all occurrences of *pat* in *text* with a modified BM algorithm, then, the complexity can become quadratic. The simplest counterexample is given by a text and a pattern over a one-letter alphabet. Observe a characteristic feature of this counterexample : high periodicity of the pattern. Let *p* be the period of the pattern. If we discover an occurrence of *pat* at some position in *text*, then the next shift must naturally be equal to *p*. Afterwards, we have only to check the last *p* symbols of *pat*. If they match with the text, then, we can report a complete match without inspecting all other *m-p* symbols of *pat*. This simple idea is embodied in the algorithm below. The variable named *memory* "remembers" the number of symbols which we have not to be inspected (*memory*=0 or *memory*=*m-p*). It remembers in fact the prefix of the pattern that matches the text at the current position. This technique is called *prefix memorization*. The correctness of the following algorithm is straightforward. The period of *pat* can be pre-computed from algorithms of Chapter 3 (see MP algorithm).

```
procedure BMG;
{ BM algorithm with prefix memorization; p = period(pat) }
begin
  i := 0; memory := 0;
  while i≤n-m do begin
    j := m;
    while j>memory and pat[j]=text[i+j] do j := j-1;
    if j=memory then begin
      write(i); memory := m-p;
    end else memory := 0;
    { inv2(i, j) }
    i := i+D[j];
  end;
end;
```

**Theorem 4.3**

Algorithm BMG makes $O(n)$ comparisons.

**Proof**

It is an easy consequence of the previous theorem that the complexity is $O(n+r.m)$, where $r$ is the number of occurrences of *pat* in *text*. This is because between any two consecutive occurrences of *pat* in *text*, BMG does not make more comparisons than the original BM algorithm. Hence, if $p≥m/2$, since $r≤n/p$, $n+r.m$ is $O(n)$.

It remains to consider the case $p<m/2$. In this case, we can group occurrences of the pattern into chains of positions differing only by $p$ (for two consecutive positions in a group) (see Figure 4.6).

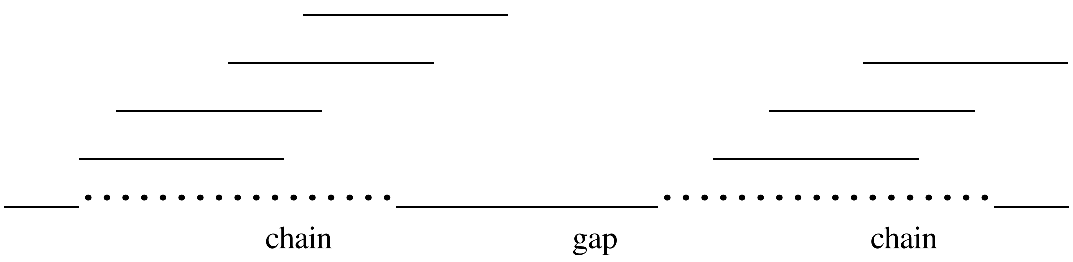


**Figure 4.6**. The text is partitioned into chains of consecutive occurrences of pattern, and gaps between them.

Within each such chain each text symbol is inspected at most once. The gaps between chains are larger than $m/2$, and, inside each such gap, BMG works is not slower than BM algorithm. Now an argument similar to that used in the case of large periods can be applied. This completes the proof. ‡

## 4.4 The Turbo_BM algorithm

We present in this section another efficient version of the Boyer-Moore algorithm. The modification looks superficial, but it actually improves the worst case complexity. The number of letter comparisons done during the search becomes less than $2.n$. The BMG algorithm of Section 4.3, implements a prefix memorization after the discovery of an occurrence of the pattern. In the present version, we implement a factor memorization. This occurs not only after occurrences of the pattern.

In the new approach no extra preprocessing is needed. The only table to keep from BM algorithm is the original table of shifts, $D$. All extra memory is of a constant size (two integers). The resulting algorithm Turbo_BM forgets all its history except the most recent one and its behavior has again a “mysterious” character. Despite that, the complexity is improved and the analysis is simple.

The main feature of Turbo_BM algorithm is that during the search of the pattern, one factor of the pattern that matches the text at the current position is memorized (this factor can be empty). This has two advantages :

— it can lead to a jump over the memorized factor during the scanning phase,

— it allows to perform what we call a *Turbo-shift*.

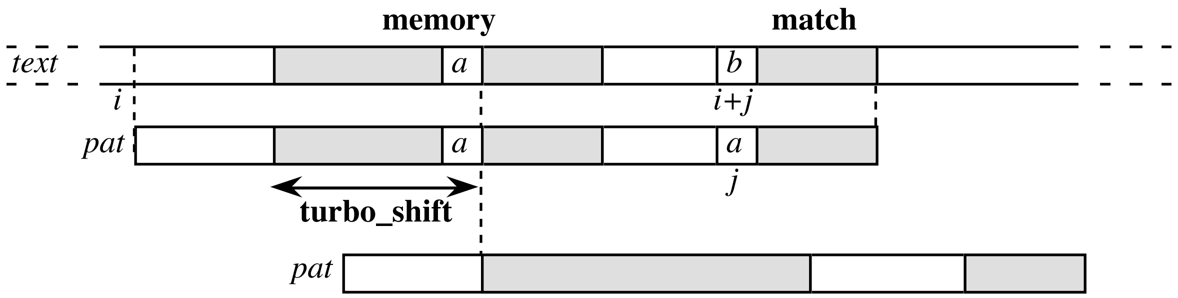


**Figure 4.7**. Turbo-shift equals *memory-match*.
Distinct letters *a* and *b* in text are at distance *h*, and *h* is a period of the right part of pattern.

In Turbo_BM algorithm, two kinds of shifts are considered : ordinary shifts of BM algorithm (called a *D*-shift), and Turbo_shifts. We now explain what is a *Turbo_shift*. Let *x* (**match**) be the longest suffix of *pat* that matches the text at a given position. Let also *y* (**memory**) be the memorized factor that matches the text at the same position. We assume that *x* and *y* do not overlap (i.e., for some non-empty word *z*, *yzx* is a suffix of *pat*). For different letters *a* and *b*, *ax* is a suffix of *pat* aligned with *bx* in the text (see Figure 4.7). The only interesting situation is when *y* is non empty, which occurs only immediately after a *D*-shift. Let *shift* its length. A *Turbo_shift* can occur when *x* is shorter than *y*. In this situation, *ax* is a suffix of *y*. Thus letters *a* and *b* occur at distance *shift* in the text. But, suffix *yzx* of *pat* has period *shift* (by definition of the *D*-shift), and thus, this word cannot overlap both occurrences of letters *a* and *b* in the text. As a consequence, the smallest safe shift of the pattern is $|y|-|x|$, which we call the *Turbo_shift*.

In a first approximation, the length of the current shift in Turbo_BM algorithm is max(*D*[*j*], *Turbo_shift*). In fact, in case a *D*-shift does not apply (*D*[*j*] is smaller than *Turbo_shift*), the length of the actual shift is made greater than the length of the matched suffix of *pat*. The proof of correctness of this second feature is similar to the above argument. It is explained in Figure 4.8.

From the above discussion, and the analysis of BM algorithm itself, it is straightforward to derive a correctness proof of Turbo_BM algorithm. The algorithm, given below, finds all occurrences of the pattern, not only the first one, as BM algorithm does.

```
procedure Turbo_BM;  { BM algorithm with factor memorization }
begin
  i:=0; memory:=0;
  while i ≤ n-m do begin
    j := m;
    while j > 0 and  pat[j] = text[i+j] do
      if memory ≠ 0 and j = m-shift then j := j-memory { jump }
      else j := j-1;
    if j = 0 then report match at position i;
    match := m-j; Turbo_shift := memory-match;
    shift := max(D[j], Turbo_shift);
    if shift > D[j] then begin
      i := i+max(shift, match+1); memory := 0;
    end else begin
      i := i+shift; memory := min(m-shift, match);
    end;
  end;
end;
```

In the above Turbo_BM algorithm, we deal only with ordinary shifts of BM algorithm. We have discussed, at the end of Section 4.1, how to incorporate into BM algorithm occurrence shifts. The version of Turbo_BM including occurrence shifts is obtained by a simple modification of the instruction computing variable *shift*. It becomes

$$shift := \max(D[j],\ j-last(t[i+j]),\ Turbo\_shift).$$

In case an occurrence shift is possible, the length of the shift is made greater than *match*. This is similar to the case where a turbo-shift applies. The proof of correctness is also similar, and explained by Figure 4.8. The length of the *D*-shift of BM algorithm is a period of the segment *match* of the text (Figure 4.8). At the same time, we have two distinct symbols *a*,*b* whose distance is the period of the segment. Hence, the shift has length at least *match*+1. This shows the correctness of Turbo_BM algorithm with occurrence shifts.

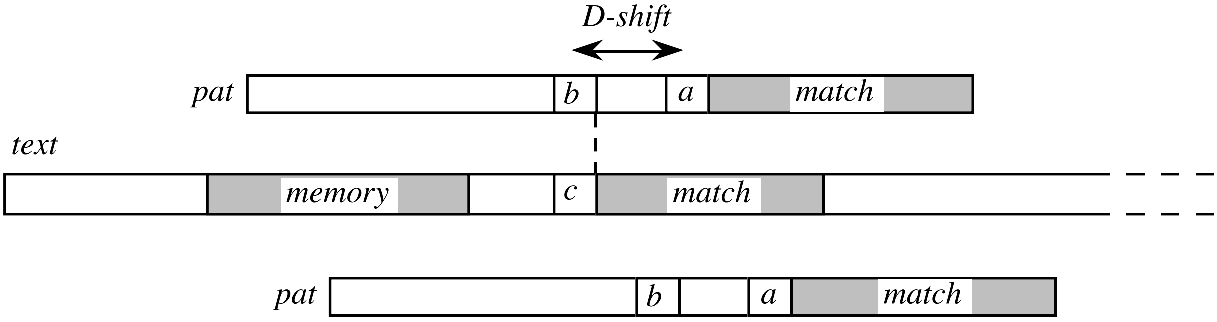


**Figure 4.8.** The occurrence-shift or Turbo-shift are greater than *D*-shift, which is a period of *match*. Letters *a* and *b* ( $a \neq b$) cannot both overlap *match*. Then the global shift must be greater than *match*.

## 4.5.* Analysis of Turbo_BM algorithm

The analysis of the time complexity of Turbo-BM is far more simpler than that of BM algorithm. Moreover, the maximum number of letter comparisons done during the search (of all occurrences of the pattern) is less the "canonical" $2.n$. Recall that it is approximatively $3.n$ for BM algorithm (to find the first occurrence of the pattern). So, Turbo_BM algorithm is superior to BM algorithm in two aspects:

— the time complexity is improved,

— the analysis is simpler.

**Theorem 4.4**

The Turbo_BM algorithm (with or without the occurrence heuristics) is linear. It makes less than $2.n$ comparisons.

**Proof**

We decompose the search into stages. Each stage is itself divided into the two operations : scan and shift. At stage $k$ we call $Suf_k$ the suffix of the pattern that matches the text and $suf_k$ its length. It is preceded by a letter that does not match the aligned letter in the text (in the case $Suf_k$ is not the $p$ itself). We also call $shift_k$ the length of the shift done at stage $k$.

Consider 3 types of stages according to the nature of the scan, and of the shift:

(i) stage followed by a stage with jump,

(ii) no type (i) stage with long shift.

(iii) no type (i) stage with short shift,

We say that the shift at stage $k$ is short if $2.shift_k < suf_k+1$. The idea of the proof is to amortize comparisons with shifts. We define $cost_k$ as follows :

— if stage $k$ is of type (i), $cost_k = 1$;

— if stage $k$ is of type (ii) or (iii), $cost_k = suf_k+1$.

In the case of type (i) stage, the cost corresponds to the mismatch comparison. Other comparisons done during the same stage are reported to the cost of next stage. So, the total number of comparisons executed by the algorithm is the sum of costs. We want to prove $\Sigma costs < 2.\Sigma shifts$. In the second $\Sigma$, the length of the last shift is replaced by $m$. Even with this assumption, we have $\Sigma shifts \leq |t|$, and if the above inequality holds, so is the result $\Sigma costs < 2.|t|$.

For stage $k$ of type (i), $cost_k$ (=1) is trivially less than $2.shift_k$, because $shift_k > 0$. For stage $k$ of type (ii), $cost_k = suf_k+1 \leq 2.shift_k$, by definition of long shifts.

It remains to consider stages of type (iii). Since in this situation, we have $shift_k<suf_k$,, the only possibility is that a $D$-shift is applied at stage $k$. Then memory is set up. At next stage $k+1$, the memory is not empty, which leads to a potential turbo-shift. The situation at stage k+1 is the general situation when a turbo-shift is possible (see Figure 4.9). Before continuing the proof, we first consider two cases and establish inequalities (on the cost of stage k) that are used later.

CASE (a) **:** $suf_k+shift_k \leq |p|$

By definition of the turbo-shift, we have $suf_k - suf_{k+1} \leq shift_{k+1}$. Thus,

$$cost_k = suf_k+1 \leq suf_{k+1}+shift_{k+1}+1 \leq shift_k+shift_{k+1}.$$

CASE (b) **:** $suf_k+shift_k > |p|$

By definition of the turbo-shift, we have $suf_{k+1}+shift_k+shift_{k+1} \geq m$. Then

$$cost_k \leq m \leq 2.shift_k-1+shift_{k+1}.$$

We can consider that at stage $k+1$ case (b) occurs, because this gives the higher bound on $cost_k$ (this is true if $shift_k \geq 2$; the case $shift_k=1$ can be treated directly).

If stage $k+1$ is of type (i), then $cost_{k+1} = 1$, and then $cost_k+cost_{k+1} \leq 2.shift_k+shift_{k+1}$, an even better bound than expected.

If stage $k+1$ is of type (ii), or even if $suf_{k+1} \leq shift_{k+1}$, we get what expected, $cost_k+cost_{k+1} \leq 2.shift_k+2.shift_{k+1}$.

The last situation to consider is when stage $k+1$ is of type (iii) with $suf_{k+1} > shift_{k+1}$. This means, as previously mentioned, that a $D$-shift is applied at stage $k+1$. Thus, the above analysis also applies at stage $k+1$, and, since only case (a) can occur then, we get $cost_{k+1} \leq shift_{k+1}+shift_{k+2}$. We finally get $cost_k+cost_{k+1} \leq 2.shift_k+2.shift_{k+1}+shift_{k+2}$.

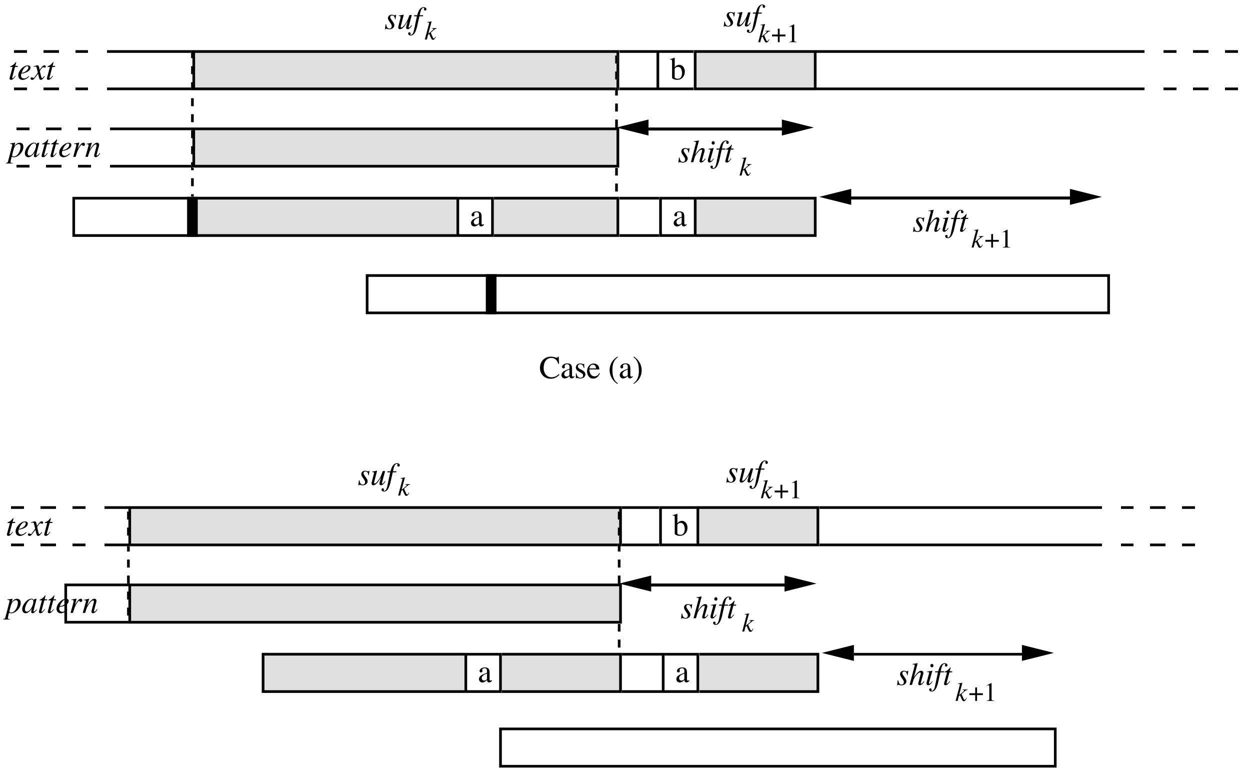
The last argument proves the first step of an induction : if all stages $k$ to $k+j$ are of type (iii) with $suf_k > shift_k$, …., $suf_{k+j} > shift_{k+j}$, then

$$cost_k+....+cost_{k+j} \leq 2.shift_k+....+2.shift_{k+j}+shift_{k+j+1}.$$

Let $k'$ be the first stage after stage $k$ such that $suf_{k'} \leq shift_{k'}$. Integer $k'$ exists because the contrary would produce an infinite sequence of shifts with decreasing lengths. We then get

$$cost_k+....+cost_{k'} \leq 2.shift_k+....+2.shift_{k'}.$$

Which shows that $\Sigma cost_k \leq 2.\Sigma shift_k$, as expected. ‡



Case (a)

Case (b)

**Figure 4.9.** Costs of stages $k$ and $k$+1 correspond to shadowed areas plus mismatches. If $shift_k$ is small, then $shift_k$+$shift_{k+1}$ is big enough to partially amortize the costs.

## 4.6 Other variations of Boyer-Moore algorithm

We describe in this section several possible improvements on BM algorithm. The first one is called AG algorithm. Its basic idea is to avoid checking the segments of the text which have already been examined. These segments have a very simple structure. They are all suffixes of pattern *pat*. Call these segments *partial matches*. Their length is the number of symbols which matched in one stage of BM algorithm.

It is convenient to introduce a table $S[j]$, analogue to $Bord[i]$ in the sense that *Bord* is defined in terms of prefixes, while $S$ is defined in terms of suffixes. Value $S[j]$ is the length of the longest suffix of $pat[1\ldots j]$ which is also a suffix of $pat[1\ldots n]$.

Suppose that we scan text *text* right-to-left and compare it with pattern *pat* as in BM algorithm. Let us consider the situation when segment $pat[j+1\ldots n]$ of *pat* has just been scanned. At this moment, the algorithm attempts to compare the $j$-th symbol of *pat* with the ($i$+$j$)-th of *text*. We further assume that, is attached to the current position of the text the fact that a partial match of length $k$ has previously ended here. Hence, we know that the next $k$ positions to the left in the text give a suffix of the pattern. If $k \le S[j]$, then we know that we can skip these

$k$ symbols (because they match), and continue comparing *pat* with *text* further to left. Otherwise, we know that our actual match is a failure because no suffix of length $k$ ends at the current position of the pattern (except when $S[j]=j$). In AG algorithm, a variable *skip* remembers how many symbols can be skipped. More precisely, the condition which enables us to make a skip is:

$$cond(k, j) : k \leq S[j] \text{ or } (S[j]=j \text{ and } j \leq k).$$

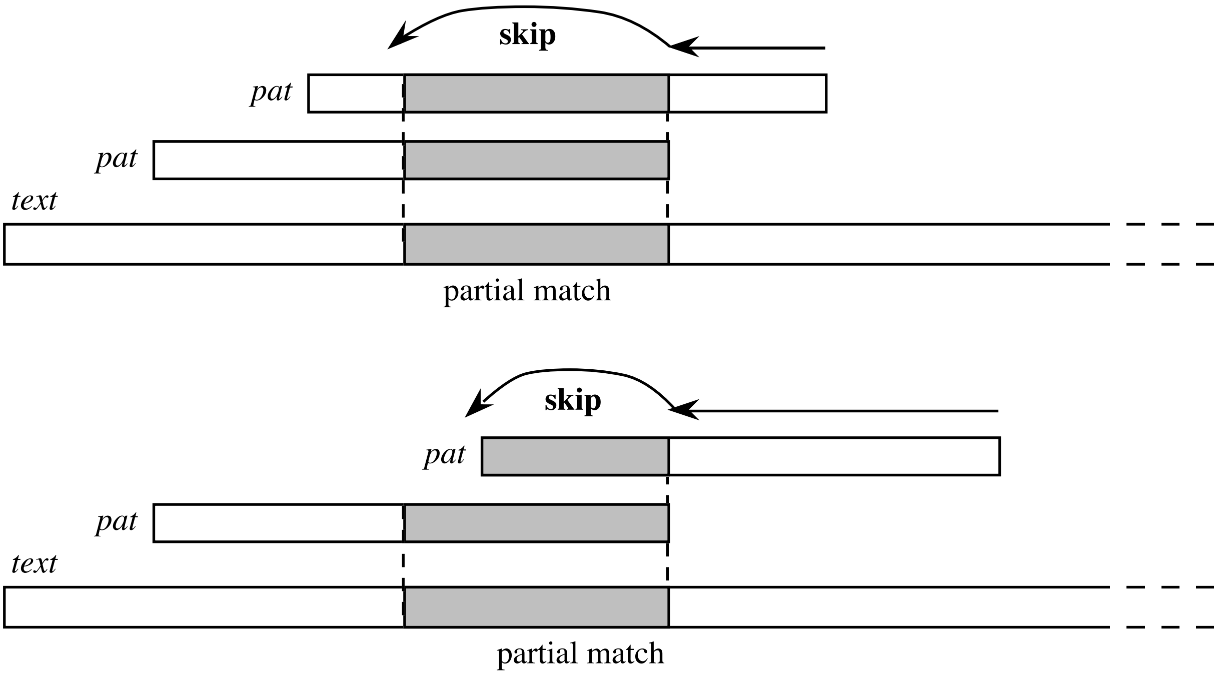


**Figure 4.10**. Two possible situations allowing a skip. A skip of length $k$ saves $k$ symbol comparisons. The skipped part is always a suffix of the pattern.

```
function AG : boolean;
{ another improved version of brute_force2 }
begin
  i := 0; { PM is the table of partial matches,
            all its entries are initially set to zero }
  while i≤n-m do begin
    j := m;
    while j>0 and ((PM[i+j]≠0 and cond(PM[i+j]) or
                   (PM[i+j]=0 and pat[j]=text[i+j])) do
      j := j-max(1, PM[i+j]);
    if j=0 then return(true);
    PM[i+m] := m-j;
    { inv2(i, j) }
    i := i+D[j];
  end;
  return(false);
end;
```

Recall that we assume a lazy evaluation from left to right of boolean expression in algorithms. Then it is easily seen that each symbol of the text is examined at most twice during a run of AG algorithm. We get a bound $2.n$ on the number of all symbol comparisons. Also, the number of times table *PM* is accessed is easily seen to be linear. Hence, AG algorithm has time complexity generally much better than that of BM algorithm. Moreover, the number of symbol comparisons made by AG algorithm never exceeds the number of comparisons made by BM algorithm. The main advantage of the latter algorithm is that it is extremely fast for many inputs (reading only small parts of text). This advantage is preserved by the AG algorithm. Note that AG algorithm requires $O(m)$ extra space due to table *PM*.

We go to the computation of table *S* used in AG algorithm. Table *S* can be computed in linear time, in a similar manner as table *Bord*; one possibility is to compute it as a by-product of MP algorithm (when text=pattern). Indeed, instead of computing *S*, one can compute a more convenient table *PREF*. It is defined by

$$PREF[i]=\max\{\, j : pat[i\ldots i+j-1] \text{ is a prefix of } pat\}.$$

The computation of table *S* is directly reducible to the computation of *PREF* for the reversed pattern. One of many alternative algorithms is based on the following observation :

$$\text{if } Bord[i]=j \text{ then } pat[i-j+1\ldots i] \text{ is a prefix of } pat.$$

This leads to the following algorithm.

```
procedure compute_PREF;
begin
  for i := 1 to n do PREF[i] :=0;
  for i := 1 to n do begin
    j := Bord[i]; PREF[i-j+1] := max(PREF[i-j+1], j);
  end;
end;
```

Though useful, this algorithm is not entirely correct. In the case of one letter alphabet only one entry of table *PREF* will be properly computed. But its incorrectness is quite "weak". If *PREF*[*k*]>0 after the execution of the algorithm then it is properly computed. Moreover, *PREF* is computed for "essential" entries. The entry *i* is essential iff *PREF*[*i*]>0 after applying this algorithm. These entries partition interval [1...*m*] into subintervals for which the further computation is easy.

The computation of the table for nonessential entries is done as follows: traverse the whole interval left-to-right and update *PREF*[*i*] for each entry *i*. . Take the first (to the left of *i*, including i) essential entry *k* with *PREF*[*k*]≥*i*-*k*+1 then we execute *PREF*[*i*]=min(*PREF*[*i*-*k*+1], *PREF*[k]-(*i*-*k*)). If there is no such essential entry then *PREF*[*i*]=0. Apply this for an example pattern over one-letter alphabet to look how it works.

BM algorithm is especially fast for large alphabets, because then, shifts are likely to be long. For small alphabets, the average number of symbol comparisons is linear. We now design an algorithm making *O*(*n* log(*m*)/*m*) comparisons on the average. Hence, if *m* is of the same order as *n*, the algorithm makes only *O*(log *n*) comparisons. It is essentially based on the same strategy as in BM algorithm, and can be treated as another variation of it. We assume, for simplicity, that the alphabet has only two elements, and that each symbol of the text is chosen independently with the same probability. Let *r*=2.log*m*.

```
Algorithm fast_on_average;
begin
  i = m;
  while i≤n do begin
    if text[i-r…i] is a factor of pat then
      compute occurrences of pat starting in [i-m…i-r]
      applying KMP algorithm
    else /* pattern does not start in [i-m…i-r] */
      i = i+m-r;
  end;
end;
```

**Theorem 4.5**

The *fast_on_average* algorithm above works in $O(n \log m/m)$ expected time and (simultaneously) $O(n)$ worst-case time if the pattern is preprocessed. The preprocessing of the pattern takes $O(m)$ time.

**Proof**

A preprocessing phase is needed to efficiently check if *text*$[i\text{-}r\ldots i]$ is a factor of *pat* in $O(r)$ time. Any of the data structures developed in chapters 5 and 6 (a suffix tree or a dawg) can be used. Assume that text *text* is a random string. There are $2^r \geq m^2$ possible suffixes of *text*, and less than $m$ factors of *pat* of length $r$. Hence, the probability that the suffix of length $r$ of *text* is a factor of *pat* is not greater than $1/m$. The expected time spent in each of the subintervals $[1\ldots m]$, $[m\text{-}r\ldots 2.m\text{-}r]$, … is $O(m.1/m+r)$. There are $O(n/m)$ such intervals. Thus, the total expected time of the algorithm is of order $(1+r)n/m = n(\log(m)+1)/m$. This completes the proof. ‡

## Bibliographic notes

The tight upper bound of approximately $3.n$ for the number of comparisons in BM algorithm has been recently discovered by Cole [Co 90]. The proof of the $4.n$ bound reported in Section 4.2 is from the same paper. A previous proof of the $4.n$ bound was given before in by Guibas and Odlyzko [GO 80], but with more complicated arguments. These authors also conjectured a $2.n$ bound which turns out to be false. Another combinatorial estimation of the upper bound on the number of comparisons needed by Boyer-Moore algorithm may be found in [KMP 77]. We recommend to read these proofs for readers interested in combinatorics on words.

The computation of the table of shifts, *D*, in the Boyer-Moore algorithm is from [Ry 80]. The algorithm presented in [KMP 77] contains a small flaw. The improved versions of the algorithm BM, BMG and AG algorithms, are from Galil [Ga 79], and Apostolico and Giancarlo [AG 86] respectively. The Boyer-Moore algorithm is still a theoretically fascinating algorithm: an open problem related to the algorithm asks about the number of states of a finite-automaton version of the strategy "Boyer-Moore". It is not known whether this number is exponential or not. The problem appears in [KMP 77]. Baeza-Yates, Choffrut and Gonnet discuss the question in [BCG 93] (see also [Ch 90]), and they design an optimal algorithm to build the automaton.

The Turbo_BM algorithm has been discovered recently when working on another algorithm based on automata that is presented in Chapter 6. It is from Crochemore et alii [C-R 92].

## Selected references

[BM 77] R.S. BOYER, J.S. MOORE, A fast string searching algorithm, *Comm. ACM* 20 (1977) 762-772.

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# 5. Suffix trees

The basic data structures in the book are data structures representing all factors of a given word. Their importance follows from a multitude of applications. We shall see some of these applications at the end of the present chapter, and in the next one.

This chapter is mainly devoted to the first of such basic data structures - the suffix tree. A related concept of subword graphs is also introduced in this chapter, but its full treatment is postponed until the next chapter.

The basic object which is to be represented is the set *Fac*(*text*) of all factors of the text *text* of length *n*. It should be represented efficiently : this means that basic operations related to the set *Fac*(*text*) should be performed fast. In this chapter, we examine closely the structure of the set *Fac*(*text*). Its size is usually quadratic, but it has succinct representations that are only of linear size. We introduce three such representations in this chapter, namely, suffix trees, subword graphs and suffix arrays. We shall see that the subword graph of a text has the same origin as its suffix tree: uncompressed trie of suffixes of the text. This is the reason why we introduce them together with suffix trees.

We need a representation useful to answer efficiently to a class of problems. Since *Fact*(*text*) is a set, the most typical problem is the membership problem : check if a given word *x* is in *Fac*(*text*). Denote the corresponding predicate by *FACTORIN*(*x*, *text*). The usefulness of the data structure for this problem means that *FACTORIN*(*x*, *text*) can be computed in time $O(|x|)$, even if *x* is much shorter than *text*. The complexity here is computed according to the basic operation of the data structure, *branching*, that takes a unit of time. Under the comparison model, branching can be implemented in order to take $O(\log|A|)$ time (*A* is the alphabet). Since it is common in practice to work on a fixed alphabet, such as the ASCII alphabet, we can also consider that $\log|A|$ is a constant.

Note that most algorithms of chapters 3 and 4 compute the value of *FACTORIN*(*x*, *text*) in time $O(|text|)$ once the word *x* has been preprocessed. The present data structure is thus well suited when the text is fixed. Such a data structure is also needed for example in chapter 4 (see, Section 4.6). We want that the preprocessing time, used to build the representation of the text, is realized in linear time with respect to the size of the text. Let us call representations satisfying these requirements "good" representations of *Fac*(*text*). We can summarize it in the following definition. The data structure *D* representing the set *Fac*(*text*) is *good* iff :

(1) *D* has linear size;

(2) *D* can be constructed in linear time;

(3) *D* allows to compute *FACTORIN*(*x*, *text*) in $O(|x|)$ time.

The main goal of this chapter is to show that suffix trees are *good* data structures. We also introduce in this chapter a third data structure, suffix array, which is "*almost*" *good*, but simpler. The "goodness" of subword graphs is the subject of the next chapter. The important algorithm of the section is McCreight's algorithm (Section 5.3). It processes the text from left to right, while the equivalent Weiner's algorithm traverses the text in the opposite direction.

## 5.1. Prelude to McCreight and Weiner algorithms

In this section we deal only with simple data structure for *Fac*(*text*), namely trees called *tries*. Algorithms presented here are intermediate steps in the understanding and design of McCreight and Weiner suffix tree construction (Sections 5.2 and 5.3, respectively). The goal is to construct such trees in time proportional to their size.

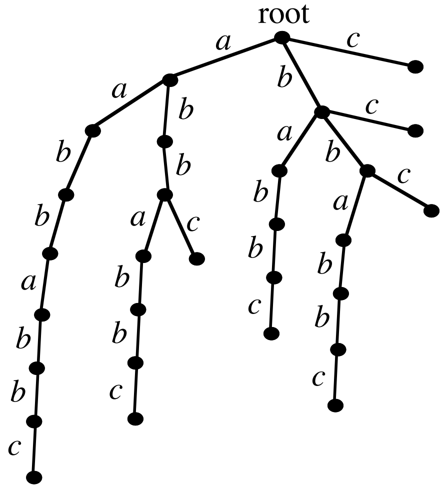


**Figure 5.1**. Trie of factors of *aabbabbc*.
It has eight leaves corresponding to the eight non-empty suffixes.

Figure 5.1 shows the trie associated to text *aabbabbc*. In these trees, the links from a node to its sons are labelled by letters. In the tree associated to *text*, a path down the tree spells a factor of *text*. All paths from the root to leaves spell suffixes of *text*. And all suffixes of *text* are labels of paths from the root. In general, these paths not necessarily end in a leaf. But for the ease of the description, we assume that the last letter of *text* occurs only once and serves as a **marker**. With this assumption, no suffix of *text* is a proper prefix of another suffix, and all suffixes of *text* label paths from the root of the trie to its leaves.

Both Weiner and McCreight algorithms are incremental algorithms. They compute the tree considering suffixes of the text in a certain order. The tree is computed for a subset of the suffixes. Then, a new suffix is inserted into the tree. This continues until all suffixes are included in the tree. Let *p* be the next suffix to be inserted in the current tree *T*. We define the *head of p*, *head*(*p*, *T*), as the longest prefix of *p* occurring in *T* (as the label of a path from the rrot). We identify *head*(*p*, *T*) with its corresponding node in the tree. Having this node, only the remaining part of *p* needs to be grafted on the tree. After adding the path, below the head to a new leaf, the tree contains a new branch label by $p$, and this produces the next tree of the construction. Below is the general scheme of both McCreight's and Weiner's algorithm. Then, are explained the method used to find the next head, and the grafting operation.

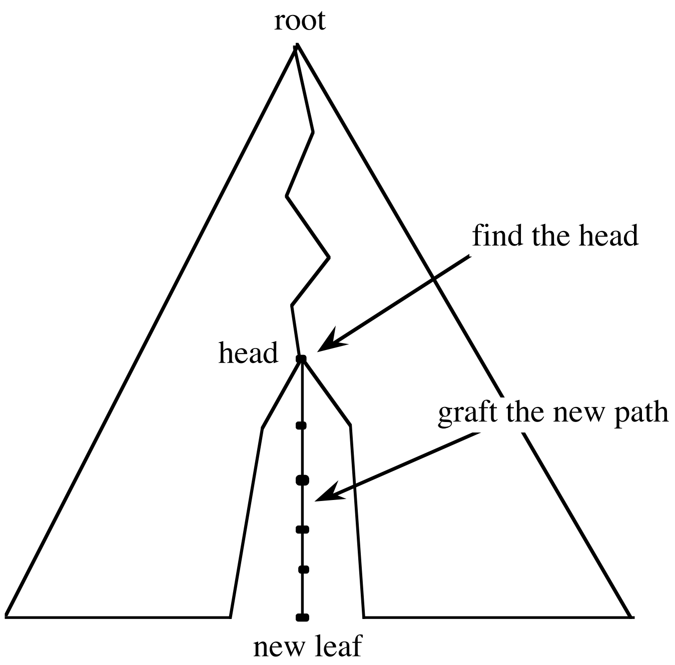


**Figure 5.2**. Insertion of the next suffix.

```
Algorithm general-scheme;
begin
  compute initial tree T for the first suffix;
  leaf:= leaf of T;
  for i := 2 to n do begin
    { insert next suffix }
    localize next head as head(current suffix, T);
    let π be the string corresponding to path from head to leaf;
    create new path starting at head corresponding to π;
    leaf:= lastly created leaf;
  end;
end.
```

The main technique used by subsequent algorithms is called *UP-LINK-DOWN*. It is the key to an improvement on a straightforward construction. It is used to find, from the lastly created leaf of the tree, the node (the head) where a new path must be grafted. The data structure incorporates links that provide shortcuts in order to fasten the search for heads. The strategy Up_link_down works as follows : it goes up the tree from the last leaf until a shortcut through an existing link is possible; it then go through the link and starts going down the tree to find the new head (see Figure 5.3). This is done by the procedure Up_Link_Down that works on the current tree and modifies it. This is somehow an abstract procedure, which admits two instances. The link mentioned in the procedure should be understood as conceptual. The actual links used afterwards depends on which algorithm is used to build the suffix tree.

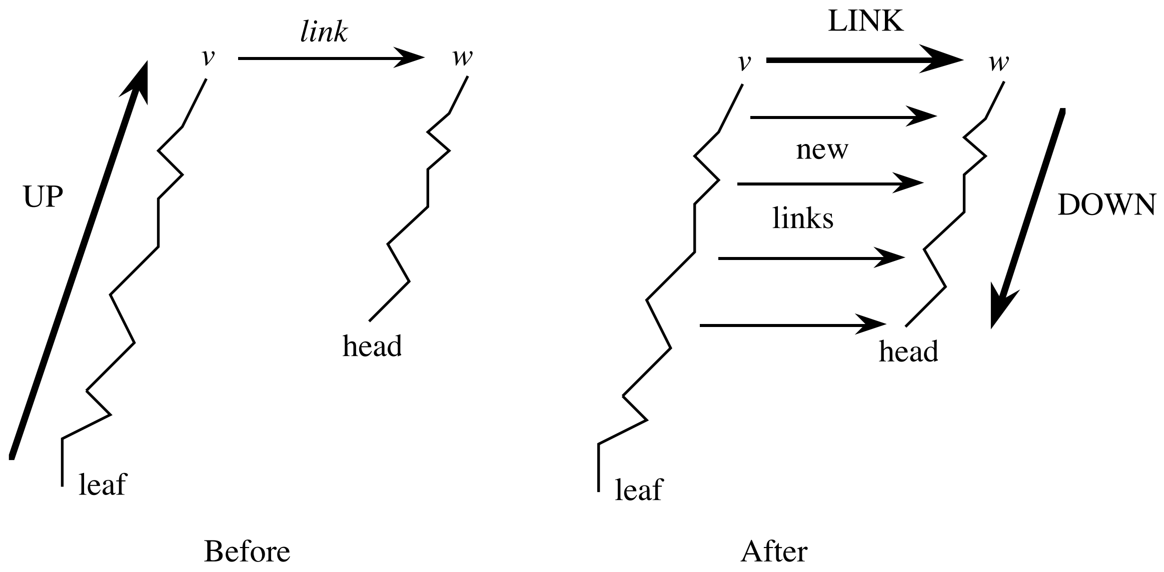


**Figure 5.3**. Strategy for finding the next head.

```
function Up_Link_Down(link, q) : node;
{ finds new head, from leaf q }
begin
{ UP, going up from leaf q }
  v := first node v on path from q to root s.t. link[v]≠nil;
  if no such node then return nil;
  let $\pi = a_j a_{j+1} \ldots a_n$ be the string, label of path from v to q;
{ LINK, going through suffix link }
  head := link[v];
{ DOWN, going down to new head, making new links }
  while son(head, $a_j$) exists do begin
    v := son(v,$a_j$); head := son(head,$a_j$);
    link[v] := head; j := j+1;
  end;
  return (v, head);
end
```

We also define the procedure Graft. Its aim is to construct a path of new nodes from the current head to a new created leaf. It also updates links from the branch containing the previous leaf, for nodes which should point to newly created nodes.

```
procedure Graft(link, v, head, $a_ja_{j+1}...a_n$);
begin w := head;
  for k := j to n do begin
    v := son(v,$a_k$); w := createson(w,$a_k$); link[v] := w;
  end;
{ w is the last leaf }
end
```

Function Up_Link_Down (or a variant in case of compressed representation of tree) is the basic tool used by algorithms that build suffix trees, and even also DAWG's. The time of a single call to Up_Link_Down can be proportional to the length of the whole pattern. But the sum of all costs is indeed linear. When used to create a compressed suffix tree, a careful implementation of the function yields also an overall linear time complexity.

For the pattern *text* = $a_1a_2...a_n$, we define $p_i$ as the suffix $a_ia_{i+1}...a_n$. *Trie*($p_1$, $p_2$ ..., $p_i$) is the tree whose branches are labelled with suffixes $p_1$, $p_2$ ..., $p_i$. In this tree, $leaf_i$ is the leaf corresponding to suffix $p_i$. And $head_i$ is the first (bottom-up) ancestor of $leaf_i$ having at least two sons; it is the root if there is no such node.

For a node corresponding to a non-empty factor *aw*, we define the *suffix link* from *aw* to *w*, by *suf*[*aw*] = *w* (see Figure 5.7). Table *suf* will serve to make shortcuts during the construction of *Trie*($p_1$, $p_2$ ..., $p_n$). It is the link mentioned in the procedure Up_Link_Down. In *Trie*($p_1$, $p_2$ ..., $p_i$) it can happen that *suf*[*v*] is undefined, for some node *v*. This situation does not happen for (compressed) suffix trees. Below is the algorithm Left_to_Right that builds the suffix tree of *text*. It processes suffixes from $p_1$ to $p_n$.

**Basic property of** *Trie*($p_1$, $p_2$ ..., $p_i$):

let *v* be the first node on the path from $leaf_{i\text{-}1}$ to root such that *suf*[*v*]≠nil in *Trie*($p_1$, $p_2$ ..., $p_{i\text{-}1}$). Then $head_i$ (in *Trie*($p_1$, $p_2$ ..., $p_i$)) is a descendant of *suf*[*v*].

```
Algorithm Left_to_Right($a_1a_2...a_n$, n>0);
begin
  $T$ := $Trie(p_1)$ with suffix link (from son of root to root);
for $i$:=2 to $n$ do begin
{ insert next suffix $p_i = a_ia_{i+1}...a_n$ into $T$ }
  { FIND new head }
  ($v$, $head$) := Up_Link_Down($suf$, $leaf_{i-1}$); { $head = head_i$ }
  if $head$ = nil then begin
  { root situation }
    let $v$ be the son of root on the branch to $leaf_{i-1}$;
    $suf[v]$ := root; $head$ := root;
  end;
  { going down from $head_i$ to $leaf_i$ creating a new path }
    let $a_j...a_n$ be the label of the path from $v$ to $leaf_{i-1}$;
    Graft($suf$, $v$, $head$, $a_ja_{j+1}...a_n$);
  end;
end.
```

**Theorem 5.1**

The algorithm Left_to_Right constructs the $T$=*Trie*(*text*) in time O(|$T$|).

**Proof**

The time is proportional to the number of created links (*suf*) which is obviously proportional to the number of internal nodes, and then to the total size of the tree. ‡

The next algorithm, Right_to_Left, builds the suffix tree of *text*, as does the algorithm Left_to_Right, but processes the suffixes in reverse order, from $p_n$ to $p_1$. The notion of link is modified. The node corresponding to a (non-empty) factor *aw* (*a* a letter) is linked to *w*. The link is called a *a*-link, and we note $link_a[w] = aw$ (see Figure 5.10). These links have the same purpose as the suffix link of the previous algorithm. The procedure Up_Link_Down will now use the *a*-links.

```
Algorithm Right_to_Left;
$T$ := $Trie(p_n)$ with $link_{a_n}$ from root to its son;
for $i$ := $n$-1 downto 1 do begin
{ insert next suffix $p_i = a_i a_{i+1} ... a_n$ into $T$ }
  { FIND new head }
  $head$ := Up_Link_Down($link_{a_i}$, $leaf_{i+1}$); { $head = head_i$ }
  if $head$ = nil then begin
  { root situation }
    $v$ := root; $head$ := createson($v$,$a_i$); $link_{a_i}[v]$ := $head$;
  end;
  { GRAFT, going down from $head_i$ to $leaf_i$ creating a new path }
    let $a_j a_{j+1} ... a_n$ be the label of the path from $v$ to $leaf_{i-1}$;
    Graft($link_{a_i}$, $v$, $head$, $a_j a_{j+1} ... a_n$);
  end;
end.
```

**Basic property of** *Trie*$(p_i, p_{i+1} ..., p_n)$:

let $v$ be the first node on the path from $leaf_{i+1}$ with $link_{a_i}[v]$≠nil in *Trie*$(p_{i+1}, p_{i+2} ..., p_n)$. Then $head_i$ (in *Trie*$(p_i, p_{i+1} ..., p_n)$) is a descendant of $link_{a_i}[v]$.

**Theorem 5.2**

The algorithm Right_to_Left constructs the trie *Trie*$(p_1, p_2 ..., p_n)$ in time O(|*T*|).

**Proof**

The time is proportional to the number of links in the tree *Trie*$(p_1, p_2 ..., p_n)$. Note that reversed links are exactly the suffix links (considered in McCreight algorithm). Since there is one link out to each internal node, we get the result. ‡

The next two sections present versions of algorithms Left_to_Right and Right_to_Left respectively, adapted to the construction of suffix trees, that is, compacted tries

## 5.2. Two compressed versions of the naive representation

Our approach to compact representations of the set of factors of a text is graph-theoretical. Let *G* be an acyclic rooted directed graph whose edges are labelled with symbols or with words: *label*(*e*) denotes the *label* of edge *e*. The *label* of a path π (denoted by *label*(π)) is the composition of labels of its consecutive edges. The edge-labelled graph *G* represents the set:

*words*(*G*) = { *label*(π) : π is a directed path in *G* starting at the root }.

And we say that the labelled graph *G* represents the set of factors of *text* iff

$$words(G)=Fac(text).$$

The first approach to representing *Fac*(*text*) in a compact way, is to consider graphs which are trees. The simplest type of labelled graphs *G* are trees in which edges are labelled by single symbols. These trees are the *subword tries* considered in the previous section. Two examples of tries are shown in Figures 5.1 and 5.4. However, tries are not "good" representation of *Fac*(*text*), because they can be too large. If $text=a^nb^na^nb^nd$, for instance, then *Trie*(*text*) has a quadratic number of nodes.

We consider two kinds of succinct representations of the set *Fac*(*text*). They both result by compressing the tree *Trie*(*text*). Two types of the compression can be applied, separately or simultaneously:

(1) compressing chains (paths consisting of nodes of out-degree one), which produces the *suffix tree* of the text,

(2) merging isomorphic subtrees (e.g. all leaves are to be identified), which leads to the *directed acyclic word graph* (dawg) of the text.

Each of these methods has its advantages and disadvantages. The first one produces a tree, and this is an advantage because in many cases it is easier to deal with trees than with other types of graphs (especially in parallel computations). Moreover, in the tree structure leaves can be assigned particular values. The disadvantage of the method is the varying length of the labels of edges. An advantage of the second method (use of dawg's) is that each edge is labelled by a single symbol. This allows us to attach information to symbols on edges. And the main disadvantage of dawg's is that they not trees !

The linear size of suffix trees is a trivial fact, but the linear size of dawg's is much less trivial. It is probably one of the most surprising fact related to representations of *Fac*(*text*).

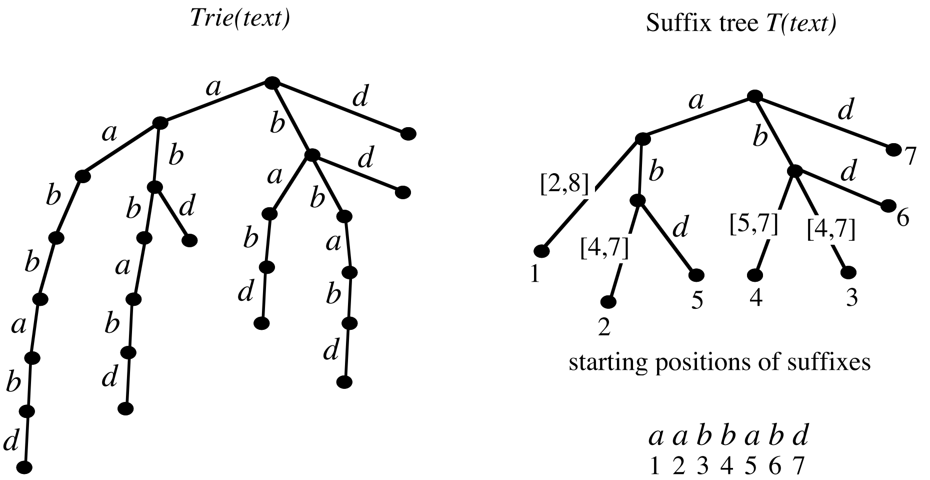


**Figure 5.4**. The tree *Trie*(*text*) and its compacted version, the suffix tree *T*(*text*), for *text* = *aabbabd*. *Trie*(*text*) has 24 nodes, *T*(*text*) has only 11 nodes.

Since we assume that no suffix of *text* is a proper prefix of another suffix (because of the right end marker), leaves of *Trie*(*text*) are in one-to-one correspondence with (non-empty) suffixes of *text*. Let *T*(*text*) be the compacted version of *Trie*(*text*) (see Figure 5.4). Each chain $\pi$ (path consisting of nodes of out-degree one) is compressed into a single edge *e* with *label*(*e*)=[*i*, *j*], where *text*[*i*…*j*]=*label*($\pi$) (observe that a compact representation of labels is also used). Note that there is a certain nondeterminism here, because there can be several possibilities to choose *i* and *j* representing the same factor *text*[*i*…*j*] of *text*. We accept any such choice. In this context we identify the label [*i*, *j*] with the word *text*[*i*…*j*]. The tree *T*(*text*) is called the suffix tree of the word *text*. The Figure 5.4 presents the suffix tree *T*(*text*) for *text*=*aabbabd*.

For a node *v* of *T*(*text*), let *val*(*v*) be *label*($\pi$), where $\pi$ is the path from root to *v*. Whenever it is unambiguous we identify nodes with their values, and paths with their labels. In this sense, the set of leaves of suffix tree is the set of suffixes of *text* (since no suffix is a prefix of another suffix). This motivates the name: suffix tree. Such trees are also called subword (factor) trees.

Note that the suffix tree obtained by compressing chains has the following property : the labels of edges starting at a given node are words having different first letters. So, the branching operation performed to visit the tree reduces to comparisons on the first letters of the labels of outgoing edges.

In the following we consider the notion of *implicit nodes* that is defined now. The aim is to restore the nodes of *Trie*(*text*) inside the suffix tree *T*(*text*). We say that a pair (*w*, $\alpha$) is an implicit node in *T* iff *w* is a node of *T* and $\alpha$ is a proper prefix of the label of an edge from *w* to a son of *w*. If *val*(*w*) = *x*, then *val*((*w*, $\alpha$)) = *x*$\alpha$. For example, in Figure 5.6, (*w*, *ab*) is an implicit node. It corresponds to a place where later a real node is created. The implicit node (*w*, $\alpha$) is said a "real" node if $\alpha$ is the empty word. In this case (*w*, $\varepsilon$) is identified with the node *w* itself.

**Lemma 5.3**

The size of the suffix tree *T*(*text*) is linear (O(|*text*|)).

**Proof**

Let *n*=|*text*|. The tree *Trie*(*text*) has at most *n* leaves, hence *T*(*text*) also has at most *n* leaves. Thus, *T*(*text*) has at most *n*-1 internal nodes because each internal node has at least two sons. Hence |*T*(*text*)| ≤ 2*n*-1. This completes the proof. ‡

There is a result similar to Lemma 5.3 on the size of dawg's. The question is the subject of Section 6.1.

## 5.3. McCreight's algorithm

A straightforward approach to the construction of *T*(*text*) could be : first build *Trie*(*text*), next compress all its chains. The main drawback of this scheme is that the size of *Trie*(*text*) can be quadratic, resulting in a quadratic time and space algorithm. Two other approaches are given in the present section (McCreight's algorithm) and the next one (Weiner's algorithm).

Both Weiner's algorithm and McCreight's algorithm are incremental algorithms. The tree is computed for a subset of consecutive suffixes. Then, the next suffix is inserted into the tree, and this continues until all (non-empty) suffixes are included in the tree.

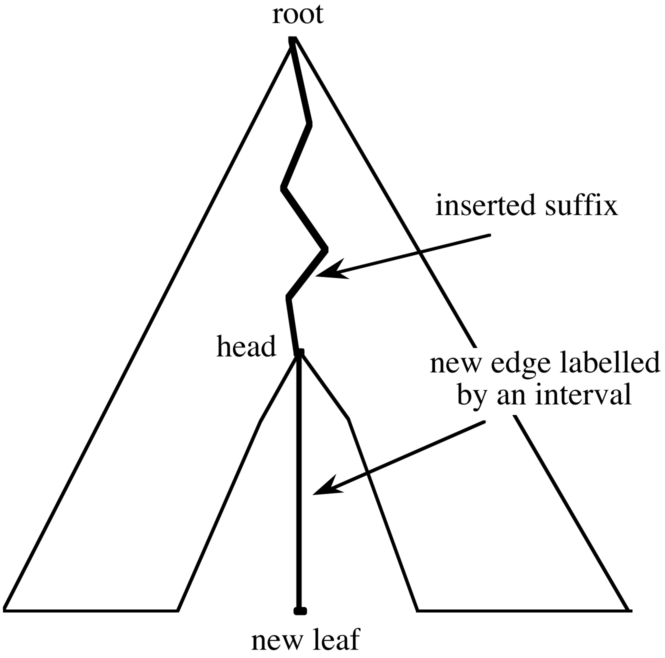


**Figure 5.5**. Insertion of a suffix in the tree.

Consider the structure of the path corresponding to a new suffix *p* inserted into the tree *T*. Such a path is indicated in Figure 5.5 by the bold line. Denote by *insert*(*p, T*) the tree obtained from *T* after insertion of the string *p*. The path corresponding to *p* in *insert*(*p, T*) ends in the last created leaf of the tree. Denote by *head* the father of this leaf. It may happen that the node *head* does not already exist in the initial tree *T* (it is only an implicit node at that moment of the construction), and has to be created during the insert operation. For example, this happens if we try to insert the path *p* = *abcdeababba* starting at *v* in Figure 5.6. In this case, one edge of *T* (labelled by *abadc*) has to be split. This is why we consider the operation *break* defined below.

The notion of implicit nodes introduced in Section 5.2 is conceptually considered in the construction. Let ($w$, $\alpha$) be an implicit node of the tree *T* ($w$ is a node of *T*, $\alpha$ is a word). The operation *break*($w$, $\alpha$) on the tree *T* is defined only if there is an edge outgoing the node $w$ whose label $\delta$ has $\alpha$ as a prefix. Let $\beta$ such that $\delta = \alpha\beta$. The (side) effect of the operation *break*($w$, $\alpha$) is to break the corresponding edge: a new node is inserted at the breaking point, and the edge is split into two edges of respective labels α and β. The value of *break*($w$, α) is the node created at the break point.

Let $v$ be a node of the tree $T$, and let $p$ be a subword of the input word *text* represented by a pair of integers $l$, $r$, where $p$ = *text*[$l$...$r$]. The basic function used in the suffix tree construction is the function *find*. The value *find*($v$, $p$) is the last implicit node along the path starting in $v$ and labelled by $p$. If this implicit node is not real, it is ($w$, α) for some nonempty α, and the function *find* converts it into the "real" node *break*($w$, α) (see Figure 5.6).

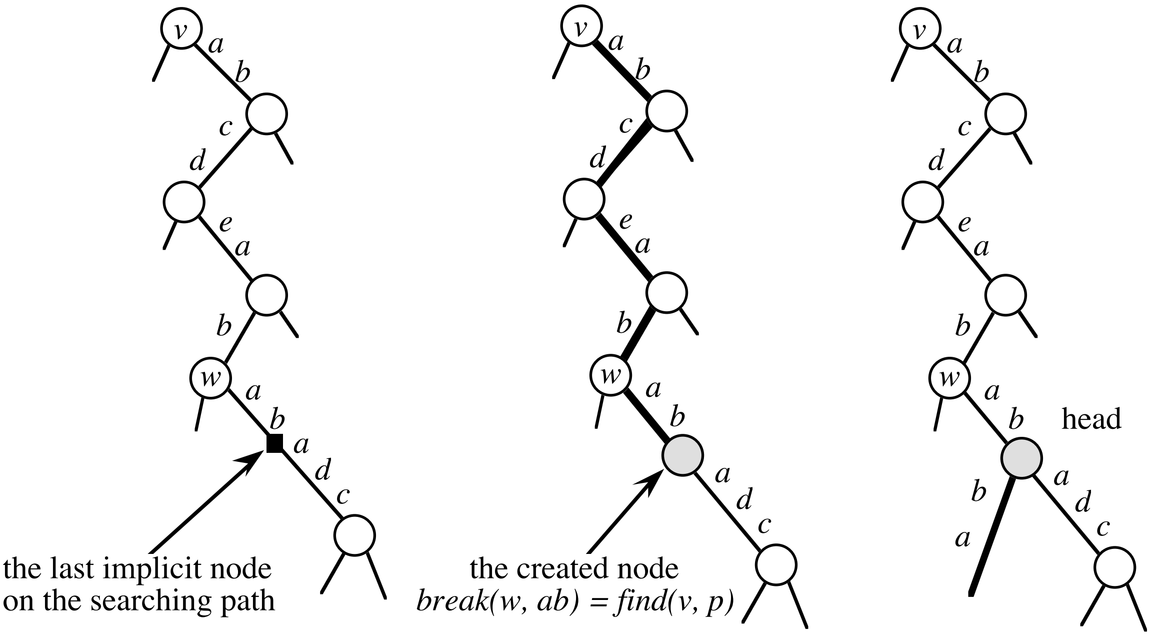


**Figure 5.6**. We attempt to insert the string $p$ = *abcdeababba*, the result of *fastfind* and *slowfind* is the newly created node *find*($v$, $p$), *fastfind* makes only 5 steps, while *slowfind* would make $O(|p|)$ steps.

The important point in the algorithm is the use of two different implementations of the function *find*. The first one, called *fastfind*, deals with the situation when we know in advance that the searching path labelled by $p$ is fully contained in some path starting at $v$. This knowledge allows us to find the searched node much faster using the compressed edges of the tree as shortcuts. If we are at a given node $u$, and if the next letter of the path is $a$, then we look for the edge outgoing from $u$ whose label starts with $a$. Only one such edge exists by definition of suffix trees. This edge leads to another node $u'$. We jump in our searching path at a distance equal to the length of the label of edge ($u$, $u'$). The second implementation of *find* is the function *slowfind* that follows its path letter by letter. The application of *fastfind* is a main feature of McCreight's algorithm, and plays a central part in its performance (toghether with links).

```
function fastfind(v : node; p string) : node;
{ p is fully contained in some path starting at v }
begin
  from node v, follow path labelled by p in the tree using
  labels of edges as shortcuts; only first symbols on each
  edge are checked;
  let (w, α) be the last implicit node;
  if α is empty then return w
  else return break(w, α);
end
```

```
function slowfind(v : node; p : string) : node;
begin
  from node v, follow the path labelled by the longest possible
  prefix of p, letter by letter;
  let (w, α) be the last implicit node;
  if α is empty then return w
  else return break(w, α);
end
```

McCreight's algorithm builds a sequence of compacted trees $T_i$ in the order $i$=1, 2 …, $n$. The tree $T_i$ contains the $i$-th longest suffixes of *text*. Note that $T_n$ is the suffix tree $T$(*text*), but that intermediate trees are not strictly suffix trees. An on-line construction is presented in Section 5.5. At a given stage of McCreight's algorithm, we have $T = T_{k\text{-}1}$, and we attempt to build $T_k$. The table of suffix links, called *suf*, plays a crucial role in the reduction of the complexity. In some sense, it is similar to the role of failure functions used in Chapter 3. If the path from the root to the node $v$ is spelled by $a\pi$ then *suf*[v] is defined as the node corresponding to the path $\pi$ (see Figure 5.7). In the algorithm, the table *suf* is computed at a given stage for all nodes, except for leaves and except maybe for the present head.

McCreight's algorithm is a rather straightforward transformation of the algorithm Left_to_Right of Section 5.2. Here most of the nodes become implicit nodes. But the algorithm works similarly. The main difference appears inside the procedure Up_Link_Down where *fastfind* is used whenever it is possible.

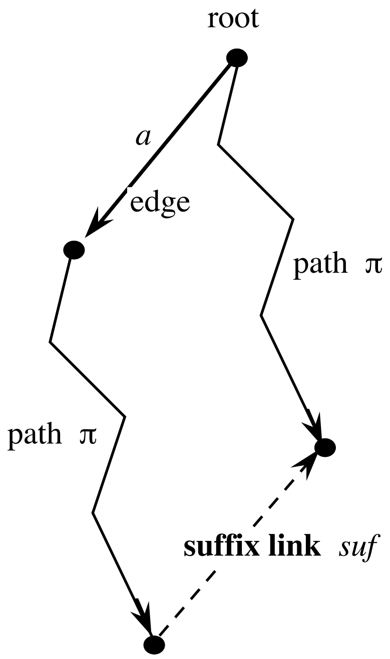


**Figure 5.7**. A suffix link *suf*.

```
Algorithm scheme of McCreight's algorithm;
{ left-to-right suffix tree construction }
begin
  compute the two-node tree $T$ with one edge labelled $p_1$=$text$;
  for $i$:=2 to n do begin
    { insert next suffix $p_i$ = $text[i..n]$ }
    localize $head_i$ as $head(p_i, T)$,
    starting the search from $suf$[father($head_{i-1}$)],
    using $fastfind$ whenever possible;
    $T$ := $insert(p_i, T)$;
  end
end.
```

The algorithm is based on the following two obvious properties:

**(1)** *head*$_i$ is a descendant of the node *suf*[*head*$_{i-1}$],

**(2)** *suf*[*v*] is a descendant of *suf*[father(*v*)] for any *v*.

The basic work done by McCreight's algorithm is spent in localizing heads. If it is done in a rough way (top-down search from the root) then the time is quadratic. The key to the improvement is the relation between *head*$_i$ and *head*$_{i-1}$ (Property 1). Hence, the search for the next head can start from some node deeply in the tree, instead of from the root. This saves some work and the amortized complexity is linear.

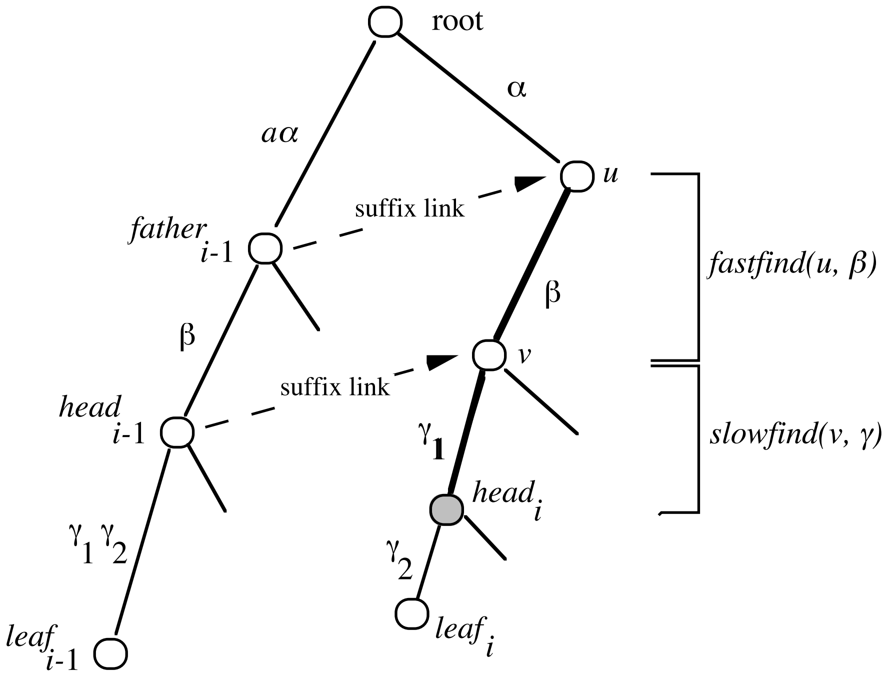


**Figure 5.8**. McCreight's algorithm : the case when *v* is an existing node.

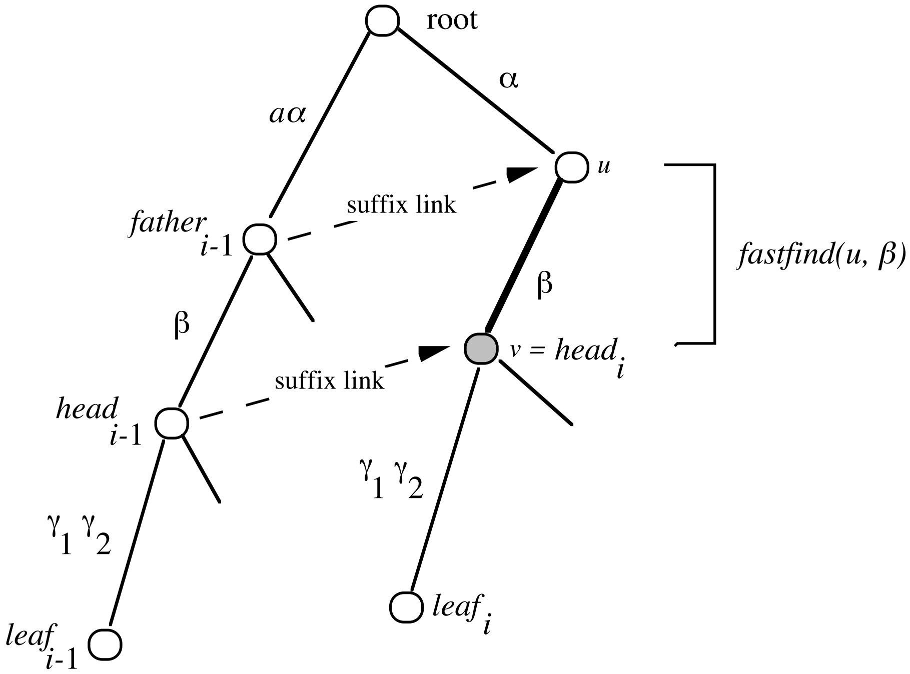


**Figure 5.9**. McCreight's algorithm : the case when $v = head_i$ is a newly created node.

```
Algorithm McCreight;
begin
  T := two-node tree with one edge labelled by $p_1$=text;
  for i:=2 to n do begin
    { insert next suffix $p_i$ = text[i..n] }
    let β be the label of the edge (father[$head_{i-1}$], $head_{i-1}$);
    let γ be the label of the edge ($head_{i-1}$, $leaf_{i-1}$);
    u := suf[father[$head_{i-1}$]];
    v := fastfind(u, β);
    if v has only one son then
      { v is a newly inserted node } $head_i$ := v
    else $head_i$ := slowfind(v, γ);
    suf[$head_{i-1}$] := v;
    create a new leaf $leaf_i$; make $leaf_i$ a son of $head_i$;
    label the edge ($head_i$, $leaf_i$) accordingly;
  end
end.
```

**Theorem 5.4**

McCreight's algorithm has $O(n \log|\Sigma|)$ time complexity, where $\Sigma$ is the underlying alphabet of the text of length $n$.

**Proof**

Assume for a moment that the alphabet is of a constant size. The total complexity of all executions of *fastfind* and *slowfind* is estimated separately. Let $father_i$ = father($head_i$). The complexity of one run of *slowfind* at stage $i$ is proportional to the difference $|father_i| - |father_{i-1}|$, plus some constant. Therefore, the total time complexity of all runs of *slowfind* is bounded by $\Sigma(|father_i| - |father_{i-1}|) + O(n)$. This is obviously linear.

Similarly, the time complexity of one call to *fastfind* at stage $i$ is proportional to the difference $|head_i| - |head_{i-1}|$, plus some constant. Therefore, the total complexity of all runs of *fastfind* is also linear.

If the alphabet is not fixed, then we can look for the edge starting with a given single symbol via binary search in $O(\log|\Sigma|)$ time. This is to be added as a coefficient and gives the total time complexity $O(n \log|\Sigma|)$. This completes the proof. ‡

**Remarks**

There is a subtle point in the algorithm : the worst case complexity is not linear if the function *slowfind* is used in the place of *fastfind*. The text $text = a^n$ is a counterexample to linear time. In fact, we could perform *slowfind* in all situations except in the following : when we are at the father of $head_i$ and we have to go down by one edge. At this moment, the work on this edges is not charged to the difference $|father_i|$ - $|father_{i-1}|$ and it should be constant on this single edge. We can call it a *crucial* edge. The function *fastfind* guarantees that traversing the single edge takes constant time (only the first symbol on the edge is inspected, and a length computed), while the function *slowfind* traverses the label of the single edge letter by letter, possibly spending a linear time on just one edge. However, the strategy (use always *slowfind* except for crucial edges) cannot be used because we do not in advance whether an edge is crucial or not.

Another remark concerns a certain redundancy of the algorithm. In the case when $suf[head_{i-1}]$ already exists, we could go directly to $suf[head_{i-1}]$ without making a "up-link-down" tour. Such situation can happen frequently in practice. Despite this redundancy the algorithm is linear time. We suggest the reader to improve the algorithm by inserting a statement omitting the redundant computations. For clarity, this practical improvement is not implemented in the above version.

## 5.4. Weiner's algorithm

Weiner's algorithm builds the sequence of suffix trees $T_i = T(p_i)$ in the order $i$=$n$, $n$-1, ..., 1 (recall that $p_i = text[i\ldots n]$). At a given stage we have $T = T_{k+1}$, and we attempt to construct $T_k$. $T$ is the suffix tree of the current suffix of the text. If the current suffix is denoted by $p$, the current value of $T$ is the suffix tree $T(p)$.

Weiner's algorithm is a rather straightforward transformation of the algorithm Right_to_Left of Section 5.2. Here again (as for McCreight's algorithm) most of the nodes become implicit nodes, but the algorithm works similarly. The notion of *a*-link (see Figure 5.10) is intensively used to localize heads (see Section 5.2). Recall that $head_i$ is the node in $T_i$ which is the father of the leaf corresponding to the last inserted suffix.

```
Algorithm scheme of Weiner's algorithm;
{ right-to-left suffix tree construction }
begin
  compute the suffix tree $T$ with tables $test$ and $link$ for
  the one-letter word $text[n]$;     { $O(1)$ cost }
  for $i$ := $n$-1 downto 1 do begin
    localize $head$ as $head(p_i, T)$; { denote it by $head_i$ }
    compute $T = next(T, p_i)$;
  end
end.
```

The basic work in the above algorithm is spent in localizing heads. If it is done in a rough way (top-down search from the root) then the total time is quadratic. The key to the improvement is the relation between $head_i$ and $head_{i+1}$. If we append the symbol $a = text[i]$ to $val(head_{i+1})$ then we obtain a prefix of $val(head_i)$ (recall that for a node $v$ of the tree $val(v)$ is the word, label of the path from the root to $v$). Hence, in the search we can start from the node corresponding to this prefix, instead of from the root. This saves some work, and the amortized complexity becomes linear. However, the algorithm also becomes more complicated, as we need extra data structures for links.

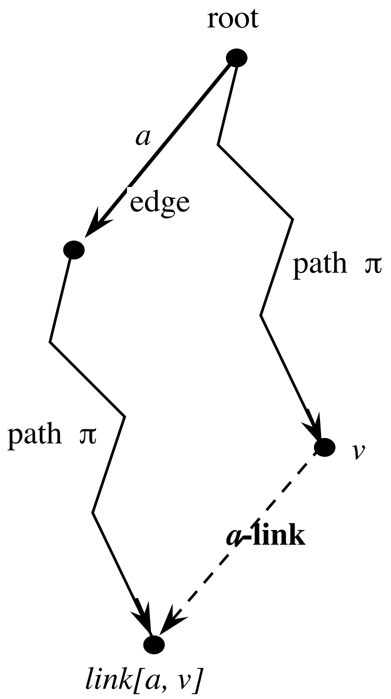


**Figure 5.10**. An *a*-link ($link_a$).

To implement this idea described above, we maintain two additional tables *link* and *test* related to internal nodes of the current tree $T$. They satisfy invariants ($p$ current suffix):

(1) $test[a, v]$ = true iff $ax \in Fac(p)$, where $x = val(v)$;

(2) $link[a, v] = w$ if $val(w) = ax$ for some node $w$ of $T$,

$link[a, v] = nil$ if there is no such node.

These tables inform us about possible left extensions of a given factor (label of node $v$).

Let us define the function $breaknode(w1, w2, v1, v2)$. This function is only defined for nodes $w1 \neq w2$ such that the label $x$ of the path from $v1$ to $v2$ is a proper prefix of the label $y$ of the edge $(w1, w2)$. The value of $breaknode(w1, w2, v1, v2)$ is a (newly created) node $w$. As a side-effect of the function, there are two created edges $(w1, w)$ and $(w, w2)$ with respective labels $x$ and $x'$ ($x'$ is such that $y = xx'$). Moreover, $test[s, w]$ is set to $test[s, w2]$ for each symbol $s$ and $link[s, w]$ is set to $nil$. Hence, the edge $(w1, w2)$ with label $y$ is decomposed into two edges with labels *x* and *x*' such that *y*=*xx*'. In the example of Figures 5.11 and 5.12, *x*=*text*[6…7], *x*'=*text*[8…14] and *y*=*text*[6…14]. It is clear that the cost to compute *breaknode*(*w*1, *w*2, *v*1, *v*2) is proportional to the length of the path from *v*1 to *v*2.

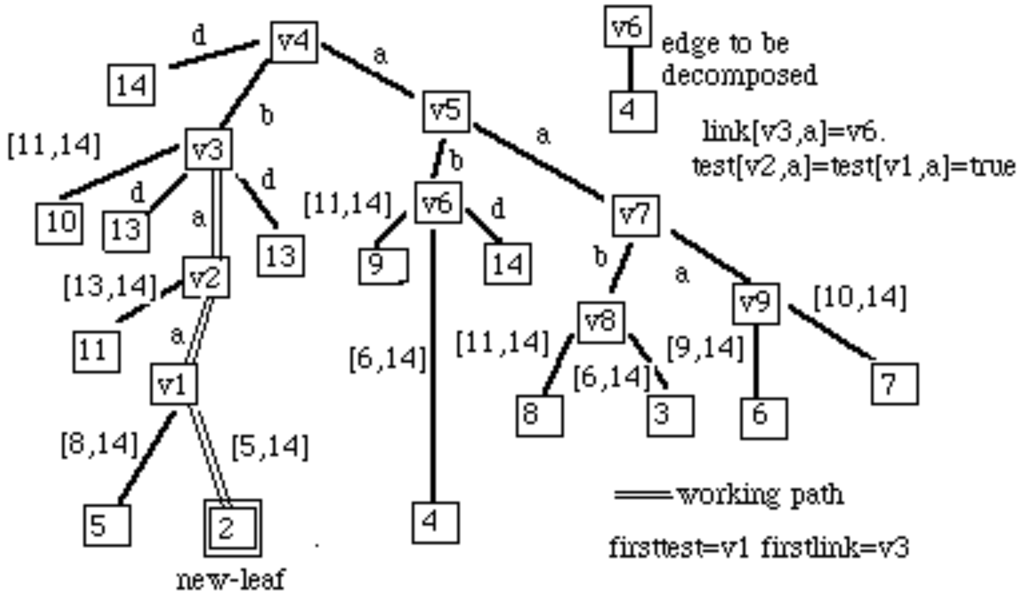


**Figure 5.11**. The suffix tree $T_2$=$T$(*text*[2…*n*]) for *text*=*abaabaaaabbabd*. The working path starts in leaf 2 and goes up to the first node *v* such that *link*[*a*, *v*]≠*nil*, here, *v* = *v*3. Let *firsttest* be the first node *v*' on this path with *test*[*a*, *v*']=true; *w*1=*link*[*a*, *v*]=*v*6, *depth*(*w*1) ≤ *depth*(*v*)+1. The cost of one stage can be charged to the difference between depths of leaves *i*+1 and *i*.

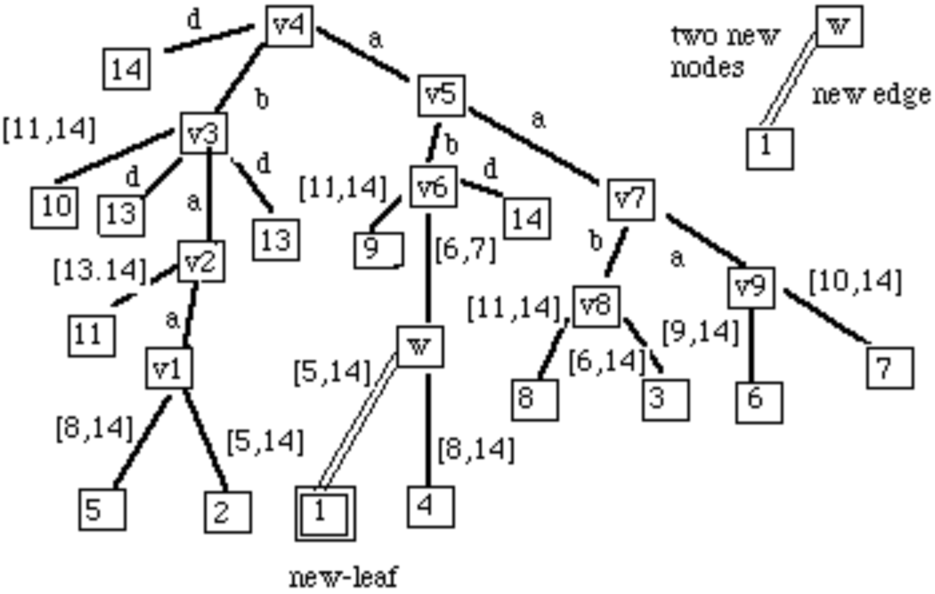


**Figure 5.12**.The suffix tree $T_1$ for *text=abaabaaaabbabd*.. The edge ($v$6, 4) of $T_2$ has been split into two edges. Generally, the tree $T_i$ is a modification of tree $T_{i+1}$ (in the example $i$=1). The edge ($w$1, $w$2) is splits into ($w$1, $w$) and ($w$, $w$2). Here, we have $w$=*breaknode*($v$6, 4, $v$3, $v$1). The leaf 1 becomes the new active leaf.

We describe separately the simpler case of transforming $T_{i+1}$ into $T_i$ when $a$=*text*[$i$] does not occurs in *text*[$i$+1…$n$]: $a$ is a symbol not previously scanned. Define the procedure *newsymbol*($a$). This function is defined only for the case described above. Let *active_leaf* be the lastly created leaf of $T_{i+1}$. The working path consists of all nodes on the path from *active_leaf* to root.

```
procedure newsymbol(a);
begin
  A new leaf i is created and connected directly to root;
  for all nodes v on the working path do test[a, v]:=true;
  link[a, active_leaf]:=i; active_leaf:=i;
end
```

```
Algorithm Weiner;
{ right-to-left suffix tree construction }
begin
  compute the suffix tree T with tables test and link for
  the one-letter word text[n]; { O(1) cost }
  active_leaf := the only leaf of T;
  for i := n-1 downto 1 do begin
  { T = T($p_{i+1}$), active_leaf = i+1, construct T($p_i$) }
    a := text[i];
    if a does not occur in $p_{i+1}$ then newsymbol(a) else begin
      firsttest := the first node v on the path up from
                     active_leaf such that test[a, v]=true;
      firstlink :=  the first node v on the path up from
                     active_leaf such that link[a, v]≠nil;
      w1 := link[a, firstlink];
      if firstlink = firsttest then
      { no edge is to be decomposed } head := w1
      else begin
        w2 := son of w1 such that the label of path from
              firstlink to firsttest starts with
              the same symbol as the label of edge (w1, w2);
        head  :=  breaknode(w1, w2, firstlink, firsttest);
      end;
      link[a, firsttest] := head; create new leaf with number i;
      link[a, active_leaf] := i;
      for each node v on the working path do test[a, v]:=true;
      active_leaf := i;
    end;
  end;
end.
```

The whole algorithm above is a version of Weiner's algorithm. One stage of the algorithm consists essentially of traversing a working path: from *active_leaf* to the first node (*firstlink*) such that *link*[*a*, *v*]≠*nil*. On this way, the node *firsttest* is found. The tree is modified locally using the information about nodes *firstlink*, *firsttest* and *w*=*link*[*a*, *firstlink*]. One edge is added and (sometimes) one edge is split into two edges. The tables *link* and *test* are updated for nodes on the working path. The newly created leaf becomes the next active leaf (*active_leaf*).

**Theorem 5.5**

Weiner algorithm builds the suffix tree of a text in linear time (on fixed alphabet).

**Proof**

One iteration (one stage) of the algorithm has a cost proportional to the length $L$ of the working path (number of nodes on this path). However, it can be easily proved that

$$depth(link[a, firstlink]) \leq depth(firstlink)+1.$$

The cost of one stage can thus be charged to the difference between depths of leaves $i$+1 and $i$ (plus a constant $c$). The sum of all these differences ($depth(i)$-$depth(i+1)+c$) is obviously proportional to $n$. This completes the proof. ‡

The main inconvenience of Weiner's algorithm is that it requires tables indexed simultaneously by nodes of the tree and letters. From this point of view, McCreight's algorithm is lighter because it requires only one additional link independent of the alphabet.

## 5.5. Ukkonen's algorithm

In this section we give a sketch of an on-line construction of suffix trees. We drop the assumption that a suffix of the text cannot be a proper prefix of another suffix. So, no marker at the end of the text is assumed. We denote by $p^i$ the prefix of length $i$ of the text. We add a constraint on the suffix-tree construction : not only we want to build $T(text)$, but we also want to build intermediate suffix trees $T(p^1)$, $T(p^2)$, ... $T(p^{n-1})$. However, we do not keep in memory all these suffix trees, because the overall would take a quadratic time. We rather transform the current tree, and its successive values are exactly $T(p^1)$, $T(p^2)$, ... $T(p^n)$. Doing so, we also require that the construction takes linear time (on fixed alphabet).

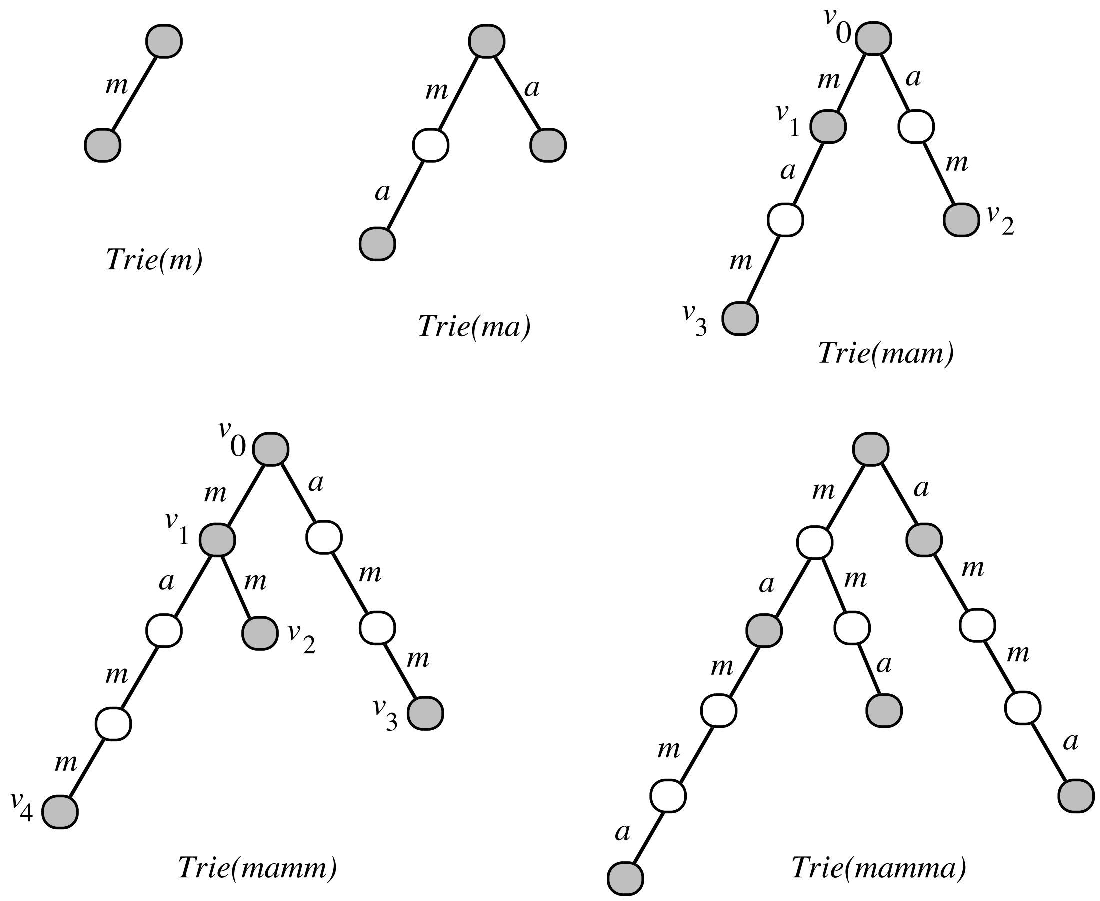
**Goal1 (on-line suffix-tree construction):**

compute the sequence of suffix trees $T(p^1)$, $T(p^2)$, ... $T(p^n)$ in linear time.

We shall first consider the uncompressed tree of suffixes of *text*, $Trie(text)$. For simplicity, we assume that the alphabet is fixed. Our first goal is an easier problem, an on-line construction of $Trie(text)$ in reasonable time, i.e. proportional to the size of the output tree.

**Goal2 (on-line uncompressed suffix-tree construction):**

compute the sequence of suffix trees $Trie(p^1)$, $Trie(p^2)$, ... $Trie(p^n)$ in $O(Trie(p^n))$ time.



*Trie(m)* *Trie(ma)* *Trie(mam)*

*Trie(mamm)* *Trie(mamma)*

**Figure 5.13**. The sequence of uncompressed suffix trees for prefixes of text *mamma*. The (compressed) suffix trees result by deleting nodes of out-degree one and composing the labels. Accepting nodes are painted.

Let us closely examine how the sequence of uncompressed trees is constructed in Figure 5.13. The nodes corresponding to suffixes of the current text $p^i$ are painted. Let $v_k$ be the suffix of length $k$ of the current prefix $p^i$ of the text. Identify $v_k$ with its corresponding node in the tree. The nodes $v_k$ are called *essential* nodes. In fact, additions in the tree, to make it grow up, are "essentially" done at such essential nodes. Consider the sequence $v_i$, $v_{i\text{-}1}$, ..., $v_o$ of suffixes in decreasing order of their length. Compare such sequences in trees for $p^3$=*mam*, and for $p^4$=*mamm* respectively (Figure 5.13). The basic property of the sequence of trees *Trie*($p^i$) is related to the way they grow. It is easily described with the sequence of essential nodes.

**Basic growing property:**

(*) Let $v_j$ be the first node in the sequence $v_{i\text{-}1}$, $v_{i\text{-}2}$, ..., $v_o$ of essential nodes, such that son($v_j$, $a_i$) exists. Then, the tree *Trie*($p^i$) results from *Trie*($p^{i\text{-}1}$) by adding a new outgoing edge labelled $a_i$, simultaneously creating a new son, to each of the nodes $v_{i\text{-}1}$, $v_{i\text{-}2}$, ..., $v_{j\text{-}1}$. If there is no such node $v_j$ then a new outgoing edge labelled $a_i$ is added to each of the nodes $v_{i\text{-}1}$, $v_{i\text{-}2}$, ..., v$_0$.

Let *suf* be the same suffix link table as in Section 5.3. Recall that, if the node *v* corresponds to a factor *ax* (for a letter *a*), *suf*[*v*] is the node associated to *x*. We also assume that *suf*[*root*]=*root*. The sequence of essential nodes can be generated by taking iteratively suffix links from its first element, the leaf whose value is the whole prefix read so far.

**Basic property of the sequence of essential nodes:**

(**) $(v_i, v_{i\text{-}1}, ..., v_0) = (v_i, suf[v_i], suf^2[v_i], ..., suf^i[v_i])$.

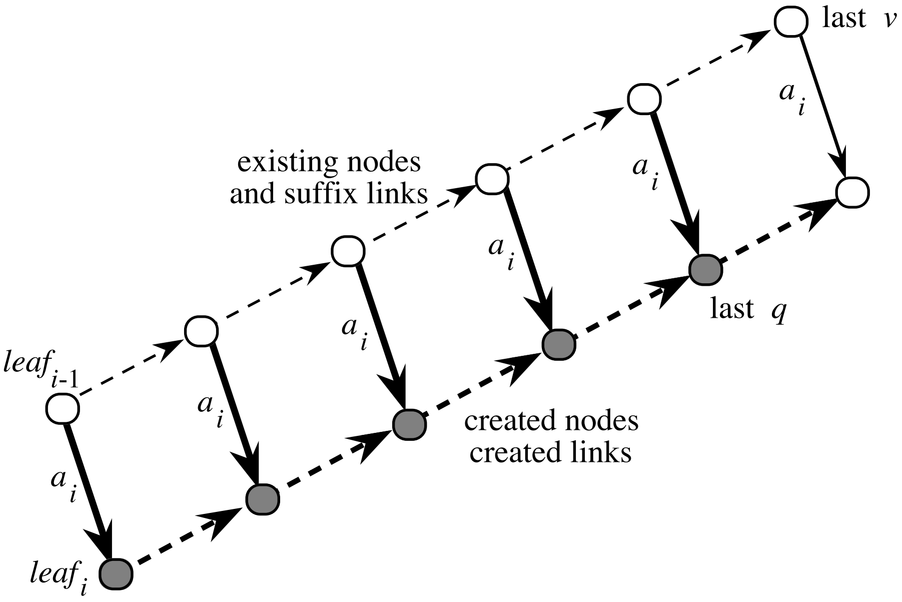


**Figure 5.14**. One iteration in the construction of *Trie*(*text*).
Bold arrows are created at this step.

In order to describe easily the on-line construction of *Trie*(*text*), we introduce the procedure *createson*. Let *v* be a node of the tree, and let *a* be a letter. Then, *createson*(*v*, *a*) connects a new son of the node *v* with an edge labelled by letter *a*. The procedure returns the created son of *v*. Using properties (*) and (**), one iteration of the algorithm looks as suggested in Figure 5.14. An informal construction is given below. A more concrete description of the on-line algorithm is given thereafter.

```
algorithm on_line_trie; { informal version }
begin
  create the two-node tree $Trie(a_1)$ with suffix links;
  for $i$ := 2 to m do begin
    $v_{i-1}$ := deepest leaf of $Trie(p^{i-1})$;
    $k$ := smallest integer such that son($suf^k[v_{i-1}]$,$a_i$) exists;
    create $a_i$-sons for $v_{i-1}$, $suf[v_{i-1}]$, ..., $suf^{k-1}[v_{i-1}]$,
    creating suffix links (see Figure 5.14);
  end;
end
```

```
algorithm on_line_trie;
begin
  create the two-node tree $T$ = $Trie(p^1)$ with suffix links;
  for $i$ := 2 to m do begin
    $v$ := deepest leaf of $T$;
    $q$ := $createson(v, a_i)$; $v$ := $suf[v]$;
    while son($v$,$a_i$) undefined do begin
      $suf[q]$ := $createson(v, a)$;
      $q$ := $suf[q]$; $v$ := $suf[v]$;
    end;
    if $q$ = son($v$,$a_i$) then { $v$ = $root$ } $suf[q]$ := $root$
    else $suf[q]$ := son($v$,$a_i$);
  end
end
```

**Theorem 5.6**

The algorithm *on-line-trie* builds the tree *Trie*(*text*) of suffixes of *text* in an on-line manner. Its works in time proportional to the size of *Trie*(*text*).

**Proof**

The correctness follows directly from properties (*) and (**). The complexity follows from the fact that the work done in one iteration is proportional to the number of created edges (calls to *createson*). This completes the proof. ‡

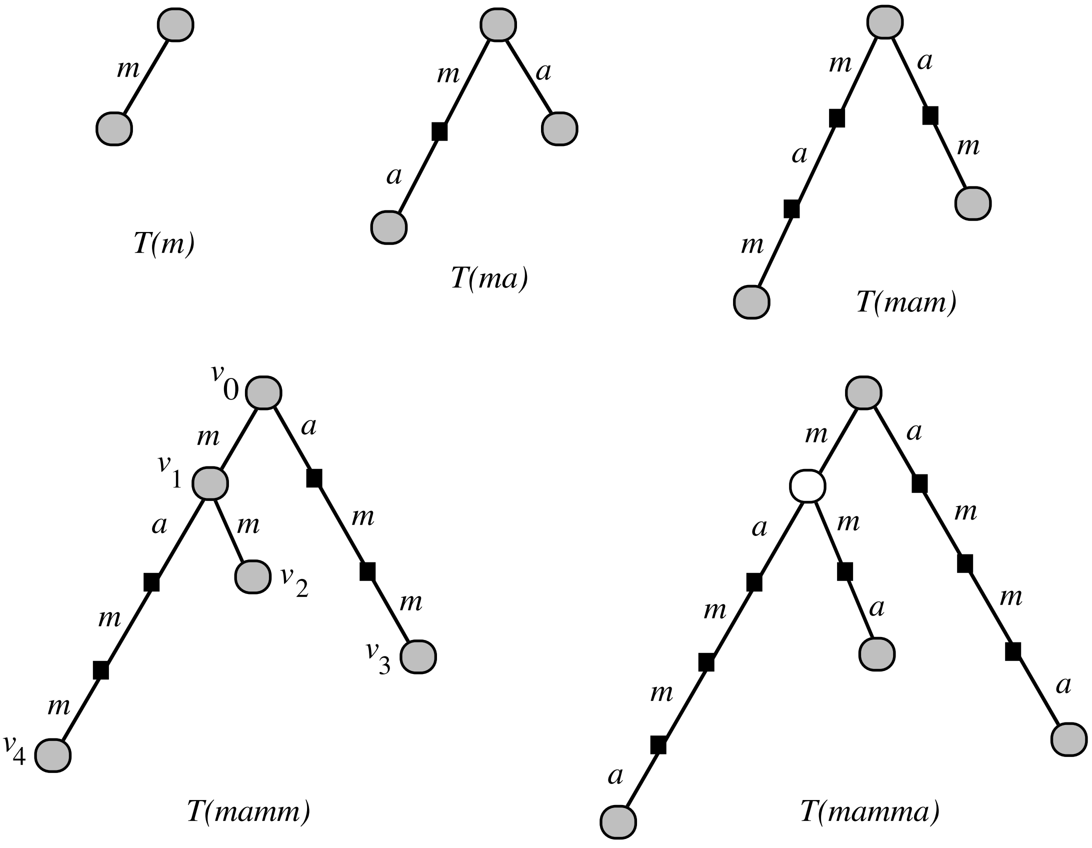


**Figure 5.15**. The sequence of (compressed) suffix trees
(with implicit nodes marked as ■).

The *i*-th iteration done in the previous algorithm can be adapted to work on the compressed suffix tree $T(p^{i-1})$. Each node of $Trie(p^{i-1})$ is treated as an implicit node. Hence, the new algorithm simulates the version *on_line_trie*. Here again the notion of implicit nodes from Section 5.2 is useful. Recall that a pair $(v, \alpha)$ is an implicit node in $T$ iff $v$ is a node of $T$ and $\alpha$ is a prefix of the label of an edge from $v$ to a son of it. The implicit node $(v, \alpha)$ is said a "real" node iff $\alpha$ is the empty word.

Let $v$ be a node of the tree $T$, and let $p$ be a subword of the input word *text* (represented by a pair of integers $l$, $r$, where $p = text[l\ldots r]$). The basic function used in McCreight's algorithm is the function *find*$(v, p)$. This function follows a path labelled by $p$ from node $v$, possibly creating a new node. In the present algorithm we use a similar strategy, except that the creation of a possible node is postponed. The corresponding function is called *normalize* and applies to a pair $(v, p)$. The value of *normalize*$(v, p)$ is the last implicit node $(v, \alpha)$ on the path spelled by $p$ from $v$. Whenever this function is applied, the word $p$ is fully contained in the followed path, hence, the *fastfind* implementation of Section 5.3 can be adapted to the work.

We have to interpret the suffix links and sons (by single letters) of implicit nodes in the compressed tree. In the algorithm we use the notation *son*' and *createson*'. They are interpreted as follows ($a$ is a letter, and $(v, \alpha)$ is an implicit node, identified to $v$ if $\alpha$ is empty):

(1) $son'((v, \alpha), a)$ exists iff the path $\alpha$ originated at node $v$ can be extended by the letter $a$; in this case $son'((v, \alpha), a) = (v, \alpha a)$, which can be a real node.

(2) The procedure $createson'((v, \alpha), a)$ first checks if $\alpha$ is nonempty. If so, the procedure first makes $(v, \alpha)$ a real node (applying $break(v, \alpha)$ of Section 5.3, for instance). Then, the procedure creates an $a$-son of the node.

There is still one important implementation detail. If the node $v$ is a leaf then there is no need to extend the edge coming from its father by a single symbol. If the label of the edge is a pair of positions $(l, r)$ then, after updating it, it should be $(l, r+1)$. We can omit such updatings by setting $r$ to infinity for all leaves. This infinity is automatically understood as the last scanned position $i$ of the pattern. Doing so cuts the amount of work during one iteration of the algorithm. If $v_i$, $v_{i-1}$, ..., $v_0$ is the sequence of essential nodes, and if we know that $v_i$, $v_{i-1}$, ..., $v_k$ are leaves, then we can skip processing them because this is done automatically by the trick with infinity. We thus start processing essential nodes from $v_{k-1}$. In the algorithm we call $v$ the current node that run through essential nodes. Since there is no sense to deal with the situation when $v$ is a leaf, at a given iteration, the first value of $v$ is the $a_i$-son of the last value of $v$ (from the preceding iteration), instead of starting from the deepest leaf as in the on-line construction of *Trie*(*text*). All that gives the on-line suffix tree construction below.

```
algorithm of Ukkonen;
begin
  create the two-node tree $T(a_1)$ with suffix links;
  $(v, \alpha)$ := (root of the tree, $\varepsilon$);
  for $i$ = 2 to $m$ do begin
    if $son'((v,\alpha),a_i)$ undefined then $createson'((v,\alpha),a_i)$;
    repeat
      $(q, \beta)$ := $son'((v, \alpha), a_i)$;
      $(v, \alpha)$ := $normalize(suf[v], \alpha)$;
      if $son'((v,\alpha),a_i)$ undefined then $createson'((v,\alpha),a_i)$;
      if $\beta$ is empty then $suf[q]$ := $son'((v,\alpha),a_i)$;
      $(v,\alpha)$ := $son'((v,\alpha),a_i)$;
           { here, the length of $\alpha$ can only be increased by one }
    until no edge created or $v$ = root;
    if $v$ = $root$ then $suf[son'(v,a_i)]$ := $root$;
  end
end
```

**Theorem 5.7**

Ukkonen algorithm builds the compressed tree $T(text)$ in an on-line manner. It works in linear time (on fixed alphabet).

**Proof**

The correctness follows from the correctness of the version working on uncompressed tree. The new algorithm is just a simulation of it.

To prove the $O(|text|)$ time bound it is sufficient to prove that the total work is proportional to the size of $T(text)$, which is linear. The work is proportional to the work done by all *normalize* operations. The cost of one *normalize* operation is proportional to the decrease of the length of $\alpha$. On the other hand, the length of $\alpha$ is increased by at most one per iteration. Hence, the total number of reduction in length of $\alpha$'s is linear. This completes the proof. ‡

## 5.6. Suffix arrays: an alternative data structure

There is a clever and rather simple way to deal with all suffixes of a text : to have their list in increasing lexicographic order in order to perform binary searches on them. The implementation of this idea leads to a data structure called *suffix array*. It is not exactly a "good representation" in the sense defined at the beginning of the chapter. But it is "almost good". This means that it satisfies the following conditions:

(1) it has $O(n)$ size,

(2') it can be constructed in $O(n.\log n)$ time,

(3') it allows to compute $FACTORIN(x, text)$ in $O(|x| + \log n)$ time.

So the time to construct and use the structure is slightly larger than that to compute the suffix tree (it is $O(n.\log|A|)$ for the latter). But suffix arrays have two advantages:

— their construction is rather simple; it is even commonly admitted that, in practice, it behaves better than the construction of suffix trees;

— it consists of two linear size arrays which, in practice again, take little memory space (typically four times less space than suffix trees).

Let $text = a_1a_2\ldots a_n$, and let $p_i = a_ia_{i+1}\ldots a_n$ be the $i$-th suffix of the text. Let $Pos[k]$ be the position $i$ where starts the $k$-th smallest suffix of *text* (according to the lexicographic order of the suffixes). In other terms, the $k$-th smallest suffix of *text* is $p_{Pos[k]}$. Denote by $LCPREF[i, j]$ the length of the longest common prefix of suffixes $p_i$ and $p_j$. We assume, for simplicity, that the size of the pattern is a power of two. If not, we can add a suitable number of endmarkers at the end of *text* to meet the condition. Let us call the whole interval $[1\ldots n]$ *regular*, and define regular subintervals by the rule : if an interval is regular, then its halves are also regular. We say that an interval $[i\ldots j]$ is regular iff it can be obtained in this way from the whole interval. Finally, observe that there are exactly $2n$-1 regular intervals.

The suffix array of *text* is the data structure consisting of both the array *Pos*, and the values $LCPREF[i, j]$ for each regular interval $[i\ldots j]$. Hence, the whole data structure has $O(n)$ size, and satisfies condition (1). To show that the condition (2') is satisfied we can apply results of Chapter 9, related to another data structure called the dictionary of basic factors. Its definition is postponed to this chapter. In fact, this dictionary is an alternative "almost good" representation of the set of factors. Note that condition (2') is rather intuitive because it concerns sorting $n$ words having strong mutual dependencies. But, in our point of view, the most interesting property of suffix arrays is that they satisfy condition (3').

**Theorem 5.8**

Assume the suffix array of *text* is computed (are computed the table *Pos* and the table *LCPREF* for regular intervals). Then, for any word $x$, we can compute *FACTORIN*($x$, *text*) in $O(|x| + \log|text|)$ time.

**Proof**

Let $min_x = \min\{k\ /\ x \le p_{Pos[k]}\}$ and $max_x = \max\{k\ /\ x \ge p_{Pos[k]}\}$, where ≤ and ≥ denote inequalities in the sense of the lexicographic ordering. Then, all occurrences of the subword $x$ in *text* are at positions given in the table *Pos* between indices $min_x$ and $max_x$. There is at least one occurrence of $x$ inside *text* iff $min_x \le max_x$.

We show how to compute $min_x$. The computation of $max_x$ is symmetrical. We start with an extremely simple algorithm having $O(x.\log n)$ running time. It is a binary search for $x$ inside the sorted sequence of suffixes. Let $suf(k) = p_{Pos[k]}$. Hence $suf(k)$ is the $k$-th suffix in the lexicographic numbering. We describe the computation of $min_x$ recursively. The value of $min_x$ is assumed to be found inside the interval [*Left*…*Right*].

```
function find(Left, Right);
begin
  if Left = Right then return Left;
  Middle := right position of the left half of [Left..Right];
  if x ≤ suf(Middle) then return find(Left, Middle)
  else return find(Middle+1, Right)
end
```

Let $l = LCPREF(suf(Left), x)$, and $r = LCPREF(suf(Right), x)$. The basic property of the function find is the following fact.

**Basic property:**

Let $l$, $r$ be the respective values of *Left* and *Right* at a given call of the function *find.* And let $l'$, $r'$ be the values of *Left* and *Right* at the next call of *find.* Then, $\max(l, r) \le \max(l',$

$r'$). If we know the values of $l$, $r$, then we can check the inequality $x \leq suf(Middle)$, and compute $l'$, $r'$ in time $O(\Delta)$, where $\Delta = \max(l', r') - \max(l, r)$.

The proof is left to the reader. Several cases are to be considered, depending on the relations between numbers $l$, $r$, *LCPREF*(*Left*, *Middle*) and *LCPREF*(*Middle*+1, *Right*). The sum of all $\Delta$'s is O(|$x$|), since $l$, $r \leq |x|$. Hence, the total complexity is $O(|x| + \log n)$ because the function *find* makes log$n$ recursive calls. ‡

The computation of *LCPREF* is discussed at the end of the next section.

## 5.7. Applications

There is a data structure slightly different from the suffix tree, known as the position tree. It is the tree of position identifiers. The *identifier* of position $i$ on the text is the shortest prefix of *text*[$i$…$n$] which does not occur elsewhere in *text*. Identifiers are well defined when the last letter of *text* is a marker. Once we have the suffix tree of *text*, computing its position tree is fairly obvious, see Figure 5.16. Moreover, this shows that the construction works in linear time.

**Theorem 5.9**

The position tree of a given text can be computed in linear time (on a fixed alphabet).

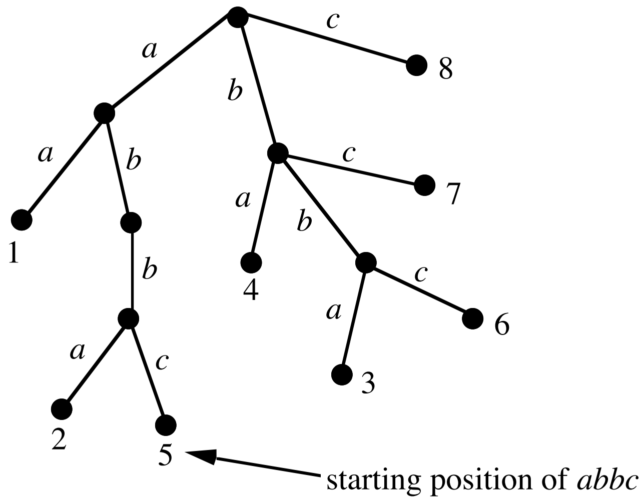


**Figure 5.16**. The position tree of *text* = *aabbabbc*.
Compare with its suffix tree in Figure 5.1.

One of the main application of suffix trees is for the situation when the text *text* is like a dictionary. In this situation, the suffix tree or the position tree act as an index on the text. The index virtually contains all the factors of the text. With the data structure, the problem of locating a word $w$ in the dictionary can be solved efficiently. But we can also perform rapidly other operations, such as computing the number of occurrences of $w$ in *text*.

**Theorem 5.10**

The suffix tree of *text* can be preprocessed in linear time so that, for a given word $w$, the following queries can be done on-line in $O(|w|)$ time:

— find the first occurrence of $w$ in *text*;

— find the last occurrence of $w$ in *text*;

— compute the number of occurrences of $w$ in *text*.

We can list all occurrences of $w$ in *text* can be listed in time $O(|w|+k)$, where $k$ is the number of occurrences.

**Proof**

We can preprocess the tree, computing bottom-up, for each node, values *first*, *last* and *number* corresponding to respectively the first position in the subtree, the last position in the subtree, and the number of positions in the subtree. Then, for a given word $w$, we can (top-down) retrieve these informations in $O(|w|)$ time (see Figure 5.17). They give the answer to the first three queries of the statement.

To list all occurrences, we first access the node corresponding to the word $w$ in $O(|w|)$ time. Then, we traverse all leaves of the subtree to collect the list of positions of $w$ in *text*. Let $k$ be the number of leaves of the subtree. Since all internal nodes of the subtree have at least two sons, the total size of the subtree is less than $2.k$, and the traversal takes $O(k)$ time. This completes the proof. ‡

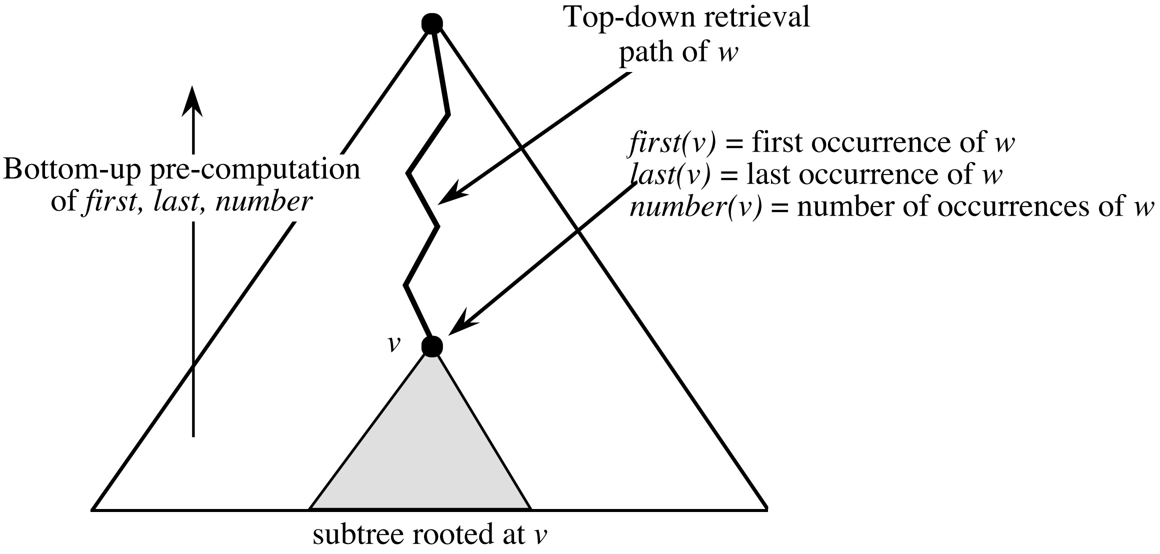

Top-down retrieval path of *w*
*first(v)* = first occurrence of *w*
*last(v)* = last occurrence of *w*
*number(v)* = number of occurrences of *w*
Bottom-up pre-computation of *first, last, number*
*v*
subtree rooted at *v*

**Figure 5.17**. We can preprocess the tree to compute (bottom-up), for each node, its corresponding values *min*, *max* and *size*. Then, for a given word *w*, we can retrieve these informations in $O(|w|)$ time.

The longest common factor problem is a natural example of a problem easily solvable in linear time using suffix trees, and very hard to solve efficiently without any essential use of "good" representation of the set of factors. In fact, it has been believed for a long time that no linear time solution to the problem is possible, even if the alphabet is fixed.

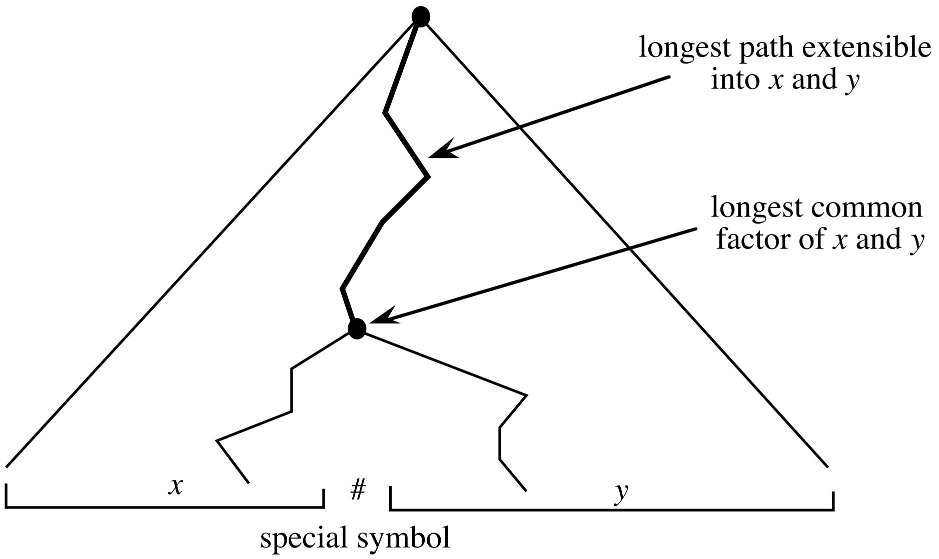

longest path extensible into *x* and *y*
longest common factor of *x* and *y*
*x*
#
*y*
special symbol

**Figure 5.18**. Finding longest common factors with suffix trees.

**Theorem 5.11**

The longest common factor of $k$ words can be found in time linear in the size of the problem, i.e. the total length of words ($k$ is a constant, alphabet is fixed).

**Proof**

The proof for case $k$=2 is illustrated by Figure 5.18. The general case, with $k$ fixed, is solved similarly. We compute the suffix tree of the text consisting of the given words separated by distinct markers. Then, for each node, exploring the tree bottom-up, is computed a vector informing, for each $1 \leq i \leq k$, whether a leaf corresponding to a position inside the $i$-th subword is in the subtree of this node. The deepest node with positive information of this type for each $i$ ($1 \leq i \leq k$) corresponds to the longest common factor. The total time is linear. This completes the proof. ‡

Another solution to the problem of the longest common factor of two words is given is Chapter 6. It uses the suffix dawg of only one pattern, and processes the other word in on-line manner.

The next figure shows an application of suffix tree to the problem of finding the longest repeated factor inside a given text. The solution is analogue to the solution of the longest common factor problem, considering that $k$=1. Problems of this type (related to regularities in strings) will be treated in more details in chapter 8, where we give also an almost linear time algorithm ($O(n \log n)$). This latter algorithm is simpler and does not use suffix trees or equivalent data structure. This algorithm will cover also the two-dimensional case, where our "good" representations (considered in the present chapter) are not well suited.

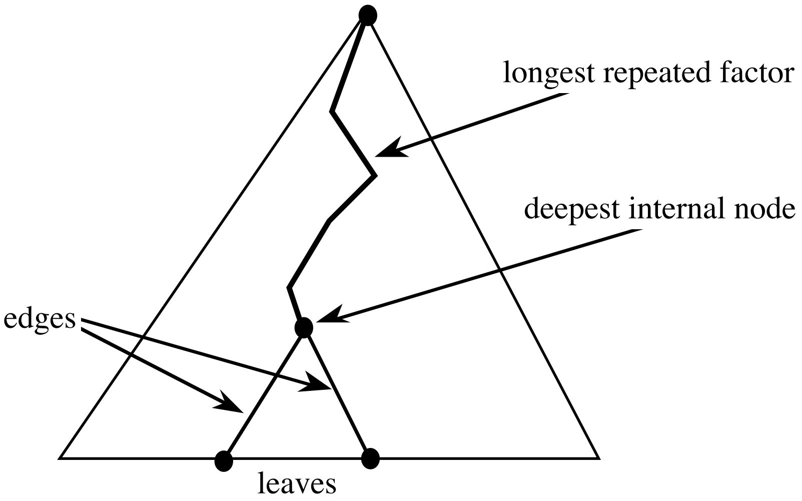


**Figure 5.19**. Computation of the longest repeated factor.

Let $LCPREF(i, j)$ denote, as in Section 5.6, the length of the longest common prefix starting at positions $i$ and $j$ in a given text of size $n$. In the chapter on two-dimensional matching we use frequently the following fact.

**Theorem 5.12**

It is possible to preprocess a given text in linear time so that each query *LCPREF*($i$, $j$) can be answered in constant time, for any positions $i$, $j$. A parallel preprocessing in $O(\log n)$ time with $O(n/\log n)$ processors of an EREW PRAM is also possible (on a fixed alphabet).

Let *LCA*($u$, $v$) denote the lowest common ancestor of nodes $u$, $v$ in a given tree $T$. The proof of Theorem 5.12 easily reduces to a preprocessing of the suffix tree which enables *LCA* queries in constant time. The value *LCPREF*($i$, $j$) can be computed as the size of the string corresponding to the node *LCA*($v_i$, $v_j$), where $v_i$, $v_j$ are leaves of the suffix tree corresponding to suffixes starting at positions $i$ and $j$.

**Theorem 5.13**

It is possible to preprocess a given tree $T$ in linear time in such a way that each query *LCA*($u$, $v$) can be answered in constant time. A parallel preprocessing in $O(\log n)$ time with $O(n/\log n)$ processors of an EREW PRAM is also possible (on a fixed alphabet).

The beautiful proof of Theorem 5.13 is beyond the scope of this book. It is based on a preprocessing corresponding to the two following simple subcases:

— $T$ is single path; then *LCA*($u$, $v$) is the node ($u$ or $v$) closer to the root; it is enough to associate to each node its distance to the root, to efficiently answer further queries;

— $T$ is the complete binary tree with $2^{k-1}$ nodes; identify nodes $u$, $v$ with their numbers in the inorder numbering of the tree; then, the number of *LCA*($u$, $v$) is given by a simple arithmetic formula of constant size; in this case, the preprocessing consists in computing the inorder number of the nodes of the tree.

In the general case, the proof is based on a transformation $F$ of the tree $T$ into a complete binary tree $F(T)$. The transformation is such that $F^{-1}(q)$ is a path in $T$, for any node $q$ in $F(T)$.

All applications discussed so far show the power of suffix trees. However, the data structure of the next chapter, dawg, can be applied as well (except maybe for the computation of *LCPREF*). Dawg's are structurally equivalent to suffix trees. We present now explicitly how to use alternatively suffix trees or dawg's on the next problem: compute the number of distinct factors of *text* (cardinality of the set *Fac*(*text*)). This problem also falls into the category of problems for which efficient algorithms without essential use of any of "good" data structures is hardly imaginable.

**Lemma 5.14**

We can compute the number of factors of a text (cardinality of the set *Fac*(*text*)) in linear time.

**Proof 1** — suffix tree application
Let *T* be the suffix tree of the text. The weight of an edge in *T* is defined as the length of its label. Then, the required number is the sum of weights of all labels. ‡

**Proof 2** — dawg application
Let *D* be the suffix dawg of the text. Compute the number *M* of all paths in *D* starting from the root (not necessarily ending at the sink). Then, *M*=|*Fac*(*text*)|. The number *M* is computed bottom-up in linear time. ‡

Illustrated by Lemma 5.14, we conclude the chapter with the following general "metatheorem": suffix trees and dawg's are "good" representations for the set of factors of a text.

## Bibliographic notes

The two basic algorithms for suffix tree construction are from Weiner [We 73] and McCreight [McC 76]. Our exposition of Weiner's algorithm uses a version of Chen and Seiferas [CS 85]. This paper also describe the relation between dawg's and suffix trees. An excellent survey on applications of suffix trees has been done by Apostolico in [Ap 85].

The on-line algorithm of Section 5.5 has been recently discovered by Ukkonen [U 92]. Note that the algorithm of McCreight is not on-line because it has to look ahead symbols of the text.

The notion of suffix array has been invented by Manber and Myers [MM 90]. They use a different approach to the construction of suffix arrays than our exposition (which refers to the dictionary of basic factors of Chapter 8). The worst case complexities of the two approaches are identical, though the average complexity of the original solution proposed by Manber and Myers is better. An equivalent implementation of suffix arrays is considered by Gonnet and Baeza-Yates in [GB 91], and called *PAT trees*.

As reported in [KMP 77], Knuth conjectured in 1970 that a linear time computation of the longest common factor problem was impossible to achieve. Theorem 5.11 shows that it is indeed possible on a fixed alphabet.

A direct computation of uncompacted position trees, without use of suffix trees, is given in [AHU 74]. The algorithm is quadratic because uncompacted suffix trees can have quadratic size.

Theorem 5.13, related to the lowest common ancestor problem in trees, is by Schieber and Vishkin [SV 88]. We refer the reader to this paper for more details. In [HT 84] an alternative proof is given. However, their solution is much more complicated, and only a sequential preprocessing is given.

## Selected references

[GB 91] G.H. GONNET, R. BAEZA-YATES, *Handbook of algorithms and data structures*, Addison-Wesley, Reading, Mass., 1991.

[MM 90] U. MANBER, E. MYERS, Suffix arrays: a new method for on-line string searches, in: (*Proc. of 1st ACM-SIAM Symposium on Discrete Algorithms*, American Mathematical Society, Providence, 1990) 319-327.

[McC 76] E.M. MCCREIGHT, A space-economical suffix tree construction algorithm, *J. ACM* 23:2 (1976) 262-272.

[U 92] E. UKKONEN, Constructing suffix trees on-line in linear time, in: (*IFIP*'92).

[We 73] P. WEINER, Linear pattern matching algorithms, in: (*Proc. 14th IEEE Annual Symposium on Switching and Automata Theory*, Institute of Electrical Electronics Engineers, New York, 1973) 1-11.

# 6. Subword graphs

The directed acyclic word graph (dawg) is a good data structure representing the set *Fac*(*text*) of all factors of the word *text* of length *n*. It is an alternative to suffix trees of Chapter 5. The graph *DAWG*(*text*), called the suffix dawg of *text*, is obtained by identifying isomorphic subtrees of the uncompacted tree *Trie*(*text*) representing *Fac*(*text*) (see Figure 6.1). An advantage of dawg's is that each edge is labelled by a single symbol. It is somehow more convenient to use it when information is to be associated to edges rather than to nodes. We consider only dawg's representing the set *Fac*(*text*), but it is clear that the approach also applies to other set of words, such as the set of subsequences of a string.

The linear size of suffix trees is a trivial fact (Chapter 5), but the linear size of suffix dawg's is much less trivial, and probably it is the most surprising fact related to representations of *Fac*(*text*).

Applications of suffix dawg's are essentially the same as applications of suffix trees, such as those presented in Section 5.7. Indexing is the main purpose of these data structure. Theorem 5.11 can also be proved with dawg's. But we present in the present chapter two quite surprising uses of dawg's in Section 6.5. There, the suffix dawg of the pattern serves to search it inside a text. The second method turns out to lead to one of the most efficient algorithm to search a text.

## 6.1. Size of suffix DAWG's

A node in the graph *DAWG*(*text*) naturally corresponds to a set of factors of the text: factors having the same right context. It is not hard to be convinced that all these factors have the following property : their first occurrences end at the same position in *text*. The converse is not necessarily true, but the remark gives the intuition of the next definition.

Let $x$ be a factor of *text*. We denote by *end-pos*($x$) (ending positions) the set of all positions in *text* at which ends an occurrence of $x$. Let $y$ be another factor of *text*. Then, the subtrees of *Trie*(*text*) rooted at $x$ and $y$ (recall that we identify the nodes of *Trie*(*text*) with their labels) are isomorphic iff *end-pos*($x$) = *end-pos*($y$) (when the text ends with a special endmarker). In the graph *DAWG*(*text*) paths $x$ having the same set *end-pos*($x$) lead to the same node. Hence, the nodes of $G$ correspond to nonempty sets of the form *end-pos*($x$). The root of the dawg corresponds to the whole set of positions $\{0, 1, 2, \ldots, n\}$ on the text. From a theoretical point of view, nodes of $G$ can be identified with such sets (especially when analyzing the construction algorithm). But, from the practical point of view, the sets are never maintained explicitly. The *end-pos* sets, usually large, cannot directly name nodes of $G$, because the sum of sizes of all such sets can happen to be nonlinear. An explicit representation of each *end-pos* sets by a list of its elements is too large. Figure 6.1 presents both the trie of the text *aabbabd*, and *DAWG*(*text*) for the same word. The graph has 10 nodes and 15 arcs. If we allow labels of edges to have varying length then its size can be further reduced to 7 nodes and 12 arcs (by compressing chains).

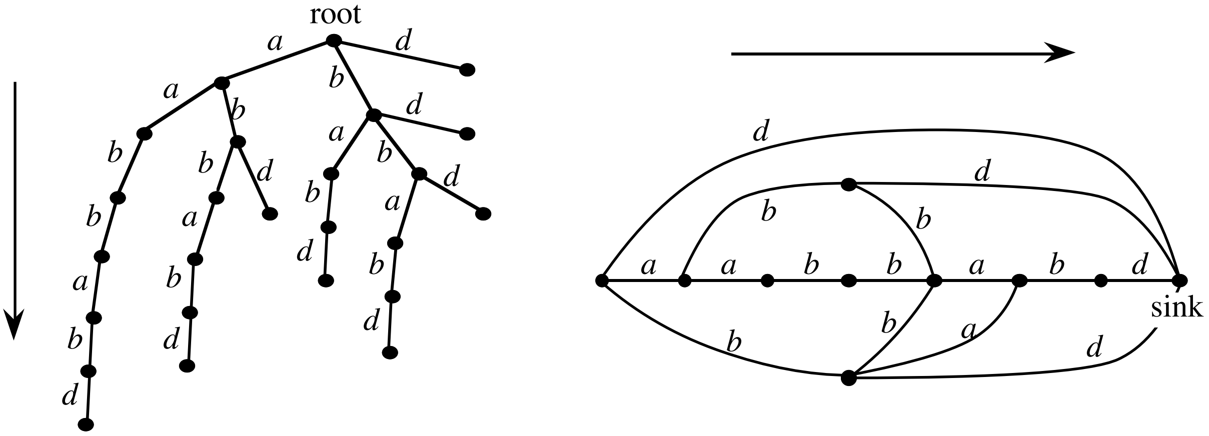


**Figure 6.1**. The uncompacted suffix tree *Trie*(*aabbabd*), and the direct acyclic word graph *DAWG*(*text*).

The small size of dawg's is due to the special structure of the family Φ of sets *end-pos*. We associate to each node *v* of the dawg its value *val*(*v*) equal to the longest word leading to it from the root. The nodes of the dawg are, in fact, equivalence classes of nodes of the uncompacted tree *Trie*(*text*), where the equivalence is meant as subtree isomorphism. In this sense, *val*(*v*) is the longest representative of its equivalence class. It can also be considered that nodes of the dawg are equivalence classes of factors of the text because nodes in *Trie*(*text*) are in one-to-one correspondence with factors of *text*.

The notion of failure function, intensively used in Chapter 3, has an exact counterpart in dawg's. Let *v* be a node of *DAWG*(*text*) distinct from the *root*. We define *suf*[*v*] as the node *w* such that *val*(*w*) is the longest suffix of *val*(*v*) non equivalent to it. In other terms, *val*(*w*) is the longest suffix of *val*(*v*) corresponding to a node different from *v*. Note that the definition implies that *val*(*w*) is a proper suffix of *val*(*v*). By convention, we define *suf*[*root*] as *root*. In the implementation it is meant that *suf* is represented as a table. The table *suf* is analogue to the table *Bord* defined in Chapter 3. We also call the table *suf* the table of *suffix links* (edges (*v*, *suf*[*v*]) are "suffix links").

The suffix links in *DAWG*(*dababd*) are presented in Figure 6.2. Since the value of *suf*[*v*] is a word strictly shorter than *val*(*v*), *suf* induces a tree structure on the set of nodes. The node *suf*[*v*] is interpreted as the father of *v* in the tree. It happens that the tree of suffix links is the same as the tree structure of sets in Φ induced by the inclusion relation.

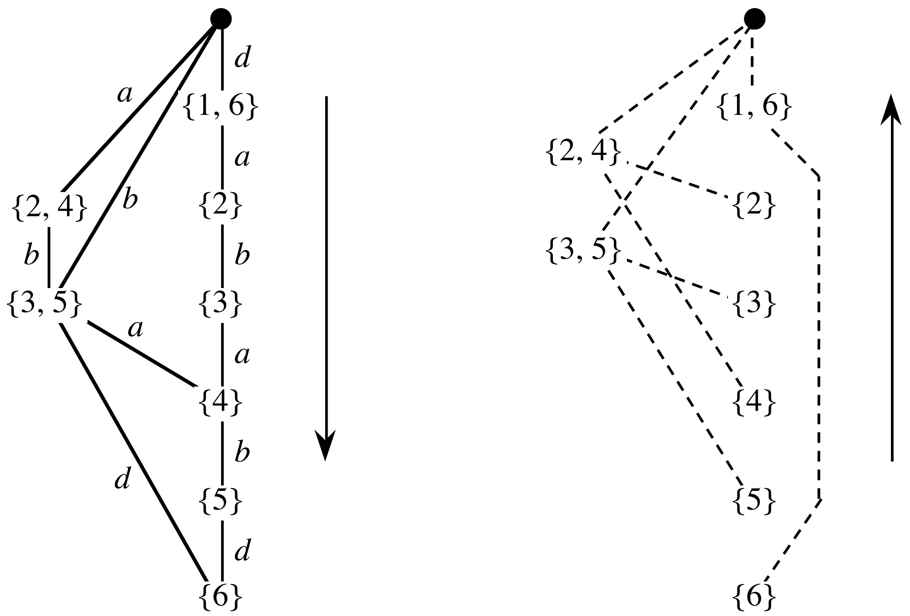


**Figure 6.2**. *DAWG*(*dababd*) (left) and its suffix links (right).
This shows the structure of the family Φ of *end-pos* sets.

**Theorem 6.1**

The size of *DAWG*(*text*) is linear. More precisely, if *N* is the number of nodes of *DAWG*(*text*) and *n*=|*text*|>0, then *N* < 2*n*. Moreover, *DAWG*(*text*) has less than *N*+*n*-1 edges. This is independent of the size of the alphabet.

**Proof**

The main property used here directly comes from the definition of *end-pos* sets : any two subsets of Φ are either disjoint or one is contained in the other. The family Φ thus have a tree structure (see Figure 6.2). All leaves are pairwise disjoint subsets of {1, 2, …, *n*} (we do not count position 0 that is associated to the root, because it is not contained in any other *end-pos* set). Hence, there is at most *n* leaves. This does not directly imply the thesis because it can happen that some internal nodes have only one son (as in the example of Figure 6.2).

We partition nodes into two (disjoint) subsets according the fact that *val*(*v*) is a prefix of *text* or not. The number of nodes in the first subset is exactly *n*+1 (number of prefixes of *text*). We now count the number of nodes in the other subset of the partition.

Let *v* be a node such that *val*(*v*) is not a prefix of *text*. Then *val*(*v*) is a non-empty word that occurs in at least two different right contexts in *text*. But then, we can deduce that at least two different nodes *p* and *q* (corresponding to two different factors of *text*) are such that *suf*[*p*] = *suf*[*q*] = *v*. This show that nodes like *v* have at least two sons in the tree inferred by *suf*. Since the tree has at most *n* leaves (corresponding to non-empty prefixes), the number of such nodes is less than *n*. Additionally note that if *text* contains two different letters the root has at least two sons but cannot be counted in the second subset because *val*(*root*)=ε is prefix of *text*. If *text* is

of the form $a^n$, the second subset is empty. Therefore, the cardinality of the class is indeed less than $n$-1. This finally shows that there is less than $(n+1)+(n-1) = 2n$ nodes.
To prove the bound on the number of edges, we consider a spanning tree $T$ over *DAWG*(*text*), and count separately the edges belonging to the tree and the edges outside the tree. The tree $T$ is chosen to contain the branch labelled by the whole text. Since there are $N$ nodes in the tree, there are $N$-1 edges in the tree. Let us count the other edges of *DAWG*(*text*). Let $(v, w)$ be such an edge. We associate to it the suffix $xay$ of *text* defined by : $x$ is the label of the path in $T$ going from the root to $v$, and $a$ is the label of the edge $(v, w)$, $y$ is any factor of *text* extending $xa$ into a suffix of *text* ($x, y \in A^*$, $a \in A$). It is clear that the correspondence is one-to-one. Moreover, the empty suffix is not consider, nor *text* itself because it is in the tree. It remains $n$-1 suffixes, which is the maximum number of edges outside $T$.
Finally, the number of edges in *DAWG*(*text*) is less than $N+n$ -1. ‡

Although the size of *DAWG*(*text*) is linear, it is not always strictly minimal. If minimality is understood in terms of finite automata (number of nodes, for short), then *DAWG*(*text*) is the minimal automaton for the set of suffixes of *text*. The minimal automaton for *Fac*(*text*) can indeed be slightly smaller.

## 6.2. A simple off-line construction

Our first construction of dawg's consists essentially in a transformation of suffix trees. The basic procedure is the computation of equivalent classes of subtrees. It is based on a classical algorithm concerning tree isomorphism (see [AHU 74] for instance). We just recall the result without proof.

**Lemma 6.2** ([AHU 74])

Let $T$ be a rooted ordered tree whose edges are labelled by letters (assumed to be of constant size). Then, isomorphic classes of all subtrees of $T$ can be computed in linear time.

We call *compacted dawg*, the dawg in which edges are labelled by words, and no node has only one outgoing edge (chains of nodes are compacted). A simple application of Lemma 6.2 provides a construction of compacted dawg's, that leads to the construction of dawg's.

**Theorem 6.3**

*DAWG*(*text*) and its compacted version can be built in linear time (on fixed alphabet).

**Proof**

We illustrate the algorithm on the example text string *w*=*baaabbabb*. The suffix tree of *w#* is constructed by any method of Chapter 5. For technical reasons, inherent to the definition of suffix trees, the endmarker # is added to the word *w*. But this endmarker is later ignored in the constructed dawg (it is only needed at this stage).

Then, by the algorithm of the preceding lemma the equivalence classes of isomorphic subtrees are computed. The roots of isomorphic subtrees are identified, and we get the compacted version *G*' of *DAWG*(*w*), see figure below. The whole process takes linear time.

The difference between the actual structure and the dawg is related to lengths of strings which are labels of edges. In the dawg each edge is labelled by a single symbol. The "naive" approach could be to decompose each edge labelled by a string of length *k* into *k* edges. But the resulting graph could have a quadratic number of nodes. We apply such an approach with the following modification. By the weight of an edge we mean the length of its label. For each node *v* we compute the heaviest (with the largest weight) incoming edge. Denote this edge by *inedge*(*v*). Then, in parallel for each node *v* we perform a local transformation *local_action*(*v*). It is crucial that all these local transformations *local_action*(*v*) are independent and can be performed simultaneously for all *v*.

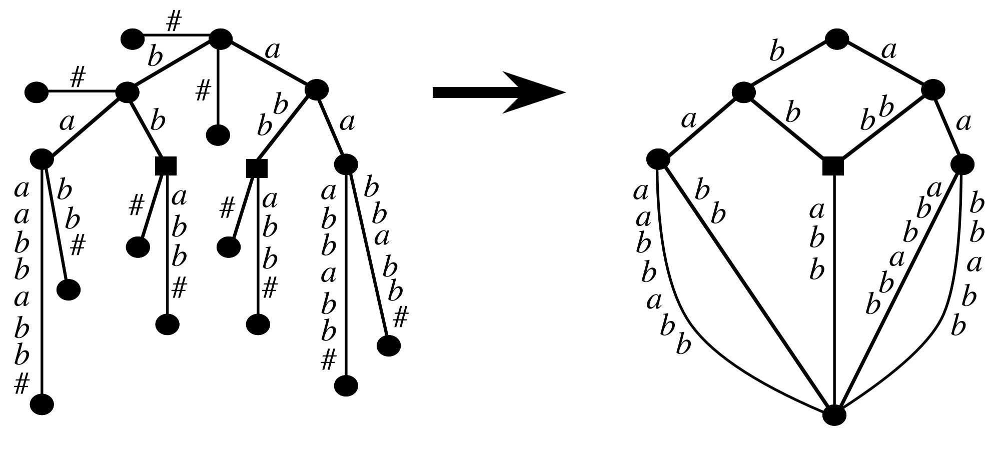


**Figure 6.3**. Identification of isomorphic classes of nodes of the suffix tree. In the algorithm the labels of the edges are constant-sized names of the corresponding strings.

The transformation *local_action*(*v*) consists in decomposing the edge *inedge*(*v*) into *k* edges, where *k* is the length of the string *z*, label of this edge. The label of *i*-th created edge is *i*-th letter of *z*. There are interleaved *k*-1 new nodes : (*v*, 1), (*v*, 2), ..., (*v*, *k*-1). The node (*v*, *i*) is at the distance *i* from *v*. For each other incoming edge of *v*, *e* = (*v*1, *v*) we perform the following additional action. Suppose that the string, label of *e* has length *p*, and that its first letter is *a*. If *p*>1 then we remove the edge *e* and create an edge from *v*1 to (*v*, *p*-1) whose label is the letter *a*. This is graphically illustrated in the figure below.

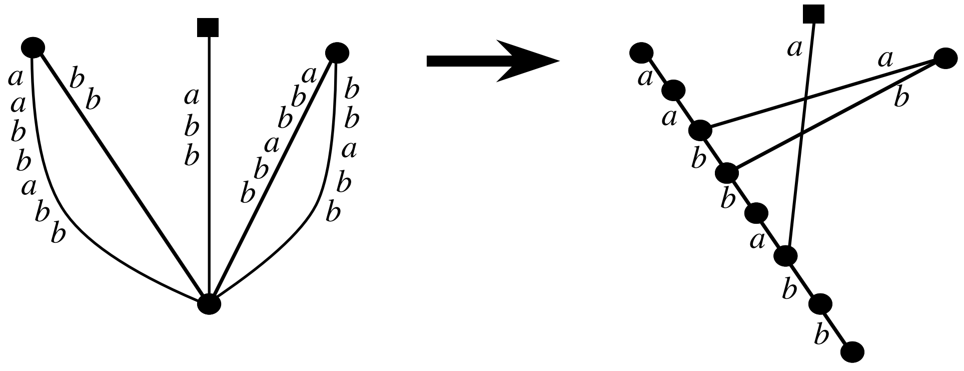


**Figure 6.4**. Local transformation.
New nodes are introduced on the heaviest incoming edge.

Then we apply to all nodes *v*, except the root, the action *local_action*(*v*).
The resulting graph for our example string *w* is presented in the next figure. This graph is the required *DAWG*(*w*). This completes the proof. ‡

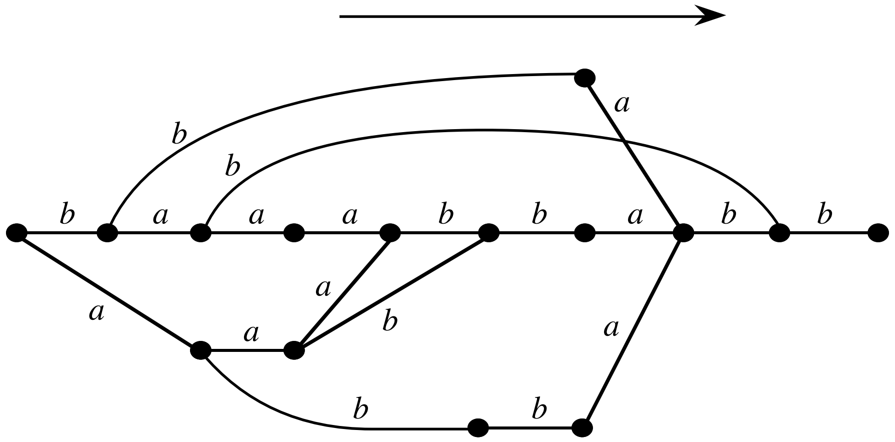


**Figure 6.5**. The suffix dawg of *baaabbabb*.

The proof of the previous statement shows how the dawg *DAWG*(*text*) can be built. The role of the end marker in the preceding proof is allow the suffix tree construction. Whenever it is removed in the data structure produces the same graph. In particular, the algorithm of the proof cannot be directly used to build the smallest subword graph accepting *Fac*(*text*), in the sense of automata theory. We do not consider these graphs because their on-line construction is more technical than that of suffix dawg given in the next section.

## 6.3. On-line construction

We describe in this section an on-line linear time algorithm for suffix dawg computation. The algorithm processes the text from left to right. At each step, it reads the next letter of the text and updates the dawg built so far. In the course of the algorithm, two types of edges in the dawg are considered : solid edges (bold ones in Figure 6.6), and non-solid edges. The solid edges are those contained in longest paths from the root. In other terms, non-solid edges are those creating shortcuts in the dawg. The adjective *solid* means that once these edges are created, they are not modified during the rest of the construction. On the contrary, the target of non-solid edges may change after a while.

In Algorithm *suffix-dawg* we compute successively *DAWG*(*text*[1]), *DAWG*(*text*[1…2]), ..., *DAWG*(*text*[1…*n*]). Figures 6.6 and 6.7 show an application of the algorithm to *text* = *aabbab*.

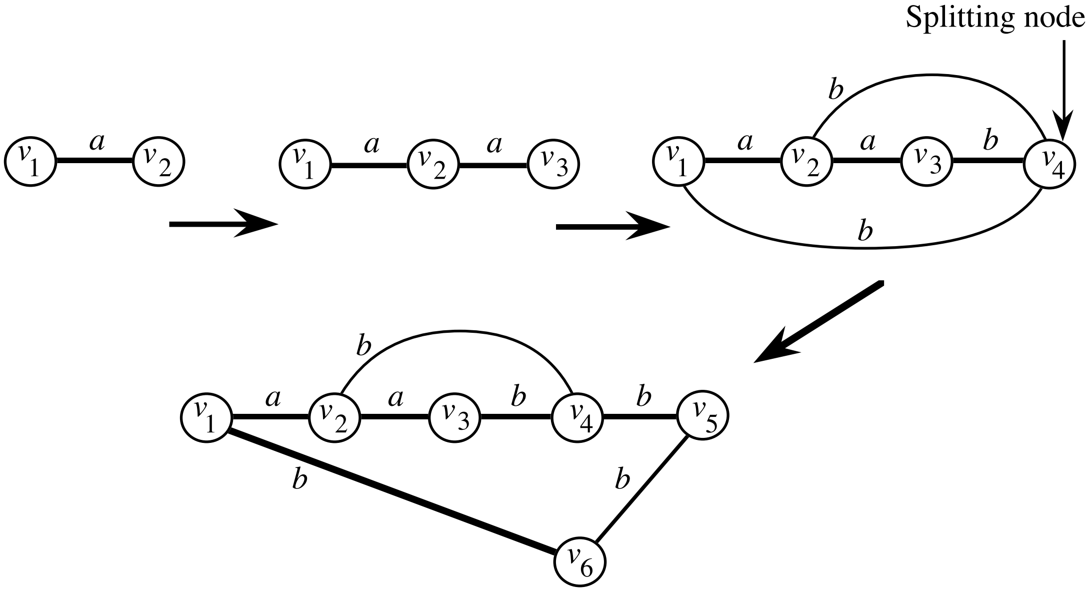


**Figure 6.6**. Iterative computation of *DAWG*( *aabb*).
Solid edges are bold faced.

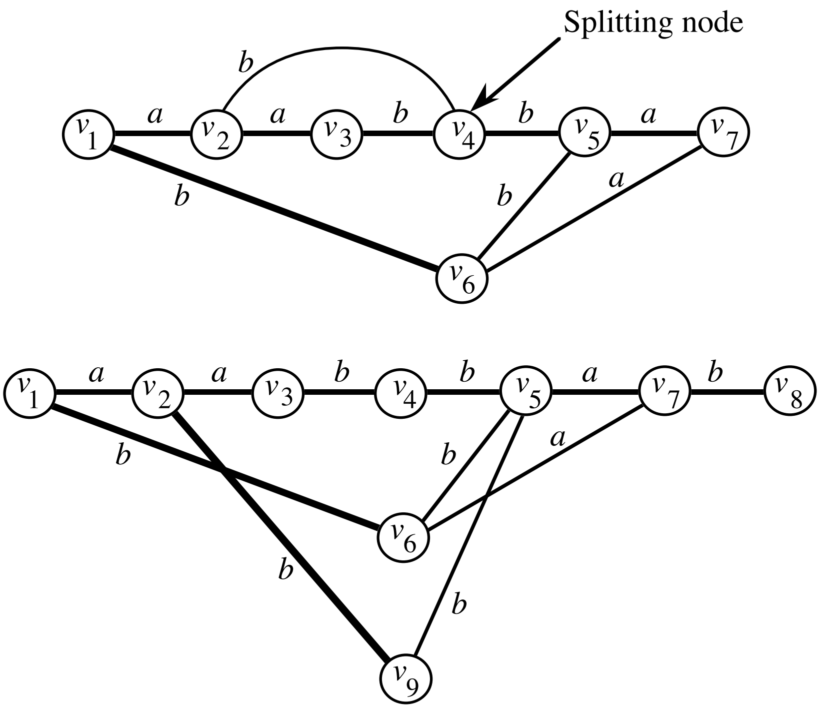


**Figure 6.7**. Transformation of *DAWG*(*aabba*) into *DAWG*(*aabbab*).
The node $v_9$ is a clone of $v_4$.

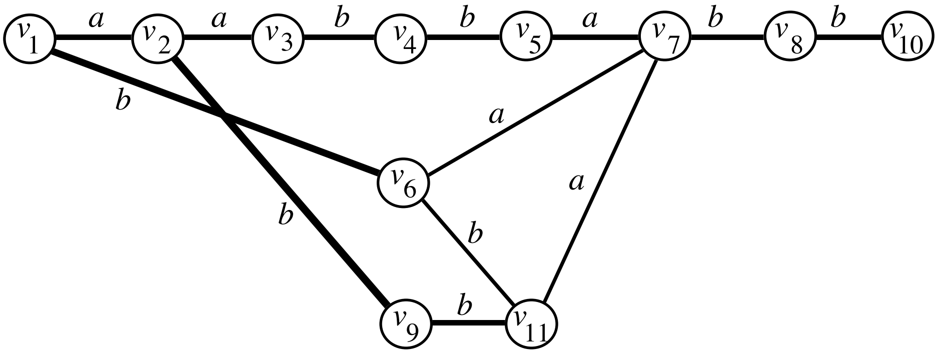


**Figure 6.8**. The suffix dawg of *aabbabb*.

The schema of one stage of the algorithm is graphically presented in Figure 6.7. It is the transformation of *DAWG*(*aabba*) into *DAWG*(*aabbab*), which points out a crucial operation of the algorithm. Addition of letter *b* to *aabba* adds new factors to the set *Fac*(*aabba*). They are all suffixes of *aabbab*. In *DAWG*(*aabba*), nodes corresponding to suffixes of *aabba*, namely, *v*1, *v*2, *v*7, will now have an outgoing *b*-edge. Consider node *v*2 in *DAWG*(*aabba*) . It has an outgoing non-solid *b*-edge. The edge is a shortcut between *v*2 and *v*4, compared with the longest path from *v*2 to *v*4 which is labelled by *ab*. The two factors *ab* and *aab* are associated to the node *v*4. But in *aabbab*, only *ab* becomes a suffix, not *aab*. This is the reason why the node *v*4 is split into *v*4 and *v*9 in *DAWG*(*aabbab*). Doing so will cause no problem for the rest of the construction, if ever *v*4 and *v*9 get different behaviors. But note that the splitting operation is not necessary if the text ends here, because nodes *v*4 and *v*9 of *DAWG*(*aabbab*) have the same outgoing edge.

When splitting a node, it may also happen that some edges have to be re-directed to the created node. The situation is illustrated in Figure 6.8 by *DAWG*(*aabbabb*). In *DAWG*(*aabbab*), the node *v*5 corresponds to factors *bb*, *abb*, and *aabb*. In *aabbabb*, just *bb* and *abb* are suffixes. Hence, in *DAWG*(*aabbabb*), paths labelled by *bb* and *abb* should reach the node *v*11, a clone of node *v*5 obtained by the splitting operation.

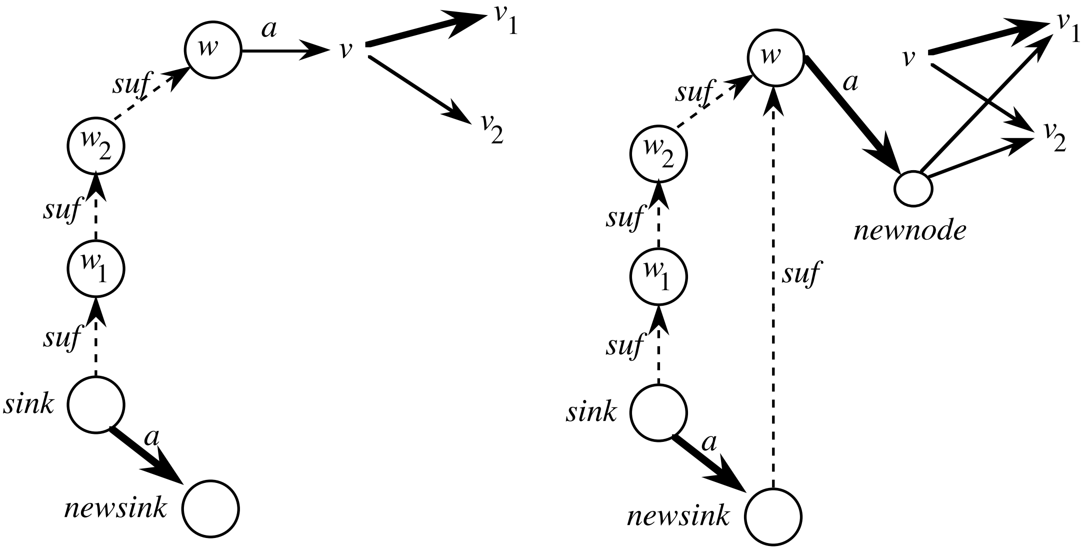


**Figure 6.9**. One stage of the algorithm, with the current letter *a*. The non-solid *a*-edge from *w* is transformed into a solid edge onto a clone of *v*.

In the algorithm, we denote by *son*(*w*, *a*) the son *v* of node *w* such that *label*(*w*, *v*)=*a*. We assume that *son*(*w*, *a*)=*nil* if there is no such node *v*.

On nodes of *DAWG*(*text*) is defined a suffix link called *suf*. It makes lists of *working paths* as shown in Figure 6.9. There, the working path is *w*1, *w*2=*suf*[*w*1], *w*3=*suf*[*w*2], *w*=*suf*[*w*3]. Generally, the node *w* is the first node on the path having an outgoing edge (*w*, *v*) labelled by letter *a*. If this edge is non-solid, then *v* is split into two nodes : *v* itself, and *newnode*. The latter is clone of node *v*, in the sense that outgoing edges and the suffix-pointer for *newnode* are the same as for *v*. The suffix link of *newsink* is set to *newnode*. Otherwise, if edge (*w*, *v*) is solid, the only action made at this step is to set the suffix link of *newsink* to *v*.

```
Algorithm suffix-dawg;
begin
  create the one-node graph G = DAWG(ε);
  root := sink := the node of G; suf[root] := nil;
  for i := 1 to n do begin
    a := text[i];
    create a new node newsink;
    make a solid edge (sink, newsink) labelled by a;
    w := suf[sink];
    while (w≠nil) and (son(w, a)=nil) do begin
      make a non-solid a-edge (w, newsink); w := suf[w];
    end;
    v := son(w, a);
    if w=nil then suf[newsink] := root
    else if (w, v) is a solid edge then suf[newsink] := v
    else begin { split the node v }
      create a node newnode;
      newnode has the same outgoing edges as v
      except that they are all non-solid;
      change (w, v) into a solid edge (w, newnode);
      suf[newsink] := newnode;
      suf[newnode] := suf[v]; suf[v]:=newnode;
      w := suf[w];
      while (w≠nil) and ((w, v) is a non-solid a-edge) do begin
      {*} redirect this edge to newnode; w :=suf[w];
      end;
    end;
    sink:=newsink;
  end;
end.
```

**Theorem 6.4**

Algorithm *suffix-dawg* computes *DAWG*(*text*) in linear time.

**Proof**

We estimate the complexity of the algorithm. We proceed similarly as in the analysis of the suffix tree construction. Let $sink_i$ be the sink of *DAWG*(*text*[1…*i*]). What we call the working path consists of nodes *w*1=suf[*sink*], *w*2=*suf*[*w*1] … *w*=*suf*[$w_k$]. The complexity of one iteration is proportional to the length $k_1$ of the working path plus the number $k_2$ of redirections made at step (*) in the algorithm. Let $K_i$ be the value of $k_1+k_2$ at the $i$-th iteration. Let *depth*($u$) be the depth of node $u$ in the graph of suffix links corresponding to the final dawg (the depth is the number of applications of *suf* needed to reach the root). Then, the following inequality can be proved (we leave it as an exercise):

$$depth(sink_{i+1}) \leq depth(sink_i) - K_i + 2,$$

and this implies

$$K_i \leq depth(sink_i) - depth(sink_{i+1}) + 2.$$

Hence, the sum of all $K_i$'s is linear, which in turn implies that the total time complexity is linear. This completes the proof that the algorithm works in linear time. ‡

**Remark 1**

Algorithm *suffix-dawg* gives another proof that the number of nodes of *DAWG*(*text*) is less than 2|*text*| : at each step $i$ of the algorithm at most 2 nodes are created, except at step 1 and 2 where only one node is created.

**Remark 2**

We classify edges of *DAWG*(*text*) into solid and non-solid ones. Such classification is an important feature of the algorithm, used to know when a node has to be split. However, we can avoid remembering explicitly whether an edge is solid or not. The category of an edge can be tested from the value *length*($v$) associated to node $v$. This information happens to be useful for other purposes. We can store in each node $v$ the length *length*($v$) of the longest path from the root to $v$. Then, the edge ($v$, $w$) is solid iff $|length(v)|+1=|length(w)|$. Function *length* plays a central role in the algorithm of the next section.

## 6.4.* Further relations between suffix trees and suffix dawg's

There is a very close relation between our two "good" representations for the set of factors *Fac*(*text*). This is an interesting feature of these data structures. The relation is intuitively obvious because suffix trees and dawg's are compacted versions of the same object — the uncompacted tree *Trie*(*text*).

Throughout this section (with a short exception) we assume that the pattern *text* starts with a symbol occurring only at the beginning of *text*. In this case the relation between dawg's and suffix trees is especially tight and simple.

**Remark**

The uniqueness of the leftmost symbol is not the crucial point for the relation between dawg's and suffix trees. Even if the leftmost symbol is not unique our construction essentially can be applied. However, the uniqueness case is easier to deal with in the framework of suffix and factor automata.

Two factors of *text*, $x$ and $y$, are equivalent iff their *end-pos* sets are equal. This means that one of the word is a suffix of the other (say $y$ is a suffix of $x$) and whenever $x$ appears then $y$ also appears in *text*. However, what happens if instead of *end-pos*itions we consider start-positions? Let us look from the "reverse perspective" and look at the reverse of the pattern. Then suffixes become prefixes, and end-positions become first-positions. Denote by *first-pos*($x$) the set of first positions of occurrences of $x$ in *text*.

Recall that a chain in a tree is a maximal path whose nodes have out-degree one except the last one. The following obvious lemma is crucial in understanding the relation between suffix trees and dawg's (see figure below):

**Lemma 6.5**

Assume that *text* has a unique leftmost symbol. Then the following three equalities are equivalent :

*end-pos*($x$)=*end-pos*($y$) in *text*;

*first-pos*($x^R$)=*first-pos*($y^R$) in *text*$^R$ ;

$x^R$, $y^R$ are contained in the same chain of the uncompacted tree *Trie*(*text*$^R$).

**Remark**

The first two equalities in the lemma are always true, however the third one can be damaged if text starts with a non-unique symbol. If *text*=*abba* then *text*=*text*$^R$ and the nodes $a$, $ab$ are contained in the same chain. However, *first-pos*($a$)={1, 4} but *first-pos*($ab$)={1}. Fortunately with a unique leftmost symbol such a situation is impossible.

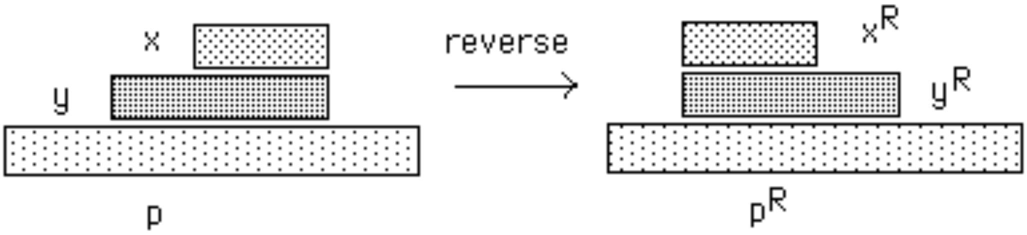


**Figure 6.10**. When the text has a unique leftmost symbol :
*end-pos*($x$)=*end-pos*($y$) in *text* iff *first-pos*($x^R$)=*first-pos*($y^R$) in *text*$^R$
iff $x^R$, $y^R$ are contained in the same chain of the uncompacted tree *Trie*(*text*$^R$).

**Corollary 6.6**

The reversed values of nodes of the suffix tree $T(text^R)$ are the longest representatives of equivalence classes of factors of *text*. Hence nodes of $T(text^R)$ can be treated as nodes of *DAWG*(*text*).

We consider first the relation : suffix trees → dawg's. Let *T* be a suffix tree. We define shortest extension links (*sext* links, in short) in *T*, dented by *sext*[*a*, *v*]. The value of *sext*[*a*, *v*] is the node *w* whose value *y*=*val*(*w*) is a shortest word having prefix *ax*, where *x*=*val*(*v*). If there is no such node *w* then *sext*[*a*, *v*]=*nil*. Observe that *sext*[*a*, *v*]≠*nil* iff *test*[*a*, *v*]=true. If *link*[*a*, *v*]≠*nil* then *sext*[*a*, *v*]=*link*[*a*, *v*].

**Lemma 6.7**

If we are given a suffix tree *T* with tables *link* and *test* computed then table *sext* can be computed in linear time.

**Proof**

The algorithm is top down. For the root sext links are easy to compute. If table *sext* was computed for entries related to *v*1=*father*(*v*) then for each symbol a the value of *sext*[*a*, *v*] is computed in constant time as follows :

```
    if test[a, v]=false then sext[a, v]:=nil else
    if link[a, v1]=nil then sext[a, v]:=sext[a, v1] else
    sext[a, v]:=the son w of link[a, v1] such that the label of edge from link[a, v1] to w has
the same first symbol as label of edge (v1, v).
```

The whole computation takes linear time because it takes constant time for each pair (*a*, *v*). This completes the proof. ‡

**Remark**

In fact, we could easily modify the algorithm for the construction of suffix trees by removing table test and replacing tables link and test by a more powerful table *sext*. Table *sext* contains essentially the same information as tables link and test together. This could improve the space complexity of the algorithm (by a constant factor). Time complexity does not change much. We leave as an easy exercise a suitable modification of the algorithm.

However we feel that tables link and test make the algorithm easier to understand. Moreover as we shall see later table link gives solid edges of the dawg for reversed pattern and table *sext* (in cases when link has value *nil*) gives non-solid edges. Also in applications it is better to have choice of several alternative data structures.

The figure below presents the uncompacted suffix tree for the text *text*=*babaad*.

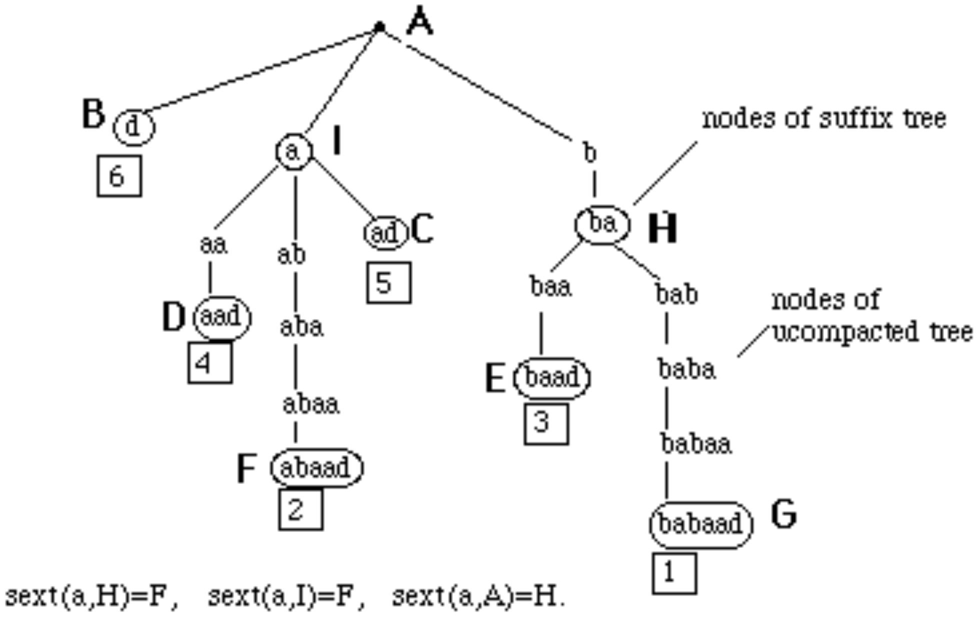


**Figure 6.11**. The uncompacted node-labelled tree $T1(text)$ for *text*=*babaad*. The nodes of the suffix tree are circled. For example *sext*[*a*, H] is the shortest extension of a word $x$ = (*a val*(H)), it is the node F such that $x$ is a prefix of *val*(F).

The next figure presents the uncompacted suffix tree from the "reverse perspective". The equivalence classes of words of the text of *text*$^R$=*daabab* are circled.

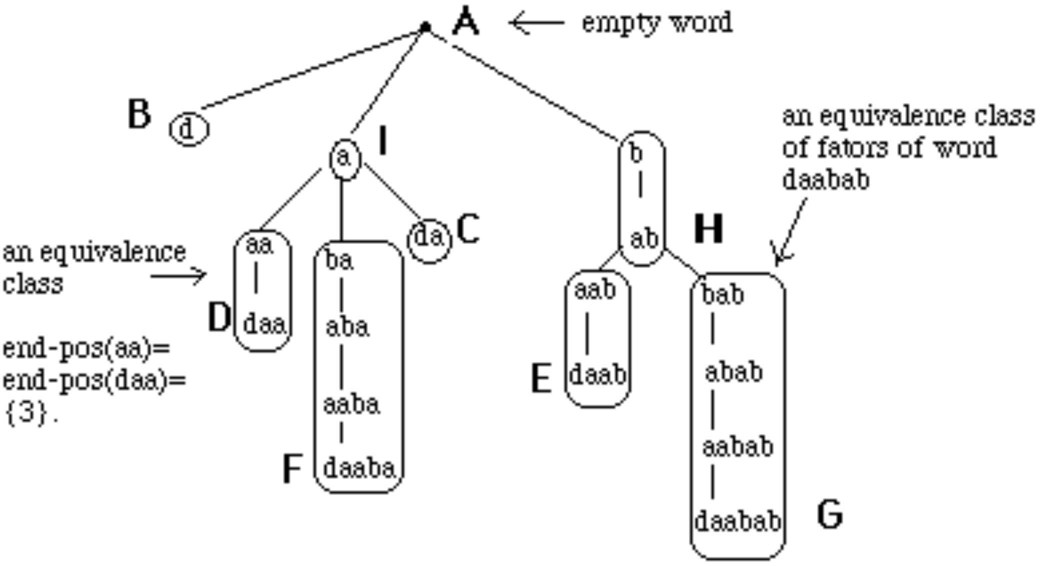


**Figure 6.12**. The previous uncompacted subword tree with the values of nodes reversed.

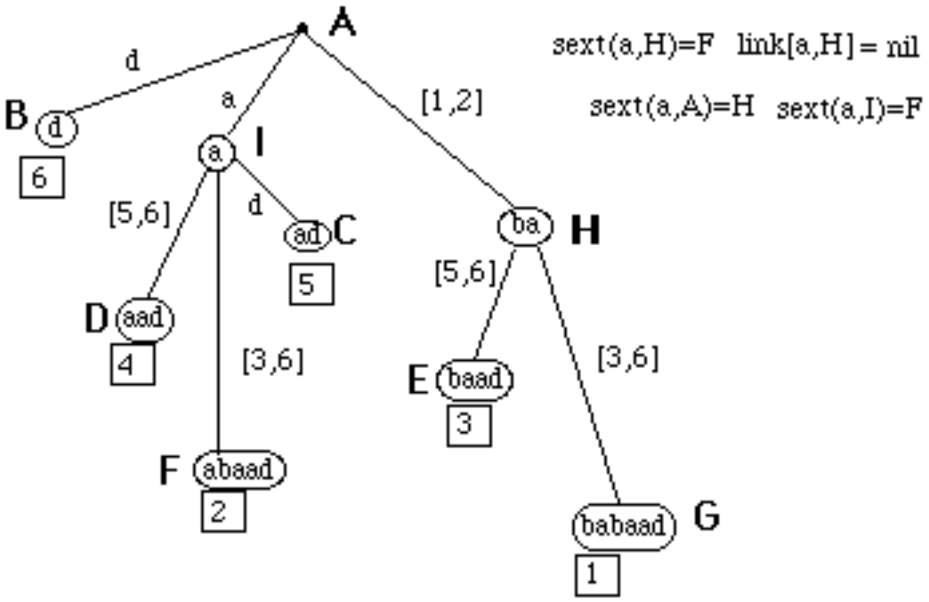


**Figure 6.13**. The suffix tree *T*(*babaad*) with examples of sext links.

**Theorem 6.8**

If *text* has the unique leftmost symbol then *DAWG*(*text*) equals the graph of sext links of suffix tree *T*=*T*($text^R$). Solid edges of the dawg of *text* are given by table *link* of *T*.

**Proof**

The thesis follows directly from the preceding lemma. The corollary from the lemma says that nodes of the dawg correspond to nodes of *T*. In the dawg for *text* the edge labelled *a* goes from the node *v* with *val*(*v*)=*x* to node *w* with *val*(*w*)=*y* iff *y* is the longest representative of the class of factors which contain word *xa*. If we consider the reversed text then it means that $ax^R$ is the longest word $y^R$ such that *first-pos*($y^R$)=*first-pos*($ax^R$) in $text^R$. This exactly means that $y^R$ =*sext*[*a*, $x^R$]. $|y^R|$=$|x^R|$+1 iff *y*=*xa* and *link*[*a*, $x^R$]=$y^R$. According to the remark ending the previous section this means that table link gives exactly all solid edges.

This completes the proof. ‡

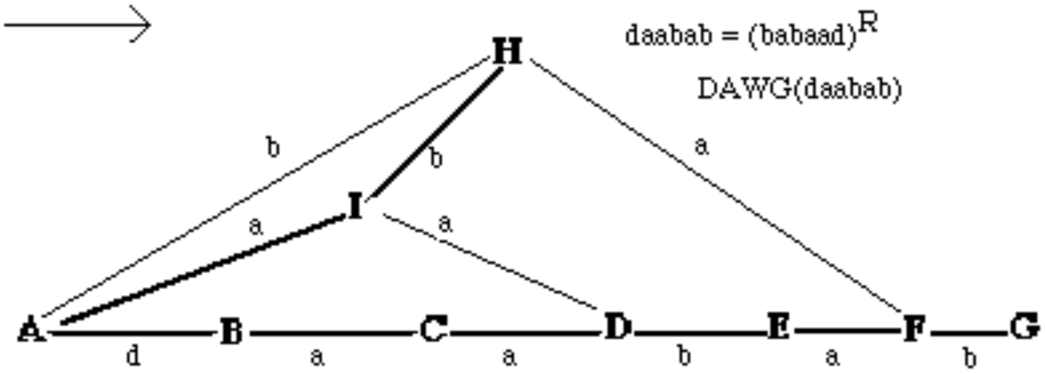


**Figure 6.13**. *DAWG*(daabab) = graph of sext links of *T*(babaad).
Solid edges are given by table link of *T*( *babaad*).

**Remark**

If one wants to construct a dawg using suffix trees and the string *text* does not start with the left marker then we can take the string *p*' = *dp* which has a left marker *d*. After constructing the dawg for *p*' we simply erase the first edge labelled *d* and delete the nodes inaccessible from the root. The first edge leading to a node of the old longest path becomes solid. The transformation of the dawg from Figure 6.13 is shown below.

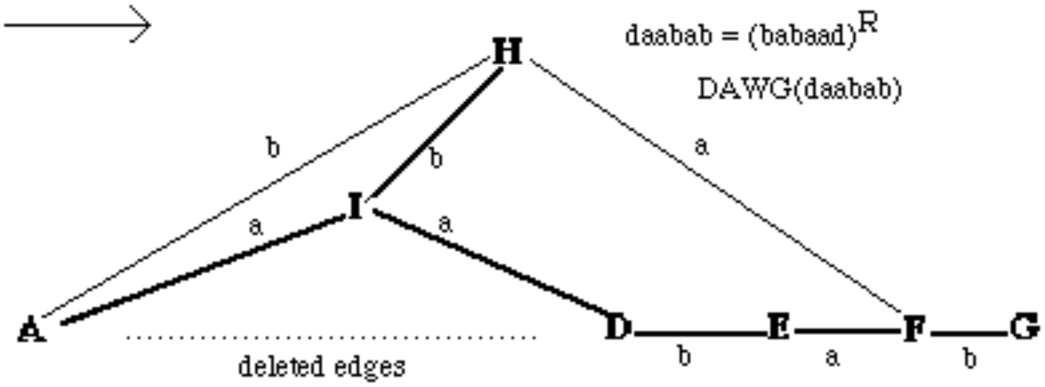


**Figure 6.14**. *DAWG*(*aabab*) results from *DAWG*(*daabab*), see Figure 6.13.
The edge labelled *d* is removed. Then nodes inaccessible from the root are deleted :
A and B are deleted. Edge (I, D) becomes solid.

Let us deal now with the relation : dawg's → suffix trees. An unexpected property of the dawg construction algorithm is that it computes also the suffix tree of the reversed text if *text* starts with a symbol occurring only at the first position (see Figure 6.15).

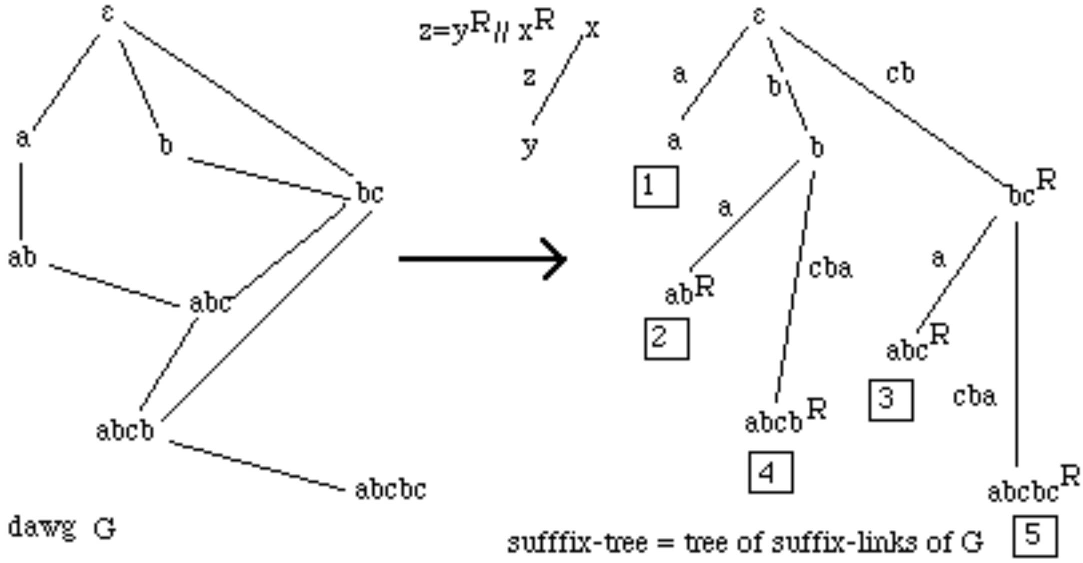


**Figure 6.15**. Tree of suffix-links of *DAWG*( *abcbc*) = suffix tree *T*(*cbcba*).
If text *text* start with the symbol occurring only at first position then the graph of suffix-links of *DAWG*(*text*) gives the suffix tree *T*(*text*$^R$).
We give values of nodes of the dawg and labels of edges of the suffix tree.
Hence the dawg construction gives also an alternative algorithm to construct suffix trees.

Given the dawg *G* of text *text* we can easily obtain the suffix tree for the reverse of *text*. Let *T* be a tree of suffix links of *G*; *suf*[*v*] is the father of *v*. The edge (*v*, *suf*[*v*]) is labelled by the word $z=y^R//x^R$, where $x=val(suf[v]$, $y=val(v)$. The operation // consists of cutting the prefix *x* of *y*. $z=y^R//x^R$ iff $y^R=x^Rz$. This operation is well defined in the context ($y=val(v)$, $x=val(suf[v])$). The tree *T* is called the tree of suffix links. This tree is automatically constructed during the computation of *DAWG*(*text*).

**Theorem 6.9**

If *text* starts with a unique leftmost symbol then the tree of suffix links of *DAWG*(*text*) equals the suffix tree *T*(*text*$^R$).

**Proof**

The same arguments as in the proof of the previous theorem can be applied. ‡

**Remark**

There is a functional symmetry between suffix tree and dawg's : essentially they have the same range of applications. They are closely related : the structure of one of them is "contained" in the structure of the other. However one of these data structures is a tree while the other is not. As it was written in [CS 85] : it is remarkable that such functional symmetry is efficiently achieved by such an integrated asymmetric construction.

From the point of view of applications the dawg can be compressed. This will result in a considerable saving in space. Such compression allows to see a relation between $G=DAWG(text)$ and $G'=DAWG(text^R)$. It is also possible to make a symmetric version of a dawg : a good data structure *SymRep*(*text*) which can efficiently represent simultaneously *Fac*(*text*) and *Fac*($text^R$).

Let us look at a relation between $G$ and $G'$. Take the example text *text*=*aabbabd*. Then $G$ is as presented in Figure 6.1 and it has 10 nodes. The graph $G'$ is presented in Figure 6.17 and it has 11 nodes.

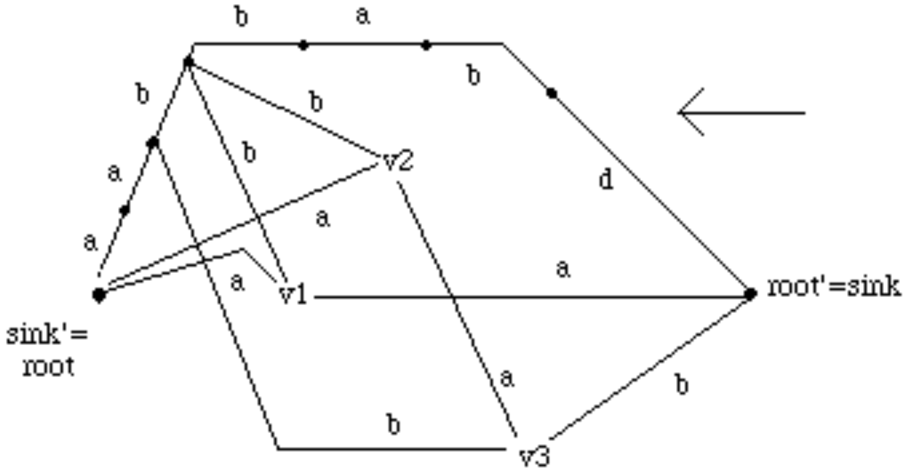


**Figure 6.17**. The graph $G'=DAWG(text^R)$.
There are three nodes of out-degree greater than 1 (edges go right-to-left).

At first sight it is hard to see any relation between $G$ and $G'$. Let *root* and *sink* be the names of the root and the sink of $G$, and let *root*', *sink*' be the root and the sink of $G'$. We have *root*=*sink*' and *sink*=*root*' (we can call these nodes external, while other nodes can be called internal). Let us look at internal nodes with out-degree bigger than one. Call such nodes essential. There are three essential nodes $v1$, $v2$, $v3$ in $G$ and also three essential nodes in $G'$. It happens that there is a one-to-one correspondence between these nodes. Let values of nodes in $G'$ be words spelled right-to-left (words from the "reverse perspective"). Then we have the same set of values of essential nodes in $G$ and that in $G'$. We leave the general proof of this fact to the reader. We can identify internal nodes of $G$ and $G'$. Now we define the compressed versions of *G* and *G*' to be graphs consisting only of essential and external nodes (all other nodes disappear by compressing chains). Hence the compressed versions are two graphs with the same set of nodes. Therefore these graphs can be combined (by taking union of edges of both graphs) and we get a labelled graph which is a symmetric representation *SymRep*(*text*). There will be two kinds of edges in such graph : left-to-right and right-to-left edges. *SymRep* is a good representation of *Fac*(*text*) and satisfies : *SymRep*(*text*)=*SymRep*(*text*$^R$).

More precisely : a compressed version *compr*(*G*) of the dawg *G* is the graph whose nodes are essential (internal) and external nodes of *G*. The graph *compr*(*G*) results by compressing all chains of *G* - each internal node of out-degree one is removed and its incoming edges are redirected. Figures 6.18 and 6.19 show the compressed versions of dawg's for the word *aabbabd* and its reverse. The nodes of *compr*(*G*) correspond to so called prime factors, see [BBHME 87], page 580, for a definition. Intuitively these are factors that appear in two distinct left contents (if extendable to the left) and two distinct right contexts (if extendable to the right).

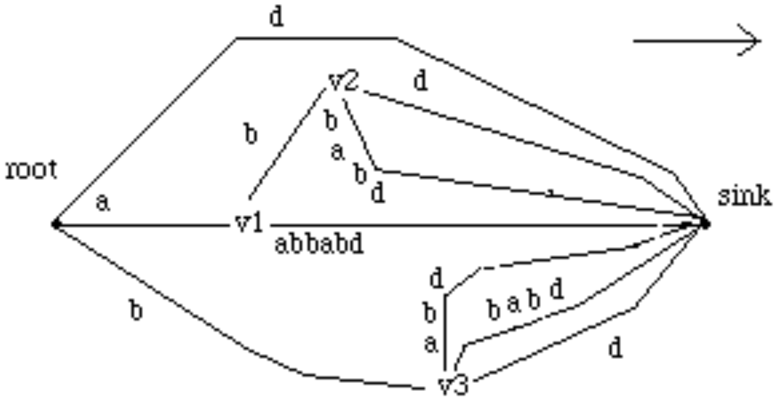


**Figure 6.18**. The graph compr(*G*) for *text*=*aabbabd*.

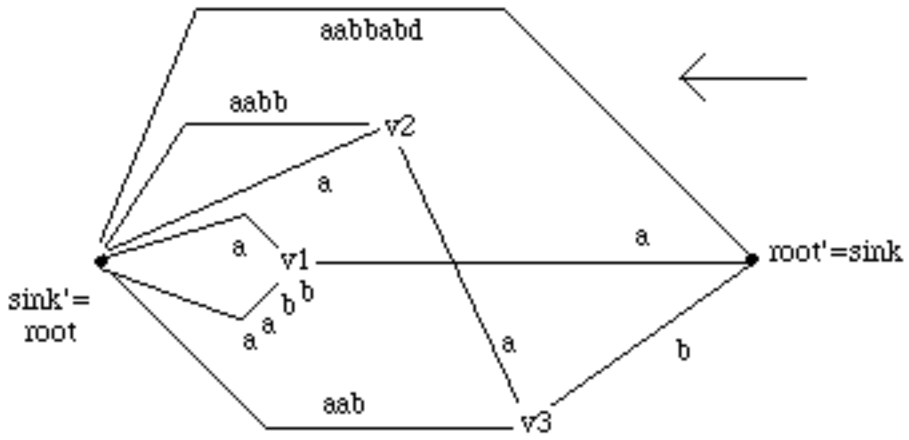


**Figure 6.19**. The graph *compr*(*G*') for $text^R$=*dbabbaa*. The direction of edges is right-to-left. The labels of edges are to be read also right-to-left. *SymRep*(*text*) = *compr*(*G*')□∪*compr*(*G*).

The constructed data structure can be used to "travel" in the dawg in two directions. We can find some useful information for the factor *x*, then for its left extension *ax*, and then for the right extension *axb*.

## 6.5. String-matching using suffix dawg's

In this section, we describe two other string-matching algorithms. They apply the strategy developed in Chapter 3 and 4 respectively, but are based on suffix dawg's built on the pattern. For fixed alphabets, the first algorithm yields a real-time search, while the second searching algorithm is optimal on the average.

A simple application of subword dawg gives an efficient algorithm to compute the longest common factor of two strings. We have already discussed an algorithm for that purpose in Chapter 5. There, the solution is based on suffix trees. The present solution is quite different by several aspects. First, it computes the longest common factor while processing one of the two input words (a priori, the longer word) in an on-line way. Second, it uses the dawg of only one word (a priori, the shorter word), which makes the whole process cheaper according to the space used. The overall algorithm can be adapted from the string-matching algorithm presented below.

The first string-matching of the present section searches the text for factors of the pattern. It computes the longest factor of the pattern ending at each position in the text. It is called the *forward-dawg-matching* algorithm (*FDM* for short) because factors are scanned from left to right. The algorithm can be viewed as another variation of algorithm *MP* (Chapter 3). In this latter algorithm, the text is searched for prefixes of the pattern, and shifts are done immediately when a mismatch is found. We explain the principles of *FDM* algorithm.

Let *pat* and *text* be the two words. Let *DAWG*(*pat*) be the dawg of the pattern. The text is scanned from left to right. At a given step, let *p* be the prefix of *text* that has just been processed. Then, we know the longest suffix *s* of *p* which is a factor of *pat*, and we have to compute the same value associated to the next prefix *pa* of *text*. It is clear that *DAWG*(*pat*) can help to compute it efficiently if *sa* is a factor of *pat*. But, this is still true if *sa* is not a factor of *pat* because in this situation we can use the suffix link of the dawg in a similar as the failure function is used in *MP* algorithm (Chapter 3).

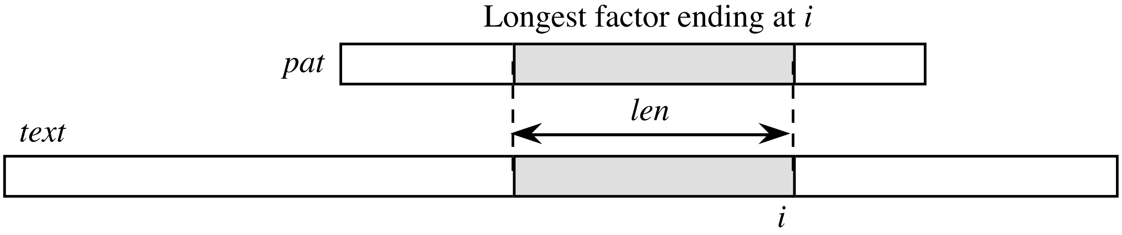


**Figure 6.20**. Current configuration in *FDM* algorithm.

In a current situation of the forward-factor algorithm, we memorize a state of *DAWG*(*pat*).
But, the detection of an occurrence of *pat* in *text* cannot be done only based on the state of *DAWG*(*pat*), because states are usually reachable through different paths. To cope with this problem, in addition to the current state of *DAWG*(*pat*), we compute the length *len* of the longest factor of *pat* ending at the present position in the *text*. When suffix links are used to compute the next factor, the algorithm resets the value of *len* with the help of the function *length* defined on states of *DAWG*(*pat*). Recall that *length*(w) is the length of the longest path form the root of *DAWG*(*pat*) to the node *w*. The next property shows why the computation of *len* is valid when going through a suffix link.

**Property of** *DAWG*(*pat*)

Let *x* be the label of any path from the root of *DAWG*(*pat*) to *w*.
Let *y* be the label of the longest path from the root of *DAWG*(*pat*) to *v*.
If *suf*[*w*] = *v*, the word *y* is a suffix of *x*.

The property is an invariant of the dawg construction of Section 6.3. Note that each time a suffix link is created in algorithm *suffix-dawg* the target of the suffix link is also the target of a solid edge. This is assumed by the splitting operation. So the proof follows by induction.

```
function FDM : boolean; { forward-dawg-matching algorithm }
{ it computes longest factors of pat occurring in text }
begin
  D := DAWG(pat);
  len := 0; w := root of D; i := 0;
  while not i≤|text| do begin
    if there is an edge (w, v) labelled by text[i] then begin
      len := len+1; w := v;
    end else begin
      repeat w := suf[w];
      until (w undefined) or
            (there is (w, v) labelled by text[i]);
      if w undefined then begin
        len := 0; w := root of D;
      end else begin
        let (w, v) be the edge labelled by text[i] from w;
        len := length(w)+1; w := v;
      end;
    { len = larger length of factor of pat ending at i in text }
      if len=|pat| then return(true);
      i := i+1;
  end;
  return(false);
end;
```

Algorithm *FDM* can still be improved. The modification is similar to the transformation of algorithm *MP* into algorithm *KMP*. It is done through a modified version of the failure function. The criterion to be considered is the delay of the search, that is, the time spent on a given letter of the text. Algorithm *FDM* has delay $O(|pat|)$ (consider the pattern $a^n$). The transformation of *FDM* is realized on the suffix link *suf* as explain below.

Assume that during the search the current letter of the text is *a* and the current node of the dawg is *w*. If no *a*-edge starts from *w*, then we would expect that some *a*-edge starts from v=*suf*[*w*]. But it happens that, sometimes, outgoing edges on *v* have the same label as outgoing edges on *w*. Then, node *v* does not play its presumed role in the computation, and *suf* has to be iterated at the next step. This iteration can in fact be preprocessed because it is independent of the text.

We define the context of node *w* of *DAWG*(*pat*) as the set of letters, which are labels of edges starting from *w* :

$$Context(w) = \{a \text{ ; there is an } a\text{-edge } (w, w') \text{ in } DAWG(pat)\}.$$

Then, the improved suffix link is *SUF* defined as (v=*suf*[*w*])

$$SUF(w) = v, \text{ if } Context(w) \neq Context(v),$$
$$SUF(w) = suf[v], \text{ otherwise.}$$

Note that *SUF*(*w*) can be left undefined with this definition because *suf*[*root*] is undefined).

In practice, for the computation of *SUF*, no context of node is indeed necessary. This is due to a special feature of dawg's. When v=*suf*[*w*], *Context*(*w*) is included in *Context*(*v*), because the value of *suf*[*w*] is a suffix of the value of *w*. Thus, tests to compute *SUF* can be made only on the sizes of context sets. The following is an equivalent definition of *SUF* :

$$SUF(w) = v, \text{ if } |Context(w)| \neq |Context(v)|,$$
$$SUF(w) = suf[v], \text{ otherwise.}$$

Then, computing *SUF* is done with a standard breadth-first exploration of *DAWG*(*pat*). Quantities |*Context*(*w*)| can be stored in each node during the construction of *DAWG*(*pat*), to help afterwards computing *SUF*.

It is clear that the number of time *SUF* can be applied consecutively is bounded by the size of the alphabet. This leads to the next theorem that summarized the overall.

**Theorem 6.10**

Algorithm *FDM* searches for *pat* in *text*, and computes longest factors of *pat* ending at each position in *text*, in linear time (on fixed alphabet). The delay of the search can be bounded by $O(|A|)$.

**Proof**

The correctness comes from the discussion above. If we modify the algorithm *FDM*, replacing *suf* by *SUF*, then the delay of the new algorithm is obviously $O(|A|)$. ‡

We now present the second string-searching of the section. It is called *backward-dawg-matching* algorithm (*BDM* for short), and is somehow a variant of *BM* algorithm (Chapter 4). Algorithm *BM* searches for a suffix of the pattern *pat* at the current position of the text *text.* In *BDM* algorithm we search for a factor *x* of *pat* ending at the current position in the text. Shifts use a pre-computed function on *x*.

The advantage of the approach is to produce an algorithm very fast on the average, not only on large alphabets, but also for small alphabets. The strategy of *BDM* algorithm is more "optimal" than that of *BM* algorithm: the smaller the cost of a given step, the bigger the shift. In practice, on the average, the match (and the cost) at a given iteration is usually small, hence, the algorithm, whose shifts are reversely proportional to local matches, is close to optimal. If the alphabet is of size at least 2, then the average time complexity of *BDM* algorithm is $O(n \log(m)/m)$. This reaches the lower bound for the problem. It is however quadratic in the worst case. But, rather standard techniques, as those applied on *BM* algorithm (see Chapter 4) lead to an algorithm that is both linear in the worst case and optimal on the average.

Algorithm *BDM* makes a central use of the dawg structure. The current factor $x$ of *pat* found in *text*, is identified with the node corresponding to $x^R$ in *DAWG*($pat^R$). We use the reverse pattern because we scan the window on the text from right to left. A constant-sized memory is sufficient to identify $x$. On the current letter $a$ of the text, we further try to match $ax$ with a factor of *pat*. This just remains to find an $a$-edge in *DAWG*($pat^R$) from the current node. If no appropriate $a$-edge is found, a shift occurs.

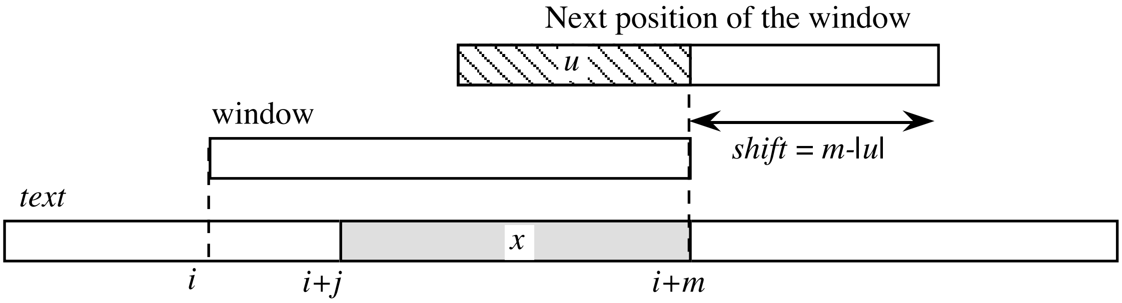


**Figure 6.21**. One iteration of Algorithm *BDM*.
Word $x$ is the longest factor of *pat* ending at $i+m$.
Word $u$ is the longest prefix of the pattern that is a suffix of $x$.

```
Algorithm BDM; { backward-dawg-matching algorithm }
{ use the suffix dawg DAWG($pat^R$) }
begin
  i := 0;
  while $i \le n-m$ do begin
    j:=m;
    while j>1 and text[i+j..i+m]∈Fac(pat) do j:=j-1;
    if j = 0 then report a match at position i;
    shift := BDM_shift[node of DAWG($pat^R$)];
    i := i+shift;
  end;
end.
```

We add to each node of *DAWG*($pat^R$) an information telling whether words corresponding to that node are suffixes of the reversed pattern $pat^R$ (i.e. prefixes of *pat*). We traverse this graph when scanning the text right-to-left in *BDM* algorithm. Let again $x$ be the longest word which is a factor of *pat*, found at a given iteration. The time spent to scan $x$ is proportional to $|x|$. The multiplicative factor is constant if a matrix representation is used for transitions in the data structure. Otherwise, it is $O(\log|A|)$ (where $A$ can be restricted to the pattern alphabet), which applies for arbitrary alphabets.

We now define the shift *BDM_shift*. Let $u$ be the longest suffix of $x$ which is a proper prefix of the pattern *pat*. We can assume that we always know the current value of $u$. It is associated to the last node on the scanned path in *DAWG*(*pat*) corresponding to a suffix of $pat^R$. Then, the shift *BDM_shift*[$x$] is $m$-$|u|$ (see Figure 6.21).

The expected time complexity of *BDM* algorithm is given in the next statement. We analyze the average running time of *BDM* algorithm, considering the situation when the text is random. The probability that a specified letter occurs at any position in the text is $1/|A|$, independently of the position of the letter.

**Theorem 6.11**

Let $c = |A| > 1$. Under independent equiprobability condition, the expected number of inspections done by *BDM* algorithm is $O((n/\log_c m)/m)$.

**Proof**

We first count the expected number of symbol inspections necessary to shift the pattern $m/2$ places to the right. We show that $O(\log_c m)$ inspections are sufficient to achieve that goal. Since there are $2n/m$ segments of text of length $m/2$, we get the expected time $O((n\backslash\log_c m)/m)$.

Let $r = 3.\lfloor\log_c m\rfloor$. There are more than $m^3$ possible values of the suffix *text*[$j$-$r$…$j$]. But, the number of subwords of length $r$+1 ending in the right half of the pattern is at most $m/2$ (provided $m$ is large enough). The probability that *text*[$j$-$r$…$j$] matches a subword of the pattern, ending in its right half, is then $1/(2m^2)$. This is also the probability that the corresponding shift has length less than $m/2$. In this case, we bound the number of inspections by $m(m/2)$ (worst behavior of the algorithm making shifts of length 1). In the other case, the number of inspections is bounded by $3.\log_c m$.

The expected number of inspections that lead to a shift of length at least $m/2$ is thus less than

3.log$_c$ $m$ (1-**Error!**) + $m$($m$/2) **Error!**;,

which is $O(\log_c m)$. This achieves the proof. ‡

Theorem 6.11 shows that *BDM* algorithm realizes an optimal search of the pattern in the text when branching in the dawg takes constant time. However, the worst-case time of search can be quadratic.

To speed up *BDM* algorithm we use the prefix-memorization technique. The prefix $u$ of size *m-shift* of the pattern (see Figure 6.22) that matches the text at the current position is kept in memory. The scan, between the part $v$ of the pattern and the part of the text align with it (Figure 6.22), is done from right to left. When we arrive at the boundary between $u$ and $v$ in a successful scan (all comparisons positive), then, we are at a *decision point***.** Now, instead of scanning $u$ until a mismatch is found, we need only scan (again) a part of $u$, due to combinatorial properties of primitive words. The part of $u$ which is scanned again in the worst case has size *period*($u$) The crucial point is that if we scan successfully $v$ and the suffix of $u$ of size *per*(*u*) then we know what shift to do without any further calculation: many comparisons are saved precisely at this moment, and this speeds up *BDM* algorithm.

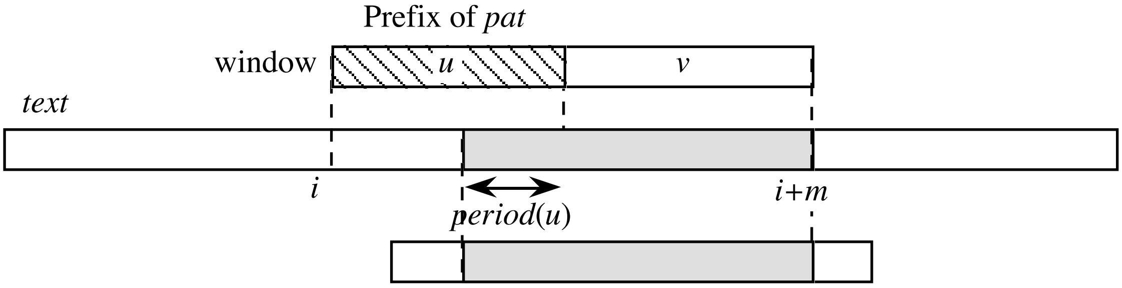


**Figure 6.22**. Prefix memorization (*u* prefix of *pat*). At most *period*(*u*) symbols of *u* are scanned again. However, this extra work is amortized by next shifts. The symbols of *v* are scanned for the first time.

```
Algorithm Turbo_BDM;
{ linear-time backward-dawg-matching algorithm }
begin
  i := 0; u := empty;
  while $i \le n-m$ do begin
    j := m;
    while $j>|u|-period(u)$ and $text[i+j..i+m] \in Fac(pat)$ do
      j := j-1;
    if $j=|u|-period(u)$ and $text[i+j..i+m]$ suffix of pat
    then report a match at position i;
    shift := BDM_shift(x);
    i := i+shift; u := prefix of pattern of length m-shift;
  end;
end.
```

The proof of *Turbo_BDM* algorithm essentially relies on the next lemma. It is stated with the notion of *displacement* of factors of *pat*, which is incorporated in *BDM* shifts. If $y \in Fac(pat)$, we denote by *displ*(*y*) the smallest integer *d* such that $y = pat[m\text{-}d\text{-}|y|+1..m\text{-}d]$ (see Figure 6.23).

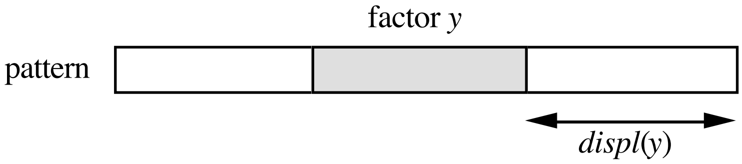


**Figure 6.23**. Displacement of factor *y* in the pattern.

**Lemma 6.12** (key lemma)

Let *u*, *v* be as in Figure 6.22. Let *z* be the suffix of *u* of length *period*(*u*), and let *x* be the longest suffix of *uv* that belongs to *Fac*(*pat*). Then

$$zv \in FACT(p) \text{ implies } BDM\_shift(x)=displ(zv).$$

**Proof**

It follows from the definition of *period*(*u*), as the smallest period of *u*, that *z* is a primitive word. The primitivity of *z* implies that occurrences of *z* can appear from the end of *u* only at distances which are multiples of *period*(*u*). Hence, *displ*(*zv*) should be a multiple of *period*(*u*), and this easily implies that the smallest proper suffix of *uv* which is a prefix of *pat* has size |*uv*|-*displ*(*zv*). Hence the next shift executed by the algorithm, *BDM_shift*(*x*), should have length *displ*(*zv*). This proves the claim. ‡

The transformation of *BDM* algorithm into *Turbo_BDM* algorithm can be done as follows. The variable *u* is specified by only one pointer to the text. The values of displacements are incorporated in the data structure *DAWG*(*pat*), and similarly the values of periods *period*(*u*) for all prefixes of the pattern can be precomputed and stored in *DAWG*(*pat*). In fact, the table of periods can be removed and values of *period*(*u*) can be computed dynamically inside *Turbo_BDM* algorithm using constant additional memory. This is quite technical and omitted here.

**Theorem 6.13**

On a text of length *n*, *Turbo_BDM* algorithm runs in linear time (for a fixed alphabet). It makes at most 2*n* inspections of text symbols.

**Proof**

In *Turbo_BDM* algorithm at most *period*(*u*) symbols of factor *u* are scanned. Let *extra_cost* be the number of symbols of *u* scanned at the actual stage. Since the next shift has length at least *period*(*u*), *extra_cost* ≤ *next_shift*. Hence, all extra inspections of symbols are amortized by the total sum of shifts, which gives together at most *n* inspections. The symbols in parts *v* (see Figure 6.22) are scanned for the first time at a given stage. These parts are disjoint in distinct stages. Hence, they give together at most *n* inspections too. The work spent inside segments *u*, and inside segments *v* altogether is thus bounded by 2*n*. This completes the proof. ‡

## Bibliographic notes

Probably the most impressive fact of the chapter is the linear size of dawg's first discovered by Blumer, Blumer, Ehrenfeucht, Haussler, and McConnell [BBEHC 83]. They have simultaneously designed a linear time algorithm for the construction of dawg's. After marking nodes of the dawg associated to suffixes of the text as terminal states, it becomes an automaton recognizing the suffixes of the text. In fact, this is even the minimal automaton for the set of suffixes of the text. This point is discussed in [Cr 85] where it is also given an algorithm to built the minimal automaton recognizing the set of all factors of the text (the factor automaton can be slightly smaller than *DAWG*(*text*)). Constructions of *DAWG*(*text*) by Blumer et alii [BBEHCS 85] and Crochemore [Cr 86] are essentially the same.

The standard application of dawg's is for building efficient dictionaries of factors of many strings, see [BBHME 87]. The relation between dawg's and suffix trees is described nicely in [CS 85].

The application of dawg's to find the longest common factor of two words (Section 6.5) is presented in [Cr 86] (see also [Cr 87]).

The average-optimal algorithm *BDM* is from [C-R 92]. The paper also contains several variations on the implementation of the algorithm.

## Selected references

[BBEHCS 85] A. BLUMER, J. BLUMER, A. EHRENFEUCHT, D. HAUSSLER, M.T. CHEN, J. SEIFERAS, The smallest automaton recognizing the subwords of a text, *Theoret. Comput. Sci.* 40 (1985) 31-55.

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# 7. Automata-theoretic approach

Finite automata can be considered both as simplified models of machine, and as mechanisms used to specify languages. As machines, their only memory is composed of a finite set of states. In the present chapter, both aspects are considered and lead to different approaches to pattern matching. Formally, a (deterministic) automaton G is a sequence ($A$, $Q$, *init*, δ, $T$), where $A$ is an input alphabet, $Q$ is a finite set of states, *init* is the initial state (an element of $Q$) and δ is the transition function. For economy reasons we allow δ to be a partial function. The value $\delta(q, a)$ is the state reached from state $q$ by the transition labelled by input symbol $a$. The transition function extends in a natural way to all words, and, for the word $x$, $\delta(q, x)$ denotes, if it exists, the state reached after reading the word $x$ in the automaton from the state $q$. The set $T$ is the set of accepting states, or terminal states of the automaton.

The automaton $G$ accepts the language:

$$L(G) = \{x : \delta(init, x) \text{ is defined and belongs to } T\}.$$

The size of $G$, denoted by *size*($G$) is the number of all transitions of $G$: number of all pairs ($q$, $a$) ($q$ is a state, $a$ is a single symbol) for which $\delta(q, a)$ is defined. Another type of a useful size of $G$ is the number of states denoted by *statesize*($G$).

Probably the most fundamental problem in this chapter is: construct in linear time a (deterministic) finite automaton $G$ accepting the words ending by one pattern among a finite set of patterns, and gives a representation of $G$ of linear size, independently on the size of the alphabet. Another very important and useful algorithm solves the question of matching a regular expression.

## 7.1. Aho-Corasick automaton

We denote by *SMA*(*pat*), for *String-Matching Automaton*, a (deterministic) finite automaton $G$ accepting the set of all words containing *pat* as a suffix, and denote by *SMA*(∏) an automaton accepting the set of all words containing a word of the finite set of words ∏ as a suffix. In other terms, noting $A^*$ the set of all words on the alphabet $A$,

$$L(SMA(pat)) = A^*pat \text{ and } L(SMA(\Pi)) = A^*\Pi.$$

In this section we present a construction of the minimal finite automaton $G$ = *SMA*(*pat*), where minimality is understood according to the number of states of $G$. Unfortunately, the total size of $G$ depends heavily on the size of the alphabet. We show how to construct these automata in linear time (with respect to the output).

With such an automaton the following real-time algorithm *SMA* can be applied to the string-matching problem (for one or many patterns). The algorithm outputs a string of 0's and 1's that locates all occurrences of the pattern in the input text (1's mark the end position of occurrences of the pattern). The algorithm does not use the same model of computation as algorithms of Chapters 3 and 4 do. There, the elementary operation used by algorithms (*MP*, *BM*, and their variations) is letter comparison. Here, the basic operation is branching (computation of a transition).

```
Algorithm SMA { real-time transducer for string-matching }
begin
  state := init; read(symbol);
  while symbol $\neq$ endmarker do begin
    state := $\delta$(state, symbol);
    if state in T then
      write(1)   { reports an occurrence of the pattern }
    else write(0);
    read(symbol);
  end;
end.
```

We start with the case of only one pattern *pat*. And show how to build the minimal automaton *SMA*(*pat*). The function *build_SMA* builds *SMA*(*pat*) sequentially. The core of the construction consists, for each letter *a* of the pattern, to unfold the *a*-transition from the last created state *t*. This is illustrated by pattern *abaaba* in Figure 7.1.

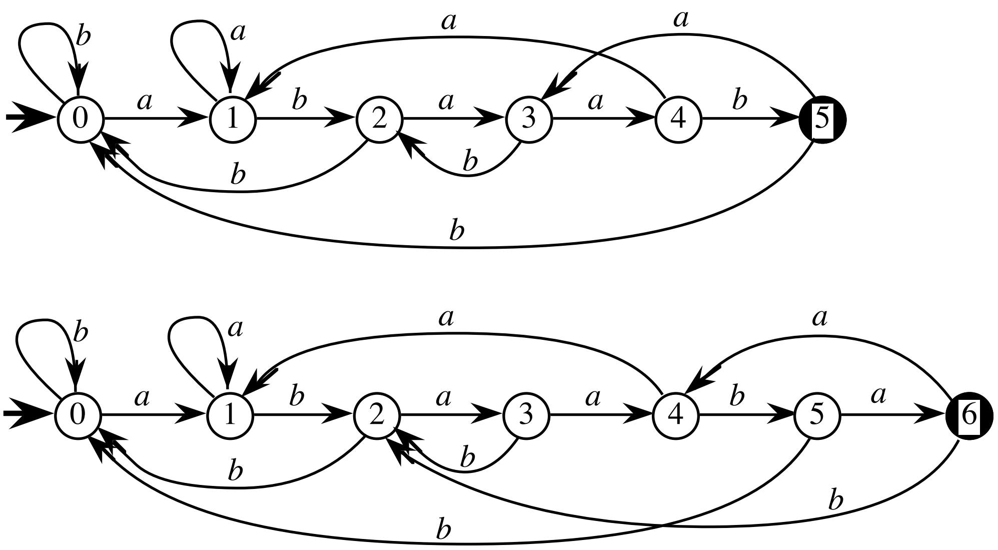

**Figure 7.1**. One step in the construction a sma: from *SMA*(*abaab*) to *SMA*(*abaaba*): unfolding the *a*-transition from state 5. Terminal states are black.

```
function build_SMA (pat) : automaton;
begin
  create a state init; terminal := init;
  for all b in A do δ(init, b) := init;
  for a := first to last letter of pat do begin
    temp := δ(terminal, a); δ(terminal, a) := new state x;
    for all b in A do δ(x, b) := δ(temp, b);
    terminal := x;
  end;
  return (A, set of created states, δ, init, {terminal});
end;
```

**Lemma 7.1**

Algorithm *build_SMA* constructs the (minimal) automaton *SMA*(*pat*) in time O(*m*.|*A*|). The automaton *SMA*(*pat*) has (*m*+1)|*A*| transitions, and *m*+1 states.

The proof of Lemma 7.1 is left as an exercise. There is an alternative construction of the automaton *SMA*(*pat*) which shows the relation between sma's and the *MP*-like algorithm of Chapter 3. Once we have computed the failure table *Bord* for pattern *pat*, the automaton *SMA*(*pat*) can be constructed as follows. We first define $Q = \{0, 1, \ldots, m\}$, $T = \{m\}$, $init = 0$. And the transition function (table) δ is computed by the algorithm below. Figure 7.2 displays simultaneously the failure links (arrows going to the left) and *SMA*(*abaaba*).

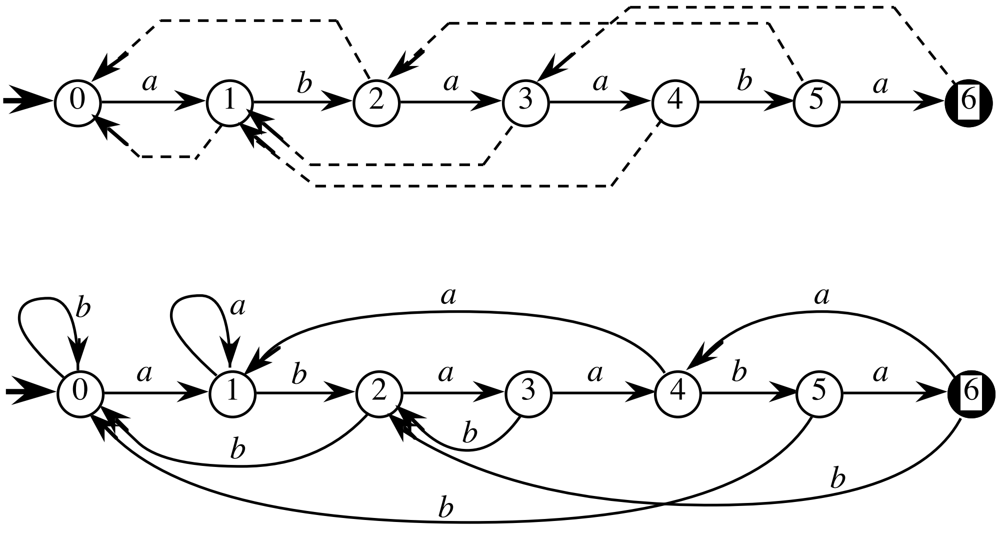

**Figure 7.2**. The function *Bord*, and the automaton *SMA*(*abaaba*).

```
Algorithm { computes the transition function of SMA(pat) }
          { assuming that table Bord is already computed }
begin
  for all a in A do δ(0, a) := 0;
  if m>0 then δ(0, pat[1]) := 1;
  for i := 1 to m do
    for all a in A do
      if i<m and a=pat[i+1] then δ(i, a) := i+1
      else δ(i, a) := δ(Bord[i], a);
end.
```

In some sense, we can consider that table *Bord* represents the transition function $\delta$ of the automaton *SMA*(*pat*). Then, *MP* algorithm becomes a mere simulation of algorithm *SMA* above. In the simulation, branching operations are substituted by letter comparisons. This remark is indeed the basis of Simon algorithm (MPS algorithm in Chapter 3). The representation of *SMA*(*pat*) by a failure function makes the size of the representation independent of the alphabet without increasing the total time complexity of the search phase.

The algorithm above shows that the transition function of *SMA*(*pat*) can be computed from the failure table *Bord*.

We next apply the same strategy for the recognition of a finite set of patterns. Assume that we have a set $\Pi$ of $r$ patterns. The $i$-th pattern is denoted by *pi*. Let $m$ be the total length (sum) of all patterns. We no longer try to build the minimal string-matching automaton corresponding to the problem. So, *SMA*($\Pi$) is not necessarily the minimal (deterministic) automaton of the language $A^*\Pi$, as it is when $\Pi$ contains only one pattern.

To construct *SMA*($\Pi$), we first consider a tree (a word trie) *Tree*($\Pi$) whose branches are labelled by elements of $\Pi$. The nodes of *Tree*($\Pi$) are identified with prefixes of words in $\Pi$. The root is the empty word $\varepsilon$. The father of a nonempty prefix *xa* is the prefix $x$. We write *father*(*xa*) = $x$, and *son*($x$, $a$) = *xa*. Nodes of *Tree*($\Pi$) are considered as states of an automaton, and they are marked as terminal or non terminal. A node is marked as terminal if the word it represents is in the set $\Pi$. All leaves are terminal states, but it may also happen that some internal node is also a terminal state. This happens when a pattern is a proper prefix of another pattern. Figure 7.3 displays *Tree*({*ab*, *babb*, *bb*}).

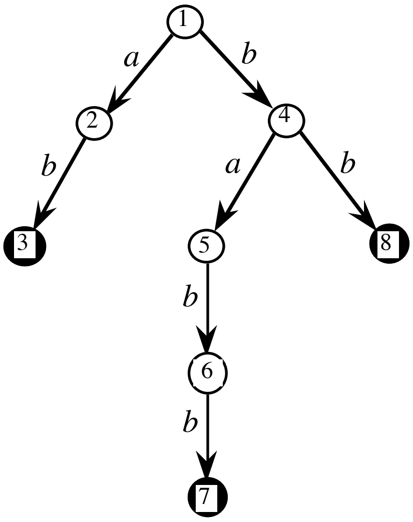

**Figure 7.3**. The word tree of set {*ab*, *babb*, *bb*}. Terminal nodes are starred.

The algorithm *build_SMA* below, applied to a set of strings Π, builds an automaton *SMA*(Π) from the tree *Tree*(Π). The states of the automaton are the nodes of the tree. The algorithm essentially transforms and completes the relation *son* into the transition δ. The algorithm is very similar to the case of a single word. Here, no state is created, because they are taken from the existing tree.

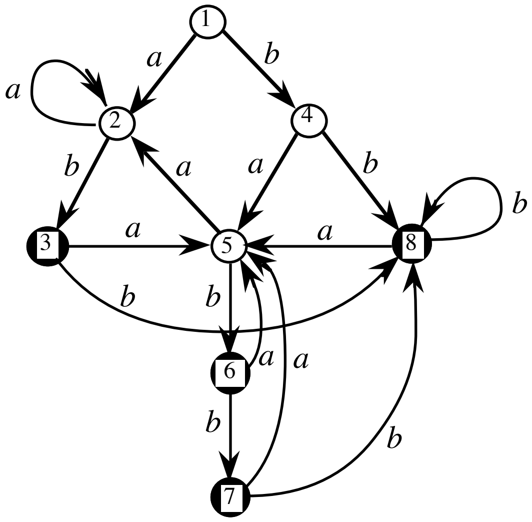

**Figure 7.4**. The automaton *SMA*(∏) for ∏ = {*ab*, *babb*, *bb*}.
Note that node 6 is terminal.

There is however a delicate point related to the computation of terminal states. It may happen that some word of Π is an internal factor of another word of the set. This is the case for the set {*ab*, *babb*, *bb*} considered in Figure 7.3. Node 6 of *Tree*({*ab*, *babb*, *bb*}) becomes a terminal state in *SMA*({*ab*, *babb*, *bb*}), because *bab* ends with the word *ab* of the set. More generally, this happens during the construction when the clone of node *x*, namely node *temp* in the algorithm, is itself a terminal node.

```
function build_SMA (Π) : automaton;
begin
{ father and son links refer to the tree Tree(Π)  }
{ states of SMA(Π) are the nodes of Tree(Π) }
  if root terminal node then T := {root} else T := ∅;
  for all b in A do δ(root, b) := root;
  for all non-root nodes x of Tree(Π) in bfs order do begin
    t := father(x); a := the letter such that x=son(t, a);
    temp := δ(t, a); δ(t, a) := x;
    if x or temp terminal nodes then add x to T;
    for all b in A do
      if son(temp, b) defined then δ(x, b) := son(temp, b)
      else δ(x, b) := δ(temp, b);
  end;
  return (A, nodes of Tree(Π), δ, root, T);
end;
```

**Lemma 7.2**

The algorithm *build_SMA* builds a deterministic automaton *SMA*(Π) having the same set of nodes as the word trie *Tree*(Π). It runs in time *O*(*statesize*(*Tree*(Π)).|*A*|).

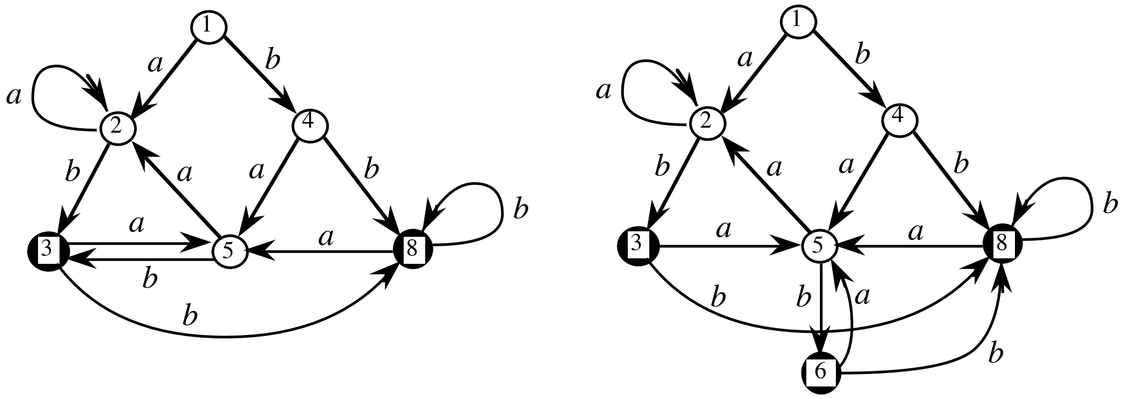

**Figure 7.5**. One step of the algorithm for the construction of *SMA*({*ab*, *babb*, *bb*}); Node 6 is a clone of δ(5, *b*)=3 (on the left). Transitions on node 6 are the same as for 3.

With the automaton *SMA*(Π) built by the previous algorithm, searching a text for occurrences of the patterns in Π can be realized by the algorithm *SMA*. The search is then performed in real time, and the space required to store the automaton is $O(statesize(Tree(\Pi)).|A|)$. Again, it is possible to represent the automaton $SMA(\Pi)$ with a failure function. Its advantage is to represent the automaton within space $O(statesize(Tree(\Pi)))$, which is independent of the alphabet. The search becomes then analogue to *MP* algorithm of Chapter 3.

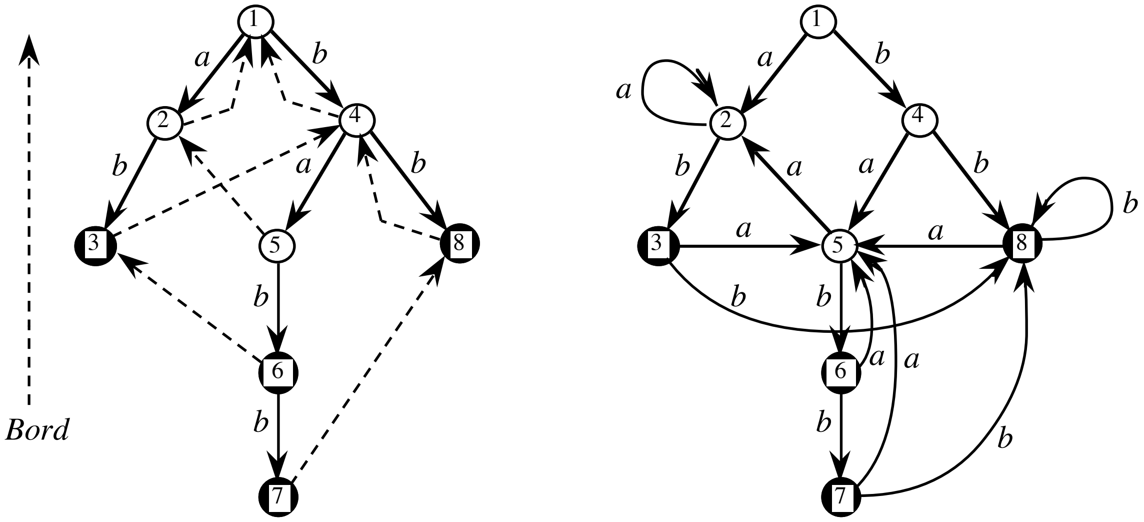

**Figure 7.6**. The tree *Tree*(∏) with suffix links *Bord* (left), and the automaton *SMA*(∏) (right), for ∏ = {*ab*, *babb*, *bb*}.

The function *Bord* related to Π is defined, for a non-empty word *u*, by

*Bord*(*u*) = longest proper suffix of *u* that is prefix of a pattern in Π.

We also denote by *Bord* the failure table defined on nodes of *Tree*(Π) (except on the root). The relation used by the following algorithm that computes table *Bord* is (*t* is a node of *Tree*(Π) different from the *root*):

$$Bord[ta] = Bord^k[t]a, \text{ for the smallest } k \text{ such that } Bord^k[t]a \in \Pi,$$
$$Bord[ta] = \varepsilon, \text{ otherwise.}$$

Note that the algorithm below also marks nodes as terminal in the same situation explained for the direct construction of *SMA*(∏).

```
procedure compute_Bord; { failure table on Tree(Π) }
begin
{ father and son refer to the tree Tree(Π) }
{ Bord is defined on nodes of Tree(Π)      }
  set Bord[ε] as undefined;
  for all a in A do Bord[a] := ε;
  for all nodes x of Tree(Π), |x|>2, in bfs order do begin
    t := father(x); a := the letter such that x=son(t, a);
    z := Bord[t];
    while z defined and za not in Tree(Π) do z := Bord[z];
    if za is in Tree(Π) then Bord[x] := za else Bord[x] := ε;
    if za is terminal then mark x as terminal;
  end;
end.
```

The complexity of the algorithm above is proportional to $m.|A|$. The analysis is similar to that for computing *Bord* for a single pattern. It is enough to estimate the total number of all executed statements "`z := Bord[z]`". This statement can be again treated as deleting some items from a store and $z$ as the number of items. Let us fix a path $\pi$ of length $k$ from the root to the leaf. Using the store principle it is easy to prove that the total number of insertions (increases of $z$) to the store for nodes of $\pi$ is bounded by $k$, hence the total number of deletions (executing "`z := Bord[z]`") is also bounded by $k$. If we sum this over all paths than we get the total length $m$ of all patterns in Π.

We can again base the construction of an automaton *SMA*(∏) on the failure table of *Tree*(Π). The transition function is defined on nodes of the tree as shown by the following algorithm.

```
Algorithm { computes transition function for SMA(Π) }
begin
  for all a not in Tree(Π) do δ(ε , a) := ε;
  for all nodes x of Tree(Π) in bfs order do
    for all a in A do
      if xa is in Tree(Π) then δ(x, a) := xa
      else δ(x, a) := δ(Bord[x], a);
end.
```

```
function AC(Tree(Π); text) : boolean;
{ Aho-Corasick multi-pattern matching }
{ uses the table Bord on Tree(Π)      }
begin
  state := root; read(symbol);
  while symbol $\neq$ endmarker do begin
    while state defined and son(state, symbol) undefined do
      state := Bord[state];
    if state undefined then state := root
    else state := son(state, symbol);
    if state is terminal then return true;
    read(symbol);
  end;
  return false;
end;
```

Algorithm *AC* is the version of algorithm *MP* for several patterns. It is a straightforward application of the notion of the failure table *Bord*. The preprocessing phase of *AC* algorithm is procedure *compute_Bord*.

Terminal nodes of *SMA*(∏) can have numbers corresponding to numbering of patterns in Π. Hence, the automaton can produce in real-time numbers corresponding to those patterns ending at the last scanned position of the text. If no pattern occurs, 0 is written. This proves the following statement.

**Theorem 7.3**

The string-matching problem for a finite number of patterns can be solved in time O($n$+$m$.|$A$|). The additional memory is of size O($m$).

The table *Bord* used in *AC* algorithm can be improved in the following sense. Assume, for instance that during the search node 6 of Figure 7.6 has been reached, and that the next letter is *a*. Since node 6 has no *a*-son in the tree, *AC* algorithm iterates function *Bord* from node 6. It finds successively nodes 3 and node 4 where the iteration stops. It is clear that the test on node 3 is useless in any situation because it has no son at all. On the contrary, node 4 plays its role because it has an *a*-son. Some iterations of the function *Bord* can be precomputed on the tree. The transformation of *Bord* is similar to the transformation of *suf* into *SUF* based on contexts of nodes described in Section 6.5. Figures 7.7 shows the result of the transformation. The optimization does not change the worst-case behavior of *AC* algorithm.

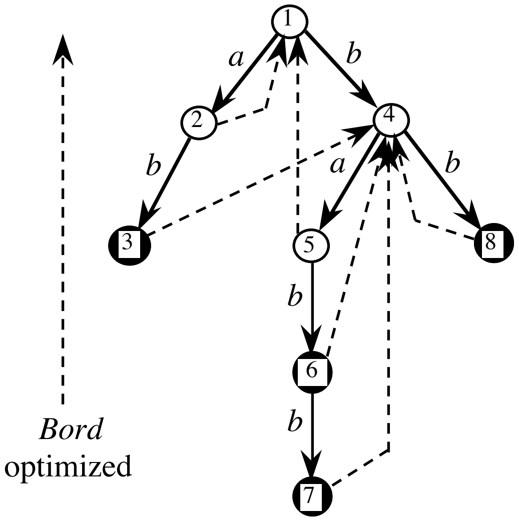

**Figure 7.7**. Optimized table *Bord* on *Tree*({*ab*, *babb*, *bb*}).
Note that the table is undefined on node 4.

## 7.2. Faster multi-pattern matching

The method presented in the preceding section is widely used, but its efficiency is not entirely satisfactory. It is similar to the method of Chapter 3. The minimum time complexity of the search phase in all these algorithms is still linear, which is rather large compared to the performance of the *BM*-type algorithms of Chapter 4. The idea is then to have the counterpart of *BM* algorithm to search for several patterns. It is possible to extend the *BM* strategy to the multi-pattern matching problem, but the natural extension becomes very technical. We present here another solution based on the use of dawg's.

The search for several patterns combines the techniques used in *AC* algorithm and in the backward-dawg-matching algorithm (*BDM* in Section 6.5). The dawg related to the set of pattern Π is used to avoid searching certain segments of the text. It must be considered as an extra mechanism added to the *AC* automaton *SMA*(Π) to speed up the search. The search is done through a window that slides along the text. The size of the window is here the minimal length of pattern in Π. In the extreme case where the minimal length is very small, the dawg is not useful, and the *AC* algorithm, on its own, is efficient enough.

The idea for speeding up *AC* algorithm is the same as the central idea used in *BM* algorithm. On the average, only a short suffix of the window has to be scanned to discover that no occurrence of a pattern in Π occurs at the current position. In order to achieve an average-optimal procedure we use the strategy of *BDM* algorithm. This approach has the further advantage to simplify the whole algorithm compared to direct extensions of *BM* algorithm to the problem.

The algorithm of the present section, for matching a finite set of patterns Π, is called *multi_BDM*. The search uses both the automaton *SMA*(Π) and the suffix dawg of reverse patterns *DAWG*($\Pi^R$). The basic work is supplied by the former structure. The role of the latter structure is to provide large shifts over the text.

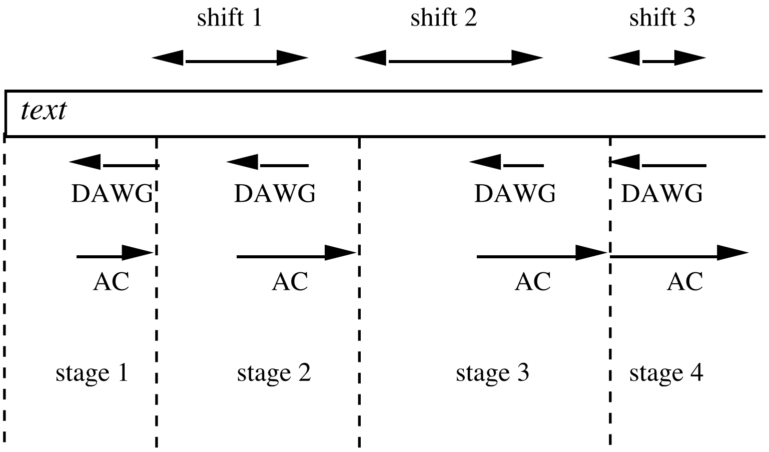

**Figure 7.8**. Series of stages in *multi_BDM* search phase.

In the current configuration of *multi_BDM* algorithm, the window is at position *i* on the text. A prefix *u* of the window has already been scanned through the *AC* automaton *SMA*(Π). The word *u* is known as a prefix of some pattern. Both the length *lp* of that prefix, and the corresponding state *state* of *SMA*(Π) are stored. They serve when extending the prefix during the present stage, if necessary. They also serve to compute the length of the next shift in some situation. Each stage is decomposed into two sub-stages. We assume that the window contains the word *uv* (*u* as above).

— **Substage I**, scan with *DAWG*($\Pi^R$). The part *v* of the window, not already scanned with *SMA*(Π), is scanned from right to left with *DAWG*($\Pi^R$). Note that the process may stop before *v* has been entirely scanned. This happens when *v* is not a factor of the patterns. This is likely to happen with high probability (at least if the window is large enough). The longest prefix *u*' of Π found during the scan is memorized to be used precisely in such a situation.

— **Substage II**, scan with *SMA*(Π). If the part *v* of the window is entirely scanned at substage I, then it is scanned again, but, with *SMA*(Π) and in the reverse direction (from left of right). Doing so, the possible matches are reported, and we get the new prefix of patterns on which the window is adjusted. If *v* is not scanned entirely at substage I, the scan with *SMA*(Π) starts from the beginning of *u*', and the rest is similar to the previous situation. This is the situation where a part of the text is ignored by the search, which leads to a faster search than with *AC* algorithm alone.

The basic assumption of Substage I is that *u* is a common prefix of the window and the patterns. Since the size of the window is fixed and is the minimal length of patterns, in particular, *u* is shorter than the shortest pattern. To meet the condition at the end of Substage II, the scan continues until the current prefix *u* is shorter than the required length.

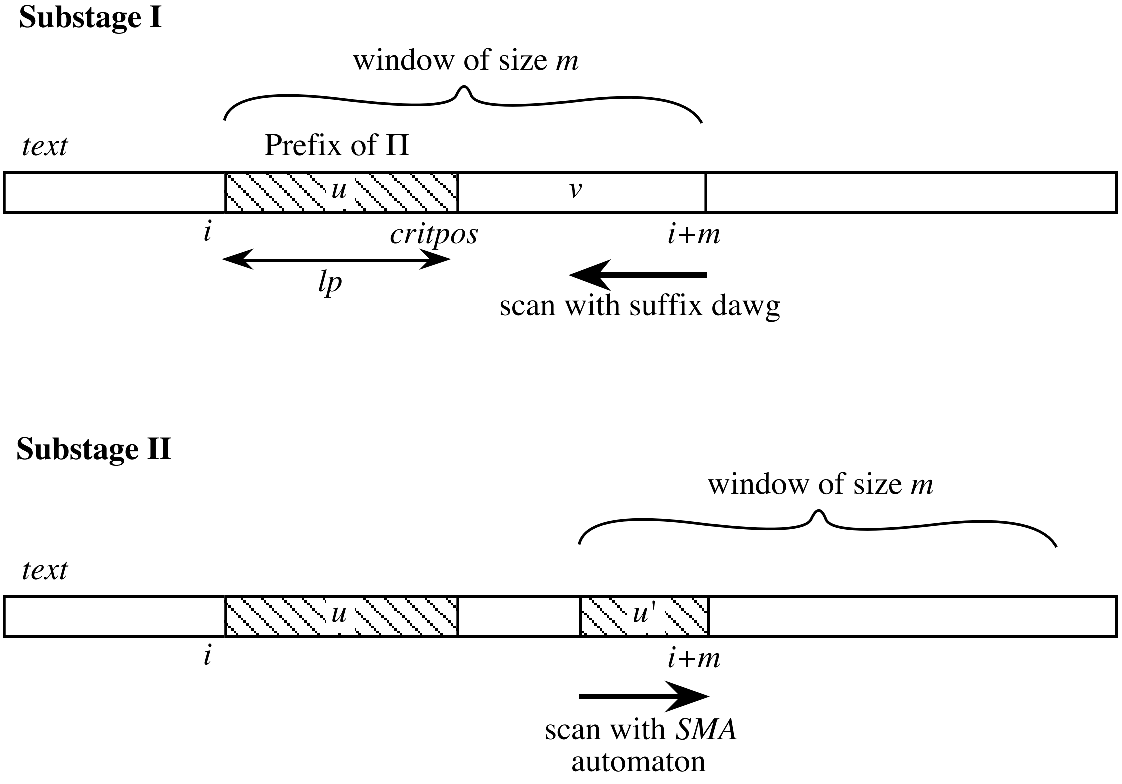

**Figure 7.9**. Substages of *multi_BDM* search phase.

The algorithm is given below. The current position of the window is *i*. Position *critpos* (≥ *i*) is the position of the input head of automaton *SMA*(Π). The corresponding state of the automaton is denoted by *state*. The first internal while loop executes Substage I. The test "*text*[*i*+*j*..*i*+*min*] Œ *Fac*($P^R$)" is assumes to be done with the help of the suffix dawg *DAWG*($\Pi^R$). The second internal while loop executes Substage II.

```
Algorithm multi_BDM;
{ searches text for the finite set of patterns $\Pi$         }
{ $G$ is $SMA(\Pi)$ ($AC$ automaton of Section 7.1),            }
{ $D$ is $DAWG(\Pi^R)$ for the reverse patterns (see Chapter 6) }
begin
  min := minimal length of patterns;
  i := 0;      { i is the position of the window on text }
  critpos := 0; state := initial state of G;
  while $i \leq n-min$ do begin
    j := min;
    while $i+j > critpos$ and $text[i+j..i+min] \in Fac(\Pi^R)$ do
      j := j-1;
    if $i+j > critpos$ then begin
      lp := length of the longest prefix of $\Pi$ found by D
            during the preceding while loop;
      state := initial state of G;
      critpos := i+min-lp;
    end;
    while not end of text and (critpos < i+min or length of
          the longest prefix of $\Pi$ found by $G \geq min$) do begin
      apply G to text[critpos+1..n], reporting matches,
      incrementing critpos;
    end;
    state := state reached by G;
    lp := length of the longest prefix of $\Pi$ found by G;
    i := critpos-lp;
  end;
end.
```

**Example**

Consider the set of patterns $\Pi$ = {*abaabaab*, *aabb*, *baaba*}, and the text *text* = *abacbaaabaabaabbccc*..... Let $D = DAWG(\Pi)$, and $G = SMA(\Pi)$.

— Stage 1. The window contains *abac*. The dawg *D* discovers that the longest suffix of the window that is prefix of $\Pi$ is the empty word. Then, *critpos* is set 4, which leads to a shift of length 4.

— Stage 2. The window contains *baaa*. The dawg *D* finds the suffix *aa* as factor of $\Pi$. The factor *aa* is scanned with *G*. The length of the shift is 2. Letter *b* is not scanned at all.

— Stage 3. The window contains *aaba*. The dawg *D* scans backward the suffix *ba* of the window, reaching the point where is the head of *G*. Then, *G* scans forward the same suffix of the window, and finds that the suffix *aba* of the window is the longest prefix of $\Pi$ found at this position. The resulting shift has length 1.

— Stage 4. The window contains *abaa*. The dawg scans only its suffix of length 1. Then, *G* scans it again. But, since the whole window is a prefix of some pattern, the scan continues along the factor *abaabb* of the text. Two occurrences (of *baaba* and *abaabaab*) are reported. The longest prefix of $\Pi$ at this point is *b*. The next contents of the window is *bccc*. ‡

The following statement shows that *multi_BDM* algorithm makes a linear search of patterns provided branching in the automata is realized in constant time. The search takes $O(n.\log|A|)$ otherwise, where *A* can be restricted to the alphabet of the patterns in $\Pi$. The second statement gives the average behavior of *multi_BDM* algorithm. The theorem makes evident that the longer is the smallest pattern, the faster is the search.

**Lemma 7.4**

The algorithm *multi_BDM* executes at most $2n$ inspections of text characters.

**Proof**

Text characters are not scanned more than once by $D = DAWG(\Pi^R)$, nor more than once by $G = SMA(\Pi)$. So, the search executes at most $2n$ inspections of text characters. ‡

**Theorem 7.5**

Let $c=|A|>1$, and $m>1$ be the length of the shortest pattern of $\Pi$. Under independent equiprobability condition, the expected number of inspections made by *multi_BDM* algorithm on a text of length *n* is $O((n.\log_c m)/m)$.

**Proof**

The proof is similar to the corresponding proof for *BDM* algorithm in Chapter 6. ‡

## 7.3. Regular expression matching

In this section we consider a problem more general than string searching. The pattern is a set of string specified by a regular expression. The problem, called *regular expression matching*, or sometimes only *pattern matching*, contains both the string-matching and the multiple string matching problems. However, since patterns are more general their recognition becomes more difficult, and it happens that solutions to pattern matching are not as efficient as to string-matching.

The pattern is specified by a regular expression on the alphabet $A$ with the regular operations : concatenation, union, and star. For instance, $(a+b)^*$ represents the set of all strings on the alphabet $\{a, b\}$, and the expression $ab^*+a^*b$ represents the set $\{a, ab, abb, abbb, \ldots, b, aab, aaab, aaaab, \ldots\}$.

Let recall the meaning of regular operations. Assume that $e$ and $f$ are regular expressions representing respectively the sets of strings (regular languages) $L(e)$ and $L(f)$. Then,

— $e.f$ (also denoted by $ef$) represents $L(e)L(f) = \{uv : u \in L(e) \text{ and } v \in L(f)\}$,

— $e+f$ represents the union $L(e) \cup L(f)$,

— $e^*$ represents the set $L(e)^* = \{u^k : k \geq 0 \text{ and } u \in L(e)\}$.

Elementary regular expression are 0, 1, and $a$ (for $a \in A$), which represents respectively the empty set and the singletons $\{\varepsilon\}$ and $\{a\}$.

The formalism of regular expressions is equivalent to that of finite automata. It is the latter that is used for the recognition of the specified patterns.

The pattern matching algorithm consists of two phases. First, the regular expression is transformed into an equivalent automaton. Second, the search on the text is realized with the help of the automaton.

We consider only specific automata having good properties according to the space used for their representations. We call them *normalized automata*. They are not necessarily deterministic, as it is in previous section of the chapter. Such an automaton $G$ is given by the tuple $(Q, i, F, t)$, assuming that the alphabet is $A$. The set $Q$ is the finite set of states, $i$ is the only one initial state, $t$ is the only one terminal state, and $F$ is the set of edges (or arcs) labelled by letters of the alphabet $A$ or by the empty word $\varepsilon$. The language of the automaton is denoted by $L(G)$, and is the set of words, labels of paths in $G$ starting at $i$ and ending at $t$. Finally, the automaton $G$ and the regular expression $e$ are said to be equivalent if $L(G) = L(e)$. Figure 7.10 displays an automaton equivalent to $ab^*+a^*b$.

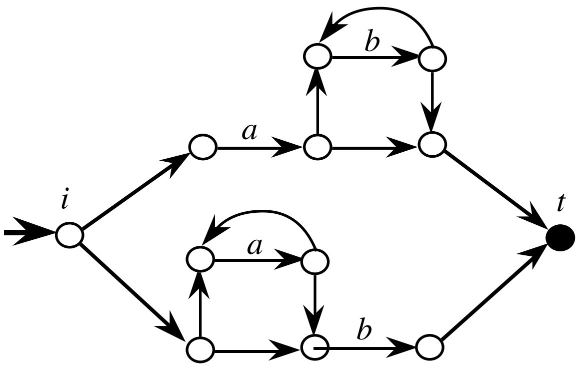

**Figure 7.10**. A normalized automaton equivalent to the regular expression *ab**+*a***b*. Edges without label are ε-transitions.

A normalized automaton $G = (Q, i, F, t)$ have specific properties listed here:

— it has a unique initial state $i$, a unique terminal state $t$, and $i \neq t$;

— no edge starts from $t$, and no edge points on $i$;

— on every state, either there is only one outgoing edge labelled by a letter of $A$, or there are at most two outgoing edges labelled by ε;

— on every state, either there is only one in-going edge labelled by a letter of $A$, or there are at most two in-going edges labelled by ε.

Note that properties satisfied by $G$ have their dual counterparts satisfied by the reverse automaton $G^R$ obtained by exchanging $i$ and $t$ and reversing directions of edges.

The pattern matching process is based on the following theorem. Its proof is given in the form of an algorithm that builds a normalized automaton equivalent to the regular expression. We can even bound the size of the automaton with respect of the size of the regular expression. We define *size*($e$) as the total number of letters (including 0 and 1), number of plus signs, and number of stars occurring in the expression $e$. Note that parenthesis and dots that may occur in $e$ are not reckoned with in the definition of *size*($e$).

**Theorem 7.6**

Let $e$ be a regular expression. There is a normalized automaton $(Q, i, F, t)$ equivalent to $e$, which satisfies $|Q| \leq 2size(e)$ and $|F| \leq 4size(e)$.

**Proof**

The proof is by induction on the size of $e$. The automaton associated to $e$ by the construction is denoted by $G(e)$. If $e$ is an elementary expression, its equivalent automaton is given in Figure 7.11.

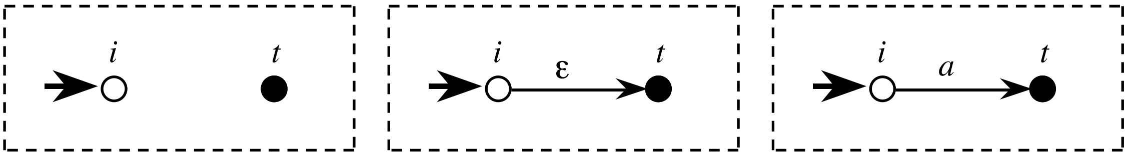

**Figure 7.11**. Normalized automata equivalent to elementary expressions 0 (empty set), 1 (set {ε}), and *a* (a letter) from left to right.

Let $G(e') = (Q', i', F', t')$, and $G(e'') = (Q'', e'', F'', t'')$ for two expressions $e'$ and $e''$. We assume that the set of states are disjoint ($Q' \cap Q'' = \emptyset$). If $e$ is a composed expression of the form $e'e''$, $e'+e''$, or $e'^*$, then $G(e)$ is respectively defined by *concat*($G(e')$, $G(e'')$), *union*($G(e')$, $G(e'')$), and *star*($G(e')$). The operations *concat*, *union*, and *star* on normalized automata are defined in Figure 7.12, Figure 7.13, and Figure 7.14. In the figure, the design of automata displays their unique initial and terminal states.

We leave it as an exercise the fact that the constructed automaton is normalized. By the way, this is clear from the figures.

In the construction, exactly two nodes are created for each element of the regular expression accounting in its size. This proves, by induction, that the number of states of $G(e)$ is at most $2size(e)$.

Then the bound on the number of edges in $G(e)$ easily comes from the properties of $G(e)$. This completes the proof of Theorem 7.6. ‡

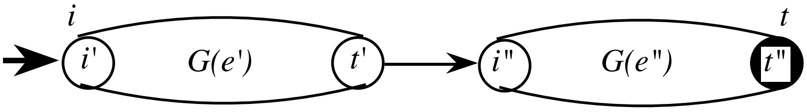

**Figure 7.12**. Concatenation of two automata

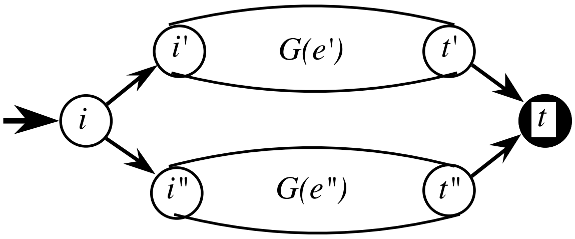

**Figure 7.13**. Union of two automata

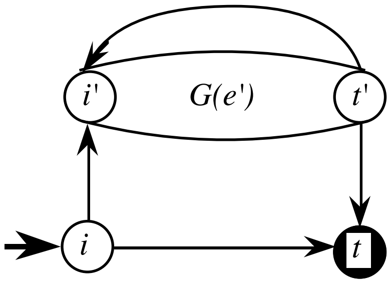

**Figure 7.14**. Star of an automaton

Figure 7.15 shows the automaton built by the algorithm of Theorem 7.6 from expression (*a*+*b**)**c*.

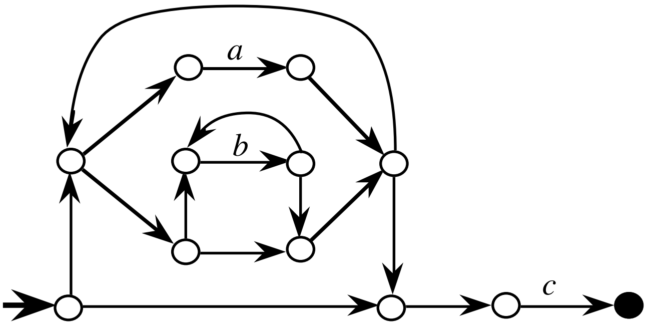

**Figure 7.15**. The normalized automaton for (*a*+*b**)**c* built by the algorithm.

To evaluate the time complexity of algorithms, it is necessary to give some hints about the data structures involved in the machine representation of normalized automata. States are simply indices on an array that stores the transitions. The array has three columns. The first corresponds to a possible edge labelled by a letter. The two others correspond to possible edges labelled by the empty word (the three columns can even be compressed into two columns because of properties of outgoing edges in normalized automata). Initial and terminal states are stored apart. This shows that the space required to represent a normalized automaton $G = (Q, i, F, t)$ is $O(|Q|)$. It is then $O(size(e))$ if $G = G(e)$.

The algorithm that proves Theorem 7.6 is given in the form of 4 functions below. The overall integrates the analysis of expression *e*. It is implemented here as a standard predictive analyzer with one look-ahead symbol (*char*). The effect of procedure *error* is to stop the analysis, in which case no automaton is produced. This happens when the input expression is not correctly written. Function *FACTOR* contains a small improvement on the construction described in the proof of Theorem 7.6 : several consecutive symbols '*' are considered as just one symbol '*'. This is because (*f**)* represents the same set of strings as *f**, for any regular expression *f*.

**Theorem 7.7**

A normalized automaton $G(e)$ equivalent to a regular expression $e$ can be built in time and space $O(size(e))$.

**Proof**

Operation *union*, *concat*, and *star* can be implemented to work in constant time with the array representation of normalized automata. Then, the algorithm *automaton* spends a constant time on each symbol of the input expression. This proves that the whole running time is $O(size(e))$. The statement on the space complexity is essentially a consequence of Theorem 7.6, after noting that the number of recursive calls is less than $size(e)$. ‡

```
function automaton(e regular expression) : normalized automaton;
{ returns the normalized automaton equivalent to e, }
{ which is defined in the proof of Theorem 7.6     }
begin
  char := first symbol of e;
  G := EXPR;
  if not end of e then error else return G;
end;
```

```
function EXPR : normalized automaton;
begin
  G := TERM;
  while char = '+' do begin
    char := next symbol of e;
    H := TERM; G := union(G, H);
  end;
  return G;
end;
```

```
function TERM : normalized automaton;
begin
  G := FACTOR;
  while char in A ∪ {'0', '1', '('} do begin
    H := FACTOR; G := concat(G, H);
  end;
  return G;
end;
```

```
function FACTOR : normalized automaton;
begin
  if char in $A \cup$ {'0', '1'} then begin
    G := the corresponding elementary automaton;
    char := next symbol of e;
  end else if char = '(' then begin
    char := next symbol of e;
    G := EXPR;
    if char = ')' then char := next symbol of e else error;
  end else error;
  if char = '*' then begin
    G := star(G);
    repeat char := next symbol of e; until char $\neq$ '*';
  end;
  return G;
end;
```

The automaton $G(e)$ can be used to test if a word $x$ belongs to the set $L(e)$ of patterns specified the regular expression $e$. The usual procedure for that purpose is to spell a path labelled by $x$ in the automaton. But their can be many such paths, and even an infinite number of them. This is the case for instance with the automaton of Figure 7.15 and $x = bc$. An algorithm using a backtracking mechanism is possible, but the usual solution is based on a kind of dynamic programming technique. The idea is to cope with path labelled by the empty word. Then, comes up the notion of *closure* of a set of states as those states accessible from them by ε-path. For $S$, a subset of states of the automaton $G(e) = (Q, i, F, t)$, we define

$$closure(S) = \{q \in Q : \text{there exist an } \varepsilon\text{-path in } G(e) \text{ from a state of } S \text{ to } q\}.$$

We also use the following notation for transitions in the automaton ($a \in A$):

$$trans(S, a) = \{q \in Q : \text{there exist an } a\text{-edge in } G(e) \text{ from a state of } S \text{ to } q\}.$$

Testing whether the word $x$ belong to $L(e)$ is implemented by the algorithm below.

```
function test(x word) : boolean;
{ test(x) = true iff x belongs to the language L(Q, i, F, t) }
begin
  S := closure({i});
  while not end of x do begin
    a := next letter of x;
    S := closure(trans(S, a));
  end;
  if t is in S then return true else return false;
end;
```

Functions *closure* and *trans* on set of states are realized by the algorithms below. With a careful implementation, based on standard manipulation of lists, the running times to compute *closure*(*S*) and *trans*(*S*, *a*) are both *O*(|*S*|). This is independent of the alphabet.

```
function closure(S set of states) : set of states;
{ closure of a set of states in the automaton (Q, i, F, t) }
begin
  T := S; File := S;
  while File not empty do begin
    delete state p from File;
    for any ε-edge (p, q) in F do
      if q is not in T then begin
        add q to T; add q to File;
      end;
  end;
  return T;
end;
```

```
function trans(S set of states; a letter): set of states;
{ transition of a set of states in the automaton (Q, i, F, t) }
begin
  T := ∅;
  for all p in S do
    if there is an a-edge (p, q) in F then
      add q to T;
  return T;
end;
```

**Lemma 7.8**

Testing whether the word $x$ belongs to the language described by the normalized automaton $(Q, i, F, t)$ can be realized in time $O(|Q|.|x|)$ and space $O(|Q|)$.

**Proof**

Each computation of *closure*($S$) and of *trans*($S$, $a$) takes time $O(|S|)$, which is bounded by $O(|Q|)$. The total time is then $O(|Q|.|x|)$.

The array representation of the automaton requires $O(|Q|)$ memory space. ‡

The recognition of expression $e$ in the text *text* uses also the automaton $G(e)$. But the problem is slightly different, because the test is done on factors of *text* and not only on *text* itself. Indeed we could consider the expression $A^*e$, and its associated automaton, to locate all occurrences of patterns like prefixes of *text*. But no transformation of $G(e)$ is even necessarily, because it is integrated in the searching algorithm. At each iteration of the algorithm, the initial state is incorporated into the current set of state, as if we restart the automaton at the new position in the text. Moreover, after each computation of set, a test is done to report a possible match ending at the current position in the text.

**Theorem 7.9**

The recognition of patterns specified by a regular expression $e$ in a text *text* can be realized in time $O(size(e).|text|)$ and space $O(size(e))$.

**Proof**

We admit that the construction of $G(e)$ can be realized in time $O(size(e))$.

The recognition itself is given by *PM* algorithm below. The detailed implementation is similar to that of function *test*. The statement is essentially a corollary of Lemma 7.8, and a consequence of Theorem 7.6 asserting that the number of states of $G(e)$ is $|Q| = 2size(e)$. ‡

```
Algorithm PM; {  Regular expression matching algorithm   }
{ searches text for the regular expression e represented }
{ by the normalized automaton (Q, i, F, t)               }
begin
  S := closure({i});
  while not end of text do begin
    a := next letter of text;
    S := closure(trans(S, a) ∪ {i}));
    if t is in S then report an occurrence;
  end;
end;
```

There is an alternative to the pattern procedure presented in this section. It is known that any (normalized finite) automaton is equivalent to a deterministic automaton (defined by a transition function). More precisely, any automaton $G$ can be transformed into a deterministic automaton $D$ such that $L(G) = L(D)$. Indeed, algorithm *PM* simulates moves in a deterministic automaton equivalent to $G(e)$. But states are computed again and again without any memorization.

It is clear that if $G(e)$ is deterministic, algorithms *PM* and *test* become much more simple, similar to algorithm *SMA* of Section 7.1. Moreover, with a deterministic automaton the time of the search becomes independent of the size of $e$ with an appropriate representation of $G(e)$. So, there seems to have only advantages to make the automaton $G(e)$ deterministic, if it is not already so. The main restriction is that the size of the automaton may grow exponentially, going from $s$ to $2^s$. This point is discussed in Section 7.4. We summarize the remark in the next statement.

**Theorem 7.10**

The recognition of patterns specified by a regular expression $e$ in a text *text* can be realized in time $O(|A|.2^{size(e)} + |text|)$ and space $O(2^{size(e)})$, where $A$ is the set of letters effectively occurring in $e$.

**Proof**

Build the deterministic version $D(e)$ of $G(e)$, and use it to scan the text. Use a matrix to implement the transition function of $D(e)$. The branching in $D(e)$ thus takes constant time, and the whole search takes $O(|text|)$. ‡

## 7.4.* Determinization of finite automata: efficient instances

We consider a certain set $S$ of patterns represented in a succinct way by a deterministic automaton $G$ with $n$ states. The set $S$ is the language $L(G)$ accepted by $G$. Typical examples of sets of patterns are $S = \{pat\}$ a singleton and $S = \{pat_1, pat_2, \ldots, pat_r\}$ a finite set of words. For the first example, the structure of $G$ is the line of consecutive positions in *pat*. The rightmost state (position) is marked as terminal. For the second example, the structure of $G$ is the tree of prefixes of patterns. All leaves of the tree are terminal states, and some internal nodes can also be terminal if a pattern is a prefix of another pattern of the set.

We can transform $G$ into a non-deterministic pattern-matching automaton, noted *loop*($G$), which accepts the language of all words having a suffix in $L(G)$. The automaton *loop*($G$) is obtained by adding a loop on the initial state, for each letter of the alphabet. The automata *loop*($G$) for two examples of the cases mentioned above are presented in Figure 7.16 and Figure 7.17. The actual non-determinism of the automata appears only on the initial state.

We can apply the classical powerset construction (see [HU 79] for instance) to a nondeterministic automaton *loop*($G$). It appears that, in these two cases of one pattern and of a finite set of patterns, doing so we obtain efficient deterministic string-matching automata. In the powerset construction, are only considered, those subsets which are accessible from the initial subset.

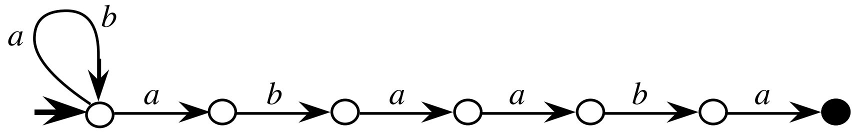

**Figure 7.16**. The non-deterministic pattern-matching automaton for *abaaba*.
The powerset construction gives the automaton *SMA*(*abaaba*) of Figure 7.2.
An efficient case of the powerset construction.

However, the idea of using altogether *loop*($G$) and the powerset construction on it is not always efficient. In Figure 7.18 a non-efficient case is presented. It is not hard to get convinced that the deterministic version of *loop*($G$), which has a tree-like structure, cannot have less than $2^7$ states. Extending the example shows that a non-deterministic automaton, even of the form *loop*($G$), with $n$+1 states can be transformed into an equivalent deterministic automaton having $2^n$ states.

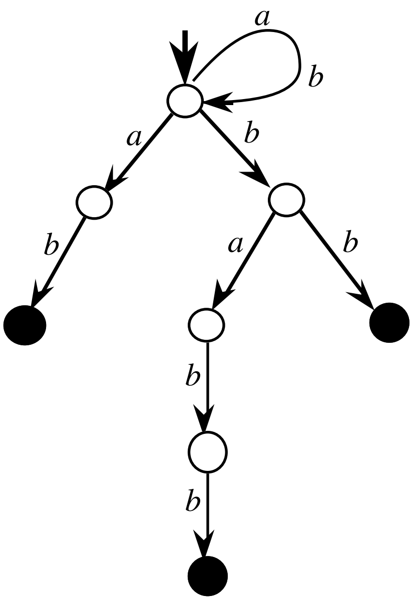

**Figure 7.17**. The non-deterministic pattern-matching automaton for the set {*ab*, *babb*, *bb*}. The powerset construction gives the automaton *SMA*({*ab*, *babb*, *bb*}) of Figure 7.4. An efficient case of the powerset construction.

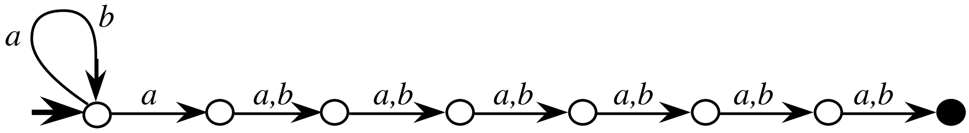

**Figure 7.18**. A non-efficient case of the powerset construction. The presented automaton results by adding the loop to the initial state of the deterministic automaton accepting words of length 7 which start with letter *a*. The smallest equivalent deterministic automaton has 128 states.

Similarly we can transform the deterministic automaton *G* accepting one word *pat* into a non-deterministic automaton *FAC*(*G*) accepting the set *Fac*(*pat*). The transformation could be done by simply saying that all states are simultaneously initial and terminal states, but we prefer creating additional edges from the single initial state to all other states and labelled by all letters. It happens that again we find an efficient case of the powerset construction if we start with the deterministic automaton accepting just a single word. The powerset construction gives the smallest deterministic automaton accepting the suffixes of *pat*.

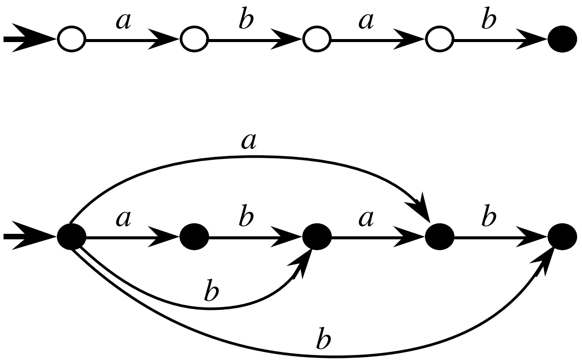

**Figure 7.19**. Efficient case of the powerset construction. Applied to *FAC*(*G*) the accepts
*Fac*(*text*)
it gives the smallest automaton for the suffixes of *pat* with a linear number of states.

The powerset construction applied on automata of the form *FAC*(*G*) is not always efficient. If we take as *G* the deterministic automaton with 2*n*+3 states accepting the set $S = (a+b)^n a(a+b)^n c$, then the automaton *FAC*(*G*) has also 2n+3 states. But the smallest deterministic automaton accepting the set of all factors of words in *S* has an exponential number of states.

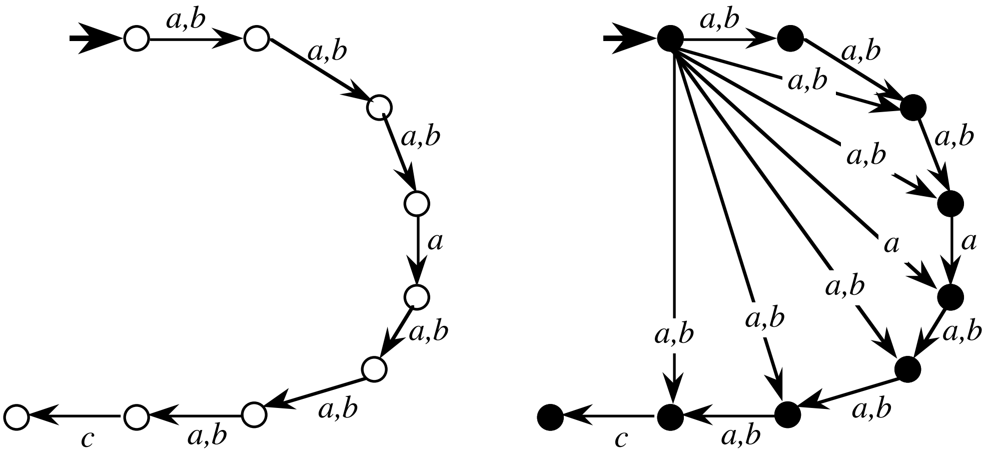

**Figure 7.20**. A non-efficient case of the powerset construction. *G* (on the left) accepts $(a+b)^n a(a+b)^n c$, for $n = 3$. A deterministic version of *FAC*(*G*) (on the right) has, in this case, an exponential number of states.

Combining *loop* and *FAC* gives sometimes an efficient powerset construction. This is done implicitly in Section 6.5. There the failure function defined on the automaton *DAWG*(*pat*) serves to represent the automaton *loop*(*DAWG*(*pat*)). The overall is efficient because both steps — from *pat* to *DAWG*(*pat*), and from *DAWG*(*pat*) to *loop*(*DAWG*(*pat*)) — are. But, in general, the whole determinization process is inefficient.

## 7.5. Two-way pushdown automata

The two-way deterministic pushdown automaton (2dpda, in short) is an abstract model of linear time decision computations on texts. A 2dpda $G$ is essentially a usual deterministic pushdown finite-state machine (see [HU 79]) which differs from the standard model in the ability to move the input head in two directions.

The possible actions of the automaton are: changing the current state of the finite control, moving the head by one position, changing locally the contents of the stack "near" its top. For simplicity, we assume that each change of the contents of the stack is of one of two types: push($a$) - pushing a symbol $a$ onto the stack; pop - popping one symbol off the stack. The automaton has access to the top symbol of the stack and to the symbol in front of the two-way head. We assume also that there are special left and right endmarkers on both ends of the input word. The output of such an abstract algorithm is 'true' iff the automaton stops in an accepting state. Otherwise, the output is 'false'. Initially the stack contains a special "bottom" symbol, and we assume that in the final moment of acceptance the stack contains also one element. When the stack is empty the automaton stops (the next move is undefined).

The problem solved by a 2dpda can be abstractly treated as a formal language $L$ consisting of all words for which the answer of the automaton is 'true' ($G$ stops in an accepting state). We say also that $G$ accepts the language $L$. The string-matching problem, for a fixed input alphabet, can be also interpreted as the formal language:

$$L_{\text{sm}} = \{\ pat\&text : pat \text{ is a factor of } text\}.$$

This language is accepted by some 2dpda. This gives an automata-theoretic approach to linear time string-matching, because as we shall see latter, 2dpda can be simulated in linear time. In fact, historically it was one of the first methods for the (theoretical) design of a linear-time string-matching algorithm.

**Lemma 7.11**

There is a 2dpda accepting the language $L_{\text{sm}}$.

**Proof**

We define a 2dpda $G$ for $L_{\text{sm}}$. It simulates the naive string-matching algorithm *brute-force1* (see Chapter 3). At a given stage of the algorithm, we start at a position $i$ in the text *text*, and at the position $j = 1$ in the pattern *pat*. The pair $(i, j)$ is replaced by the pair (stack, $j$), where $j$ is the position of the input head in the pattern (and has exactly the same role as $j$ in algorithm *brute-force1*). The contents of the stack is $text[i+1\ldots n]$ with $text[i+1]$ at the top.

The automaton tries to match the pattern starting from position $i$+1 in the text. It checks if top of stack equals the current symbol at position $j$ in the pattern; if so, then ($j := j$+1; *pop*). This action is repeated until a mismatch is found, or until the input head points on the marker '&'. In the latter case $G$ accepts. Otherwise, it goes to the next stage. The stack should now correspond to *text*[$i$+1…$n$] and $j$ = 1. It is not difficult to reach such a configuration. The stack is reconstructed by shifting the input head back simultaneously pushing scanned symbols of *pat* (which have been matched successfully against the pattern).

This shows that the algorithm *brute-force1* can be simulated by a 2dpda, and completes the proof. ‡

Similarly the problem of finding the prefix palindromes of a string, and several other problems related to palindromes can be interpreted as formal languages. Here is a sample:

$$L_{\text{prefpal}} = \{ww^Ru\text{: } u, w \in A^*, w \text{ is non-empty}\},$$

$$L_{\text{prefpal3}} = \{ww^Ruu^Rvv^Rz : w, u, v \in A^*, w, u, v \text{ non-empty}\},$$

$$L_{\text{pal2}} = \{ww^Ruu^R : w, u, v \in A^*, w, u \text{ are nonempty}\}.$$

All these languages related to symmetries are accepted by 2dpda's. We leave it as an exercise for a reader to construct the appropriate 2dpda's.

The main result about 2dpda's is that they correspond to some simple linear-time algorithms. Assume that we are given a 2dpda $G$ and an input word $w$ of length $n$. The size of the problem is $n$ (the static description of $G$ has constant size). Then, it is proved below that testing whether $w$ is in $L(G)$ takes linear time. We give the concepts that leads to the proof of the result.

The key concept for 2dpda is the consideration of *top configurations*, also called *surface configurations*. The top configuration of a 2dpda retains from the stack only its top element. The first basic property of top configurations is that they contain enough information for the 2dpda to choose the next move. The whole configuration consists of the current state, the present contents of the stack, and the position of the two-way input head. Unfortunately, there are too many such configurations (potentially infinite, as the automaton can loop when making push operations). It is easy to see that in every accepting computation the height of the stack is linearly bounded. This also does not help very much because there is an exponential number of possible contents of the stack of linear height. There comes the second basic property of top configurations: their number is linear in the size of the problem $n$.

Formally, a top configuration is a triple $C$ = (*state*, *top symbol*, *position*). The linearity of the set of top configurations follows obviously from the fact that the number of states, and the number of top symbols (elements of the stack alphabet) is bounded by a constant; it does not depend on $n$.

We can classify top configurations according to the type of next move of the 2dpda: *pop configurations* and *push configurations*. For a top configuration $C$, we define *Term*[$C$] as a pop configuration $C'$ accessible from $C$ after some number (possibly zero) of moves which are not allowed to pop the top symbol $C$. It is as if we started with a stack of height one, and at the end the height of the stack were still equal to one. If there is no such $C'$ then *Term*[$C$] is undefined. Assume (w. l. o. g.) that the accepting configuration is a pop configuration and the stack is a simple element.

The theorem below is the main result about 2dpda's. It is surprising in view of the fact that the number of moves is usually bigger than that of top configurations. In fact, a 2dpda can make an exponential number of moves and halt. But the result simply shows that shortcuts are possible.

**Theorem 7.12**

If the language $L$ is accepted by a 2dpda, then there is a linear-time algorithm to test whether $x$ belongs $L$ (for fixed size alphabets).

**Proof**

Let $G$ be a 2dpda, and let $w$ be a given input word of length $n$. Let us introduce two functions acting on top configurations:

— $P1(C) = C'$, where $C'$ results from $C$ by a push move; this is defined only for push configurations;

— $P2(C1, C2) = C'$, where $C'$ results from $C2$ by a pop move, and the top symbol of $C'$ is the same as in $C1$ ($C2$ determines only the state and the position).

Let $POP$ be the boolean function defined by: $POP(C)$ = true iff $C$ is a pop configuration.

All these functions can be computed in constant time by a random access machine using the (constant sized) description of the automaton.

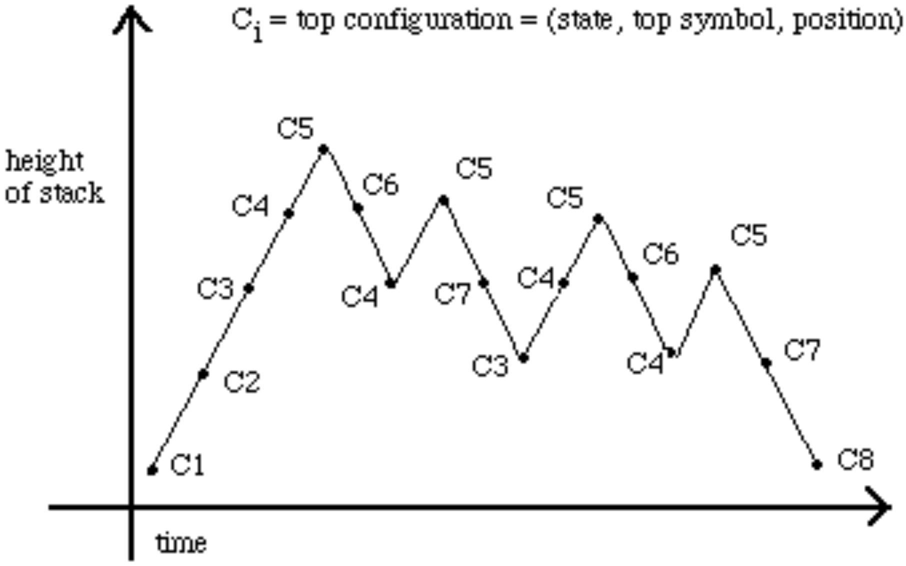

**Figure 7.21**. The diagram representing the history of the computation of a 2dpda.
$Term[C3] = C7$, $Term[C2] = Term[P2(C2, Term[P1(C2)])]$,
where $P1(C2) = C3$, $Term[C3] = C7$ and $P2(C2, C7) = C3$, $Term[C3] = C7$.

It is enough to compute in linear time the value (or find that it is undefined) of $Term[C0]$, where $C0$ is an initial top configuration. According to our simplifying assumptions about

2dpda's, if *G* accepts, then *Term*[*C*0] is defined. Assume that initially all entries of the table *Term* contain a special value "not computed".
We start with an assumption that *G* never loops, and ends with a one-element stack. In fact, if the move of *G* is at some moment undefined we can assume that it goes to a state in which all the symbols in the stack are successively popped.

```
Algorithm; { linear-time simulation of the halting 2dpda }
begin
  for all configuration C do onstack[C] := false;
  return Comp(C0);
end.

function Comp(C) ; { returns Term[C] if defined, else 'false' }
begin
  if Term[C] = "not computed" then
    Term[C] := if POP(C) then C else Comp(P2(C, Comp(P1(C))));
  return Term[C]
end;
```

The correctness and time linearity of the algorithm above are obvious in the case of an halting automaton. The statement "`Term[C] := ...` " is executed at most once for each *C*. Hence, only a linear number of push moves (using function *P*1) are applied.

```
Algorithm Simulate;
{ a version of the previous algorithm that detects loops }
begin
  for all configuration C do onstack[C] := false;
  return Comp(C0);
end.

function Comp(C) ;
{ returns Term[C] if defined, 'false' otherwise }
begin { C1 is a local variable }
  if Term[C] = "not computed" then begin
    C1 := P1(C);
    if onstack[C1] then return false { loop }
    else onstack[C1] := true;
    C1 := Comp(C1); onstack[C1] := false; { pop move };
    C1 := P2(C, C1);
    if onstack[C1] then return false { loop } else begin
      onstack[C] := false; onstack[C1] := true
    end;
    Term[C] := Comp(C1)
  end;
  return Term[C]
end;
```

The algorithm *Simulate* above is for a general case: it has also to detect a possible looping of *G* for a given input. We use the table *onstack* initially consisting of values 'false'. Whenever we make a push move then we set *onstack*[*C*1] to true for the current top configuration *C*1, and whenever a pop move is done we set *onstack*[*C*1] to false. The looping is detected if we try to put on the (imaginary) stack of top configurations a configuration which is already on the stack. If there is a loop then such situation happens.

The algorithm *Simulate* has also a linear time complexity, by the same argument as in the case of halting 2dpda's. This completes the proof. ‡

It is sometimes quite difficult to design a 2dpda for a given language *L*, even if we know that such 2dpda exists. An example of such a language *L* is:

$$L = \{ 1^n : n \text{ is the square of an integer}\}.$$

A 2dpda for this language can be constructed by a method presented in [Mo 85].

It is much easier to construct 2dpda's for the following languages:

$$\{a^nb^m : m = 2^n\}, \{a^nb^m : m = n^4\}, \{a^nb^m : m = \log^*(n)\}.$$

But it is not known whether there is a 2dpda accepting the set of even palstars, or the set of all palstars. In general, there is no good technique to prove that a specific language is not accepted by any 2dpda. In fact the "P = NP?" problem can be reduced to the question: does it exists a 2dpda for a specific language $L$. There are several examples of such languages. Generally, 2dpda's are used to give alternative formulations of many important problems in complexity theory.

## Bibliographic notes

Two "simple" pattern matching machines are discussed by Aho, Hopcroft, and Ullman in [AHU 74] and, in the case of many patterns, by Aho and Corasick in [AC 75]. The algorithms first compute failure functions, and then the automata. The construction given in Section 7.1 are direct constructions of the pattern matching machines. The algorithm of Aho and Corasick is implemented by the command "fgrep" of the Unix system.

A version of *BM* algorithm adapted to the search for a finite set of pattern has been first sketched by Commentz-Walter [Co 79]. The algorithm has been completed by Aho [Ah 90]. Another version of Commentz-Walter's algorithm is presented in [BR 90]. The version of multiple search of Section 7.2 is from Crochemore et alii [C-R 93], where are presented experiments on the real behavior of the algorithm.

The recognition of regular expressions is a classical subject treated in many books. The first algorithm is from Thompson [Th 68]. The equivalence between regular expressions and finite automata is due to Kleene [Kl 56]. The equivalence between deterministic automata an non-deterministic automata is from Rabin and Scott [RS 59]. The very useful command "grep" of Unix implements the pattern algorithm based on non-deterministic automata (Theorem 7.9). The command "egrep" makes the search with a deterministic automaton (Theorem 7.10). But the states of the automaton are computed only when they are effectively reached during the search (see [Ah 90]).

The determinization of automata can be found in the standard textbook of Hopcroft and Ullman [HU 79]. The question of efficient determinization of automata is from Perrin [Pe 90]. This paper is a survey on the main properties and last discoveries about automata theory.

The reader can refer to [KMP 77] for a discussion about the 2dpda approach to string-matching (see also [KP 71]).

The linear-time simulation of 2dpda's is from Cook [Co 71] (see also the presentation by Jones [Jo 77]). Our presentation is from Rytter [Ry 85]. This paper also gives a different algorithm similar to the efficient recognition of unambiguous context-free languages. We refer to Galil [Ga 77] for the theoretical significance of 2dpda's, and interesting theoretical other questions. An example of interesting 2dpda computation can be found in [Mo 84].

## Selected references

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# 8. Regularities in texts: symmetries and repetitions

This chapter presents algorithms dealing with regularities in texts. By a regularity we mean here a similarity between one factor and some other factors of the text. Such a similarity can be of two kinds: one factor is an exact copy of the other, or it is a symmetric copy of the other. Algorithmically, an interesting question is to detect situations in which similar factors are consecutive in the text. For exact copies we get repetitions of of the same factor of the form $xx$ (squares). In the case of symmetric copies we have words of the form $xx^R$, called even palindromes. Odd palindromes are also interesting regularities: words of the form $xax^R$, where $x$ is a nonempty word. The compositions of very regular words are in some sense also regular: a palstar is a composition of palindromes and analogously a squarestar is a composition of squares. Algorithms of the chapter are aimed at discovering regularities in text.

## 8.1. KMR algorithm: longest repeated factors in words and arrays

We start with a search for copies of the same factor inside a text. Let us denote by *lrepfac*(*text*) the length of the *longest repeated factor* of *text*. It is the longest word occurring at least twice in *text* (occurrences are not necessarily consecutive). When there are several such longest repeated factors, we compute any of them. Let also $lrepfac_k(text)$ be the longest factor which occurs at least $k$ times in *text*.

The central notion used in algorithms of the section is called *naming* or *numbering*. It serves to compute longest repeated factors, but its range of application is much wider. The algorithm that attributes numbers is called *KMR*, and described below.

To explain the technique of numbering, we begin with the search for repetitions of factors of a given length $r$. The algorithm will be an example of the reduction of a string problem to a sorting problem. Suppose that there are $k$ distinct factors of length $r$ (in fact $k$ is computed by the algorithm) in the *text*. Let $fac(1), fac(2),\dots, fac(k)$ be the sequence of these $k$ different factors in lexicographic order. The algorithm computes the vector $NUM_r$ of length $n\text{-}r$, whose $i$-th component is (for $i = 1\dots n\text{-}r\text{+}1$):

$$NUM_r[i] = j \text{ iff } text[i\dots i\text{+}r\text{-}1] = fac(j).$$

In other words, for each position $i$ ($i = 1\dots n\text{-}r$), $NUM_r$ identifies the rank or index $j$, inside the ordered list, of the factor of length $r$ which starts at this position. For example if $text = ababab$ and $r = 4$ we have $fac(1) = abab$, $fac(2) = baba$ and $NUM_4 = [1, 2, 1]$. In this sense, we compute equivalence classes of positions: two positions are $r$-equivalent iff the factors of length $r$ starting at these positions are equal. We denote the equivalence on positions by $\equiv_r$. Then, for two position $i$ and $j (1 \le i, j \le n\text{-}r\text{+}1)$,

$$i \equiv_r j \text{ iff } NUM_r[i] = NUM_r[j].$$

The equivalences on *text* are strongly related to the suffix tree of *text*.

**Remark**

String-matching can be easily reduced to the computation of the table $NUM_m$ defined on *text*, for a pattern *pat* of length *m*. Consider the string *w* = *pat*&*text*, where & is a special symbol not in the alphabet. If $NUM_m[1] = q$ then the pattern *pat* starts at all positions *i* in *text* (relative to *w*) such that $NUM_m[i] = q$.

The algorithm *KMR* described below is aimed at computing $NUM_r$. For simplicity, we start with the assumption that *r* is a power of two. Later the assumption is dropped. We describe a special function RENUMBER(*x*) used at each step of *KMR* algorithm. The value of RENUMBER applied to the vector *x* is the vector $NUM_1$ associated to *x* which is treated as a text. Doing so, the alphabet of *x* consists of all distinct entries of *x*; its size can be large, but it does not exceed the length of *x*. The function RENUMBER realizes one step of *KMR* algorithm.

Let *x* be a vector (an array) of size *n* containing elements of some linearly ordered set. The function RENUMBER assigns to *x* a vector *x*'. Let *val*(*x*) be the set of values of all entries of *x*. The vector *x*' satisfies:

(a) if $x[i] = x[j]$ then $x'[i] = x'[j]$, and

(b) *val*(*x*') is a subset of [1…*n*].

There are two variations of the procedure depending on whether the following condition is also satisfied:

(c) $x'[i]$ is the rank of $x[i]$ in the ordered list of elements of *val*(*x*).

Note that condition (c) implies the two others, and can be used to define *x*'. But the real values $x'[i]$'s are of no importance because their role is to identify equivalence classes. We require also that the procedure computes as a side effect the vector *POS*: if *q* is in val(*x*') then *POS*[*q*] is any position *i* such that $x'[i] = q$.

The main part of the algorithm RENUMBER (satisfying conditions (a-c)) is the lexicographic sort. We explain the action of RENUMBER on the following example:

$$x = [(1, 2), (3, 1), (2, 2), (1, 1), (2, 3), (1, 2)].$$

We give a method to compute a vector *x*' satisfying conditions (a) and (b). We first create the vector *y* of composite entries $y[i] = (x[i], i)$. Then, the entries of *y* are lexicographically sorted. So, we get the ordered sequence

$$((1, 1), 4), ((1, 2), 1), ((1, 2), 6), ((2, 2), 3), ((2, 3), 5), ((3, 1), 2).$$

Next, we partition this sequence into groups of elements having the same first component. These groups are consecutively numbered starting from 1. The last component *i* of each element is used to define the output vector: $x'[i]$ is the number associated to the group of the element. So, in the example, we get

$$x'[4] = 1, x'[1] = 2, x'[6] = 2, x'[3] = 3, x'[5] = 4, x'[2] = 5.$$

Doing so is equivalent to computing the vector $NUM_1$ for $x$. A vector $POS$ associated to $x'$ is

$$POS[1] = 4, POS[2] = 1, POS[3] = 3, POS[4] = 5, POS[5] = 2. ‡$$

**Lemma 8.1**

If the vector $x$ has size $n$, and its components are pairs of integers in the range (1, 2, ..., $n$), RENUMBER($x$) can be can be computed in time $O(n)$.

**Proof**

The linear time lexicographic sorting based on bucket sort can be applied (see [AHU 83], for instance). In this way, procedure RENUMBER has the same complexity as sorting $n$ elements of a special form. ‡

The crucial fact that gives the performance of algorithm *KMR* is the following simple observation:

(*) $NUM_{2p}[i] = NUM_{2p}[j]$ iff $(NUM_p[i] = NUM_p[j])$ and $(NUM_p[i+p] = NUM_p[j+p])$.

This fact is used in *KMR* algorithm to compute vectors $NUM_r$. Let us look at how the algorithm works for the example string *text* = *abbababba* and $r = 4$. The first vector $NUM_1$ identifies the letters in *text*:

$$NUM_1 = [1, 2, 2,1, 2,1, 2, 2,1].$$

Then, the algorithm computes successively vectors $NUM_2$, and finally $NUM_3$.

$$NUM_2 = [1, 3, 2, 1, 2,1, 3, 2];$$
$$NUM_4 = [2, 5, 3, 1, 4, 2].$$

```
Algorithm KMR;
{ relatively to text, computes the vector $NUM_r$ (r is a power}
{ of two) and, as a side effect, vectors $NUM_p$ ($p = 2^q < r$)     }
begin
  $NUM_1$ := x := RENUMBER(text); { text considered as a vector }
  p := 1;
  while p < r do begin
    for i := 1 to n-2p+1 do y[i] := (x[i], x[i+p]);
    $NUM_{2p}$ := RENUMBER(y);
    p := 2.p;
  end;
end.
```

Once all vectors $NUM_P$, for all powers of two smaller than $r$, are computed we can easily compute for each integer $q < r$ the vector $NUM_q$ in linear time. Let $q'$ be the greatest power of two not greater than $q$. We can compute $NUM_q$ using a fact similar to (*):

$$NUM_q[i] = NUM_q[j] \text{ iff } (NUM_{q'}[i] = NUM_{q'}[j]) \text{ and } (NUM_{q'}[i+q-q'] = NUM_{q'}[j+q-q']).$$

Equivalences on positions of a text (represented by vectors $NUM_P$) computed by *KMR* algorithm, capture the repetitions in the text. The algorithm is a general strategy that can serve several purposes. A first application, provides a longest factor repeated at least $k$ times in the text (recall that its length is denoted by $lrepfac_k(text)$). And it can produce at the same cost the position of such a factor. Let us call it $REP_k(r, text)$. If $r$ is its length, and if the vector $NUM_r[i]$ on *text* is known, then $lrepfac_r(text)$ can be trivially computed in linear time.

**Theorem 8.2**

The function $lrepfac_k(text)$ can be computed in $O(n.\log n)$ time for alphabets of size $O(n)$.

**Proof**

We can assume that length $n$ of the text is a power of two; otherwise a suitable number of "dummy" symbols can be appended to text. The algorithm *KMR* can be used to compute all vectors $NUM_p$ for powers of two not exceeding $n$. Then we apply a kind of binary search using function $REP_k(r, text)$: the binary search looks for the maximum $r$ such that $REP_k(r, text) \neq$ nil. If the search is successful than we return the longest ($k$ times) repeated factor. Otherwise we report that there is no such repetition. The sequence of values of $REP_k(r, text)$ (for $r = 1, 2, \ldots, n\text{-}1$) is "monotonic" is the following sense: if $r1 < r2$ and $REP_k(r2, text) \neq$ nil, then $REP_k(r1, text) \neq$ nil. The binary search behaves like searching an element in a monotonic sequence. It has $\log n$ stages; in each stage the value $REP_k(r, text)$ is computed in linear time. Altogether the computation takes $O(n.\log n)$ time. This completes the proof. ‡

**Remark**

We give later in Section 8.2 a linear time algorithm for this problem. However it will be more sophisticated, and it uses one of the structures from Chapters 5 and 6.

The longest repeated factor problem generalizes in a straightforward way to an equivalent two-dimensional problem. It is called the *longest repeated sub-array* problem. We are given an $n\times n$ array $T$. The size of the problem is $N = n^2$. For this problem *KMR* algorithm gives $O(N.\log N)$ time complexity, which is the best upper bound known up to now. The algorithm works as well for finding repetitions in trees.

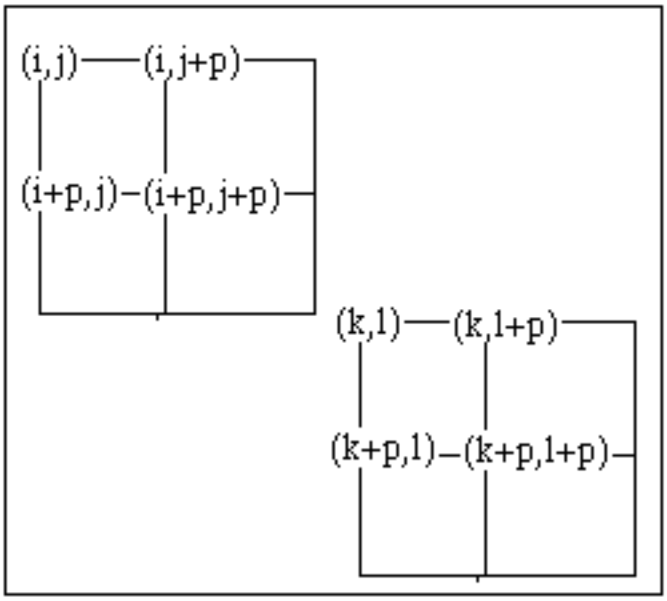

**Figure 8.1**. A repeated sub-array of size 2*p*×2*p*. The occurrences can overlap.

Still, numbering is used on sub-arrays. Let $NUM_r[i, j]$ be the number of the *r*×*r* sub-array of the array *T* having its upper-left corner at position (*i*, *j*). There is a fact, analogue to (*), illustrated by Figure 8.1:

$$(**)\ NUM_{2p}[i, j] = NUM_{2p}[k, l] \text{ iff}$$
$$NUM_p[i, j] = NUM_p[k, l] \text{ and } NUM_p[i+p, j] = NUM_p[k+p, l] \text{ and}$$
$$NUM_p[i, j+p] = NUM_p[k, l+p] \text{ and } NUM_p[i+p, j+p] = NUM_p[k+p, l+p].$$

Using fact (**) all the computation of repeating 2*p*×2*p* sub-array reduces to the computation of repeating *p*×*p* sub-arrays. The matrix $NUM_{2p}$ is computed from $NUM_p$ by a procedure analogue to RENUMBER. Now, the internal lexicographic sorting is done on elements having four components (instead of two for texts). But, Lemma 8.1 still holds in this case, such as *KMR* algorithm that is deduced from RENUMBER. This proves the following.

**Theorem 8.3**

The size of a longest repeated sub-array of an *n*×*n* array of symbols can be computed in $O(N.\log N)$ time, where $N = n^2$.

The longest repeated factor problem for texts can be solved in a straightforward way if we have already constructed the suffix tree *T*(*tree*) (see Section 5.7). The value *lrepfac*(*text*) is the longest path (in the sense of length of word corresponding to the path) leading from the root of *T*(*tree*) to an internal node. Generally, $lrepfac_k(text)$ is the length of a longest path leading from the root to an internal node whose subtree contains at least *k* leaves. The computation of such a path can be accomplished easily in linear time. The preprocessing needed to construct the suffix tree makes the whole algorithm much more complicated than the one applying the strategy of *KMR* algorithm. Nevertheless, this proves that the computation takes linear time.

**Theorem 8.4**

The function $lrepfac_k$ can be computed in time linear in the length of the input text, for fixed size alphabets.

## 8.2. Finding squares

It is a nontrivial problem to find a square factor in linear time, that is, a non-empty factor of the form *xx*. A naive algorithm gives cubic bound on the number of steps. A simple application of failure function gives a quadratic algorithm. For that purpose, we can compute a failure function $Bord_i$ for each suffix *text*[*i*...*n*] of the text. Then, there is a square starting at position *i* in the text iff $Bord_i[j] \geq j/2$, for some *j* ($1 \leq j \leq n\text{-}i+1$). Since each failure function is computed in linear time, the whole algorithm takes quadratic time.

The notions introduced in Section 8.1 are useful to find a square of a given length *r*. Using $NUM_r$ the test takes linear time, giving an overall $O(n.\log n)$ time algorithm. In fact, values of $NUM_r$, for all sensible values of *r*, can help to find squares at a similar cost, but *KMR* algorithm does not provide all these vectors.

We develop now an $O(n.\log n)$ algorithm that test the squarefreeness of texts. And design afterwards a linear time algorithm (for fixed alphabets). The first method is based on a divide-and-conquer approach. The main part of both algorithms is a fast implementation of the boolean function *test*(*u*, *v*) which tests whether the word *uv* contains a square for two squarefree words *u* and *v*. Then, if *uv* contains a square, it necessarily begins in *u* and ends in *v*. Thus, the operation *test* is a composition of two smaller boolean functions: *righttest* and *lefttest*. The first one searches for a square whose center is in *v*, while the second searches for a square whose center is in *u*.

We describe how *righttest* works on words *u* and *v*. We use two auxiliary tables related to string-matching. The first table *PREF* is defined on the word *v*. For a position *k* on *v*, *PREF*[*k*] is the size of longest prefix of *v* occurring at position *k* (it is a prefix of *v*[*k*+1...]. The second table is called *SUF*. The value $SUF_u[k]$ (*k* is still a position on *v*) is the size of longest suffix of *v*[1...*k*] which is also a suffix of *u*. Table $SUF_u$ is a generalization of table *S* discussed in Section 4.6. These tables can be computed in linear time with respect to |*v*| (see Section 4.6). With the two tables, the existence of a square in *uv* centered in *v* reduces to a simple test on each position of *v*, as shown by Figure 8.2.

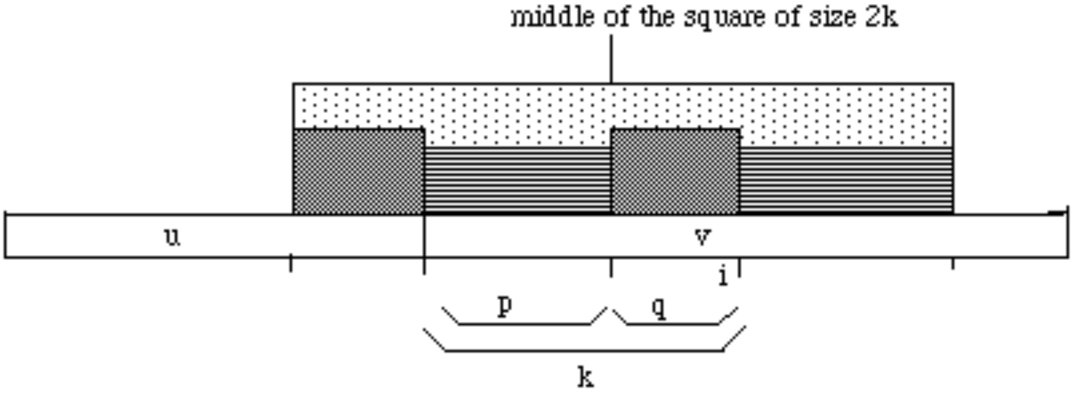

**Figure 8.2**. A square *xx* of size 2*k* occurs in *uv*. The suffix of *v*[1…*k*] of size *q* is also a suffix of *u*; the prefix of *v*[*k*+1…] of size *p* is a prefix of *v*. $PREF[k]+SUF_u[k] \geq k$.

**Lemma 8.5**

The boolean value *righttest*(*u*, *v*) can be computed in *O*(|*v*|) time (independently of the size of *u*).

**Proof**

The computation of tables *PREF* and $SUF_u$ takes *O*(|*v*|) time. It is clear (see Figure 8.2) that there exists a square centered in *v* iff for some position *k* $PREF[k]+SUF_u[k] \geq k$. All these tests take again *O*(|*v*|) time. ‡

**Corollary 8.6**

The boolean value *test*(*u*, *v*) can be computed in O(|*u*|+|*v*|) time.

**Proof**

Compute *righttest*(*u*, *v*) and *lefttest*(*u*, *v*). The value *test*(*u*, *v*) is the boolean value of *righttest*(*u*, *v*) or *lefttest*(*u*, *v*). The computation takes respectively *O*(|*v*|) (Lemma 8.5), and *O*(|*u*|) time (by symmetry from Lemma 8.5). The result follows. ‡

We give another very interesting algorithm computing *righttest*(*u*, *v*) in linear time according to *v*, but requiring only a constant additional memory space. It is based on the following combinatorial fact:

— if *u*, *v* are squarefree, and we have a situation as in Figure 8.3 (where segments painted with same color indicate which factors are equal) then $i' < \max(j, i/2)$ and $i'+j' < test$.

The proof is rather technical and is left to the reader as an excellent exercise on word combinatorics.

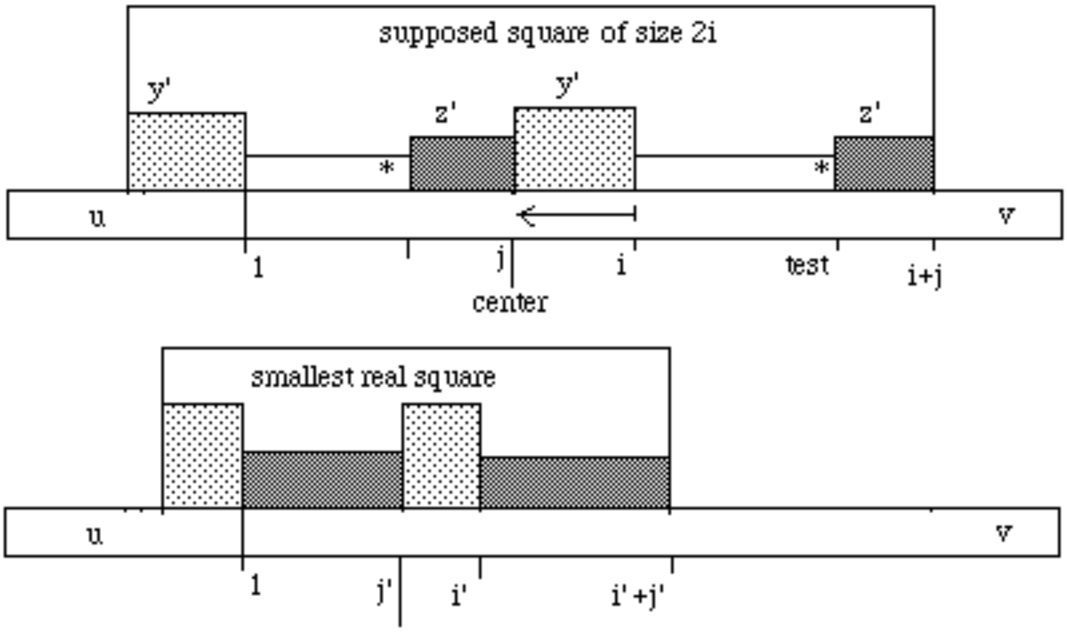

**Figure 8.3**. One stage of an algorithm to compute *righttest*(*u*, *v*): start at *i* and check right-to-left until a mismatch at *j*; then, assume the middle of a square at *j*, and check from *i*+*j* right-to-left until a mismatch occurs at position *test*. Parts of text painted with the same pattern match. Each part can be empty, but not all together.

One stage of the algorithm consists in finding largest matching segments painted with ░, and then, (if *i*+*j* < *test*) in finding largest matching segments painted with ▓. If we reach position 1 then a square is found. Otherwise we set *i* := *i*', where *i*' can be taken small according to the combinatorial fact above. Then, we start the next (similar) stage.

```
function righttest($u$, $v$) : boolean;
{ return true iff $uv$ contains a square centered in $v$ }
begin
  $i := |v|$; $test := |v|+1$;
          { initially, no reasonable bound on $i+j$ is known }
  while $i \geq 1$ do begin
    $j := i$;
    { traversing right-to-left segments painted with ░ }
    while $j \geq 1$ and $|u|-i+j \geq 1$ and $u[|u|-i+j] = v[j]$ do
        $j := j-1$;
    if $j = 0$ then return true;
    $k := i+j$;
    if $k < test$ then begin
      $test := k$;
    { traversing right-to-left segments painted with ▓ }
      while $test > i$ and $v[test] = v[j-k+test]$ do
          $test := test-1$;
      if $test = i$ then return true;
    end; { if }
    $i := \max(j, \lceil i/2 \rceil)-1$;
  end; { main while loop }
  return false; { no square centered in $v$ }
end;
```

We leave as an exercise the proof that the algorithm makes only a linear number of steps. Symmetrically *lefttest* can be accomplished in linear time using also a constant-sized memory. So can implemented the function *test*.

**Lemma 8.7**

The function *test* can be computed in linear time using only O(1) auxiliary memory.

The recursive algorithm *SQUARE* for testing occurrences of squares in a text is designed with the divide-and-conquer method, for which function *test* has been written.

**Theorem 8.8**

Algorithm *SQUARE* tests whether the text *text* of length *n* contains a square in time $O(n.\log n)$ with $O(1)$ additional memory space.

**Proof**

The algorithm has $O(n.\log n)$ time complexity, because *test* can be computed in linear time. The recursion has a highly regular character, and can be organized without using a stack. It is enough to remember the depth of recursion and the current interval. The tree of recursion can be computed in a bottom-up manner, level-by-level. This completes the proof. ‡

```
function SQUARE(text) : boolean;
{ checks if text contains a square, $n$ = |text| }
begin
  if $n > 1$ then begin
    if SQUARE(text[1..$\lfloor n/2 \rfloor$]) then return true;
    if SQUARE(text[$\lfloor n/2 \rfloor$+1..$n$]) then return true;
    if test(text[1..$\lfloor n/2 \rfloor$], text[$\lfloor n/2 \rfloor$+1..$n$]) then return true;
    return false;   { if value true not already returned }
end;
```

The algorithm *SQUARE* inherently runs in $O(n.\log n)$ time. This is due to the divide-and-conquer strategy for the problem. But, it can be shown that the algorithm extends to the detection of all squares in a text. And this shows that the algorithm becomes optimal, because some texts may contain exactly $O(n.\log n)$ squares, namely Fibonacci words.

We show that the question of testing the sqaurefreeness of a word can be done in linear time on a fixed alphabet. This contrasts with the above problem. The strategy will be again to use a kind of divide-and-conquer, but with an unbalanced nature. It is based on a special factorization of texts. The interest is mainly theoretical because of a rather large overhead in memory usage: the extra memory space is of linear size (instead of $O(1)$ for *SQUARE*), and an efficient data structure for factors of the text has to be used. But the algorithm, or more exactly the factorization defined for the purpose, is related to data compressions methods based on elimination of repetitions of factors. The algorithm shows another deep application of data structures developed in Chapters 5 and 6 for storing all factors of a text.

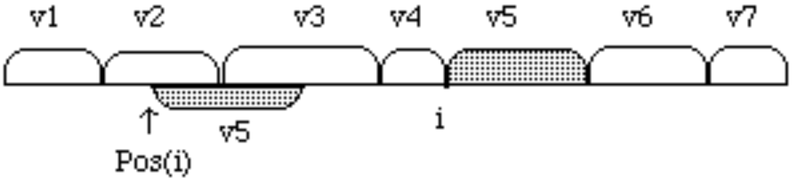

**Figure 10.5**. Efficient factorization of the source.
$v_5$ is the longest factor occurring before.

We first define the *f*-factorization of *text* (the *f* stands for factors). It is a sequence of nonempty words $(v_1, v_2,\ldots, v_m)$, where

— $v_1 = text[1]$, and

— for $k > 1$, $v_k$ is defined as follows. If $|v_1v_2\ldots v_{k-1}| = i$ then $v_k$ is the longest prefix $u$ of $text[i+1\ldots n]$ which occurs at least twice in $text[1\ldots i]u$. If there is no such $u$ then $v_k = text[i+1]$. Denote by $pos(v_k)$ the smallest position $l < i$ (where $i = |v_1v_2\ldots v_{k-1}|$) such that an occurrence of $v_k$ starts at $l$. If there is no such position then take $pos(v_k) = 0$.

The *f*-factorization of a *text*, and the computation of values $pos(v_k)$ can be done in linear time with the directed acyclic word graphs $G = DAWG(text)$ (also with the suffix tree $T(text)$). Indeed, the factorization is computed while the dawg is built. The overall has the same asymptotic linear bound as just building the dawg. This leads to the final result of the section, consequence of the following observation whose proof is left as an exercise.

**Lemma 8.9**

Let $(v_1, v_2,\ldots, v_m)$ be the *f*-factorization of *text*. Then, *text* contains a square iff for some $k$ at least one of the following conditions holds:

(1) $pos(v_k)+|v_k|\geq|v_1v_2\ldots v_{k-1}|$ (selfoverlapping of $v_k$),

(2) $lefttest(v_{k-1}, v_k)$ or $righttest(v_{k-1}, v_k)$,

(3) $righttest(v_1v_2\ldots v_{k-2}, v_{k-1}v_k)$.

```
function linear-SQUARE(text) : boolean;
{ checks if text contains a square, n = |text| }
begin
  compute the f-factorization ($v_1$, $v_2$, .., $v_m$) of text;
  for k :=1 to m do
    if (1) or (2) or (3) hold then { Lemma 8.9 }
      return true;
  return false;
end;
```

**Theorem 8.10**

Function *linear-SQUARE* tests whether a text of length $n$ contains a square in time $O(n)$ (on a fixed alphabet), with $O(n)$ additional memory space.

**Proof**

The key point is that the computation of $righttest(v_1v_2...v_{k-2}, v_{k-1}v_k)$ can be done in $O(|v_{k-1}v_k|)$ time. The total time is thus proportional to the sum of length of all $v_k$'s, hence, it is linear. This completes the proof. ‡

## 8.3. Symmetries in texts

We start with a decision problem which consists in verifying if a given text has a prefix which is a palindrome (such palindromes are called prefix palindromes). There is a very simple linear time algorithm to search for a prefix palindrome:

— compute the failure function *Bord* for $text\&text^R$ (of length $2n+1$),

— then, text has a prefix palindrome iff $Bord(2n+1) \neq 0$.

However, this algorithm has two drawbacks: it is not an on-line algorithm, and moreover, we could expect to have an algorithm which computes the smallest prefix palindrome in time proportional to the length of this palindrome (if a prefix palindrome exists). It will be seen later in the section (when testing palstars) why we impose such requirement.

For time being, we restrict ourselves to even palindromes. We proceed in a similar way as in the derivation of *KMR* algorithm. An efficient algorithm will be derived from an initial *brute_force* algorithm by examining its invariants. However here more combinatorics on words is used (as compared with *KMR* algorithm).

Observe a strong similarity between this algorithm and the first algorithm for string-matching, *brute_force1*. The time complexity of the algorithm is quadratic (in worst case). A simple instance of a worst text for the algorithm is $text = ab^n$. On the other hand, the same analysis as for algorithm *brute_force1* (string-matching) shows that the expected number of comparisons (if symbols of text are randomly chosen) is linear.

```
Algorithm brute_force;
{ looking for prefix even palindromes }
begin
  i := 1;
  while i ≤ ⌊n/2⌋ do begin
    { check if text[1..2i] is a palindrome }
    j := 0;
    while j < i and text[i-j] = text[i+1+j] do j := j+1;
    if j = i then return true;
    { inv(i, j): text[i-j] ≠ text[i+1+j] }
    i := i+1;
  end;
  return false;
end.
```

The key to the improvement is to make an appropriate use of the information gathered by the algorithm. This information is expressed by invariant

$$w(i, j) : text[i\text{-}j\ldots i] = text[i+1\ldots i+j].$$

The maximum value of $j$ satisfying $w(i, j)$ for a given position $i$ is called the radius of the palindrome centered at $i$, and denoted by $Rad[i]$. Hence, algorithm *brute_force* computes values of $Rad[i]$ but does not profit from their computation. The information is wasted. At the next iteration, the value of $j$ is reset to 0. Instead of that, we try to make use of all possible information, and, for that purpose, the computed values of $Rad[i]$ are stored in a table for further use. The computation of prefix palindromes easily reduces to the computation of table *Rad*. Hence, we convert the decision version of algorithm *brute_force* into its optimized version computing *Rad*. For simplicity assume that the text starts with a special symbol. So a palindrome centered in $i$ is actually a prefix palindrome iff $Rad[i] = i\text{-}1$.

The key to the improvement is not only a mere recording of table *Rad*, but also a surprising combinatorial fact about symmetries in words. Suppose that we have already computed $Rad[1]$, $Rad[2]$,...., $Rad[i]$. It happens that we can sometimes compute many new entries of table *Rad* without comparing any symbols. The following fact enables to do it.

**Lemma 8.11**

If $1 \le k \le Rad[i]$ and $Rad[i\text{-}k] \ne Rad[i]\text{-}k$, then $Rad[i+k] = \min(Rad[i\text{-}k], Rad[i]\text{-}k)$.

**Proof**

Two cases are considered.

— Case (a): *Rad*[*i-k*] < *Rad*[*i*]-*k*.

The palindrome of radius *Rad*[*i*+*k*] centered at *i-k* is contained completely in the longest palindrome centered in *i*. Position *i-k* is symmetrical to *i*+*k* with respect to *i*. Hence, by symmetry (with respect to position *i*) the longest palindrome centered in *i*+*k* has the same radius as the palindrome centered at *i-k*. This implies the conclusion in this case.

— Case (b): *Rad*[*i-k*] > *Rad*[*i*]-*k*.

The situation is displayed in Figure 8.4. The maximal palindromes centered at *i*, *i*+*k* and *i-k* are presented. Symbols *a*, *b* are distinct because of the maximality of the palindrome centered in *i*. Hence, *Rad*[*i*+*k*] = min(*Rad*[*i-k*], *Rad*[*i*]-*k*).

This completes the whole proof of the lemma. ‡

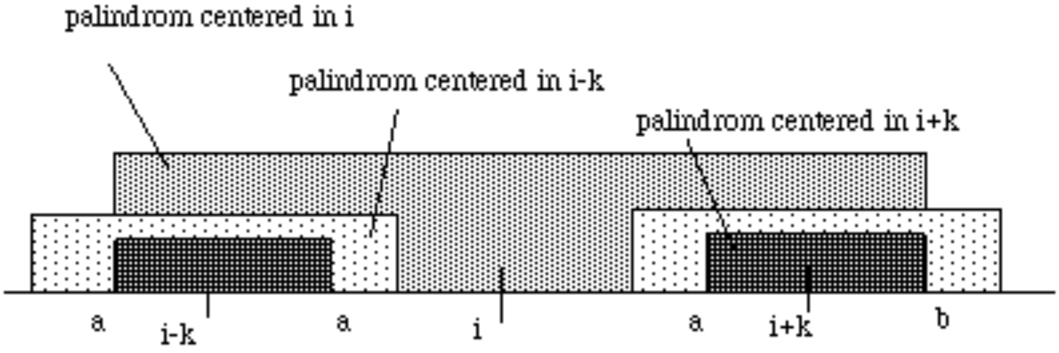

**Figure 8.4**. Case (b) of proof of Lemma 8.11.

In one stage of the algorithm that computes prefix palindromes, we can update *Rad*[*i*+*k*] for all consecutive positions *k* = 1, 2,... such that *Rad*[*i-k*] ≠ *Rad*[*i*]-*k*. If the last such *k* is, say, *k*' then we can later consider the next value of *i* as *i*+*k*', and start the next stage. This is similar to shifts applied in string-matching algorithms is whose values result form a precise consideration on invariants. We obtain the following algorithm for on-line recognition of prefix even palindromes and computation of the table of radii. All positions *i* satisfying *Rad*[*i*] = *i*-1 (occurrences of prefix palindromes) are output.

```
Algorithm Manacher;
{ on-line computation of prefix even palindromes,                }
{ and of table Rad; text starts with a unique left endmarker     }
begin
  i := 2; Rad[1] := 0; j := 0; { j = Rad[i] }
  while i ≤ ⌊n/2⌋ do begin
    while text[i-j] = text[i+1+j] do j := j+1;
    if j = i then write(i); Rad[i] := j;
    k := 1;
    while Rad[i-k] ≠ Rad[i]-k do begin
      Rad[i+k] := min(Rad[i-k], Rad[i]-k); k := k+1;
    end;
    { inv(i, j): text[i-j] ≠ text[i+1+j] }
    j := max(j-k, 0);
    i := i+k;
  end;
end.
```

The solution presented for the computation of prefix even palindromes adjusts easily to the table of radii of odd palindromes. They can also be computed in linear time. So are longest palindromes occurring in the text. Several other problems can be solved in a straightforward way using the table *Rad*.

**Theorem 8.12**

The longest symmetrical factor and the longest (or shortest) prefix palindrome of a text can be computed in linear time. If *text* has a prefix palindrome, and if *s* is the length of the smallest prefix palindrome, then *s* can be computed in time $O(s)$.

We now consider another question about regularities in texts. Let $P^*$ be the set of words which are compositions of even palindromes, and let $PAL^*$ denote the set of words composed of any type of palindromes (even or odd). Recall that one-letter words are not palindromes according to our definition (their symmetry is too trivial to be considered as an "interesting" symmetry).

Our aim is now to test whether a word is an *even palstar*, i.e. a member of $P^*$, or a *palstar*, i.e. a member of $PAL^*$. We begin with the easier case of even palstars.

Let *first*(*text*) be a function whose value is the first position *i* in text such that *text*[1…*i*] is an *even* palindrome; it is zero if there is no such prefix palindrome. The following algorithm, in a natural way, tests even palstars. It finds the first prefix even palindrome, and cuts it.

Afterwards, the same process is repeated as long as possible. If we are left with an empty string then the initial word is an even palstar.

```
function PSTAR(text) : boolean; { is text an even palstar ? }
begin
  s := 0;
  while s < n do begin { cut text[s+1..n] }
    if first(text[s+1..n])=0 then return false;
    s := s+first(text[s+1..n])
  end;
  return true;
end;
```

**Theorem 8.13**

Even palstars can be tested on-line in linear time.

**Proof**

It is obvious that the complexity is linear, even on-line. In fact, Manacher algorithm computes the function *first* on-line. An easy modification of the algorithm gives an on-line algorithm operating within the same complexity.

However, a more difficult issue is the correctness of function *PSTAR*. Suppose that *text* is an even palstar. Then, it seems reasonable to expect that its decomposition into even palindromes does not necessarily start with the shortest prefix even palindrome. Fortunately and surprisingly perhaps, it happens that we have always a good decomposition (starting with the smallest prefix palindrome) if *text* is an even palstar. So the greedy strategy of function *PSTAR* is correct. To prove this fact, we need some notation related to decompositions. It is defined only for texts that are even palindromes. Let

$$parse(text) = \min\{s : text[1\ldots s] \in P \text{ and } text[s+1\ldots n] \in P^*\}.$$

Now the correctness of the algorithm follows directly from the following fact about even nonempty palstars text.

**Claim:** $parse(text) = first(text)$.

**Proof** of the claim.

It follows from the definitions that $first(text) \le parse(text)$, hence it is sufficient to prove that the reverse inequality holds. The proof is by contradiction. Assume that *text* is an even palstar such that $first(text) < parse(text)$. Consider two cases,

— case (a): $parse(text)/2 < first(text) < parse(text)$,

— case (b): $2 \le first(text) \le parse(text)/2$.

The proof of the claim according to these cases is given in Figure 8.5. This completes the proof of the correctness and the whole proof of the theorem. ‡

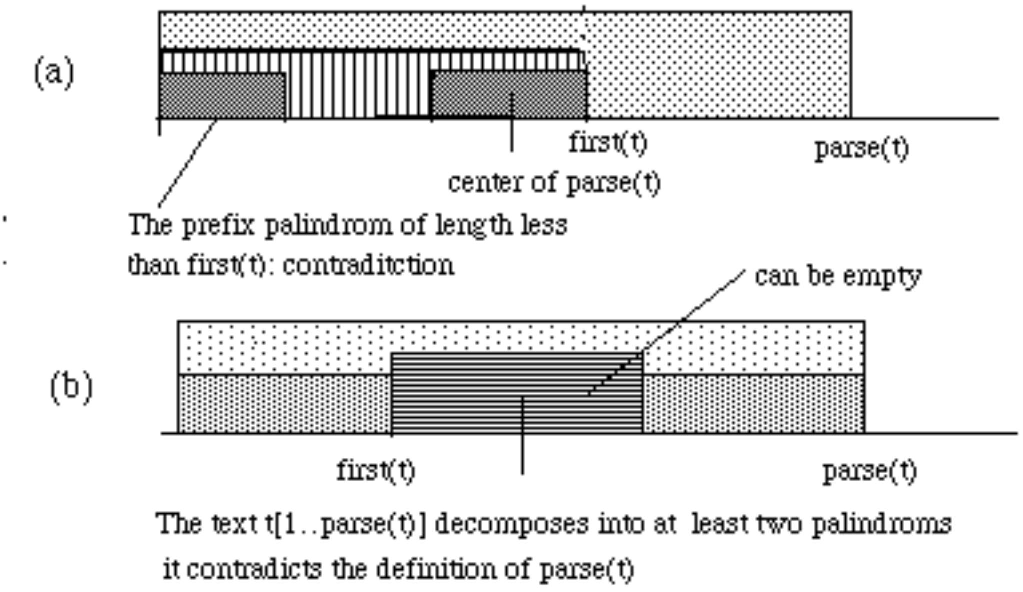
(a)
first(t)
parse(t)
center of parse(t)
The prefix palindrom of length less
than first(t): contraditction
can be empty
(b)
first(t)
parse(t)
The text t[1..parse(t)] decomposes into at least two palindroms
it contradicts the definition of parse(t)

**Figure 8.5** The proof of the claim (by contradiction).

If we try to extend the previous algorithm to all palstars, we are led to consider functions *first*1 and *parse*1, analogue to *first* and *parse* respectively, as follows:

$$parse1(text) = \min\{s : text[1\ldots s] \in PAL \text{ and } text[s+1\ldots n] \in PAL^*\},$$

$$first1(text) = \min\ \{s : text[1\ldots s] \in PAL\}.$$

Unfortunately, when *text* is a palstar the equality *parse*1(*text*) = *first*1(*text*) is not always true. A counterexample is the text *text* = *bbabb*. We have *parse*1(*text*) = 5 and *first*1(*text*) = 2. If *text* = *abbabba*, then *parse*1(*text*) = 7 and *first*1(*text*)=4. For *text* = *aabab*, we have *parse*1(*text*) = *first*1(*text*).

Observe that for the first text, we have *parse*1(*text*) = 2.*first*1(*text*)+1; for the second text, we have *parse*1(*text*) = 2.*first*1(*text*)-1; and for the third text, we have *parse*1(*text*) = *first*1(*text*). It happens that this is a general rule that only these cases are possible.

**Lemma 8.14**

Let *text* be a nonempty palstar, then

$$parse1(text) \in \{first1(text), 2.first1(text)\text{-}1, 2.first1(text)\text{+}1\}.$$

**Proof**

The proof is similar to the proof of the preceding lemma. In fact, the two special cases (2.*first*1(*text*)-1, 2.*first*1(*text*)+1) are caused by the irregularity implied at critical points by considering together odd and even palindromes. Let *f* = *first*1(*text*), and *p* = *parse*1(*text*). The proof of the impossibility of the situation ($f < p < 2.f$-1) is essentially presented in the case (a) of the Figure 8.5. The proof of the impossibility of two other cases ($p = 2.f$) and ($p > 2.f$+1) are similar. ‡

Assume that we have computed the tables $F[i]$ = *first*1(*text*$[i+1\ldots n]$) and $PAL[i]$=(*text*$[i+1\ldots n]$ is a palindrome) for $i$ = (0, 1, …, $n$). Then, the following algorithm recognizes palstars.

```
function PALSTAR(text): boolean; { palstar recognition }
begin
  palstar[n] := true; { the empty word is a palstar }
  for i := n-1 downto 0 do begin
    f := F[i];
    if f = 0 then palstar[i] := false
    else if PAL[i] then palstar[i] := true
    else palstar[i] := (palstar[i+f] or palstar[i+2f-1]
                                        or palstar[i+2f+1]);
  end;
  return palstar[0];
end.
```

**Theorem 8.15**

Palstars can be tested in linear time.

**Proof**

Assuming the correctness of function *PALSTAR*, to prove that it works in linear time, it is enough to show how to compute tables $F$ and $PAL$ in linear time. The computation of $PAL$ is trivial if the table *Rad* is known. This latter can be computed in linear time. More difficult is the computation of table $F$. For simplicity we restrict ourselves to odd palindromes, and compute the table

$$F1[j] = \min \{s : text[1\ldots s] \text{ is an odd palindrome, or } s = 0\}.$$

Assume *Rad* is the table of radii of odd palindromes. The radius of the palindrome of size $2k+1$ equals $k$. We say that $j$ is in the range of an odd palindrome centered at $i$ iff $i\text{-}j+1 \leq Rad[i]$ (see Figure 8.6).

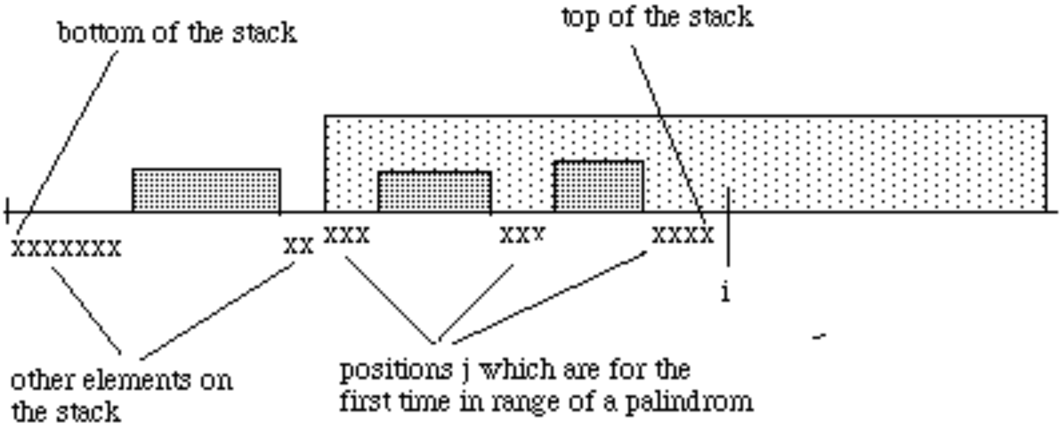

**Figure 8.6**. Stage(*i*): **while** the top position *j* is in the range of palindrome centered at *i* **do begin** *pop*(*stack*); *F*1[*j*] := 2(*j*-*i*)+1 **end**; *push*(*i*).

A stack of positions is used. Its convenient to have some special position at the bottom. Initially the first position 1 is pushed onto the stack, and *i* is set to 2. One stage begins with the situation depicted in the Figure 8.6. All x's are on the stack (entries of *F*1 waiting for their values). The whole algorithm is:

```
for i := 2 to n do stage(i);
for all remaining elements j on the stack do
{j is not in a range of any palindrome} F1[j] := 0.
```

The treatment of even palindromes is similar. Then *F*[*i*] is computed as the minimum value of even or odd palindromes starting at position *i*. This completes the proof. ‡

**Remark**

In fact the algorithm *PALSTAR* can be transformed into an on-line linear time algorithm. But this is outside the scope of the book.

It is perhaps surprising that testing whether a text is a composition of a fixed number of palindromes seems more difficult than testing for palstars. Recall that *P* denotes here the set of even palindromes. It is very easy to recognize compositions of exactly two words from *P*. The word *text* is such a composition iff for some internal position *i* *text*[1…*i*] and *text*[*i*+1…*n*] are even palindromes. This can be checked in linear time if table *Rad* is already computed. But this approach does not give directly a linear-time algorithm for $P^3$. Fortunately, there is another nice combinatorial property of texts useful for that. Its proof is omitted.

**Lemma 8.16**

If $x \in P$, then there is a decompositions of $x$ into words $x[1...s]$ and $x[s...n]$ such that both are members of $P$, and that either the first word is the longest prefix palindrome of $x$, or the second one is the longest suffix palindrome of $x$.

One can compute the tables of all longest palindromes starting or ending at positions of the word by a linear time algorithm very similar to that for table $F$. Assume now that we have such tables, and also the table *Rad*. Then one can check if any suffix or prefix of text is a member of $P^2$ in constant time because of Lemma 8.16 (only two positions to be checked using preprocessed tables). Now we are ready to recognize elements of $P^3$ in linear time. For each position $i$ we just check in constant time if $text[1...i] \in P^2$ and $text[i+1...n] \in P$. Similarly, we can test elements of $P^4$. For each position $i$ we check in constant time if $text[1...i] \in P^2$ and $text[i+1...n] \in P^2$. We have just sketched the proof of the following statement.

**Theorem 8.17**

The compositions of two, three and four palindromes can be tested in linear time.

As far as we know, there is presently no algorithm to test compositions of exactly five palindromes in linear time.

We have defined palindromes as nontrivial symmetric words (words of size at least two). One can say that for a fixed $k$, palindromes of size smaller than $k$ are also uninteresting. This leads to the definition of $PAL_k$ as palindromes of size at least $k$. Generalized palstars (compositions of words from $PAL_k$) can also be defined. For a fixed $k$, there are linear time algorithms for such palstars. The structure of algorithms, and the combinatorics of such palindromes and palstars are analogous to what has been presented in the section.

## Bibliographic notes

The algorithm *KMR* of the first section is from Karp, Miller and Rosenberg [KMR 72]. Another approach is presented in [Cr 81]. It is based on a modification of Hopcroft's partitioning algorithm [Ho 71] (see [AHU 74]), and the algorithm computes vectors $NUM_r$ for all sensible values of $r$. It yields an optimal computation of all repetitions in a word. The same result has been shown by Apostolico and Preparata [AP 83] as an application of suffix trees, and by Main and Lorentz [ML 84].

The first $O(n.\log n)$ algorithm for searching a square is by Main and Lorentz [ML 79] (see also [ML 84]). The procedure *righttest* of Section 8.2 is a slight improvement on the original algorithm proposed by these authors. The linear time algorithm of Section 8.2 is from

Crochemore [Cr 83] (see also [Cr 86]). A different method achieving linear time has been proposed by Main and Lorentz [ML 85].

The algorithm for prefix palindrome in Section 8.3 is from Manacher [Ma 75]. The material of the rest of the section is mainly from Galil and Seiferas [GS 78]. The reader can refer to [GS 78] for the proof of Lemma 8.16, or an on-line linear time algorithm for *PALSTAR*.

## Selected references

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# 9. Almost optimal parallel algorithms

By an efficient parallel algorithm we mean an NC-algorithm (see Chapter 2). Especially efficient are optimal and almost optimal parallel algorithms. By optimal we mean an algorithm whose total number of elementary operations is linear, while an almost optimal algorithm is one which is optimal within a polylogarithmic factor. From the point of view of any application, the difference between optimal and almost optimal algorithms is extremely thin. In this chapter, we present almost optimal algorithms for two important problems: string-matching, and suffix tree construction. In the first section we present an almost optimal parallel string-matching algorithm ($O(\log^2 n)$ time, $O(n)$ processors) which is based on a parallel version of the Karp-Miller-Rosenberg algorithm of Chapter 8, and is called *Parallel-KMR*. In fact, it is possible to design a string-matching algorithm using only $n/\log^2 n$ processors (which is strictly optimal), but such an algorithm is much more complicated to describe, and its structure is quite different than that of KMR algorithm. KMR algorithm is conceptually very powerful. The computation of regularities in Section 9.3 is derived from it. And, in the Section 9.4, we present an almost optimal parallel algorithm for the suffix tree construction that can be also treated as an advanced version of KMR algorithm.

Methodologically we apply two different approaches for the construction of efficient parallel algorithms:

(1) — design of a parallel version of a known sequential algorithm,

(2) — construction of a new algorithm with a good parallel structure.

The method (1) works well in the case of almost optimal parallel string-matching algorithms, and square finding. The known KMR algorithm, and the Main-Lorentz algorithm (for squares) have already a good parallel algorithmic structure. However, method (1) works poorly in the case of suffix tree construction, and Huffman coding, for instance. Generally, many known sequential algorithms look inherently sequential, and are hard to parallelize. All algorithms of Chapter 5 for the problem of suffix tree construction, and the algorithm of Chapter 10 for Huffman coding are inherently sequential. For these problems, we have to develop some new approaches, and construct different algorithms. In fact, the sequential version of our parallel algorithm for suffix tree construction gives a new simple and quite efficient sequential algorithm for this problem (working in $O(n.\log n)$ time). This shows a nice application of parallel computations to efficient sequential computations for textual problems.

Our basic model of parallel computations is a parallel random access machine without write conflicts (PRAM). But the PRAM model with write-conflicts (concurrent-writes) is also discussed (see Chapter 2). The PRAM model is best suited to work with tree structured objects or tree-like (recursive) structured computations. As a starter we show such a type of computation. One of the basic parallel operations is the (so-called) *prefix computation*.

Given a vector *x* of *n* values compute all prefix products: $y[1] = x[1]$, $y[2] = x[1]\otimes x[2]$, $y[3] = x[1]\otimes x[2]\otimes x[3]$, …. Denote by *prefprod*(*x*) the function which returns the vector *y* as value. We assume that ⊗ is an associative operation computable on a RAM in O(1) time. We also assume for simplicity that *n* is a power of two. The typical instances of ⊗ are arithmetic operations +, *min* and *max*. The parallel implementation of *prefprod* works as follows. We assign a processor to each entry of the initial vector of length *n*.

```
function prefprod(x); { the size of x is a power of two }
begin
  n : = size(x);
  if n = 1 then return x else begin
    $x_1$ := first half of x; $x_2$ := second half of x;
    for each $i \in \{1,2\}$ do in parallel $y_i$ : = prefprod($x_i$);
    midval : = $y_1[n/2]$;
    for each $1 \le j \le n/2$ do in parallel $y_2[j]$ : = midval$\otimes y_2[j]$;
    return concatenation of vectors $y_1$, $y_2$;
  end;
end.
```

**Lemma 9.1**

Parallel prefix computation can be accomplished in $O(\log n)$ time with $n/\log n$ processors.

**Proof**

The algorithm above for computing *prefprod*(*x*) takes $O(\log n)$ time and uses *n* processors. The reduction of the number of processors by a factor log*n* is technical. We partition the vector *x* into segments of length log*n*. A processor is assigned to each segment. All such processors simultaneously compute all prefix computations locally for their segments. Each processor makes it by a sequential process. Then, we compress the vector by taking from each segment a representative (say the first element). A vector *x*' of size *n*/log*n* is obtained. The function *prefprod* is applied to *x*' (now *n*/log*n* processors suffice because of the size of *x*'). Finally, all processors assigned to segments update values for all entries in their own segments using a (globally) correct value of the segment representative. This again takes $O(\log n)$ time, and uses only *n*/log*n* processors. This completes the proof. ‡

Prefix computation will be used in this paper, for instance, to compute the set of maximal (in the sense of set inclusion) subintervals of an $O(n)$ set of subintervals of $\{1, 2, …, n\}$.

Another basic parallel method to construct efficient parallel algorithms is the (so-called) *doubling technique*. Roughly speaking, it consists in computing at each step objects whose size is twice bigger as before, knowing the previously computed objects. The word "doubling" is often misleading because in many algorithms of such type the size of objects grows with a ratio $c > 1$, not necessarily with ratio $c = 2$. The typical use of this technique is in the proof of the following lemma (see [GR 88]). Suppose we have a vector of size $n$ with some of the positions marked. Denote by *minright*[*i*] (resp. *maxleft*[*i*]) the nearest marked position to the right (resp. to the left) of position *i*. Computing vectors *minright* and *maxleft* takes logarithmic parallel time.

**Lemma 9.2**

From a vector of size $n$ with marked positions, vectors *minright*, and *maxleft* can be computed in $O(\log n)$ time with $n/\log n$ processors.

The doubling technique is also the crucial feature of the structure of the Karp-Miller-Rosenberg algorithm in a parallel setting. In one stage, the algorithm computes the names for all words of size $k$. In the next stage, using these names, it computes names of words having size twice bigger. We explain now how the algorithm KMR of Chapter 8 can be parallelized.

To make a parallel version of KMR algorithm, it is enough to design an efficient parallel version of one stage of the computation, and this essentially reduces to the parallel computation of RENUMBER($x$). If this procedure is implemented in $T(n)$ parallel time with $n$ processors, then we have a parallel version of KMR algorithm working in $T(n).\log n$ time with also $n$ processors. This is due to the doubling technique, and the fact that there are only $\log n$ stages. Essentially, the same problems as computed by a sequential algorithm can be computed by its parallel version in $T(n).\log n$ time.

The time complexity of computing RENUMBER($x$) depends heavily on the model of parallel computations used. It is $T(n) = \log n$ without concurrent writes, and it is $T(n) = O(1)$ with concurrent writes. In the latter case, one needs a memory bigger than the total number of operations used by what is called a *bulletin board* (auxiliary table with $n^2$ entries; or, by making some arithmetic tricks, with $n^{1+\varepsilon}$ entries). This looks slightly artificial, though entries of auxiliary memory have not to be initialized. The details related to the distribution of processors are also very technical in the case of concurrent writes model. Therefore, we present most of the algorithms using the PRAM model without concurrent writes. This generally increases the time by a logarithmic factor. This logarithmic factor gives also a big margin of time for technical problems related to the assignment of processors to elements to be processed. We shortly indicate how to remove this logarithmic factor when concurrent writes are used. The main difference is the implementation of the procedure RENUMBER, and the computation of equivalent classes (classes of objects with the same name).

## 9.1. Building the dictionary of basic factors in parallel

Given the string *text*, we say that two positions are *k*-equivalent iff the factors of length *k* starting at these positions are equal. Such an equivalence is best represented by assigning at each position *i* a name or a number to the factor of length *k* starting at this position. The name is denoted by $NUM_k[i]$. This is the *numbering* technique presented in Chapter 8 (Section 6.1). We shall compute names of all factors of a given length *k* for *k* running through 1, 2, 4, …. We consider only factors whose length is a power of two. Such factors are called *basic factors*. The *name of a factor*, denoted by is its rank in the lexicographic ordering of factors of a given length. We also call these names *k-names*. Factors of length *k*, and their corresponding *k*-names can be considered as the same object. For each *k*-name *r* we also require (for further applications) a link *POS*[*r*, *k*] to any one position at which an occurrence of the *k*-name *r* starts. We consider only factors starting at positions [1.. *n*-1]. The *n*-th position contains the special endmarker #. The endmarker has highest rank in the alphabet. We can generally assume w. l. o. g. that n-1 is a power of two, adding enough marker otherwise.

The tables *NUM* and *POS* are called together the *dictionary of basic factors*. This dictionary is the basic data structure used in several applications.

```
                     i    = 1 2 3 4 5 6 7 8
                  text    = a b a a b b a a #######
                            _______________
k = 1      NUM[i,k] = 1 2 1 1 2 2 1 1
k = 2      NUM[i,k] = 2 4 1 2 5 4 1 3
k = 4      NUM[i,k] = 3 6 1 4 8 7 2 5

                     r    = 1 2 3 4 5 6 7 8
                            _______________
k = 1      POS[r,k] = 1 2 undefined
k = 2      POS[r,k] = 3 1 8 2 5 undefined
k = 4      POS[r,k] = 3 7 1 4 8 2 6 5
```

**Figure 9.1**. The dictionary of basic factors: tables of names of *k*-names, and of their positions. The *k*-name at position *i* is the factor *text*[*i*…*i*+*k*-1]; its name is its rank according to lexicographic ordering of all factors of length *k* (order of symbols is: *a* < *b* < #). Integers *k* are powers of two. The tables can be stored in *O*(*n*.log*n*) memory.

Figure 9.1 displays the data structure for *text* = *abaabbaa#*. Six additional #'s are appended to guarantee that each factor of length 8 starting in [1…8] is well defined. The figure presents tables *NUM* and *POS*. In particular, the entries of *POS*[*, 4] give the lexicographically sorted sequence of factors of length 4. This is the sequence of factors of length 4 starting at positions 3, 7, 1, 4, 8, 2, 6, 5. The ordered sequence is:

*aabb*, *aa##*, *abaa*, *abba*, *a###*, *baab*, *baa#*, *bbaa*.

In the case of arrays, basic factors are $k \times k$ subarrays, where $k$ is a power of two. In this situation, $NUM[(i, j), k]$ is the name of the $k \times k$ subarray of a given array *text* having its upper-left corner at position $(i, j)$. We will discuss mostly the construction of dictionaries of basic factors for strings. The construction in the two-dimensional case is an easy extension of that for one-dimensional data.

The central machinery of KMR algorithm is the procedure RENUMBER that is defined now. Let $x$ be a vector or an array of total size $n$ containing elements of some linearly ordered set. We recall the definition of procedure RENUMBER (see chapter 8). The function RENUMBER assigns to $x$ a vector $x'$. Let $val(x)$ be the set of values of all entries of $x$ (the alphabet of $x$). The vector $x'$ satisfies:

(a) if $x[i] = x[j]$ then $x'[i] = x'[j]$, and

(b) $val(x')$ is a subset of $[1\ldots n]$.

As a side effect, the procedure also computes the table $POS$ : if $q$ is in $val(x')$ then $POS[q]$ is any position $i$ such that $x'[i] = q$. Conditions (a) and (b) are obviously satisfied if $x'[i]$ is defined as the rank of $x[i]$ inside the ordered list of values if $x[j]$'s. But we do not generally assume such definition because it is often harder to compute.

**Lemma 9.3**

Let $x$ be a vector of length $n$.

(1) RENUMBER($x$) can be computed in $O(\log n)$ time with $n$ processors on an exclusive-write PRAM.

(2) Assume that $val(x)$ consists of integers or pairs of integers in the range $[1\ldots n]$. Then, RENUMBER($x$) can be computed in $O(1)$ time with $n$ processors on a concurrent-write PRAM. In this case, the size of auxiliary memory is $O(n^{1+\varepsilon})$.

**Proof**

(1) The main part of the procedure is the sorting (see chapter 8). Sorting by a parallel merge sort algorithm is known to take $O(\log n)$ time with $n$ processors. Hence, the whole procedure RENUMBER has the same complexity as sorting $n$ elements. This completes the proof of point (1).

(2) Assume that $val(x)$ consists of pairs of integers in the range $[1\ldots n]$. In fact, RENUMBER is used mostly in such cases. We consider an $n \times n$ auxiliary table $BB$. This table is called the bulletin board. The processor at position $i$ writes its name into the entry $(p, q)$ of table $BB$, where $(p, q) = x[i]$. We have many concurrent writes here because many processors attempt to write their own position into the same entry of the bulletin board. We assume that one of them (for instance, the one with smallest position) succeeds and writes its position $i$ into the entry $BB[p, q]$. Then, for each position $j$, the processor sets $x'[i]$ to the value of $BB[p, q]$, where $(p, q)$ is the value of $x[j]$. The computation is graphically illustrated in Figure 9.2. The time is

constant (two steps). Doing so, we use quadratic memory. But applying some arithmetic tricks it can be reduced to O($n^{1+\varepsilon}$). This completes the proof. ‡

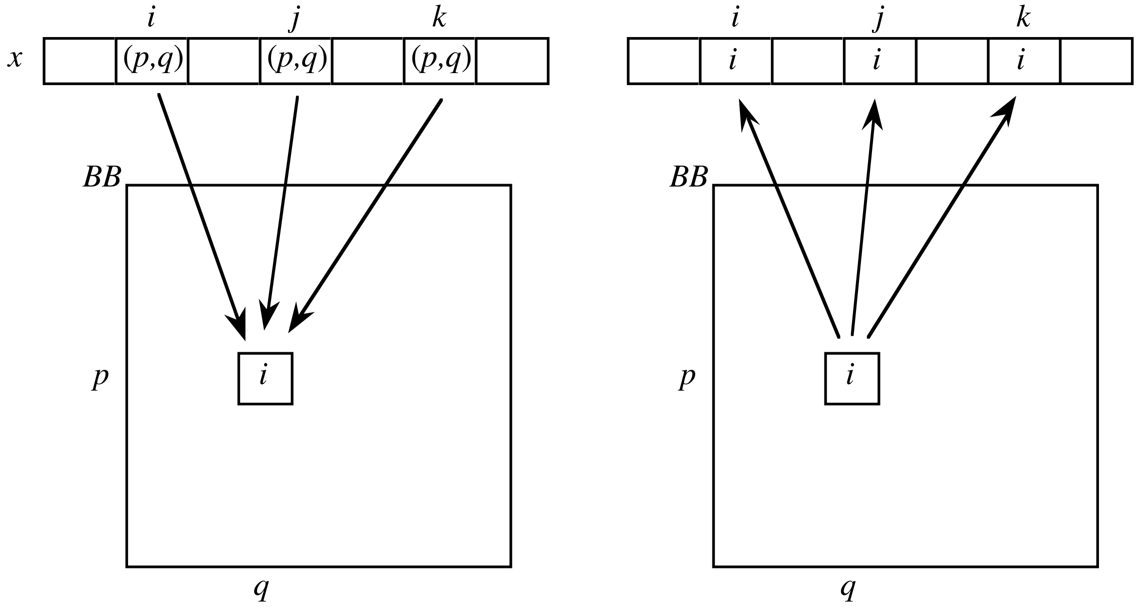


**Figure 9.2**. Use of a bulletin board. $x[i] = x[j] = x[k] = (p, q)$. Then the values of $x$ at positions $i, j, k$ are changed, in two parallel steps (with concurrent writes), to the same value $i$.

**Theorem 9.4**

The dictionary of basic factors (resp. basic subarrays) of a string (resp. array) of size $n$ can be computed with $n$ processors in $O(\log^2 n)$ time on an exclusive-write PRAM, and in O(log$n$) time on a concurrent-write PRAM (in the latter case auxiliary memory space of size $O(n^{1+\varepsilon})$ is used).

**Proof**

We describe the algorithm only for strings. The crucial fact is the property already used in Chapter 8:

(*) $NUM[i, 2k] = NUM[j, 2k]$ iff ($NUM[i, k] = NUM[j, k]$ and $NUM[i+k, k] = NUM[j+k, k]$).

The dictionary is computed by the algorithm *Parallel-KMR* below. The correctness of the algorithm follows from fact (*). The number of iterations is logarithmic, and the dominating operation is the procedure RENUMBER. The thesis follows now from the Lemma 9.3.

In the two-dimensional case, there is a fact analogous to (*), which makes the algorithm work similarly. The size of the $k$×$k$ array is $n = k^2$. This completes the proof. ‡

```
Algorithm Parallel-KMR;
{ a parallel version of the Karp-Miller-Rosenberg algorithm. }
{ Computation of the dictionary of basic factors of text;    }
{ text ends with #, |text| = n, n-1 is a power of two        }
begin
  x : = text;
  x := RENUMBER(x); { recall that RENUMBER computes POS }
  for i in 1..n do in parallel begin
    NUM[i, 1] := x[i]; POS[1, i] := POS[i];
  end;
  k := 1;
  while k < n-1 do begin
    for i in 1..n-2k+1 do in parallel x[i] := (x[i], x[i+k]);
    delete the last 2k-1 entries of x;
    x := RENUMBER(x);
    for i in 1..n-2k+1 do in parallel begin
      NUM[i, 2k] := x[i]; POS[2k, i] : = POS[i];
    end;
    k := 2k;
  end;
end.
```

## 9.2. Parallel construction of string-matching automata.

We first present a simple application of the dictionary of basic factors to string-matching. Then we describe an application to the computation of failure tables *Bord* and string-matching automata (see Chapter 7).

The table *PREF* is a close "relative" of the failure table *Bord* commonly used in efficient sequential string-matching algorithms and automata (see Chapter 3). The table *PREF* is defined by

$$PREF[i] = \max\{j\colon text[i\ldots i+j\text{-}1] \text{ is a prefix of } text\},$$

while the table *Bord* is defined by

$$Bord[i] = \max\{i : 0 \le j < i \text{ and } text[1\ldots j] \text{ is a suffix of } text[1\ldots i]\}.$$

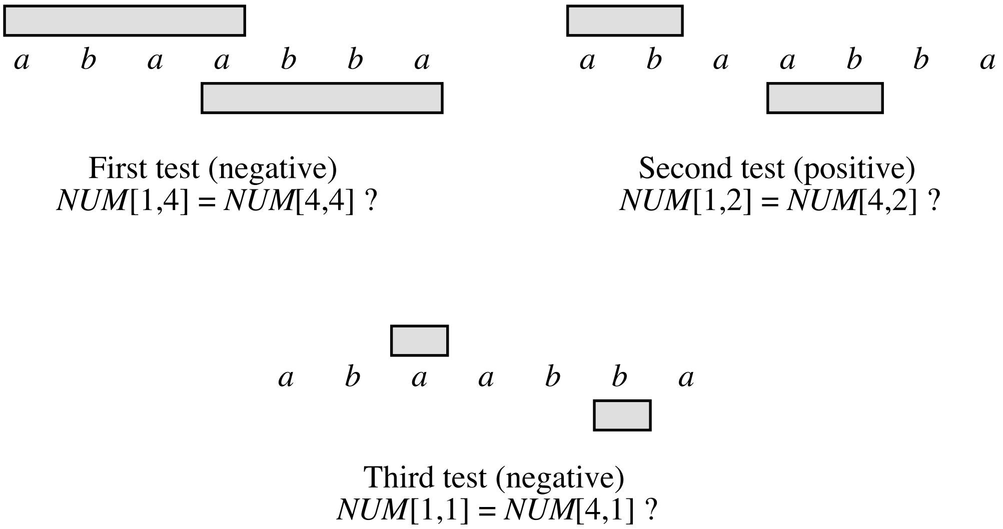
The table *PREF*, and the related table *SUF*, are crucial tables in the Main-Lorentz square-finding algorithm (Chapter 8, Section 2), for which a parallel version is given in Section 9.3.

**Theorem 9.5**

The table *PREF* can be computed in O($\log n$) time with $n$ processors (without using concurrent writes), if the dictionary of basic factors is already computed.

**Proof**

Essentially it is enough to show how to compute table *PREF* within our complexity bounds. One processor is assigned to each position $i$ of *text*, and it computes *PREF*[$i$] using a kind of binary search, as indicated in Figure 9.3. This completes the proof. ‡



First test (negative)
*NUM*[1,4] = *NUM*[4,4] ?

Second test (positive)
*NUM*[1,2] = *NUM*[4,2] ?

Third test (negative)
*NUM*[1,1] = *NUM*[4,1] ?

**Figure 9.3**. The computation of *PREF*[4] = 2 using binary search ($\log_2 8 = 3$ tests).

**Corollary 9.6**

String-matching can be solved in time $O(\log^2 n)$ time with $n$ processors in the exclusive-write PRAM model.

**Proof**

To find occurrences of *pat* in *text*, consider the word *pat#text*. Compute table *PREF* for this word. Then, occurrence of *pat* in *text* appears at positions $i$ of *text* where *PREF*[$i$] = |*pat*|. The overall takes $O(\log^2 n)$ time with $n$ processors, as a consequence of Theorems 9.4 and 9.5. ‡

**Lemma 9.7**

The failure table *Bord* for a pattern *pat* of length $n$, can be computed in $O(\log^2 n)$ time with $n$ processors without using concurrent writes (in $O(\log n)$ time if the dictionary of basic factors is already computed).

**Proof**

We can assume that the table *PREF* is already computed (Theorem 9.5). Let us consider pairs ($i$, $i$+*PREF*[$i$]-1). These pairs correspond to intervals of the form [$i$…$j$]. The first step is to compute all such intervals which are maximal in the sense of set inclusion order. It can be done with a parallel prefix computation. For each $k$, we compute the value

$$maxval(k) = \max(PREF[1], PREF[2]+1, PREF[3]+2, \ldots, PREF[k\text{-}1]+k\text{-}2).$$

Then, we "turn off" all positions $k$ such that $maxval(k) \geq PREF[k]+k\text{-}1$. We are left with maximal subintervals ($i$, $RIGHT[i]$). Let us (in one parallel step) mark all right ends of these intervals, and compute the table $RIGHT^{-1}[j]$ for all right ends $j$ of these intervals. For the other values $j$, $RIGHT^{-1}[j]$ is undefined. Again, using a parallel prefix computation, for each position $k$, we can compute $minright[k]$, the first marked position to the right of $k$.

Then, in one parallel step, we set

$Bord[k] := 0$ if $minright[k]$ is undefined, and

$Bord[k] := \max(0, k\text{-}RIGHT^{-1}[minright[k]]+1)$ otherwise (see Figure 9.4).

This completes the proof. ‡

Structure of maximal intervals ($i$, $RIGHT[i]$)

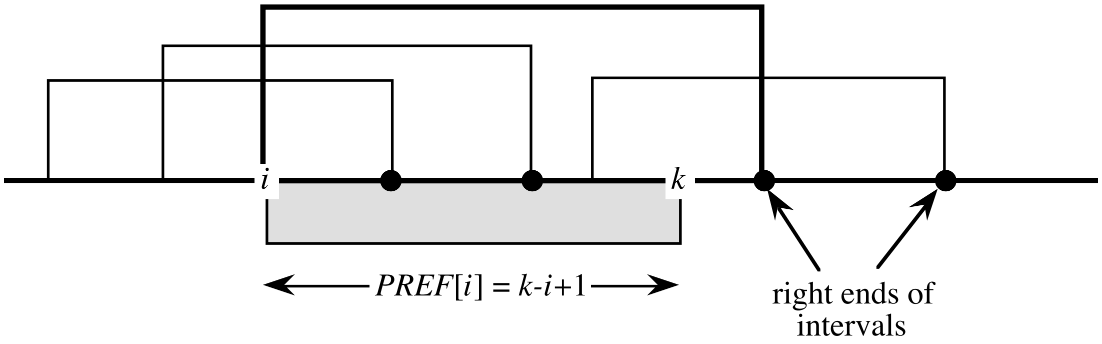


**Figure 9.4**. Computation of $Bord[k]$ in the case $i = RIGHT^{-1}[minright[k]] \leq k$.

One may observe that if the table $PREF$ is given then even $n/O(\log n)$ processors are sufficient to compute table $Bord$, because our main operations are parallel prefix computations.

**Corollary 9.8**

The periods of all the prefixes of a word can be computed in $O(\log^2 n)$ time with $n$ processors without using concurrent writes (in $O(\log n)$ time if the dictionary of basic factors is already computed).

**Proof**

The period of prefix $pat[1\ldots i]$ is $i\text{-}Bord[i]$ (Chapter 2). ‡

We now give another consequence of Lemma 9.7 related to the previous result. It is shown in Chapter 7 (Section 1) how to build the string-matching automaton for pat, $SMA(pat)$. It is the minimal deterministic automaton which accepts the language $A^*pat$. The construction of such automata is the background of several string-matching algorithms. Its sequential construction is straightforward, and can be related to the failure function $Bord$. Using this fact, we develop a parallel algorithm to compute $SMA(pat)$.

**Theorem 9.9**

Assume that the basic dictionary of *pat* is computed, and the alphabet has $O(1)$ size. Then, we can compute the string-matching automaton $SMA(x)$ in $O(\log n)$ time with $n$ processors on an exclusive-write PRAM. The same result holds for a finite set of patterns.

**Proof**

We prove only the one-pattern case. The case with many patterns can be done in essentially the same way, though trees are to be used instead of one-dimensional tables (see Chapter 7). *Parallel-KMR* algorithm works for trees as well.

We can assume that the failure table *Bord* for *pat* is already known. Our algorithm is essentially a parallel version of the construction of $SMA(x)$ shown in Section 7.1. The string-matching automaton has $\{0, 1,\ldots, n\}$ as set of states. The initial state is 0 and $n$ is the only accepting state.

Define first the transition function δ for occurrences of symbols of *pat* only: let $\delta[i, a] = i+1$ for $a = pat[i+1]$ and $\delta[0, a] = 0$ for $a \neq pat[1]$. For each symbol $a$ of the alphabet, define a modified failure table as follows:

for $i < n$, $P_a[i]$ = if $(pat[i+1] = a)$ then $i$ else $Bord[i]$,

and $P_a[n] = Bord[n]$.

Let $P_a{}^*[i] = P_a{}^k[i]$, where $k$ is such that $P_a{}^k[i] = P_a{}^{k+1}[i]$.

Tables $P_a$ are treated here as functions that can be iterated indefinitely. We can easily compute all tables $P_a{}^*[i]$ in $O(\log n)$ time with $n$ processors using the doubling technique ($\log n$ executions of $P_a[i] := P_a{}^2[i]$). Then, the transition table of the automaton is constructed as follows:

```
for each letter $a$, and position $i$ such that $\delta[i, a]$ is not already defined
do in parallel $\delta[i, a] := \delta[P_a{}^*[i], a]$.
```

This completes the proof. ‡

## 9.3. Parallel computation of regularities

We continue the applications of KMR algorithm with the problem of searching for squares in strings. Recall that a square is a nonempty word of the form *ww*. Section 8.2 gives an algorithm to find a square factor within a word in sequential linear time. But the algorithm is based on a compact representation of factors of the word. We consider here the other methods devoted to the same problem and also presented in Section 8.2.

A simple application of failure functions gives a quadratic sequential algorithm. It leads to a parallel NC-algorithm. To do so, we can compute a failure function $Bord_i$ for each suffix $pat[i\ldots n]$ of the word *pat*. We have already remarked that there is a square in *pat*, prefix of the *pat*[$i$...$n$], iff $Bord_i[j] \geq (j\text{-}i+1)/2$ for some $j > i$. Computing a linear number of failure functions leads to a quadratic sequential algorithm, and to a parallel NC-algorithm. However, with such an approach, the parallel computation requires a quadratic number of processors. We show how the divide-and-conquer method used in the sequential case saves time and space in parallel computation.

The main part of the sequential algorithm *SQUARE* for finding a square in a word (Section 8.2) is the operation called *test*. This operation applies to squarefree words $u$ and $v$, and tests whether the word $uv$ contains a square (the square begins in $u$ and ends in v). This operation is a composition of two smaller tests *righttest* and *lefttest*. The first (resp. second) operation tests whether $uv$ contains a square which center is in $v$ (resp. $u$).

The operation *test* can be realized with the two auxiliary tables *PREF* and $SUF_u$. Recall that $SUF_u[k]$ is the size of longest suffix of $v[1...k]$ which is also a suffix of $u$. This table $SUF_u$ can be computed in the same way as *PREF* (computing *PREF* for $u^R\&v^R$, for instance).

**Lemma 9.10**

Tables *PREF* and $SUF_u$ being computed, functions *righttest*($u$, $v$), *lefttest*($u$, $v$) and *test*($u$, $v$) can be computed in $O(\log n)$ time with $n/\log n$ processors. The running time is constant with a concurrent-write PRAM having $n$ processors.

**Proof**

Given tables *PREF* and $SUF_u$, the computation of *righttest*($u$, $v$) reduces to the comparison between $k$ and $PREF[k]+SUF_u[k]$. A square of length $2k$ is found iff the latter quantity is greater than or equal to $k$, as shown in Figure 8.2. The evaluation of *righttest* is done by inspecting in parallel all positions $k$ on $v$. Hence, in $O(\log n)$ time (and constant time with the concurrent-writes model), the time to collect the boolean value, we can compute *righttest*. By grouping the values of $k$ in intervals of length $\log n$ we can even reduce the number of processors to $n/\log n$. The same holds for *lefttest*, and thus for *test* which is a composition of the two others. This completes the proof. ‡

The function *test* yields a recursive parallel algorithm for testing occurrences of squares.

```
function SQUARE(text): boolean;
{ returns true if text contains a square }
{ W.l.o.g. n = |text| is a power of two  }
begin
  if n > 1 then begin
    for i ∈ {1, n/2+1} do in parallel
      if SQUARE(text[i..i+n/2-1]) then return true;
    { if the algorithm has not already stopped then ... }
    if (test(text[1..n/2], text[n/2+1..n]) then return true;
  end;
  return false; { if the "true" has not been already returned }
end;
```

**Theorem 9.11**

The algorithm *SQUARE* tests the squarefreeness of a word of length $n$ in $O(\log^2 n)$ parallel time using $n$ processors in the PRAM model without concurrent writes.

**Proof**

The complexity of the algorithm *SQUARE* essentially comes from the computation of basic factors in $O(\log^2 n)$ (Theorem 9.4). Each recursive step during the execution of the algorithm takes $O(\log n)$ time with $n$ processors as shown by Lemma 9.10. The number of step is $\log n$. This gives the result. ‡

The parallel squarefreeness test above is the parallel version of the corresponding algorithm *SQUARE* of Chapter 8. Section 8.2 contains another serial algorithm that solves the same question in linear time on fixed alphabets. We present now the parallel version of the latter algorithm.

Recall that the second algorithm is based on the *f*-factorization of *text*. It is a sequence of nonempty words $(v_1, v_2, \ldots, v_m)$ such that $text = v_1 v_2 \ldots v_m$ and defined by

— $v_1 = text[1]$, and

— for $k > 1$, $v_k$ is defined as follows. If $|v_1 v_2 \ldots v_{k-1}| = i$ then $v_k$ is the longest prefix $u$ of $text[i+1\ldots n]$ which occurs at least twice in $text[1\ldots i]u$. If there is no such $u$ then $v_k = text[i+1]$.

Recall also that $pos(v_k)$ is the position of the first occurrence of $v_k$ in *text* (it is the length of the shortest word $y$ such that $yv_k$ is a prefix of *text*).

**Theorem 9.12**

The *f*-factorization of *text* of size $n$, and the associated table *Pos*, can be computed in $O(\log n)$ time with $n$ processors of a CRCW PRAM.

**Proof**

(a) First construct the suffix tree $T(text)$ by the algorithm of [AILSV 88]. The leaves of $T(text)$ correspond to suffixes of text, and the path from the root to the leaf numbered $i$ spells the suffix starting at position $i$ in *text*.

(b) For each node $v$ of $T(text)$ compute the minimal value of the leaf in the subtree rooted at $v$. This can be done by a tree-contraction algorithm, for example the one of [GR 88].

(c) For each leaf $i$, compute the first node $v$ (bottom-up) on the path from $i$ to the root with a value $j < i$. Denote by $size(i)$ the length of the string spelled by the path from the root to the node $v$. The value $j$ equals $pos(i)$. If there is no such node then $pos(i) = i$ and $size(i) = 1$.

The computation of tables $pos(i)$ and $size(i)$ can be done efficiently in parallel as follows:

— Let $Up[v, k]$ be the node lying on the path from $v$ to the root whose distance from $v$ is $2^k$. If there is no such node then we set $Up[v, k]$ to *root*.

— For each node $v$ of the tree, compute the table $MinUp[v, k]$ for $k =1, 2, \ldots, \log n$. The value of $MinUp[v, k]$ is the node with the smallest value on the path from $v$ to $Up[v, k]$. Both tables can be easily computed in $O(\log n$ time with $O(n)$ processors.

— Next, the values of $pos(i)$ can be computed by assigning one processor to each leaf $i$. The assigned processor makes a kind of binary search to find the first $j < i$ on the path from $i$ to the root. This takes logarithmic time.

(d) Let $Next(i) = i+size(i)$. Compute in parallel all powers of *Next*. The factorization can then be deduced because the position of the element $v_{i+1}$ of $(v_1, v_2, \ldots, v_m)$ is $Next^i(1)$.

The table *pos* has been already computed at point (c). This completes the proof. ‡

The parallel version of the function *linear-SQUARE* of Section 8.2 is as follows.

Now the key point is that the computation of $righttest(v_1v_2\ldots v_{k-2}, v_{k-1}v_k)$, implied by the test of conditions (2) and (3), can be done in logarithmic time using only $O(|v_{k-1}v_k|)$ processors. All the tests can be done independently.

```
function Parallel-test(text): boolean;
begin
  compute in parallel
  the f-factorization ($v_1$, $v_2$, .., $v_m$) of text;
  for each $k \in$ {1, 2, .., m} do in parallel
    if (1) or (2) or (3) hold then { see Lemma 8.8xxx }
      return true;
  return false;
end;
```

**Theorem 9.13**

The square-freeness test for a given text *text* of size *n* can be computed in $O(\log n)$ time using $O(n)$ processors of a CRCW PRAM.

**Proof**

Each condition can be checked in the algorithm *Parallel-test* in $O(\log n)$ time using $O(|v_{k-1}v_k|)$ processors, due to Lemma 9.10. Thus, the number of processors we need is at most the total sum of all $|v_{k-1}v_k|$, which is obviously $O(n)$. This completes the proof. ‡

The next application of KMR algorithm is to algorithmic questions related to palindromes. We consider only even length palindromes: let *PAL* denote the set of such nonempty even palindromes (words of the form $ww^R$). Recall that $Rad[i]$ is the radius of the maximal even palindrome centered at position *i* in the text *text*,

$$Rad[i] = \max\{k : text[i\text{-}k+1\ldots i] = (text[i+1\ldots i+k])^R\}.$$

If *k* is the maximal integer satisfying $text[i\text{-}k+1\ldots i] = (text[i+1\ldots i+k])^{R,}$ then we say that *i* is the center of the maximal palindrome $text[i\text{-}k+1\ldots i+k]$. We identify palindromes with their corresponding subintervals of $[1\ldots n]$.

**Lemma 9.14**

Assume that the dictionaries of basic factors for *text* and its reverse, $text^R$, are computed. Then the table *Rad* of maximal radii of palindromes can be computed in $O(\log n)$ time with *n* processors.

**Proof**

The proof is essentially the same as for the computation of table *PREF*: a variant of parallel binary search is used. ‡

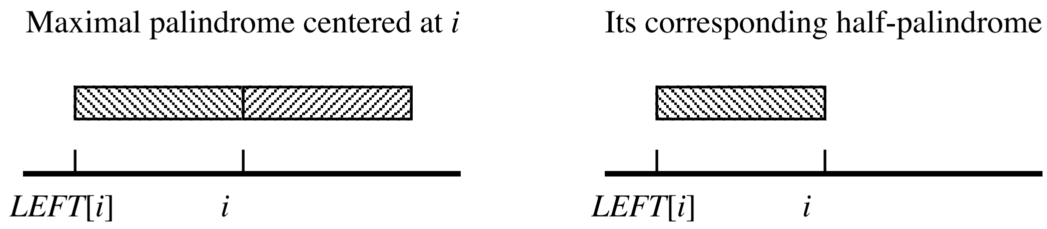
Denote by *Firstcentre*[*i*] (resp. *Lastcentre*[*i*]) the tables of first (resp. last) centers to the right of *i* (including *i*) of palindromes containing position *i*.

**Lemma 9.15**

If the table *Rad* is computed then the table *Firstcentre* (resp. *Lastcentre*) can be computed in $O(\log n)$ time with *n* processors.

**Proof**

We first describe an $O(\log^2 n)$ time algorithm. It uses the divide-and-conquer approach. A notion of half-palindrome is introduced and shown on Figure 9.5.



Maximal palindrome centered at *i*

Its corresponding half-palindrome

**Figure 9.5**. Half-palidromes.

The value *Firstcentre*[*k*] is the first (to the right of *k* including *k*) right end of an half-palindrome containing *k*.

The structure of the algorithm is recursive:

> The word is divided into two parts *x*1 and *x*2 of equal sizes. In *x*1 we disregard the half-palindromes with right end in *x*2. Then, we compute in parallel the table *Firstcentre* for *x*1 and *x*2 independently. The computed table, at this stage, gives correct final value for positions in *x*2. However, the part of the table for *x*1 may be incorrect due to the fact that we disregarded for *x*1 half-palindromes ending in *x*2. To cope with this, we apply procedure *UPDATE*(*x*1, *x*2).

The table is updated looking only at previously disregarded half-palindromes. The structure of these half-palindromes is shown on Figure 9.6.

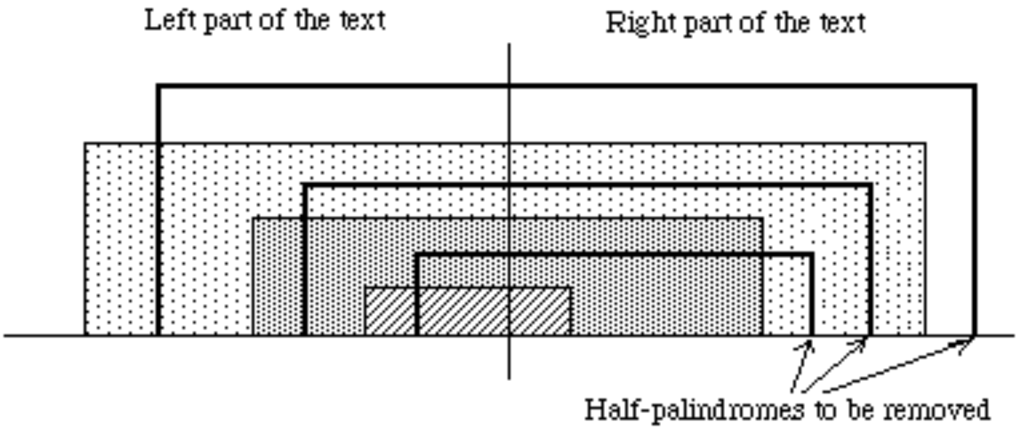


**Figure 9.6**. Structure of half-palindromes.

The half-palindromes can be treated as subintervals [*i*…*j*]. We introduce a (partial) ordering on half-palindromes as follows: [*i*…*j*]≤[*k*…*l*] iff ($i \leq k$ and $j \leq l$).

```
procedure UPDATE(x1, x2);
{ only half-palindromes starting in x1 and ending in x2 are
considered }
begin
  remove all half-palindromes but minimal ones;
{ this can be done in logn time by parallel prefix computation }
{ we are left with the situation presented in Figure 9.7      }
  we compute for each position k the first (to the left)
  starting position s[k] of an half-palindrome;
  for each position k in x1 do in parallel
    { see Figure 9.7 }
    Firstcentre[k] := min(Firstcentre[k], right end of half-
                                   palindrome starting at s[k]);
end;
```

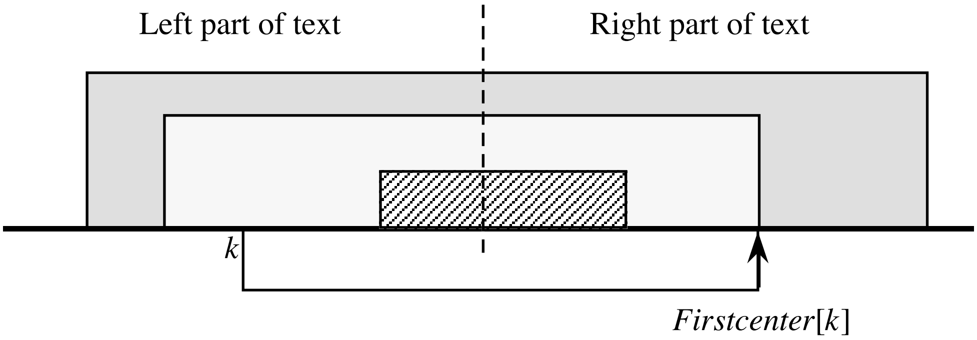


**Figure 9.7**. Table *Firstcenter*.

At the beginning of the whole algorithm *Firstcentre*[*k*] is set to +∞. One can see that the procedure *UPDATE* takes *O*(log*n*) time using |*x*1|+|*x*2| processors. The depth of the recursion is logarithmic, thus, the whole algorithm takes $O(\log^2 n)$ time.

We now briefly describe how to obtain *O*(log*n*) time with the same number of processors. We look at the global recursive structure of the previous algorithm. The initial level of the recursion is the zero level, the last one has depth log*n*-1. The crucial observation is that we can simultaneously execute *UPDATE* at all levels of the recursion. However at the *q*-th level of the recursion, instead of minimizing the value of *Firstcentre*[*k*] we store the values computed at this level in a newly introduced table $Firstcentre_q$: for each position *k* considered at this level the procedure sets $Firstcentre_q[k]$ to the right end of half-palindrome starting at *s*[*k*] (see *UPDATE*). Hence, the procedure *UPDATE* is slightly modified; at level *q* it computes the table $Firstcentre_q$. Assume that all entries of all tables are initially set to infinity.

After computing all tables $Firstcentre_q$ we assign a processor to each position $k$. It computes sequentially (for its position) the minimum of $Firstcentre_q[k]$ over recursion levels $k$ = 0, 1,..., log$n$-1. This globally takes $O(\log n)$ time with $n$ processors. But we compute $O(\log n)$ tables $Firstcentre_q$, each of size $n$, so we have to be sure that $n$ processors suffice to compute all these data in $O(\log n)$ time. The computation of $Firstcentre_q$, at a given level of recursion can be done by simultaneous applications of parallel prefix computations (to compute the first marked element to the left of each position $k$) for each pair ($x1$, $x2$) of factors (at the $q$-th level we have $2^q$ such pairs). The prefix computations at a given level take together $O(n)$ elementary sequential operations. Hence the total number of operations for all levels is n $O(\log n)$. It is easy to compute $Firstcentre_q$ for a fixed $q$ using $n$ processors. This requires $O(n.\log n)$ processors for all levels $q$, however we have only $n$ processors.

At this moment, we have an algorithm working in $O(\log n)$ time whose total number of elementary operations is $O(n\log n)$. We can apply Brent's lemma: if $M(n)/P(n) = T(n)$ then the algorithm performing the total number of $M(n)$ operations and working in parallel time $T(n)$ can be implemented to work in $O(T(n))$ time with $P(n)$ processors (see for instance [GR 88]).

In our case $M(n) = O(n.\log n)$ and $T(n) = O(\log n)$. Brent's lemma is a general principle, its application depends on the detailed structure of the algorithm as to whether it is possible to redistribute processors efficiently. However in our case we deal with computations of very simple structure: multiple applications of parallel prefix computations. Hence $n$ processors suffice to make all computations in $O(\log n)$ time. This completes the proof. ‡

**Theorem 9.16**

Even palstars can be tested in $O(\log n)$ time with $n$ processors on the exclusive-write PRAM model, if the dictionary of basic factors is already computed.

**Proof**

Let *first* be a table whose $i$-th value is the first position $j$ in *text* such that $text[i\ldots j]$ is an even nonempty palindrome; it is zero if there is no such prefix even palindrome. Define $first[n] = n$. This table can be easily computed using the values of $Firstcentre[i]$. Then, the sequential algorithm tests even palstars in the following natural way: it finds the first prefix even palindrome and cuts it; then such a process is repeated as long as possible; if we are done with an empty string then we return "true": the initial word is an even palstar. The correctness of the algorithm is then analogue to that of Theorem 8.12.

We make a parallel version of the algorithm. Compute table $first^*[i] = first^k[i]$, where $k$ is such that $first^k[i] = first^{k+1}[i]$, using a doubling technique. Now the text is an even palstar iff $first^*[1] = n$. This can be tested in one step.

This ends the proof. ‡

Unfortunately the natural sequential algorithm described above for even palstars does not work for arbitrary palstars. But, in this more general case, a similar table *first* can be defined and computed in essentially the same manner as for even palindromes. Palstar recognition then reduces to the following reachability problem: is there a path according to *first* from position 1 to *n*. It is known that the positions are nodes of a directed graph whose maximal outdegree is three. It is rather easy to solve the reachability problem in linear sequential time, but we do not know how to solve it by an almost optimal parallel algorithm. In fact, the case of even palstars can be also viewed as a reachability problem: its simplicity is related to the fact that in this case the outdegree of each vertex in the corresponding graph is just one.

**Lemma 9.17**

The table *Lastcentre* can be computed in $O(\log n)$ time with $n$ processors on the exclusive-write model.

**Proof**

We compute the maximal (with respect to inclusion) half-palindromes. We mark their leftmost positions, and then, the table *Lastcentre* is computed according to Figure 9.8. For position *k*, we have to find only the first marked position to the left of *k* (including *k*). This completes the proof. ‡

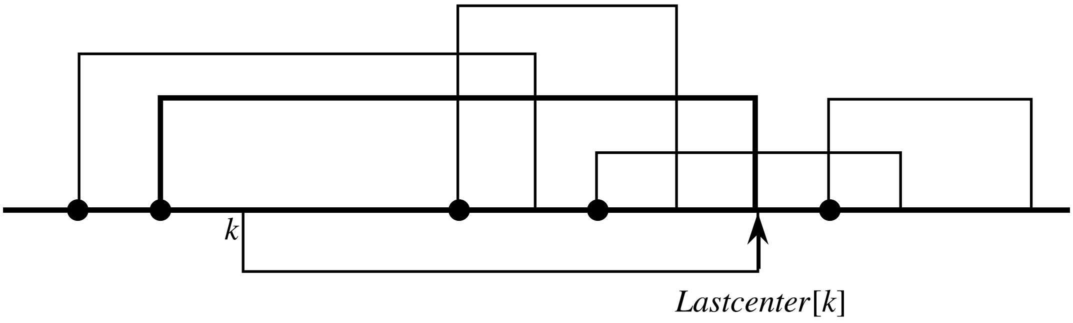


**Figure 9.8**. Table *Lastcenter*.

**Theorem 9.18**

Compositions of $k$ palindromes, for $k = 2$, 3 or 4, can be tested in $O(\log n)$ time with $n/\log n$ processors in the exclusive-write PRAM model, if the dictionary of basic factors is computed.

**Proof**

The parallel algorithm is an easy parallel version of the sequential algorithm in [GS 78] which applies to $k = 2, 3, 4$. The key point is that if a text $x$ is a composition $uv$ of even palindromes then there is a composition $u'v'$ such that $u'$ is a maximal prefix palindrome or $v'$ is a maximal suffix palindrome of $x$. The maximal prefix (suffix) palindrome for each position of the text can be computed efficiently using the table *Lastcentre* (in the case of suffix palindromes the table is computed for the reverse of the string).

Given the tables *Rad* and *Lastcentre* (also for the reversed string) the question "is the text $x[1...i]$ a composition of two palindromes" can be answered in constant time using one processor. The computation of logical "or", or questions of this type, can be done by a parallel prefix computation. The time is $O(\log n)$, and $O(n/\log n)$ processors suffice (see Lemma 9.1). This completes the proof. ‡

Several combinatorial algorithms on graphs and strings consider strings on an ordered alphabet. A basic algorithm often used in this context is the computation of maximal suffixes, or of minimal non-empty suffixes, according to the alphabetic ordering. These algorithms are strongly related to the computation of the Lyndon factorization of a word, that is recalled now. A Lyndon word is a non-empty word which is minimal among its non-empty suffixes. Chen, Fox and Lyndon proved that any word $x$ can be uniquely factorized as $l_1l_2.. l_h$ such that $h \geq 0$, the $l_i$'s are Lyndon words, and $l_1 \geq l_2 \geq \ldots \geq l_h$. It is known also that $l_h$ is the minimal non-empty suffix of $x$. In the next parallel algorithm, we will use the following characterization of the Lyndon word factorization of $x$.

**Lemma 9.19**

The sequence of non-empty words $(l_1, l_2, \ldots, l_\mathrm{h})$ is the Lyndon factorization of the word $x$ iff $x = l_1l_2.. l_h$, and the sequence $(l_1l_2\ldots l_h, l_2l_3\ldots l_\mathrm{h}, \ldots, l_h)$ is the longest sequence of suffixes of $x$ in decreasing alphabetical order.

**Proof**

We only prove the 'if' part and leave the 'only if' part to the reader.

Let $s_1 = l_1l_2\ldots l$, $s_2 = l_2l_3\ldots l_\mathrm{h}$, …, $s_h = l_h$, $s_{h+1} = \varepsilon$. As a consequence of the maximality of the sequence, one may note that, for each $i = 1, \ldots, h$, any suffix $w$ longer than $s_{i+1}$ satisfies $w > s_i$. To prove that $(l_1, l_2, \ldots, l_\mathrm{h})$ is the Lyndon factorization of $x$, we have only to show that each element of the sequence is a Lyndon word. It is the case for $l_h$ since, again by the maximality condition, $l_h$ is the minimal non-empty suffix of $x$, and thus is less than any of its non-empty suffixes. Assume, ab absurdo, that $v$ is both a non-empty proper prefix and suffix of $l_i$, and let $w$ be such that $vw = s_i$. Since $vs_{i+1}$ is a suffix of $x$ longer than $s_{i+1}$, we have $vs_{i+1} > s_i$. The latter expression implies $s_i > w$, which is a contradiction. This proves that no non-empty proper suffix $v$ of $l_i$ is a prefix of $l_i$. But since again $vs_{i+1} > s_i$, we must have $v > s_i$, and also $v > l_i$. So, $l_i$ is a Lyndon word. This ends the proof. ‡

**Theorem 9.20**

The maximal suffix of the text of length $n$, and its Lyndon factorization can be computed in $O(\log^2 n)$ time with $n$ processors on the exclusive-write PRAM.

**Proof**

We first apply the KMR algorithm of Section 3 using the exclusive-write model to the word $x\#\ldots\#$. Assume here (contrary to the previous sections) that the special character # is the minimal symbol. Essentially, it makes no difference for KMR algorithm. We then get the ordered sequence of basic factors of $x$ given by tables *POS*. After padding enough dummy symbols to the right, each suffix of $x$ becomes also a basic factor. Hence, for each position $i$, we can get $Rank[i]$: the rank of the $i$-th suffix $x[i]\ldots x[n]$ in the sequence of all suffixes. One may note that the padded character # has no effect on the alphabetical ordering since it is less than any other character.

Let us define $L[i]$ to be the position $j$ such that both $j \leq i$ and $Rank[j] = \min\{Rank[j']: 1 \leq j' \leq i\}$. By the above characterization of the Lyndon word factorization of $x$, $L[i]$ gives the starting position of the Lyndon factor containing $i$. Values $L[i]$ can be computed by prefix computation. Define an auxiliary table $G[i] = L[i]$-1. Now, it is enough to compute the sequence $G[n]$, $G^2[n]$, $G^3[n]$, ..., $G^h[n] = 0$. In fact, such sequence gives the required list of positions, starting with position $n$. It is easy to mark all positions of $[0..\ n]$ contained on this list in $O(\log^2 n)$ parallel time. These positions decompose the word into its Lyndon factorization. This completes the proof. ‡

## 9.4. Parallel computation of suffix trees

Efficient parallel computation of the suffix tree of a text is a delicate question. The dictionary of basic factors leads to a rather simple solution, but which is not optimal. As already noted in Chapter 8, the equivalences on factors of a text are strongly related to its suffix tree. And the naming technique used by KMR algorithm to compute the dictionary is precisely a technique to handle the equivalence classes.

To build the suffix tree of a text, a first coarse approximation of it is built. Afterwards the tree is refined step by step. The approximation becomes closer to the suffix tree that is reached at the end of the process. During the construction, we have to answer quickly the queries of the form: are the $k$-names (i.e. the factors of length $k$) starting at positions $i$ and $j$ identical ? This is needed to compute the $k$-equivalence relations defined on the nodes of intermediate trees. Roughly speaking, such relations help to make refinements of the tree and get better approximations of the final suffix tree.

Assume $n$-1 is a power of two. The $n$-th letter of *text* is a special symbol. A suitable number of special symbols is padded to the end of *text* in order to have well defined factors of length $n$-1 starting at positions 1, 2, ..., $n$-1. We say that two words $x$ and $y$ are $k$-equivalent if they have the same prefix of length $2^k$.

We build a series of logarithmic number of trees $T_{n-1}$, $\mathrm{T}_{(n-1)/2}$, ..., $T_1$: each successive tree is an approximation of the suffix tree. The key invariant of the construction is:

> *invar*($k$): for each internal node $v$ of $T_k$ there are no two distinct outgoing edges whose labels have the same prefix of length $k$. The label of the path from the root to the leaf $i$ equals $text[i\ldots i+n]$. There is no internal node of outdegree one.

Note that the parameter $k$ is always a power of two. This gives the logarithmic number of iterations.

**Remark**

If *invar*(1) holds, then we have the tree $T_1$ is essentially the suffix tree *T*(*text*). Just a trivial modification may be needed to delete all #'s padded for technical reasons, except one.

The core of the construction is the procedure REFINE($k$) that transforms $T_{2k}$ into $T_k$. The procedure maintains the invariant: if *invar*($2k$) is satisfied for $T_{2k}$, then *invar*($k$) holds for $T_k$ after running REFINE($k$) on $T_{2k}$. The correctness (preservation of invariant) of the construction is based on the trivial fact expressed graphically below.

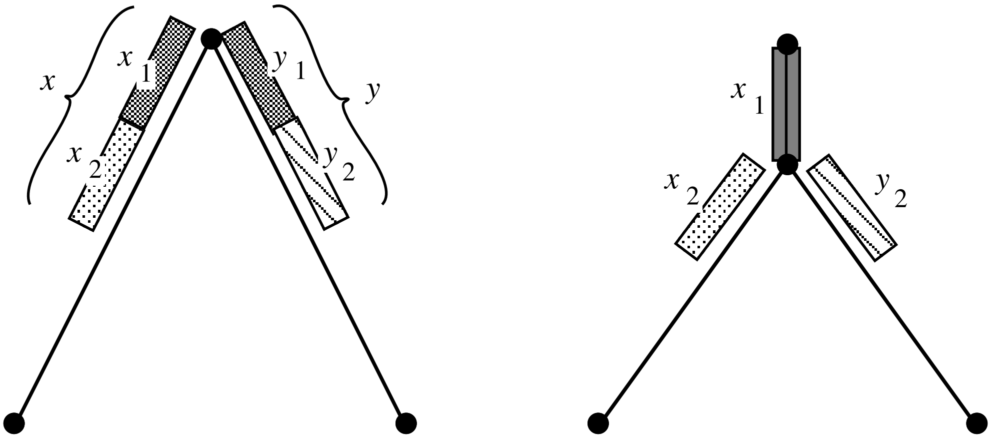


**Figure 9.9**. If $x \neq y$ and $x_1 = y_1$, then $x_2 \neq y_2$. If *invar*($2k$) is locally satisfied (on the left), after insertion of a new node, *invar*($k$) locally holds (on the right).

The procedure REFINE($k$) consists of two stages:

(1) insertion of new nodes, one per each non-singleton $k$-equivalence class;

(2) deletion of nodes of outdegree one.

In the first stage the operation *localrefine*($k$, $v$) is applied in parallel to all internal nodes $v$ of the current tree. This local operation is graphically presented in the Figure 9.10. The $k$-equivalence classes, labels of edges outgoing a given node, are computed. For each non-singleton class, we insert a new (internal) node.

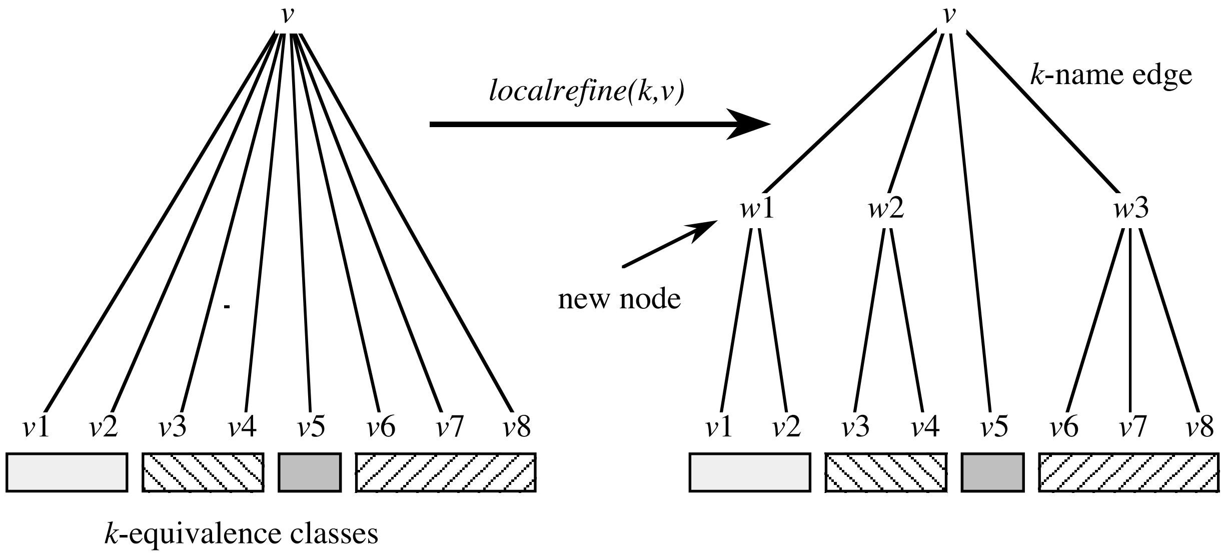


**Figure 9.10**. Local refinement. The sons (of node *v*) whose edge labels have the same *k*-prefixes are *k*-equivalent.

To achieve a more complete parallelization, each of operation *localrefine*(*k*, *v*) is performed with as many processors as the number of sons of *v* (one processor per son). Hence, each local refinement is done in logarithmic time, as well as the whole REFINE operation. Since we apply REFINE log*n* times, the global time complexity is $O(\log^2 n)$. The number of processors is linear as is the sum of outdegrees of all internal nodes.

The algorithm is informally presented on the example text *abaabbaa#*. We start with the tree *T*(8) of all factors of length 8 starting at positions 1, 2, …, 8. The tree is almost a suffix tree: the condition that is only violated is that some internal node *v* (in fact here, the root) has two distinct outgoing edges whose labels have a common nonempty prefix. We attempt to satisfy the condition by successive refinements: the prefixes violating the condition become smaller and smaller, divided by two at each stage, until they become empty.

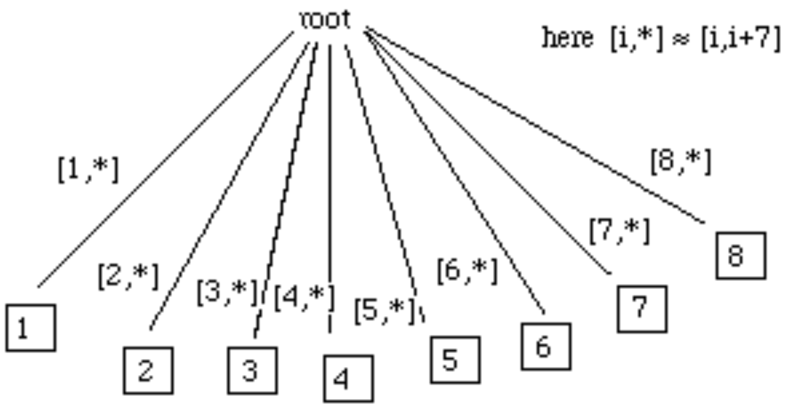


**Figure 9.11**.The tree $T(8)$ for *text* = *abaabbaa#*. The 8-equivalence is the 4-equivalence, hence $T(8) = T(4)$. But the 2-equivalence classes are {6, 2}, {3, 7}, {4, 1}, {8}, {5}. We apply REFINE(2) to get $T(2)$.

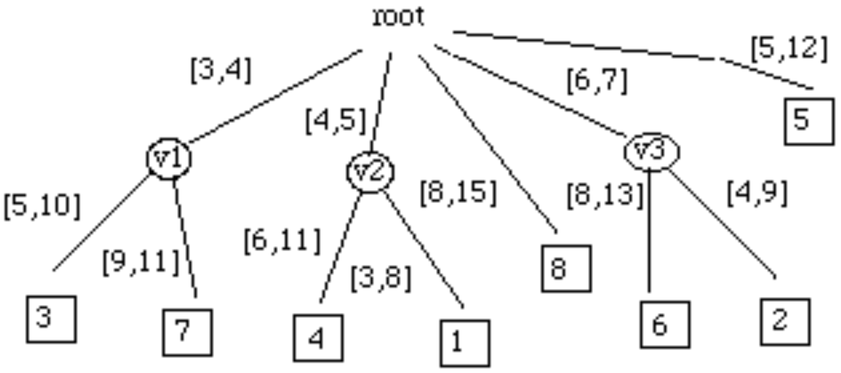


**Figure 9.12**. Tree $T(2)$. Now the 1-equivalence classes are {3}, {7}, {4}, {1}, {*v*1, v2, 8}, {6, 2}, {*v*3, 5}. Three new nodes has to be created to obtain $T(1)$.

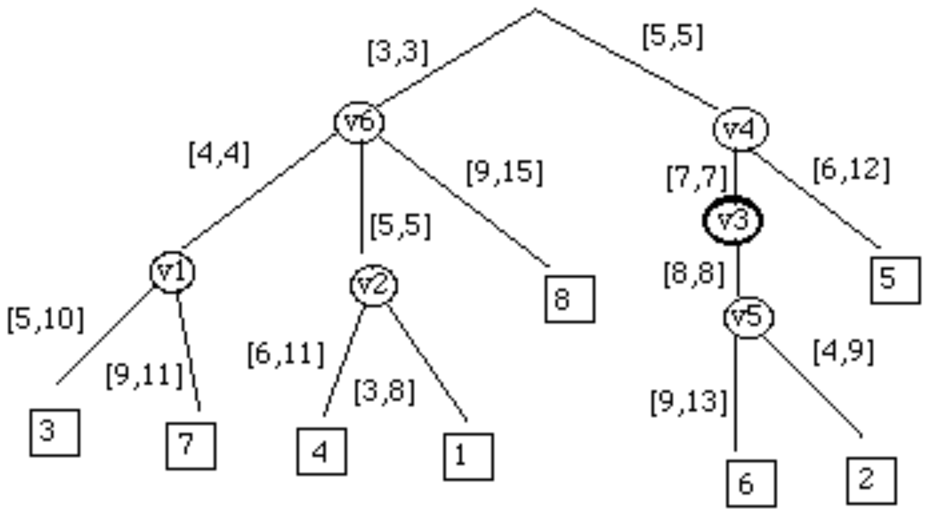


**Figure 9.13**. The tree after the first stage of REFINE(1) : insertion of new nodes *v*4, *v*5, *v*6.

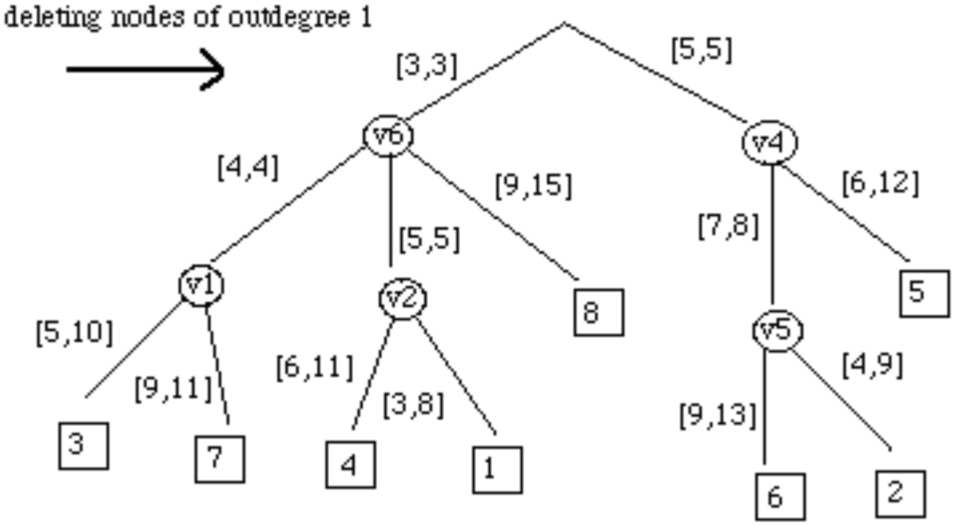


**Figure 9.14**. Tree *T*(1) after the second stage of REFINE(1):
deletion of nodes of outdegree one.

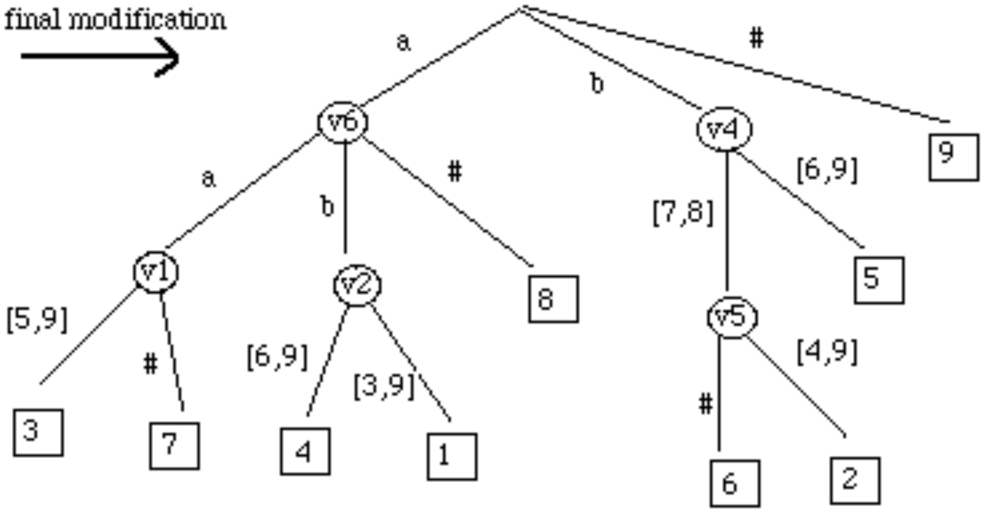


**Figure 9.15**. The suffix tree $T$(*abaabbaa#*).
It results from $T$(1) by a "cosmetic" modification, elimination of extra #.

The informal description of the construction of the suffix tree $T$(*text*) is summarized by the algorithm below.

```
Algorithm
{ parallel suffix tree construction; n-1 is a power of two }
  procedure REFINE(k);
  begin
    for each internal node v of T do in parallel begin
      localrefine(k, v); delete all nodes of outdegree one;
    end;
  end;
{ main algorithm }
begin
  let T be the tree of height 1 whose leaves are 1..n-1, and
  the label of the i-th edge is [i, i+n];
  k : = n-1;
  repeat { T satisfies invar(k) }
    k : = k/2; REFINE(k); { T satisfies invar(k) }
  until k = 1;
  delete extra #'s;
  return T;
end.
```

**Remark**

Observe that the previous strategy followed to build the suffix tree $T(text)$ can be implemented in the sequential RAM model (one processor). Then, because the computation of equivalence classes can be done by a sequential linear time algorithm (with the help of radix sorting), we get an $O(n.\log n)$ time simple new algorithm for the computation of suffix trees. The suffix tree constructions of Chapter 5 are inherently sequential, because the text is scanned from left to right or in the reverse direction. The nature of the present algorithm is "more parallel", and has almost no reason to be considered for sequential computations

**Theorem 9.21**

The suffix tree of text of length $n$ can be constructed in $O(\log^2 n)$ parallel time with $n$ processors on a PRAM with exclusive-writes. (With a more elaborated construction even read conflicts can be avoided).

**Proof**

The complexity bounds follows directly from the construction, and from the algorithm computing the dictionary of basic factors. At each stage, it is possible to calculate for each node how many new sons have to be created for this node. Then, in logarithmic time, we can assign new processors to the newly created nodes. All calculations are easy because we can calculate the number of new nodes traversing the tree in pre-order, for instance. Such traversal of the tree is easily parallelized efficiently. This completes the proof. ‡

In the construction above, the running time can be reduced by the logarithmic factor if concurrent writes are allowed. Basically, the method is analogue to the computation of the dictionary of basic factors. The bulletin board technique is used similarly. However, it becomes more difficult to assign processors to newly created nodes.

**Theorem 9.22**

Suffix trees can be built in $O(\log n)$ parallel time with $n$ processors in the PRAM with write conflicts.

## 9.5.* Parallel computation of dawg's

In this section we extend the results of the previous section to the computation of dawg's. We show how to compute efficiently in parallel the directed acyclic word graph of all factors of a text, and also its compressed version — the minimal factor automaton. The construction of dawg's given here consists essentially in a parallel transformation of suffix trees. The basic procedure is the computation of equivalent classes of subtrees. We encode the suffix tree by a string in such a way that the subtrees correspond to subwords of the coding string.

**Lemma 9.23**

Let $T$ be a rooted ordered tree whose edges are labelled with constant size letters. Then, we can compute the isomorphic classes of subtrees of $T$ with $O(n)$ processors in time $O(\log^2 n)$ in the exclusive-write PRAM model, and in time $O(\log n)$ in the concurrent-write PRAM model.

**Proof**

We use an Euler tour technique, we refer the reader to [TV 85] and [GR 88] for more detailed exposition of this technique. The edge with label $X$ is replaced by two edges: the forward edge with label $X$, and the backward edge with label $X'$. The tree becomes an Eulerian directed graph.

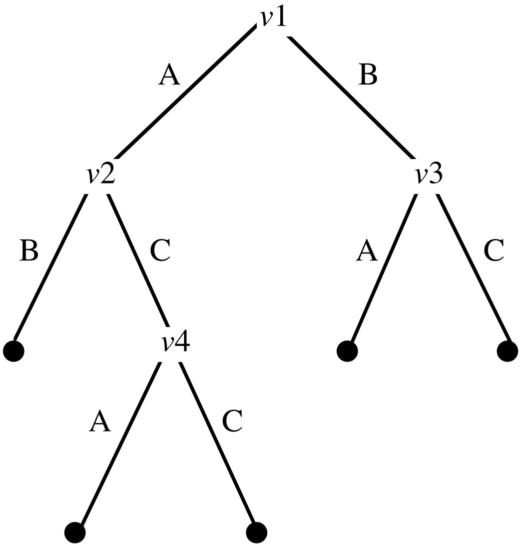


**Figure 9.16**. $code(v1)$ = "ABBCAACCCABAACCB"; $code(v3) = code(v4)$.
The code $x$ of the tree $T$ is constructed in parallel by the Euler tour method.
The labels of edges outgoing a given node are sorted. The nodes $v4$ and $v3$ are roots of isomorphic subtrees because $x[5\ldots8] = x[12\ldots15]$.

An Euler tour $x$ is computed such that the edges outgoing a given node of the tree appear in their original order. Such a tour can be computed in $O(\log n)$ time with $n$ processors [TV 85]. The main advantage of the technique is the transformation of tree problems into problems on strings. Figure 9.16 demonstrates an Euler tour technique for a sample tree.

Let $code(v)$ denote the part of the traversal sequence $x$ corresponding to the subtree rooted at $v$. It is possible to compute in $O(\log n)$ time with $n$ processors the integers $i$ and $j$ such that $code(v) = x[i\ldots j]$ for each node $v$. The subtrees rooted at $v1$ and $v2$ are isomorphic iff $code(v1) = \text{code}(v2)$.

We build the dictionary of basic factors for $x$. Then, each subtree gets a constant size name corresponding to its code. These names are given directly by the dictionary if the length is a power of two. If not, the composite name is created (decomposing the code of the subtree into two overlapping strings having length a power of two). Afterwards two subtrees are isomorphic iff they have the same names, and the crucial point is here that the names are of $O(1)$ size. The procedure RENUMBER can be applied to compute the equivalence classes of subtrees with the same name. This completes the proof. ‡

**Theorem 9.24**

*DAWG*(*text*) can be constructed in $O(\log^2 n)$ time in the exclusive-write PRAM model, and in $O(\log n)$ time in the concurrent-write PRAM model, using $O(n)$ processors.

**Proof**

We demonstrate the algorithm on the example string *text* = *baaabbabb*. We assume that the suffix tree of text is already constructed. For technical reasons, the endmarker # is added to the *text*. This endmarker is later ignored in the final dawg (however, it is necessary at this stage).

By the algorithm given in the proof of the preceding lemma, the equivalence classes of isomorphic subtrees are computed. The roots of isomorphic subtrees are identified, and we get an approximate version *G*' of *DAWG*(*text*) (see Figure 9.17). The difference between the actual structure and the dawg is related to lengths of strings which are labels of edges. In the dawg each edge is labelled by a single symbol. The "naive" approach could be to decompose each edge labelled by a string of length *k* into *k* edges and then merge some of them; but the intermediate graph could have a quadratic number of nodes. We apply such an approach with the following modification. By the weight of an edge we mean the length of its label. For each node *v*, we compute the heaviest (with the biggest weight) incoming edge. Denote this edge by *inedge*(*v*). Then, in parallel, for each node *v*, we perform a local transformation *local-action*(*v*). It is crucial that all these local transformations are independent and can be performed simultaneously for all *v*.

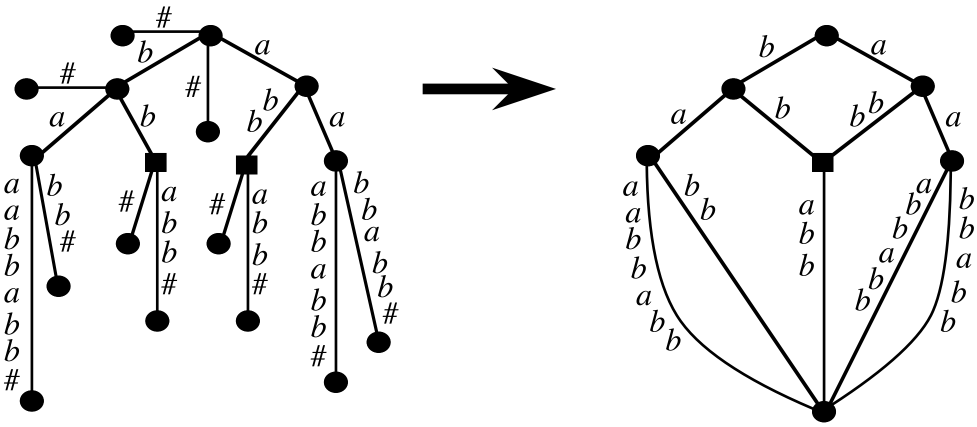


**Figure 9.17**. Identification of isomorphic classes of nodes of the suffix tree.
In the algorithm, labels of edges are constant size names corresponding to themselves.

The transformation *local-action*($v$) consists in decomposing the edge *inedge*($v$) into $k$ edges, where $k$ is the length of the label $z$ of this edge. The label of $i$-th edge is $i$-th letter of $z$. Are introduced $k$-1 new nodes: ($v$, 1), ($v$, 2), …, ($v$, $k$-1). The node ($v$, $i$) is at distance $i$ from $v$. For each other edge incoming $v$, $e$ = ($w$, $v$) we perform in parallel the following additional action. Suppose that the label of $e$ has length $p$, and that its first letter is $a$. If $p > 1$, we remove the edge $e$, and create an edge from $w$ to ($v$, $p$-1) whose label is the letter $a$. This is graphically illustrated in Figure 9.18.

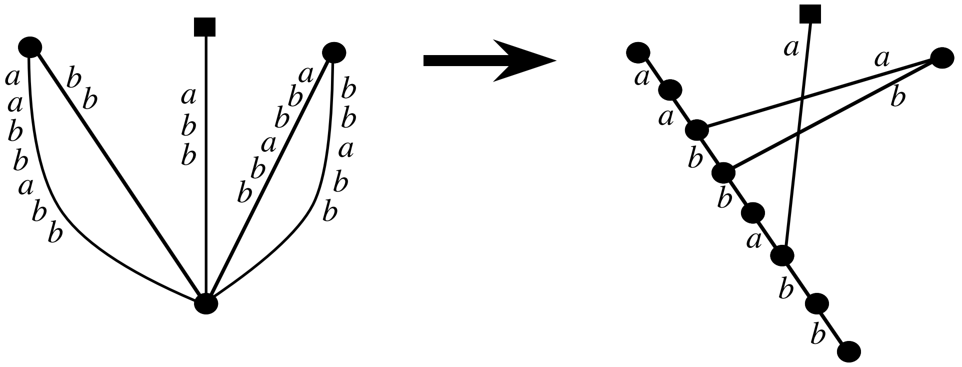


**Figure 9.18**. The local transformation. New nodes are introduced on the heaviest incoming edge.

Then we execute the statement : **for** all non-root nodes $v$ **in parallel do** *local-action*($v$). The resulting graph for our example string *text* is presented in the Figure 9.19. Generally, this graph is the required *DAWG*(*text*). This completes the proof. ‡

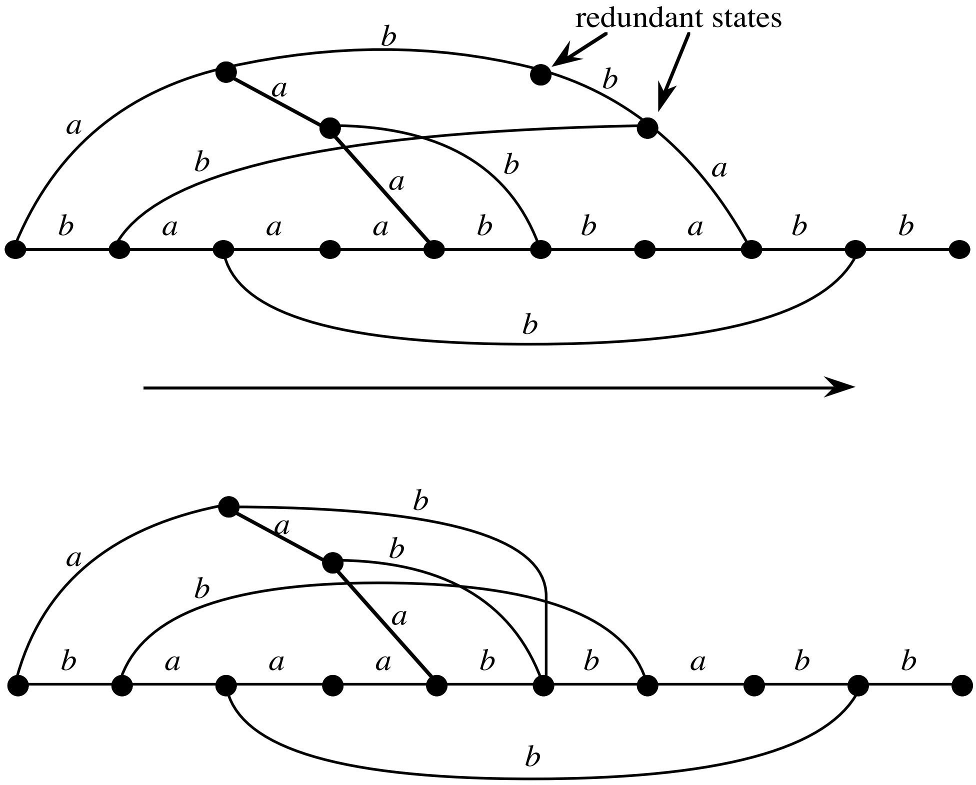


**Figure 9.19**. Dawg (top) and minimal factor automaton (bottom) of *baaabbabb*.

The dawg *DAWG*(*text*) can still be compacted. In fact, the structure can be reduced in the sense of minimization of automata. This remains to merge equivalent node according to the path starting from them. The reduction is possible if we do not mark nodes associated to suffixes of the text. In other words, the structure then accepts the set of all factors of *text* without any distinction between them. We call the resulting structure the minimal factor automaton of *text*, and denote it by *F*(*text*). Figure 9.19 illustrate the notion on the word *text* = *baaabbabb*. We first show how to determine the nodes of *DAWG*(*text*) associated to suffixes of *text*. The overall gives the minimal automaton accepting suffixes of *text*, *S*(*text*). Then, we give the construction of *F*(*text*) derived from that of *DAWG*(*text*).

**Theorem 9.25**

The minimal suffix automaton of a text of length of length $n$ can be constructed in $O(\log^2 n)$ time in the exclusive-write PRAM model, and in $O(\log n)$ time in the concurrent-write PRAM model, using $O(n)$ processors.

**Proof.**

We admit that the minimal suffix automaton *S*(*text*) is just *DAWG*(*text*) in which nodes associated to suffixes of *text* are marked as accepting states. We can assume that we know the values of nodes of the suffix tree (labels of the path from the root to nodes). In the process of identification of roots of isomorphic subtrees, we can assign names to the nodes of the dawg: the name of node *v* is the word corresponding to the longest path from the root to *v*. Then, node is an accepting state of *S*(*text*) iff its name is the suffix of the input word *text*. This can be checked for each node *v* in constant time with the dictionary of basic factors. This completes the proof. ‡

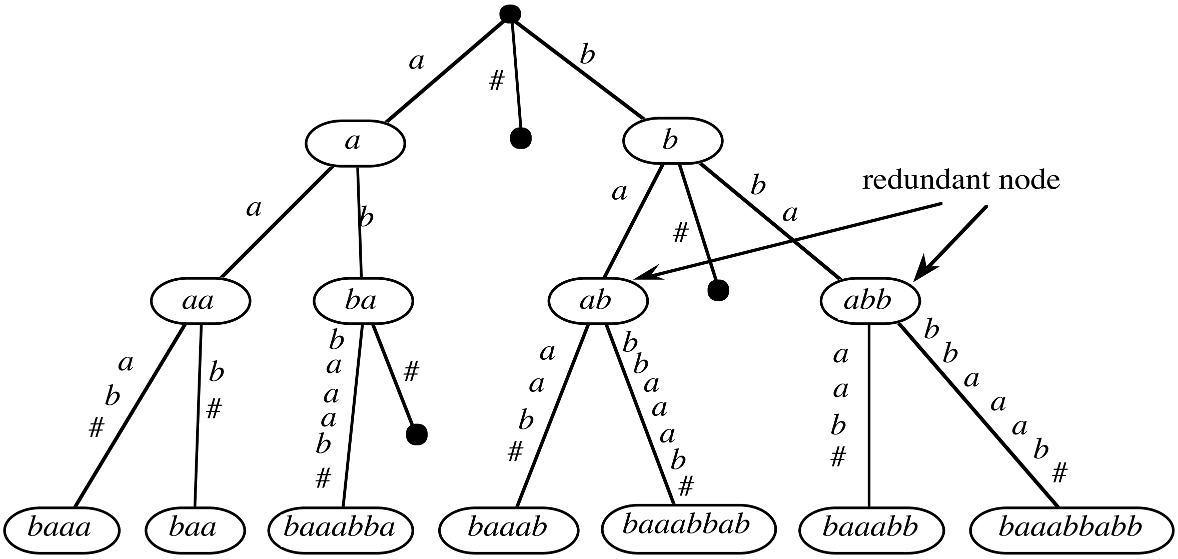


**Figure 9.20**. The suffix tree *T*(w') for *w* = *bbabbaaab#*; *w* is the reverse of *text* = *baaabbabb*, with an endmarker. We ignore nodes whose incoming edges are labelled only by *#*. The values of nodes of this tree are reverses of the labels of their paths in *T*(*w*); they correspond to the nodes of *DAWG*(*text*). The node *v* is redundant iff, simultaneously, *v* is a prefix of the father of *text*, *v* has only two sons, and at least one of them is a leaf. Hence, *a* is not redundant, but nodes *ab* and *abb* are.

**Theorem 9.26**

The minimal factor automaton of a text of length of length *n* can be constructed in $O(\log^2 n)$ time in the exclusive-write PRAM model, and in $O(\log n)$ time in the concurrent-write PRAM model, using $O(n)$ processors.

**Sketch of the proof**

Construct the suffix tree *T*' = *T*(*w*). Let *G* = *DAWG*(*text*) and *G*' = *DAWG*(*#text*). Let *w* be the reverse of *#text*. There is a one-to-one correspondence between nodes of *G*' and *T*', if we reverse all labels of nodes of *T*'. The original label of the node *v* of *T*' is the word corresponding to the path from the root to *v*. However, we modify these labels by reversing these words. We identify all nodes of *G* with their equivalents in *T*' by an efficient parallel algorithm based on the dictionary of basic factors.

The tree *T*' is the tree of so-called suffix-links of *G*'. It provides a useful information about *G*' and *G*, since *G* is a subgraph of *G*'. Let *V*' be the set of all nodes (including root) reachable in *G* from the root, after removing the edge labelled #; the subgraph *G*' induced by *V*' equals *G*.

Now the graph *G* = *DAWG*(*text*) can be treated as a finite deterministic automaton accepting all factors of text (the set *Fac*(*text*)). All nodes are accepting states. Two nodes of *G* are equivalent iff they are equivalent in the sense of this automaton. It happens that equivalence classes are very simple, each equivalence class consists of at most two nodes. It is easy to compute these equivalence classes in parallel using the tree *T*'. We say that the node (state) *v* is redundant if it is contained in a two-element equivalence class, and its partner *v*' (in the equivalence class) has a longer value. For a redundant node *v*, denote by π(*v*) the node *v*'. Essentially, the problem of the computation of the minimal factor automaton reduces to the computation of redundant nodes, and of the function π. Let us identify nodes with their values. Let *z* be the father of *text* in *T*'.

**Claim**

> The node *v* of *G* is redundant iff *v* is a prefix of *z* (not necessarily proper), *v* has only two sons in *T*', and one of its sons is a leaf.
>
> Let *b* be the letter preceding the rightmost occurrence of *z* in *text*. Assume that *v* is a redundant node, and that *v*' is a son of *v* such that the label of the edge (*v*, *v*') does not start with the letter *b*. Then π(*v*) = *v*'.

We leave the technical proof of the claim to the reader (as a non-trivial exercise !). Section 6.4 may be helpful for that purpose. In the example of Figure 9.20, *z* = *abb*, its prefixes are *a*, *ab*, and *abb*. Only *ab* and *abb* are redundant; π(*ab*) = *baaab* and π(*abb*) = *baaabb*.

The claim above allows to compute efficiently in parallel all redundant nodes, and the function π. After that, we execute: the statement

```
for each redundant node v do in parallel
    identify v with π(v), redirect all edges coming
    from non-redundant nodes to v onto π(v);
```

The computation of redundant nodes is illustrated in Figure 9.20. Once we know redundant nodes, the whole minimization process can be done efficiently in parallel. This completes the proof. ‡

The algorithm gives also another sequential linear-time construction of dawg's, as classes of isomorphic subtrees can be computed in linear sequential time traversing the tree in a bottom-up manner and using bucket sort. There is a possible different efficient parallel algorithm for dawg construction by transforming the suffix tree of the reverse input word into the dawg of the word. In this case, the correspondence between such suffix trees and dawg's, as described in chapter 6, can be used. In the presentation above, we parallelize the transformation of suffix trees into dawg's, which relies on subtrees isomorphism. It is also possible to parallelize the other transformation, but this becomes much more technical.

The parallel algorithm for dawg construction can be further extended, and applies to the computation (in parallel) of complete inverted files. This can be understood as the construction of the suffix dawg of a finite set of texts.

## Bibliographic notes

Elementary techniques for the construction of efficient parallel algorithms on a PRAM can be found in [GR 88]. It is also a source for detailed description of optimal pattern-matching algorithm for strings (see Chapter 14). The method developed in *Parallel-KMR* algorithm leads to less efficient algorithm, but is more general and easy to explain. Moreover, the running times we get with KMR algorithm are usually within a logarithmic factor of best known algorithms. The dictionary of basic factors in from [CR 91c]. Cole [Co 87] has designed a parallel merge sort that can be used for one implementation of the procedure *RENUMBER* of Section 9.1.

The material of Sections 9.2 and 9.3 is from [CR 91c]. Apostolico has given an optimal algorithm to detect squares in texts [Ap 92].

The suffix tree construction is based on the same ideas. Efficient parallel algorithms for the construction of suffix trees have been discovered independently by Landau, Schieber, Vishkin, and by Apostolico and Iliopoulos. The combined version appears in [AILSV 88]. This paper also contains the trick on the reduction of bulletin board space from $n^2$ to $n^{1+\varepsilon}$.

The construction of suffix and minimal factor automata is from [CR 90], and is based on the close relationship between suffix trees and dawg's given in [CS 84] (see Chapter 6). A more efficient algorithm to test the squarefreeness of a text, achieving an optimal speed-up, has been designed by Apostolico et alii [ABG 92] (see also [Ap 92]), but the method are much more complicated than the ones presented in this chapter.

Technical properties used to derive parallel detections of palindromes are essentially from [GS 78].

The properties required to prove Theorem 9.26 can be found in [BBEHCS 85] (see also Section 6.4).

## Selected references

[AILSV 88] A. APOSTOLICO, C. ILIOPOULOS, G.M. LANDAU, B. SCHIEBER, U. VISHKIN, Parallel construction of a suffix tree with applications, *Algorithmica* 3 (1988) 347-365.

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# 10. Text compression techniques

The aim of data compression is to provide representations of data in a reduced form. The information carried by data is left unchanged by the compression processes considered in this Chapter. There is no loss of information. In other words, compression processes that we discuss are reversible.

The main interest of data compression is of practical nature. Methods are used both to reduce the memory space required to store files on hard disks or other similar devices, and to accelerate the transmission of data in telecommunications. The question remains important even regarding the rapid increase of mass memory, because the amount of data increases accordingly (to store images produced by satellites or scanners, for instance). The same argument applies to transmission of data, even if the capacity of existing media is constantly improved.

We describe data compression methods based on substitutions. The methods are general, which means that they apply to data on which little is known. Semantic data compression techniques are not considered. So, compression ratios must be appreciate under that condition. Standard methods usually save about 50% memory space.

Data compression methods try to eliminate redundancies, regularities, and repetitions in order to compress the data. It is not surprising then that algorithms have common features with others described in preceding chapters.

After a first section on elementary notions on the compression problem, we consider the classical Huffman statistical coding (Sections 10.2 and 10.3). It is implemented by the Unix (system V) command "pack". It admits an adaptive version well suited for telecommunication, and implemented by the "compact" command of Unix (BSD 4.2). Section 10.4 deals with the general problem of factor encoding, and contains the efficient Ziv-Lempel algorithm. The "compress" command of Unix (BSD 4.2) is based on a variant of this latter algorithm.

## 10.1. Substitutions

The input of a data compression algorithm is a text. It is denoted by $s$, for *source*. It should be considered as a string on the alphabet $\{0, 1\}$. The output of the algorithm is also a word of $\{0, 1\}^*$ denoted by $c$, for *encoded text*. Data compression methods based on substitutions are often described with the help of an intermediate alphabet $A$ on which the source $s$ translates into a text *text*. The method is then defined by the mean of two morphisms $g$ and $h$ from $A^*$ to $\{0, 1\}^*$. The text *text* is an inverse image of $s$ by the morphism $g$, which means that its letters are coded with bits. The encoded text $c$ is the direct image of *text* by the morphism $h$. The set $\{(g(a), h(a)) : a \in A\}$ is called the *dictionary* of the coding method. When the morphism $g$ is known or implicit, the description of the dictionary is just given by the set $\{a, h(a)) : a \in A\}$.

We only consider data compression methods without loss of information. This implies that a *decoding function f* exists such that $s$=$f$($c$). Again, $f$ is often defined through a decoding function $h'$ such that *text* = $h'(c)$, and then $f$ itself is the composition of $h'$ and $g$. The lossless information constraint implies that the morphism $h$ is one-to-one, and that $h'$ is its inverse morphism. This means that the set $\{h(a)) : \mathrm{a} \in A\}$ is a uniquely decipherable code.

The pair of morphisms, ($g$, $h$), leads to a classification of data compression methods with substitutions. We get four principal classes according to whether $g$ is uniform (i.e. when all images of letters are words of the same length) or not, and whether the dictionary is fixed or computed during the compression process. Most elementary methods do not use any dictionary. Strings of a given length are sometimes called in this context *blocks*, while factors of variable lengths are called *variables*. A method is then qualified as *block-to-variable* if the morphism $g$ is uniform, or *variable-to-variable* if neither $g$ nor $h$ are assumed to be uniform.

The efficiency of a compression method that encodes a text $s$ into a text $c$, is measured through a *compression ratio*. It can be $|s|/|c|$, or its inverse $|c|/|s|$. It is sometimes more intuitive to compute the amount of space saved by the compression, $(|s|-|c|)/|c|$.

| | *block-to-variable* | *variable-to-variable* |
|---|---|---|
| | differential encoding | repetition encoding |
| *fixed dictionary* | statistical encoding (Huffman) | factor encoding |
| *evolutive dictionary* | sequential statistical encoding (Faller et Gallager) | Ziv and Lempel's algorithm |

The rest of the section is devoted to the description of two basic methods. They appear on the first line of the previous table: *repetition encoding* and *differential encoding*.

The aim of repetition encoding is to efficiently encode repetitions. Let *text* be a text on the alphabet $A$. Let us assume that *text* contain a certain quantity of repetitions of the form $aa\ldots a$ for some character $a$ ($a \in A$). Inside *text*, a sequence of $n$ letters $a$, can be replaced by *&an*, where "&" is a new character ($\& \notin A$). This corresponds to the usual mathematical notation $a^n$. When the repetitions of only one letter are encoded in that way, the letter itself do need not to appear, so that the repetition is encoded by *&n*. This is commonly done for "space deletion".

```
1100001 1100001 1100001 1100001 1100001 1100001
   a       a       a       a       a       a
                  encoded by
                &      a      6
            0100110 1100001 000110
```

**Figure 10.1**. Repetition coding (with ASCII code).

The string *&an* that encodes a repetition of $n$ consecutive occurrences of $a$, is itself encoded on the binary alphabet {0, 1}. In practice, letters are often represented by their ASCII code. So, the codeword of a letter belongs to $\{0, 1\}^k$ with $k$=7 or 8. There is no problem in general to choose the character "&" (in Figure 10.1, the real ASCII symbol & is used). Both symbols & and $a$ appear in the coded text $c$ under their ASCII form. The integer $n$ of the string *&an* should also by encoded on the binary alphabet. Note that it is not sufficient to translate $n$ by its binary representation, because we would be unable to localize it at decoding time inside the stream of bits. A simple way to cope with that is to encode $n$ by the string $0^l\mathrm{bin}(n)$, where bin($n$) is the binary representation of $n$, and $l$ is the length of it. This works well because the binary representation of $n$ starts with a "1" (because $n$>0). There are even more sophisticated integer representations, but not really suitable in the present situation. On the opposite, a simpler solution is to encode $n$ on the same number of bits as letters. If this number is $k$=8 for instance, the translation of any repetition of length less than 256 has length 3. It is thus useless to encode $a^2$ and $a^3$. A repetition of more than 256 identical letters is cut into smaller repetitions. These limitations reduce the efficiency of the method.

The second very useful elementary compression technique is the differential encoding, also called relative encoding. We explain it on an example. Assume that the source text $s$ is a series of dates

1981, 1982, 1980, 1982, 1985, 1984, 1984, 1981, ...

These dates appears in binary form in $s$, so at least 11 bits are necessary for each of them. But, the sequence can be represented by the other sequence

(1981, 1, -2, 2, 3, -1, 0, -3, ...),

assuming that the integer 1 in place of the second date is the difference between the second and the first dates. An integer in the second sequence, except the first one, is the difference between two consecutive dates. The decoding process is obvious, and processes the sequence from left to right, which is well adapted for texts. Again, the integers of the second sequence appear in binary in the coded text $c$. All but the first, in the example, can be represented with only 3 bits each. This is how the compression is realized on suitable data.

More generally, differential encoding takes a sequence $(u_1, u_2, \ldots, u_n)$ of data, and represents it by the sequence of differences $(u_1, u_2\text{-}u_1, \ldots, u_n\text{-}u_{n\text{-}1})$ where "-" is an appropriate operation.

Differential encoding is commonly used to create archives of successive versions of a text. The initial text is fully memorized on the tape. And, for each following version, only the differences with its preceding one is kept on the tape. Several variations on this idea are possible. For instance, $(u_1, u_2, \ldots, u_n)$ can be translated by $(u_1, u_2\text{-}u_1, \ldots, u_n\text{-}u_1)$, considering that the differences are all with the first element of the sequence. This element can also change during the process according to some rule.

Very often several compression methods are combined to realize a whole compression process. A good example of this strategy is given by the application to facsimile machines (FAX). Pages to be transmitted are made of lines, each of 1728 bits. A differential encoding is first applied on consecutive lines. So, if the $n^{\text{th}}$ line is

0101001 0101010 1001001 1101001 1011101 1000000...

and the $n$+$1^{\text{th}}$ line is

0101000 0101011 0111001 1100101 1011101 0000000...

the following line is to be sent

0000001 0000001 1110000 0001100 0000000 1000000...

Of course, no compression at all would be achieved if the line were sent as it is. There are two solution to encode the line of differences. The first solution encodes runs of "1" occurring in the line both by their length and their relative position in the line. So, we get the sequence

(7, 1), (7, 4), (8, 2), (10, 1), ...

whose representation on the binary alphabet gives the coded text. The second solution makes use of a statistical Huffman code the encode successive runs of 0's and runs of 1's. These codes are defined in the next section.

A good compression ratio is generally obtained when the transmitted image contains a written text. But it is clear that "dense" pages lead to small compression ratio, and that best ratios are reached with blank (or black) pages.

## 10.2. Static Huffman coding

The most common technique to compress a text is to redefine the codewords associated to the letters of the alphabet. This is achieved by *block-to-variable* compression methods. According to the pair of morphisms ($g$, $h$) introduced in section 10.1, this means that $g$ represents the usual code attributed to the characters (ASCII code, for instance). More generally, the source is factorized into blocks of a given length. Once this length is chosen, the method reduces to the computation of a morphism $h$ that minimizes the size of the encoded text $h(text)$. The key idea to find $h$ is to consider the frequency of letters, and to encode frequent letters by short codewords. Methods based on this criterion are called *statistical compression methods*.

Computing $h$, remains to find the set $C = \{h(a) : a \in A\}$, which must be a uniquely decipherable code in order to permit the decoding of the compressed text. Moreover, to get an efficient decoding algorithm, $C$ is chosen as an instantaneous code, i.e. a *prefix code*, which means that no word of $C$ is prefix of another word of $C$. It is quite surprising that this does not reduce the power of the method. This is because any code has an equivalent prefix code with the same distribution of codeword lengths. The property, stated in the following theorem, is a consequence of what is known as the Kraft-McMillan inequalities related to codeword lengths, which are recalled first.

**Kraft's inequality**

There is a prefix code with word lengths $l_1$, $l_1$, …, $l_k$ on the alphabet {0, 1} iff

(*) **Error!**≤ 1.

**McMillan's inequality**

There is a uniquely decipherable code with word lengths $l_1$, $l_1$, …, $l_k$ on the alphabet {0, 1} iff the inequality (*) holds.

**Theorem 10.1**

A uniquely decipherable code with prescribed word lengths exists iff a prefix code with the same word lengths exists.

Huffman's method computes the code $C$ according to a given distribution of frequencies of the letters. The method is both optimal and practical. The entire Huffman's compression algorithm proceeds in three steps. In the first step, the numbers of occurrences of letters (blocks) are computed. Let $n_a$ be the number of times letter $a$ occurs in *text*. In the second step, the set $\{n_a : a \in A\}$ is used to compute a prefix code $C$. Finally, in the third step, the text is encoded with the prefix code $C$ found previously. Note that the prefix code should be appended □□tthe coded text because the decoder needs it. It is commonly put inside a *header* (of the compressed file) that contains additional information on the file. Instead of computing exact numbers of occurrences of letters in the source, a prefix code can be computed on the base of a standard probability distribution of letters. In this situation, only the third step is applied to encode a text, which gives a very simple and fast encoding procedure. But obviously the coding is no longer optimal for a given text.

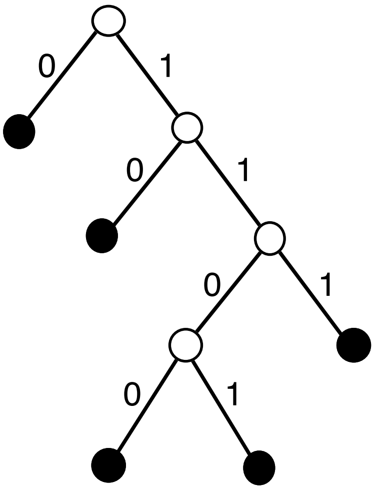


**Figure 10.2**. The trie of the prefix code {0, 10, 1100, 1101, 111}.
Black nodes correspond to codewords.

The core of Huffman's algorithm is the computation of a prefix code, over the alphabet {0, 1}, corresponding to the distribution of letters $\{n_a : a \in A\}$. This part of the algorithm builds the word trie $T$ of the desired prefix code. The "prefix" property of the code ensures that there is a one-to-one correspondence between codewords and leaves of $T$ (see Figure 10.2). Each codeword (and leaf of the trie) corresponds to some number $n_a$, and gives the encoding $h(a)$ of the letter $a$.

The size of the coded text is

$|h(text)|$ = **Error!**.

On the trie of the code $C$ the equality translates into

$|h(text)|$ = **Error!**,

where $f_a$ is the leaf of $T$ associated with letter $a$, and $level(f_a)$ is its distance to the root of $T$. The problem of computing a prefix code $C = \{h(a) : a \in A\}$ such that $|h(text)|$ is minimum becomes a problem on trees :

— find a minimum weighted binary tree $T$ whose leaves $\{f_a : a \in A\}$ have initial weights $\{n_a : a \in A\}$,

where the weight of $T$, denoted by $W(T)$, is understood as the quantity **Error!**. The algorithm below builds a minimum weighted tree in a bottom-up fashion, grouping together two subtrees under a new node. In other words, at each stage, the algorithm creates a new node that is made a father of two existing nodes. The weight of a node is the weight of the subtree below it. There are several possible trees of minimum weight. All trees that can be produced by Huffman algorithm are called *Huffman trees*.

**Example**

Let *text* = *abracadabra*. The number of occurrences of letters are

$$n_a = 5, \quad n_b = 2, \quad n_c = 1, \quad n_d = 1, \quad n_r = 2.$$

The tree of a possible prefix code built by Huffman's algorithm is shown in Figure 10.3. Weights of nodes are written on the nodes. The prefix code is :

$$h(a) = 0, \quad h(b) = 10, \quad h(c) = 1100, \quad h(d) = 1101, \quad h(r) = 111.$$

The coded text is then

0 10 111 0 1100 0 1101 0 10 111 0

which is a word of length 23. If the initial codewords of letters have length 5, we get the compression ratio 55/23 ≈ 2.4. However, if the prefix code (or its trie) has to be memorized, this additionally takes at least 9 bits, which reduces the compression ratio to 55/32 ≈ 1.7. If the initial coding of letters has also to be stored (with at least 25 bits), the compression ratio is even worse: 55/57 ≈ 0.96. In the latter case, the encoding leads to an expansion of the source text. ‡

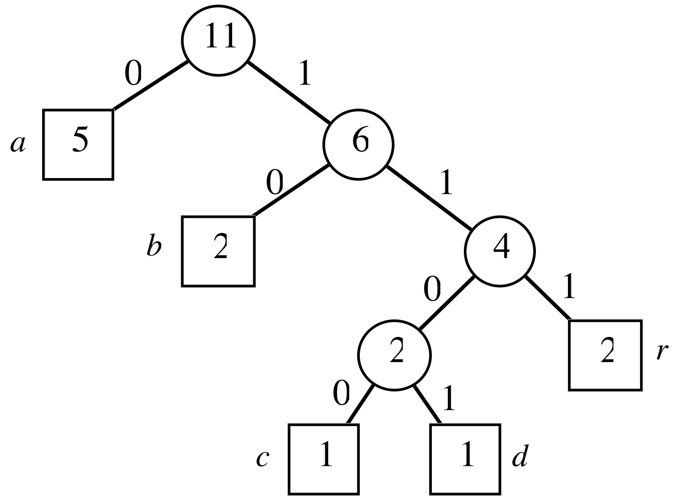


**Figure 10.3**. Huffman tree for *abracadabra*.

As noted in the previous example, the header of the coded text must often contain enough information on the coding to allow a later decoding of the text. The necessary information is the prefix code computed by Huffman's algorithm, and the initial codewords of letters. Altogether, this takes around 2|*A*|+*k*|*A*| bits (if *k* is the length of initial codewords), because the structure of the trie can be encoded with 2|*A*|-1 bits.

```
Algorithm Huffman { minimum weighted tree construction }
begin
  for $a$ in $A$ do create a one-node tree $f_a$ with weight $W(f_a) = n_a$;
  $L$ := queue of trees $f_a$ in increasing order of weights;
  $N$ := empty queue; { for internal nodes of the final tree }
  while $|L|+|N| > 1$ do begin
    let $u$ and $v$ be the elements of $L \cup N$ with smallest weights;
    { $u$ and $v$ are found from heads of lists }
    delete $u$ and $v$ from (heads of) the queues;
    create a tree $x$ with a new node as root,
                    and $u$ and $v$ as left and right subtrees;
    $W(x)$ := $W(u)+W(v)$;
    add the tree $x$ to the end of queue $N$;
  end;
  return the remaining tree in $L \cup N$;
end.
```

**Theorem 10.2**

Huffman algorithm produces a minimum weighted tree in time $O(|A|.\log|A|)$.

**Proof**

The correctness is based on several observations. First, a Huffman tree is a binary complete tree, in the sense that all internal nodes have exactly two sons. Otherwise, the weight of the tree could be decreased by replacing a one-son node by its own son. Second, there is a Huffman tree $T$ for $\{n_a : a \in A\}$ in which two leaves at the maximum level are siblings, and have minimum weights among all leaves (and all nodes too). Possibly exchanging leaves in a Huffman tree gives the conclusion. Third, let $x$ be the father of two leaves $f_b$ and $f_c$ in a Huffman tree $T$. Consider a weighted tree $T'$ for $\{n_a : a \in A\}$-$\{n_b, n_c\}$+$\{n_b + n_c\}$, assuming that $x$ is a leaf of weight $n_b + n_c$. Then,

$$W(T) = W(T')+n_b+ n_c.$$

Thus, $T$ is a Huffman tree iff $T'$ is. This is the way the tree is built by the algorithm, joining two trees of minimal weights into a new tree.

The sorting phase of the algorithm takes $O(|A|.\log|A|)$ with any efficient sorting method. The running time of the instructions inside the "while" loop is constant because the minimal weighted nodes in $L \cup N$ are at the beginning of the lists. Therefore, the running time of the "while" loop is proportional to the number of created nodes. Since exactly $|A|$-1 nodes are created, this takes $O(|A|)$ time. ‡

The performance of Huffman codes is related to a measure of information of the source text, called the *entropy of the alphabet*. Let $p_a$ be $n_a/|text|$. This quantity can be viewed as the probability that letter $a$ occurs at a given position in the text. This probability is assumed to be independent of the position. Then, the entropy of the alphabet according to the $p_a$'s is defined as

$H(A)$ = - **Error!**.

The entropy is expressed in bits (log is a based-two log). It is a lower bound of the average length of the codewords $h(a)$,

$m(A)$ = **Error!**.

Moreover, Huffman codes give the best possible approximation of the entropy (among methods based on a recoding of the alphabet). This is summarized in the following theorem whose proof relies on the Kraft-McMillan inequalities.

**Theorem 10.3**

The average length of any uniquely decipherable code on the alphabet $A$ is at least $H(A)$.

The average length $m(A)$ of a Huffman code on $A$ satisfies $H(A) \leq m(A) \leq H(A)+1$.

The average length of Huffman codes is exactly the entropy $H(A)$ when, for each letter $a$ of $A$, $p_a = 2^{-|h(a)|}$ (note that the sum of all $p_a$'s is 1). The ratio $H(X)/m(X)$ measures the efficiency of the code. In English, the entropy of letters according to a common probability distribution on letters is close to 4 bits. And the efficiency of a Huffman code is more than 99%. This means that if the English source text is an 8-bit ASCII file, Huffman compression method is likely to divide its size by two. The Morse code (developed for telegraphic transmissions), that also takes into account probabilities of letters, is not a Huffman code, and has an efficiency close 66%. This not as good as any Huffman code, but the Morse code incorporate redundancies in order to make transmissions safer.

In practice, Huffman codes are built for ASCII letters of the source text, and also for digrams (factors of length 2) occurring in the text instead of letters. In the latter case, the source is factorized into blocks of length 16 bits (or 14 bits). On large enough texts, the length of blocks can be chosen higher to capture some dependencies between consecutive letters, but the size of the alphabet grows exponentially with the length of blocks.

Huffman's algorithm generalizes to the construction of prefix codes on alphabets of size $m$ larger than two. The trie of the code is then an almost $m$-ary tree. Internal nodes have $m$ sons, except maybe one node which is father of less than $m$ leaves.

The main default of the whole Huffman's compression algorithm is that the source text must be read twice. The first time to compute the frequencies of letters, and the second time to encode the text. Only one reading of the text is possible if one uses known average frequencies of letters. But then, the compression is not necessarily optimal on a given text. The next section presents a solution avoiding two readings of the source text.

There is another statistical encoding that produces a prefix code. It is known as the Shannon-Fano coding. It builds a weighted tree, as Huffman's method does, but the process works top-down. The tree and all its subtrees are balanced according to their weights (sum of occurrences of characters associated to leaves). The result of the method is not necessarily an optimal weighted tree, so its performance is generally within that of Huffman coding.

## 10.3. Dynamic Huffman coding

We describe now an adaptive version of Huffman's method. With this algorithm, the source text is read only once. Moreover, the memory space required by the algorithm is proportional to the size of the current trie, that is, to the size of the alphabet. The encoding of letters of the source text is realized while the text is read. In some situations, the compression ratio is even better than the ratio of Huffman's method.

Assume that *za* (*z* a word, *a* a letter) is a prefix of *text*. We consider the alphabet *A* of letters occurring in *z*, plus the extra symbol # that stands for all letters not occurring in *z* but that possibly appear in *text*. Let us denote by $T_z$ any Huffman tree built on the alphabet $A \cup \{\#\}$ with the following weights:

$$n_a = \text{number of occurrences of } a \text{ in } z,$$

$$n_\# = 0.$$

We denote by $h_z(a)$ the codeword corresponding to *a*, and determined by the tree $T_z$. Note that the tree has only one leaf of zero weight, namely, the leaf associated to #.

The encoding of letters proceeds as follows. In the current situation, the prefix *z* of *text* has already been coded, and we have the tree $T_z$ together with the corresponding encoding function $h_z$. The next letter *a* is then encoded by $h_z(a)$ (according the tree $T_z$). Afterwards, the tree is transformed into $T_{za}$. At decoding time the algorithm reproduces the same tree at the same time. However, the letter *a* may not occur in *z*, in which case it cannot be translated as any other letter. Here, the letter *a* is encoded by $h_z(\#)g(a)$, that is, the codeword of the special symbol # according the tree $T_z$, followed by the initial code of letter *a*. This step also is reproduced without any problem at decoding time.

The reason why this method is practically effective comes from an efficient procedure to update the tree. The procedure UPDATE used in the algorithm below can be implemented in time proportional to the height of the tree. This means that the compression and decompression algorithms work in real-time for any fixed alphabet, as it is the case in practice. Moreover, the compression ratio obtained by the method is close to that of Huffman's compression algorithm.

```
Algorithm { adaptive Huffman coding }
begin
  z := ε; T := $T_ε$;
  while not end of text do begin
    a := next letter of text;          { h is implied by T }
    if a is not a new letter then write(h(a))
    else write(h(#)g(a)); { g(a) = initial codeword for a }
    T := UPDATE(T);
  end;
end.
```

The key-point of the adaptive compression algorithm is a fast implementation of the procedure UPDATE. It is based on a characterization of Huffman trees, known as the siblings property. The property does not hold in general for minimum weighted trees.

**Theorem 10.4** (siblings property)

Let $T$ be a complete binary weighted tree (with $p$ leaves) in which leaves have positive weights, and the weight of any internal node is the sum of weights of its sons. Then, $T$ is a Huffman tree iff its nodes can be arranged in a sequence $(x_1, x_2, \ldots, x_{2n-1})$ such that:

1 — the sequence of weights $(w(x_1), w(x_2), \ldots, w(x_{2n-1}))$ is in increasing order, and

2 — for any $i$ $(1 \leq i < n)$, the consecutive nodes $x_{2i-1}$ and $x_{2i}$ are siblings (they have the same father).

**Proof**

If $T$ is a tree built by Huffman algorithm, the ordering on nodes is just given by the order in which nodes are deleted from queues during the run of the algorithm.
The "if" part of the proof is by induction on the number $p$ of leaves. Consider the two nodes $x_1$ and $x_2$ of the list. It is rather obvious to prove that they are leaves because weights are strictly positive integers. The leaves $x_1$ and $x_2$ can be chosen first by Huffman algorithm because they have minimum weights. Let $x$ be their father. The rest of the construction is done as if we had only $p$-1 leaves, $x_1$ and $x_2$ being substituted by $x$. By induction, the existence of the ordering proves that the tree in which $x$ is a leaf is a Huffman tree. Thus, the initial tree in which $x$ is the father of $x_1$ and $x_2$, is also a Huffman tree (see the proof of Theorem 10.2). ‡

The characterization of Huffman trees by the siblings property remains true if only one leaf has a null weight. During the sequential encoding, the transformation of the current tree $T_z$ into $T_{za}$ starts by incrementing the weight of the leaf $x_i$ that corresponds to $a$. If point 1 of the siblings property is no longer satisfied after that, node $x_i$ is exchanged with the node $x_j$ for which $j$ is the greatest integer such that $w(x_j) < w(x_i)$. If necessary, the same operation is repeated on the father of $x_i$, and so on. The exchange of nodes is, in fact, the exchange of the corresponding subtrees. The tree structure is not affected by exchanges because weights strictly increase from leaves to the root (except maybe in the 3-node tree containing the leaf associated to #), so that a node cannot be exchanged with any of its ancestors. This proves that the procedure UPDATE can be implemented in time proportional to the height of the tree. Thus, we have proved the following.

**Lemma 10.5**

Procedure UPDATE can be implemented to work in time $O(|A|)$.

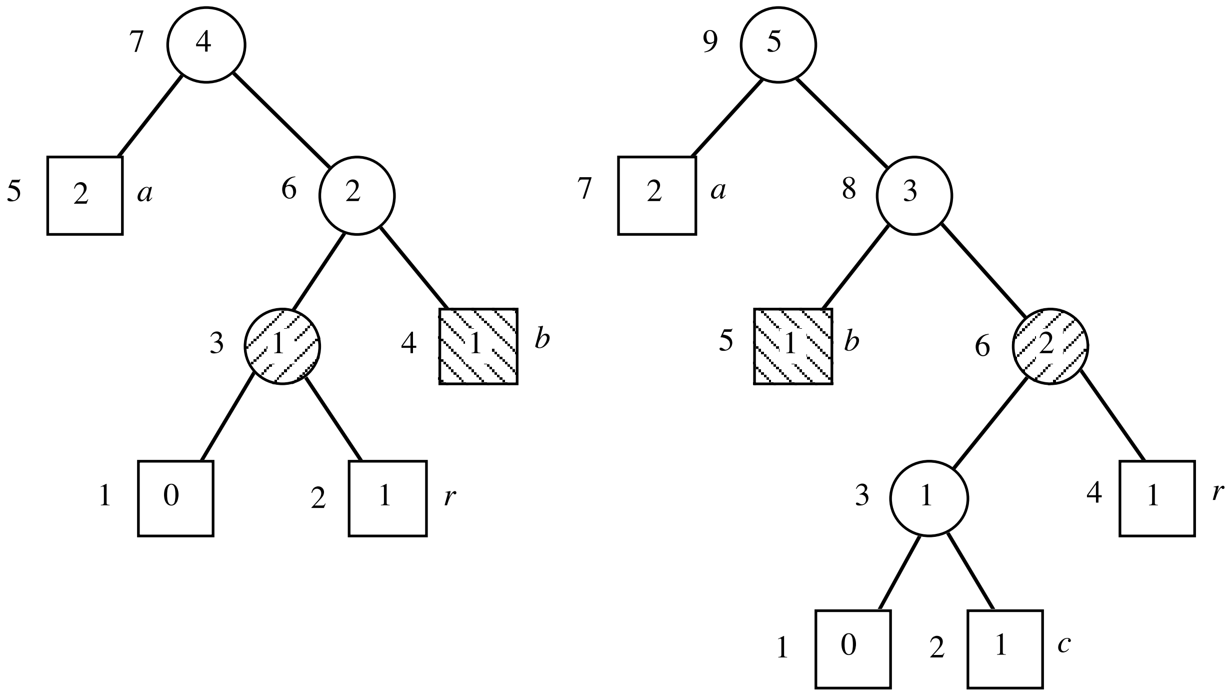


**Figure 10.4**. Transformation of $T_{abra}$ into $T_{abrac}$. Marked nodes have been excahanged. Numbers besides nodes give an ordering satisfying the siblings property.

**Example**

Figure 10.5 shows the sequential encoding of *abracadabra*. Letters are assumed to be initially encoded on 5 bits (*a* -> 00000, *b* -> 00001, *c* -> 00010, ..., *z* -> 11010). The entire translation of *abracadabra* is :

```
00000 000001 0010001 0 10000010 0 110000011 0 110 110 0
  a     b       r    a    c     a     d     a  b   r  a
```

We get a word of length 45. These 45 bits are to be compared with the 57 bits obtained by the original Huffman's algorithm. For this example, the dynamic algorithm gives a better compression ratio, say 55/45 = 1, 22. ‡

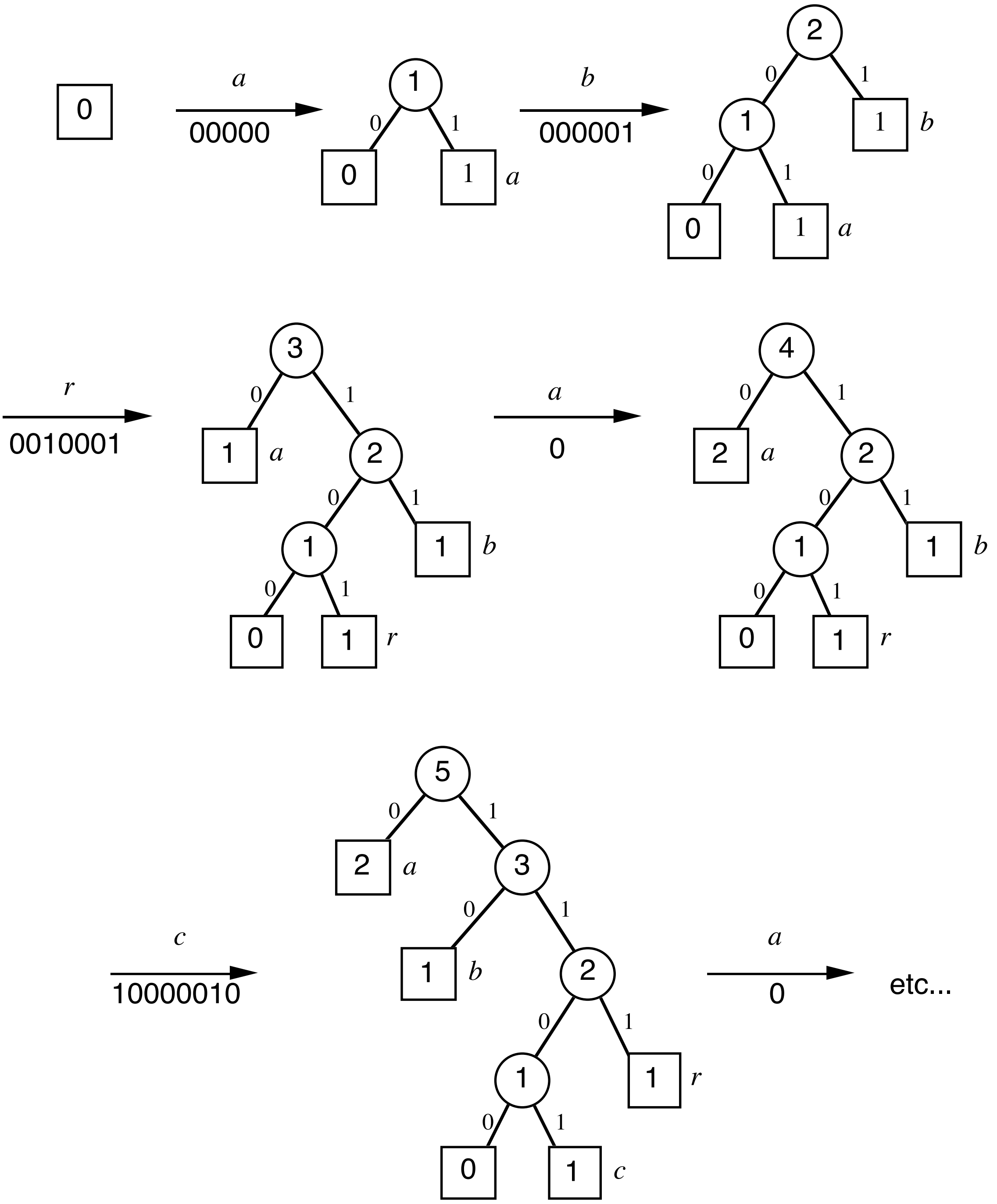


**Figure 10.5**. Dynamic Huffman compression of *abracadabra*.

The precise analysis of the adaptive Huffman compression algorithm has led to an improved compression algorithm. The idea of the improvement is to choose a specific ordering for the nodes of the Huffman tree. One may note indeed that, in the ordering given by the siblings property, two nodes of same weight are exchangeable. The improvement is based on a specific ordering that corresponds to a width-first tree-traversal of the tree from leaves to the root. Moreover, at each level in the tree, nodes are ordered from left to right, and leaves of a given weight precede internal nodes of the same weight. The algorithm derived from this is efficient even for texts of few thousands characters. The encoding of larger texts save almost one bit per character compared with Huffman's algorithm.

## 10.4. Factor encoding

Data compression methods with substitutions find all their power when the substitution applies to variable-length factors instead of blocks. The substitution is defined by a dictionary:

$$D = \{(f, c) : f \in F, c \in C\},$$

where $F$ is a (finite) set of factors of the source text $s$, and $C$ is the set of their corresponding codewords. The set $F$ acts as the alphabet $A$ of Section 10.1. The source text is a concatenation of elements of $F$.

**Example**

Let *text* be a text composed of ordinary ASCII characters encoded on 8 bits. One may choose for $C$ the 8-bit words that correspond to no letter of *text*. Then, $F$ can be a set of factors occurring frequently inside the text *text*. Replacing in *text* factors of $F$ by letters of $C$ compresses the text. This amounts to increase the alphabet on which *text* is written. ‡

In the general case of factor encoding, a data compression scheme must solve the three following points:

— find the set $F$ of factors that are to be encoded,

— design an algorithm to factorize the source text according to $F$,

— compute a code $C$ in one-to-one correspondence with $F$.

When the text is given, the computation of such an optimal encoding is a NP-complete problem. The proof can be done inside the following model of encoding. Let $A$ be the alphabet of the *text*. The encoding of *text* is a word of the form $d\#c$ where $d$ ($\in A^*$) is supposed to represent the dictionary, # is a new letter (not in $A$), and $c$ is the compressed text. The part $c$ of the encoded string is written on the alphabet $A \cup \{1, 2, \ldots, n\}\times\{1, 2, \ldots, n\}$. A pair $(i, j)$ occurring in $c$ means a reference to the factor of length $j$ which occurs at position $i$ in $d$.

**Example**

On $A = \{a, b, c\}$, let $text = aababbabbabbc$. Its encoding can be $bbabb\#aa(1, 4)a(0, 5)c$. The explicit dictionary is then

$$D = \{(babb,\ (1, 4)),\ (bbabb,\ (0, 5))\} \cup A\times A. ‡$$

Inside the above model, the length of $d\#c$ is the number of occurrences of both letters and pairs of integers that appear in it. For instance, this length is 12 in the previous example. The search for a shortest word $d\#c$ that encodes a given *text* reduces to the SCS-problem — the

Shortest Common Superstring problem for a finite set of words — which is a classical NP-complete problem.

When the set $F$ of factors is known, the main problem is to factorize the source $s$ efficiently according to the elements of $F$, that is, to find factors $f_1, f_2, \ldots, f_k \in F$ such that

$$s = f_1 f_2 \ldots f_k.$$

The problem arises from the fact that $F$ is not necesarily a unique decipherable code, so several factorizations are often possible. It is important that the integer $k$ be as small as possible, and the factorization is said to be an *optimal factorization* when $k$ is minimal.

The simplest strategy to factorize $s$ is to use a greedy algorithm. The factorization is computed sequentially. So, the first factor $f_1$ is naturally chosen as the longest prefix of $s$ that belongs to $F$. And the decomposition of the rest of the text is done iteratively in the same way.

**Remark 1**

If $F$ is a set of letters or digrams ($F \subseteq A \cup A{\times}A$), the greedy algorithm computes an optimal factorization. The condition may seem quite restrictive, but in French, for instance, the most frequent factors ("er", "en") have length 2.

**Remark 2**

If $F$ is a factor-closed set (all factors of words of $F$ are in $F$), the greedy algorithm also computes an optimal factorization.

Another factorization strategy, called here *semi-greedy*, leads to optimal factorizations under wider conditions. Moreover, its time complexity is similar to the previous strategy.

**Semi-greedy factorization strategy of *s***

— let $m = \max\{|uv| : u, v \in F$, and $uv$ is a prefix of $s\}$;

— let $f_1$ be an element of $F$ such that $f_1 v$ is prefix of $s$, and $|f_1 v| = m$, for some $v \in F$;

— let $s = f_1 s'$;

— iterate the same process on $s'$.

**Example**

Let $F = \{a, b, c, ab, ba, bb, bab, bba, babb, bbab\}$, and $s = aababbabbabbc$. The greedy algorithm produces the factorization

$$s = a\ ab\ ab\ babb\ ab\ b\ c$$

which has 7 factors. The semi-greedy algorithm gives

$$s = a\ a\ ba\ bbab\ babb\ c$$

which is an optimal factorization. Note that $F$ is prefix-closed (prefixes of words of $F$ are in $F$) after adding the empty word. ‡

The interest in the semi-greedy factorization algorithm comes from the following lemma whose proof is left as an exercise. As we shall see later in the section, the hypothesis of the set of factors $F$ arises naturally for some compression algorithms.

**Lemma 10.6**

If the set $F$ is prefix-closed, the semi-greedy factorization strategy produces an optimal factorization.

When the set $F$ is finite, the semi-greedy algorithm may be realized with the help of a string-matching automaton (see Chapter 7). This leads to a linear-time algorithm to factorize a text.

Finally, if the set $F$ is known, and if the factorization algorithm has been designed, the next step to consider in order to perform a whole compression process is to determine the code $C$. As for statistical encodings of Sections 10.2 and 10.3, the choice of codewords associated with factors of $F$ can take into account their frequencies. This choice can be done once for all, or in a dynamic way during the factorization of $s$. Here is an example of a possible strategy: the elements of $F$ are put into a list, and encoded by their position in the list. A move-to-front procedure realized during the encoding phase tends to attribute small positions, and thus short encodings, to frequent factors. The idea of encoding a factor by its position in a list is applied in the next compression method.

Factor encoding becomes even more powerful with an adaptive feature. It is realized by the Ziv-Lempel method (ZL method, for short). The dictionary is built during the compression process. The codewords of factors are their positions in the dictionary. So, we regard the dictionary $D$ as a sequence of words $(f_0, f_1, \ldots)$. The algorithm encodes positions in the most efficient way according to the present state of the dictionary, using the function $lg$ defined by:

$$lg(1) = 1 \text{ and,}$$
$$lg(n) = \lceil \log_2(n) \rceil, \text{ for } n > 1.$$

```
Algorithm ZL; { Ziv-Lempel compression algorithm }
{ encodes the source $s$ on the binary alphabet }
begin
  $D$ := {ε};  $x$ := $s$#;
  while $x \neq \varepsilon$ do begin
    $f_k$ := longest word of $D$ such that $x = f_k a y$, for some $a \in A$;
    $a$ := letter following $f_k$ in $x$;
    write $k$ on $lg|D|$ bits;
    write the initial codeword of $a$ on $lg|A|$ bits;
    add $f_k a$ at the end of $D$;
    $x$ := $y$;
  end;
end.
```

**Example**

Let $A = \{a, b, \#\}$. Assume that the initial codewords of letters are 00 for $a$, 01 for $b$, and 10 for #. Let $s = aababbabbabb\#$. Then, the decomposition of $s$ is

$$s = a \ ab \ abb \ abba \ b \ b\#$$

which leads to

$$c = 000 \ 101 \ 1001 \ 1100 \ 00001 \ 10110.$$

After that, the dictionary $D$ contains seven words:

$$D = (\varepsilon, a, ab, abb, abba, b, b\#).$$ ‡

Intuitively, ZL algorithm compresses the source text because it is able to discover some repeated factors inside it. The second occurrence of such a factor is encoded only by a pointer onto its first position, which can save a large amount of space.

From the implementation point of view, the dictionary $D$ in ZL algorithm can be stored as a word trie. The addition of a new word in the dictionary takes a constant amount of time and space.

There is a large number of possible variations on ZL algorithm. The study of this algorithm has been stimulated by its good performance in practical applications. Note, for instance, that the dictionary built by ZL algorithm is prefix-closed, so the semi-greedy factorization strategy may help to reduce the number of factors in the decomposition.

The model of encoding valid for that kind of compression method is more general than the preceding one. The encoding $c$ of the source text $s$ is a word on the alphabet $A \cup \{1, 2, \ldots, n\} \times \{1, 2, \ldots, n\}$. A pair $(i, j)$ occurring in $c$ references a factor of $s$ itself: $i$ is the position of the factor, and $j$ is its length.

**Example**

Let again $s$ = *aababbabbabb#*. It can be encoded by the word

$$c = a\ (0,\ 1)b\ (1,\ 2)b\ (3,\ 3)a\ b\ (11,\ 1)\#,$$

of length 10, which corresponds to the factorization found by ZL algorithm. ‡

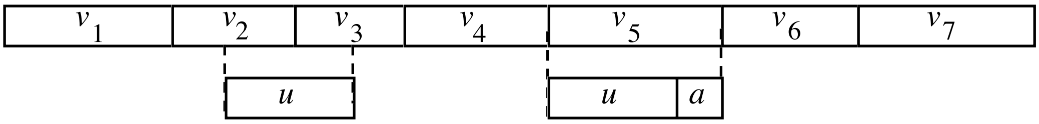


**Figure 10.6**. Efficient factorization of the source.
$v_5$ is the shortest factor not occurring on its left.

The number of factors of the decomposition of the source text reduces if we consider a decomposition of the text similar to the *f*-factorization of Section 8.2. The factorization of $s$ is a sequence of words $(f_1, f_2, \ldots, f_m)$ such that $s = f_1f_2\ldots f_m$, and that is iteratively defined by (see Figure 10.6):

$f_i$ is the shortest prefix of $f_if_{i+1}\ldots f_m$ which does not occurs before in $s$.

**Example**

The factorization of $s$ = *aababbabbabb#* is

$$(a,\ ab,\ abb,\ abbabb\#)$$

which accounts to encode $s$ into

$$c = a\ (0,\ 1)b\ (1,\ 2)b\ (3,\ 6)\#,$$

word of length 7 only, compared with the previous factorization. ‡

**Theorem 10.7**

The *f*-factorization of a string $s$ can be computed in linear time.

**Proof**

Use the directed acyclic word graph *DAWG*($s$), or the suffix tree *T*($s$). ‡

The number of factors arising in the *f*-factorization of a text measures, in a certain sense, the complexity of the text. The complexity of sequences is related to the notion of entropy of a set of strings as stated below. Assume that the possible set of texts of length $n$ (on the alphabet $A$) is of size $|A|^{hn}$ (for all length $n$). Then $h$ ($\leq 1$) is called the entropy of the set of texts. For instance, if the probability of appearance of a letter in a text does not depend on its position, then $h$ is the entropy $H(A)$ considered in Section 10.2.

**Theorem 10.8**

The number $m$ of elements of the $f$-factorization of long enough texts is upper bounded by $hn/\log n$, for almost all texts.

We end this section by reporting some experiments on compression algorithms. Table 10.1 gives the results. Rows are indexed by algorithms, and columns by types of text files. "Uniform" is a text on a 20-letter alphabet generated with a uniform distribution of letters. "Repeated alphabet" is a repetition of the word *abc…zABC…Z*. Compression of the five files have been done with Huffman method, Ziv-Lempel algorithm (more precisely, COMPRESS command of UNIX), and the compression algorithm, called FACT, based on the $f$-factorization. Huffman method is the most efficient only for the file "Uniform", which is not surprising. For other files, the results for COMPRESS and FACT are similar.

| Source | French text | C program | Lisp program | Uniform | Repeated alphabet |
|---|---|---|---|---|---|
| Initial length | 62816 | 684497 | 75925 | 70000 | 530000 |
| Huffman | 53.27 % | 62.10 % | 63.66 % | **55.58** % | 72.65 % |
| COMPRESS | **41.46** % | 34.16 % | 40.52 % | 63.60 % | 2.13 % |
| FACT | 47.43 % | **31.86** % | **35.49** % | 73.74 % | **0.09** % |

**Table 10.1**. Sizes of some compressed files
(best scores in bold).

## 10.5.* Parallel Huffman coding

The sequential algorithm for Huffman coding is quite simple, but unfortunately it looks inherently sequential. Its parallel counterpart is much more complicated, and requires a new approach. The global structure of Huffman trees must be explored deeper. In this section, we give a polylogarithmic time parallel algorithm to compute a Huffman code. The number of processors is $M(n)$, where $M(n)$ is the number of processors needed for a (min, +) multiplication of two $n$ by $n$ real matrices in logarithmic parallel time. We assume, for simplicity, that the alphabet is binary.

A binary tree $T$ is said to be *left-justified* iff it satisfies the following properties:

(1) — the depths of the leaves are in non-increasing order from left to right,

(2) — if a node $v$ has only one son, then it is a left son,

(3) — let $u$ be a left brother of $v$, and assume that the height of the subtree rooted at $v$ is at least $l$. Then the tree rooted at $u$ is full at level $l$, which means that $u$ has $2^l$ descendants at distance $l$.

For the present problem, the most important is the following property of left-adjusted trees.

**Basic property:**

Let $T$ be a left-justified binary tree. Then, it has a structure illustrated in Figure 10.7. All hanging subtrees have height at most log$n$.

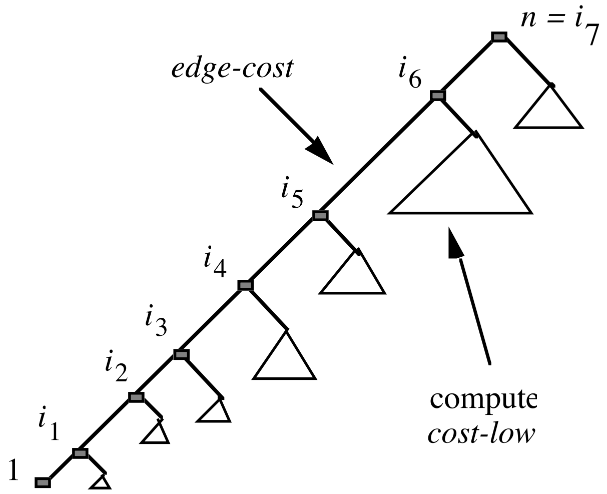


**Figure 10.7**. A left-justified Huffman tree. The hanging subtrees are of logarithmic height.

**Lemma 10.9**

Assume that the weights $p_1, p_2, ..., p_n$ are pairwise distinct and in increasing order. Then, there is Huffman tree for $(p_1, p_2, ..., p_n)$ which is left-justified.

**Proof**

We first show the following claim:

For each tree $T$ we can find a tree $T'$ satisfying (1), (2), (3), whose leaves are a permutation of leaves of $T$, and such that the depths of corresponding leaves in the trees $T$ and $T'$ are the same.

This claim can be proved by induction with respect to the height $h$ of the tree $T$. Let $T1$ be derived from $T$ by the following transformation : cut all leaves of $T$ at maximal level; the fathers of these leaves become new leaves, called special leaves in $T1$. The tree $T1$ has height $h$-1. It can be transformed into a tree $T1'$ satisfying (1), by applying the inductive assumption. The leaves of height $h$-1 of $T1'$ form a segment of consecutive leaves from left to right. They contain all special leaves. We can permute the leaves at height $h$-1 in such a way that special leaves are at the left. Then, we insert back the deleted leaves as sons of their original fathers (special leaves in $T1$ and $T1'$). The resulting tree $T'$ satisfies the claim.

Let us consider an Huffman tree $T$. It can be transformed into a form satisfying conditions (1) to (3), with the weight of the tree left unchanged. Hence, after the transformation, the tree is also of minimal weight. Therefore, we can consider that our tree $T$ is optimal *and* is left-justified. It is enough to prove that leaves are in increasing order of their weights $p_i$, from left to right. But this is straightforward since the deepest leaf has the smallest weight. Hence, the tree $T$ satisfies all requirements. This completes the proof. ‡

**Theorem 10.10**

The weight of a Huffman tree can be computed in $O(\log^2 n)$ time with $n^3$ processors. The corresponding tree can be constructed within the same complexity bounds.

**Proof**

Let $weight[i, j] = p_{i+1}+p_{i+2}+\ldots+p_j$. Let $cost[i, j]$ be the weight of a Huffman tree for $(p_{i+1}, p_{i+2}, \ldots, p_j)$, and whose leaves are keys $K_{i+1}, K_{i+2}, \ldots, K_j$. Then, for $i < j$-1, we have:

$$(*) \quad cost[i, j] = \min\{cost[i, k]+cost[k, j]+weight[i, j] : i < k < j\}.$$

Let us use the structure of $T$ shown in Figure 10.7. All hanging subtrees are shallow, they are of height at most log$n$. So, we first compute the weights of such shallow subtrees.

Let $cost\text{-}low[i, j]$ be the weight of the Huffman tree of logarithmic height, whose leaves are keys $K_{i+1}, K_{i+2}, \ldots, K_j$.

The table *cost-low* can be easily computed in parallel by applying (*). We initialize $cost\text{-}low[i, i+1]$ to $p_i$, and $cost\text{-}low[i, j]$ to ∞, for all other entries. Then, we repeat log$n$ times the same parallel-do statement:

```
for each $i, j, i < j$-1 do in parallel
    $cost\text{-}low[i, j] := \min\{cost\text{-}low[i, k]+cost\text{-}low[k, j] : i < k < j\} + weight[i, j]$.
```

We need $n$ processors for each operation "min" concerning a fixed pair $(i, j)$. Since there are $n^2$ pairs $(i, j)$, globally we use a cubic number of processors to compute cost-low's.

Now, we have to find the weight of an optimal decomposition of the whole tree $T$ into a leftmost branch, and hanging subtrees. The consecutive points of this branch correspond to points (1, $i$). Consider the edge from (1, $i$) to (1, $j$), and identify it with the edge ($i$, $j$). The contribution of this edge to the total weight is illustrated in Figure 10.8.

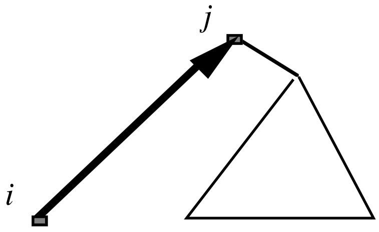


**Figure 10.8**. $edge\text{-}cost[i, j] = cost\text{-}low[i, j] + weight[1, j]$.

We assign to the edge $(i, j)$ the cost given by the formula:

$$edge\text{-}cost(i, j) = cost\text{-}low[i, j] + weight[1, j].$$

It is easy to deduce the following fact:

the total weight of $T$ is the sum of costs of edges corresponding to the leftmost branch. Once we have computed all cost-low's we can assign the weights to the edges correspondingly to the formula, and we have an acyclic directed graph with weighted edges. The cost of the Huffman tree is reduced to the computation of the minimal cost from 1 to $n$ in this graph. This can be done by $\log n$ squarings of the weight matrix of the graph. Each squaring corresponds to a (min, +) multiplication of $n \times n$ matrices, so, can be done in $\log n$ time with $n^3$ processors. Hence $\log^2 n$ time is enough for the whole process. This completes the proof of the first part of the theorem.

Given costs, the Huffman tree can be constructed within the same complexity bounds. We refer the reader to [AKLMT 89]. This completes the proof of the whole theorem. ‡

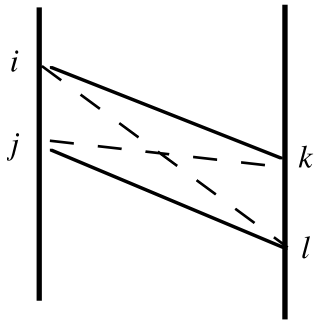


**Figure 10.9**. The quadrangle inequality: (cost of plain lines) ≤ (cost of dashed lines).

In fact the matrices which occur in the algorithm have a special property called the *quadrangle inequality*. This property allows the number of processors to be reduced to a quadratic number.

A matrix $C$ has the quadrangle inequality iff for each $i < j < k < l$ we have:

$$C[i, k] + C[j, l] \leq C[i, l] + C[j, k].$$

Let us consider matrices that are strictly upper triangular (elements below the main diagonal, and on the main diagonal are null). Such matrices correspond to weights of edges in acyclic directed graphs. Denote by © the (min, +) multiplication of matrices:

$$A © B = C \text{ iff } C[i, j] = \min\{A[i, k]+B[k, j] : i < k < j\}.$$

The proof of the following fact is left to the reader.

**Lemma 10.11**

If the matrices $A$ and $B$ satisfy the quadrangle inequality then $A$ © $B$ also satisfies this property.

For matrices occurring in the Huffman tree algorithm, the (min, +) multiplication is easier in parallel, and the number of processors is reduced by a linear factor, due to the following lemma.

**Lemma 10.12**

If the matrices $A$ and $B$ satisfy the quadrangle inequality then $A$ © $B$ can be computed in $O(\log^2 n)$ time with $O(n^2)$ processors.

**Proof**

Let us fix $j$, and denote by $CUT[i]$ the smallest integer $k$ for which the value of $A[i, k]+B[k, j]$ is minimal. The computation of $A$ © $B$ reduces to the computation of vectors $CUT$ for each $j$. It is enough to show that, for $j$ fixed, this vector can be computed in $O(\log^2 n)$ time with $n$ processors.

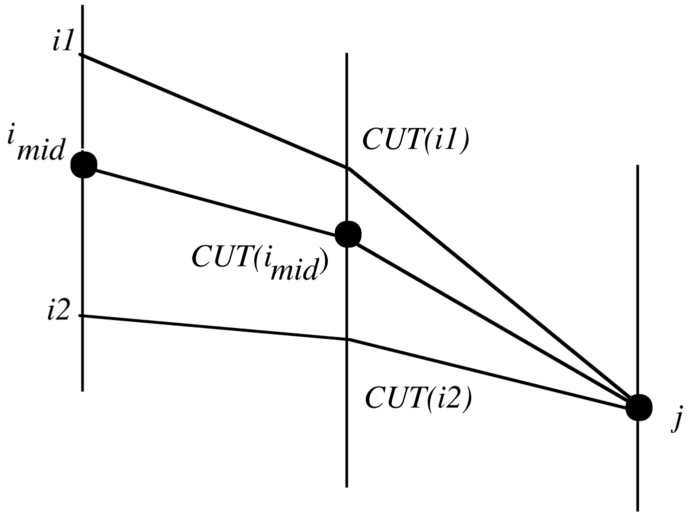


**Figure 10.10**. Computing cuts by a divide-and-conquer strategy.

The structure of the algorithm is the following:

let $i_{mid}$ the middle of interval $[1, 2, \dots, n]$; compute $CUT[i_{mid}]$ in $O(\log n)$ time with $n$ processors assuming that the value of $CUT$ is in the whole interval $[1, 2, \dots, n]$.

Afterwards it is easy to see, due to the quadrangle inequality, that

$$CUT[i] \le CUT[i_{mid}] \text{ for all } i \le i_{mid},$$

$$CUT[i] \ge CUT[i_{mid}] \text{ for all } i \ge i_{mid}.$$

Using this information we compute $CUT[i]$ for all $i \le i_{mid}$, knowing that its value is above $CUT[i_{mid}]$. Simultaneously we compute $CUT[i]$ for all $i > i_{mid}$, knowing that its value is not above $CUT[i_{mid}]$. Let $m$ be the size of the interval in which the value of $CUT[i]$ is expected to be (for $i$ in the interval of size $n$). We have the following equation for the number $P(n, m)$ of processors:

$$P(n, m) \le \max(m, P(n, m_1)+P(n, m_2)), \text{ where } m_1+m_2 = m.$$

Obviously $P(n, n) = O(n)$. The depth of the recursion is logarithmic. Each evaluation of a minimum takes also logarithmic time. Hence, we get the required total time. For a fixed $j$,

$P(n, n)$ processors are enough. Altogether, for all $j$, we need only a quadratic number of processors. This completes the proof. ‡

The lemma implies that the parallel Huffman coding problem can indeed be solved in polylogarithmic time with only a quadratic number of processors. This is still not optimal, since the sequential algorithm makes only $O(n.\log n)$ operations. We refer the reader to [AKLMT 89] for an optimal algorithm.

## Bibliographic notes

An extensive exposition of theory of codes is given in [BP 85].

Elementary methods to data compression may be found in [He 87]. Practical programming aspects of data compression techniques are presented by Nelson in [Ne 92].

The construction of a minimal weighted tree is from Huffman [Hu 51]. The Shannon-Fano method is independently by Shannon (1948) and Fano (1949), see [BCW 90].

In the seventies, Faller [Fa 73] and Gallager [Ga 78] independently designed a dynamic data compression algorithm based on Huffman's method. Practical versions of dynamic Huffman coding have been designed by Cormack and Horspool [CH 84], and Knuth [Kn 85]. The precise analysis of sequential statistical data compression has been done by Vitter in [Vi 87], where an improved version is given.

NP-completeness of various questions on data compression can be found in [St 77]. The idea of the semi-greedy factorization strategy is from Hartman and Rodeh [HR 84]. And the dynamic factor encoding using the move-to-front strategy if by Bentley, Sleator, Tarjan and Wei [BSTW 86].

In 1977, Ziv et Lempel designed the main algorithm of Section 10.4 [ZL 77] (see also [ZL 88]). The notion of word complexity, and Theorem 10.8, appears in [LZ 76]. The corresponding linear time computations are by Rodeh, Pratt and Even [RPE 81] (with suffix trees) and Crochemore [Cr 83] (with suffix dawg). A large number of variants of Ziv-Lempel algorithm may be found in [BCW 90] and [St 88]. An efficient implementation of a variant of ZL algorithm is by Welch [We 84]. The experimental results of Section 10.4 are from Zipstein [Zi 92]. References and results relating compression ratios and entropy may be found in [HPS 92].

Some data compression methods do not use substitutions. Application of arithmetic coding gives a typical example which often leads to higher efficiency because it can be combined with algorithms that evaluate or approximate the source probabilities. A software version of data compression based on arithmetic coding is by Witten, Neal and Cleary [WNC 87]. It is not clear to whom application of arithmetic coding to compression should be attributed, see [BCW 90] for historical remarks on this point.

The Huffman coding in parallel setting (Section 10.5) is from Atallah, Kosaraju, Larmore, Miller, and Teng [AKLMT 89]. The number of processors is reduced by observing that matrices are "concave". In [AKLMT 89], it is also presented an optimal parallel algorithm for constructing almost optimal prefix codes.

## Selected references

[BCW 90] T.C. BELL, J.G. CLEARY, I.H. WITTEN, *Text Compression*, Prentice Hall, Englewood Cliffs, New Jersey, 1990.

[BP 85] J. BERSTEL, D. PERRIN, *Theory of codes*, Academic Press, Orlando, Florida, 1985.

[He 87] G. HELD, *Data Compression - Techniques and Applications, Hardware and Software Considerations*, John Wiley & Sons, New York, NY, 1987. 2nd edition.

[Ne 92] M. NELSON, *The Data Compression Book*, M&T Publishing, Inc., Redwood City, California, 1992.

[St 88] J.A. STORER, *Data compression: methods and theory*, Computer Science Press, Rockville, MD, 1988.

# 11. Approximate pattern matching

In practical pattern matching applications, the exact matching is not always pertinent. It is often more important to find objects which match a given pattern in a reasonably approximate way. In this chapter, approximation is measured mainly by the so-called edit distance: the minimal number of local edit operations to transform one object into another. Such operations are well suited for strings, but they are less natural for two-dimensional patterns or for trees. The analogue for DNA sequences is called the *alignment problem*. Algorithms are mainly based on the algorithmic method called *dynamic programming*. We present also problems strongly related to the notion of edit distance, namely, the computation of longest common subsequences, string-matching allowing errors, and string-matching with don't care symbols. At the end of the chapter, we give the scheme of an algorithm to compute efficiently the edit distance in parallel.

## 11.1. Edit distance — serial computation

An immediate question arising in applications is to be able to test the equality of two strings allowing some errors. The errors correspond to differences between the two words. We consider in this section three types of differences between two strings $x$ and $y$:

*change* — symbols at corresponding positions are distinct,

*insertion* — a symbol of $y$ is missing in $x$ at corresponding position,

*deletion* — a symbol of $x$ is missing in $y$ at corresponding position.

It is rather natural to ask for the minimum number of differences between $x$ and $y$. We translate it as the smallest possible number of operations (change, deletion, insertion) to transform $x$ into $y$. This is called the *edit distance* between $x$ and $y$, and denoted by $edit(x, y)$. It is clear that it is a distance between words, in the mathematical sense. This means that the following properties are satisfied:

— $edit(x, y) = 0$ iff $x = y$,

— $edit(x, y) = edit(y, x)$ (symmetry),

— $edit(x, y) \leq edit(x, z) + edit(z, y)$ (triangle inequality).

The symmetry of *edit* comes from the duality between deletion and insertion: a deletion of the letter $a$ of $x$ in order to get $y$ corresponds to an insertion of $a$ in $y$ to get $x$.

```
ACCATGAA---ACTTCTTATCCTCACCTGCCTCGTGGCTG
|||||||    |||||| |||||  ||      ||||  |
ACCATGAGTGCACTTCTGATCCTAGCCCTT---GTGGGAG
```

**Figure 11.1**. Alignment of two DNA sequences showing changes, insertions (- in top line), and deletions (- in bottom line).

Below is an example of transformation of $x = wojtk$ into $y = wjeek$.

```
w o j t   k
  ↓         deletion
      ↓     change
        ↓   insertion
w   j e e k
```

This shows that *edit*(*wojtk*, *wjeek*) ≤ 3, because it uses three operations. In fact, this is the minimum number of edit operations to transform *wojtk* into *wjeek*.

From now on, we consider that words $x$ and $y$ are fixed. The length of $x$ is $m$, and the length of $y$ is $n$, and we assume that $n \geq m$. We define the table *EDIT* by

$$EDIT[i, j] = edit(x[1\ldots i], y[1\ldots j]),$$

with $0 \leq i \leq m$, $0 \leq j \leq n$. The boundary values are defined as follows (for $0 \leq i \leq m$, $0 \leq j \leq n$):

$$EDIT[0, j] = j,\ EDIT[i, 0] = i.$$

There is a simple formula to compute other elements

(*) $EDIT[i, j] = \min(EDIT[i\text{-}1, j]+1, EDIT[i, j\text{-}1]+1, EDIT[i\text{-}1, j\text{-}1]+\partial(x[i], y[j]))$,

where $\partial(a, b) = 0$ if $a = b$, and $\partial(a, b) = 1$ otherwise. The formula reflects the three operations, deletion, insertion, change, in that order.

There is a graph theoretical formulation of the editing problem. We can consider the grid graph, denoted by $G$, composed of nodes $(i, j)$ (for $0 \leq i \leq m$, $0 \leq j \leq n$). The node $(i\text{-}1, j\text{-}1)$ is connected to the three nodes $(i\text{-}1, j)$, $(i, j\text{-}1)$, $(i, j)$ when they are defined (i.e. when $i \leq m$, or $j \leq n$). Each edge of the grid graph has a weight according to the recurrence (*). The edges from $(i\text{-}1, j\text{-}1)$ to $(i\text{-}1, j)$ and $(i, j\text{-}1)$ have weight 1, as they correspond to insertion or deletion of a single symbol. The edge from $(i\text{-}1, j\text{-}1)$ to $(i, j)$ has weight $\partial(x[i], y[j])$. Figure 11.2 shows an example of grid graph for words *cbabac* and *abcabbbaa*. The edit distance between words $x$ and $y$ equals the length of a shortest path in this graph from the *source* (0, 0) (left upper corner) to the *sink* $(m, n)$ (right bottom corner).

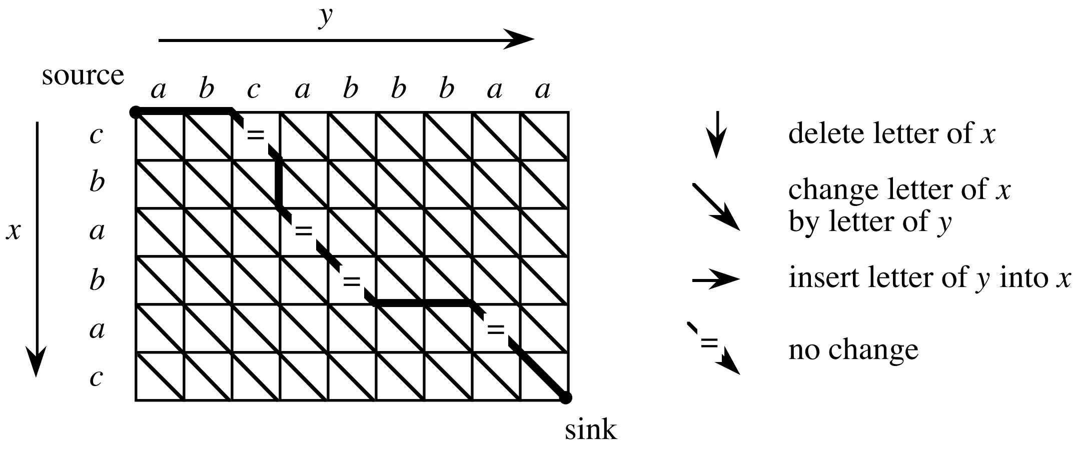


**Figure 11.2**. The path corresponds to the sequence of edit operations: *insert*(*a*), *insert*(*b*), *delete*(*b*), *insert*(*b*), *insert*(*b*), *change*(*c*, *a*).

```
function edit(x, y)  { computation of edit distance }
{ |x| = m, |y| = n, EDIT is a matrix of integers }
begin
  for i := 0 to m do EDIT[i, 0] := i;
  for j := 1 to n do EDIT[0, j] := j;
  for i := 1 to m do
    for j := 1 to n do
      EDIT[i, j] = min(EDIT[i-1, j]+1, EDIT[i, j-1]+1,
                       EDIT[i-1, j-1] + ∂(x[i], y[j]));
  return EDIT[m, n]
end.
```

The algorithm above computes the edit distance of strings *x* and *y*. It stores and computes all values of the matrix *EDIT*, although the only one entry *EDIT*[*m*, *n*] is required. This serves to save on time, and this feature is called the *dynamic programming method.* Another possible algorithm to compute *edit*(*x*, *y*) could be to use the classical Dijkstra's algorithm for shortest paths in the grid graph.

### Theorem 11.1

Edit distance can be computed in $O(mn)$ time using $O(m)$ additional memory.

**Proof**

The time complexity of the algorithm above is obvious. The space complexity follows from the fact that we have not to store the whole table. The current and the previous columns (or lines) are sufficient to carry out computations. ‡

**Remark**

We can assign specific costs to edit operations, depending on the type of operations, and on the type of symbols involved. Such a generalized edit distance can still be computed using a formula analogous to (*).

**Remark**

As noted in the proof of the previous theorem, the whole matrix *EDIT* does not need to be stored (only two rows are necessary at a given step) in order to compute only *edit*($x$, $y$). However, we can keep it in memory if we want to compute a shortest sequence of edit operations transforming $x$ into $y$. This is essentially the same process as reconstructing a shortest path from the table of sizes of all-pairs shortest paths.

## 11.2. Longest common subsequence problem

In this section, we consider a problem that is a particular case of the edit distance problem of previous section. This is the question of computing *longest common subsequences*. We denote by *lcs*($x$, $y$) the maximal length of subsequences common to $x$ and $y$. For fixed $x$ and $y$, we denote by *LCS*[$i$, $j$] the length of a longest common subsequence of $x[1\ldots i]$ and $y[1\ldots j]$.

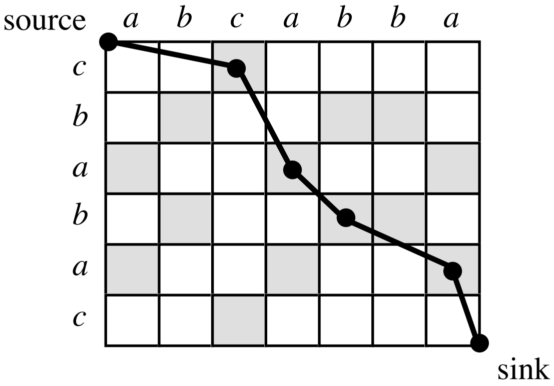


**Figure 11.3**. The size of the longest subsequence is the maximal number of shadowed boxes on a monotonically decreasing path from source to sink. Compare to Figure 11.4.

There is a strong relation between the longest common subsequence problem and a particular edit distance computation. Let $edit_{di}(x, y)$ be the minimal number of operations *delete* and *insert* to transform $x$ into $y$. This corresponds to a restricted edit distance where changes are not allowed. A change in the edit distance of Section 11.1 can be replaced by a pair of operation, deletion and insertion. The following lemma shows that the computation of *lcs*($x$, $y$) is equivalent to the evaluation of $edit_{di}(x, y)$. The statement is not true in general for all edit operations, or for edit operations having distinct costs. However, the restricted edit distance $edit_{di}$ remains to give weight 2 to changes, and weight 1 to deletions and insertions. Recall that $x$ and $y$ have respective length $m$ and $n$, and let $EDIT_{di}[i, j]$ be $edit_{di}(x[1...i], y[1...j])$.

**Lemma 11.2**

$2lcs(x, y) = m + n - edit_{di}(x, y)$, and,

for $0 \le i \le m$ and $0 \le j \le n$, $2LCS[i, j] = i + j - EDIT_{di}[i, j]$.

**Proof**

The equality can be easily proved by induction on $i$ and $j$. This is also visible on the graphical representation in Figure 11.4. Consider a path from the source to the sink in which diagonal edges are only allowed when the corresponding symbols are equal. The number of diagonal edges in the path is the length of a subsequence common to $x$ and $y$. Horizontal and vertical edges correspond to a sequence of edit operations (delete, insert) to transform $x$ into $y$. If we assign cost 2 to diagonal edges, the length of the path is exactly the sum of lengths of words, $m+n$. The result follows. ‡

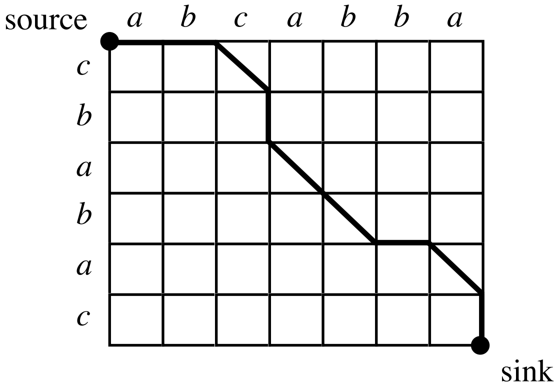


**Figure 11.4**. Assigning cost 2 to diagonal edges, the length of the path is $m+n$. Diagonal edges correspond to equal letters, others to edit operations.

As a consequence of Lemma 11.2, computing $lcs(x, y)$ takes the same time as computing the edit distance of the strings. A longest common subsequence can even be found with linear extra space (see bibliographic references).

**Theorem 11.3**

A longest common subsequence of $x$ and $y$ can be computed in $O(mn)$ time using $O(mn)$ additional memory.

**Proof**

Assume that the table $EDIT_{di}$ is computed for zero-one costs of edges. Table *LCS* can be recomputed from Lemma 11.2. A longest common subsequence can be constructed from the table *LCS*. ‡

Let $r$ be the number of shadowed boxes in Figure 11.3. More formally, it is the number of pairs $(i, j)$ such that $x[i] = y[j]$. If $r$ is small (which often happens in practice) compared to $mn$, then there is an algorithm to compute longest common subsequence faster than the previous algorithm.

The algorithm is given below. It processes the word $x$ sequentially from left to right. Consider the situation when $x[1\ldots i\text{-}1]$ has just been processed. The algorithm maintains a partition of positions on the word $y$ into intervals $I_0, I_1, \ldots, I_k, \ldots$. They are defined by

$$I_k = \{j \,;\, lcs(x[1\ldots i\text{-}1], y[1\ldots j]) = k\}.$$

In other words, positions in a class $I_k$ correspond to prefixes of $y$ having the same maximal length of common subsequence with $x[1\ldots i\text{-}1]$.

Consider, for instance, $y$ = *abcabbaba* and $x$ = *cb*…. Figure 11.5 (top) shows the partition $\{I_0, I_1, I_2\}$ of positions on $y$. For the next symbol of $x$, letter $a$, the figure (bottom) displays the modified partition $\{I_0, I_1, I_2, I_3\}$. The computation remains to shift to the right, like bowls on a wire, positions corresponding to occurrences of $a$ inside $y$.

The algorithm *lcs* below implements this strategy. It makes use of operations on intervals of positions: *CLASS*, *SPLIT*, and *UNION*. They are defined as follows. For a position $p$ on $y$, $CLASS(p)$ is the index $k$ of the interval $I_k$ to which it belongs. When $p$ is in the interval $[f, f+1, \ldots, g]$, and $p \neq f$, then $SPLIT(I_k, p)$ is the pair of intervals $([f, f+1, \ldots, p\text{-}1], [p, p+1, \ldots, g])$. Finally, *UNION* is the union of two intervals; in the algorithm, only unions of disjoint consecutive intervals are performed.

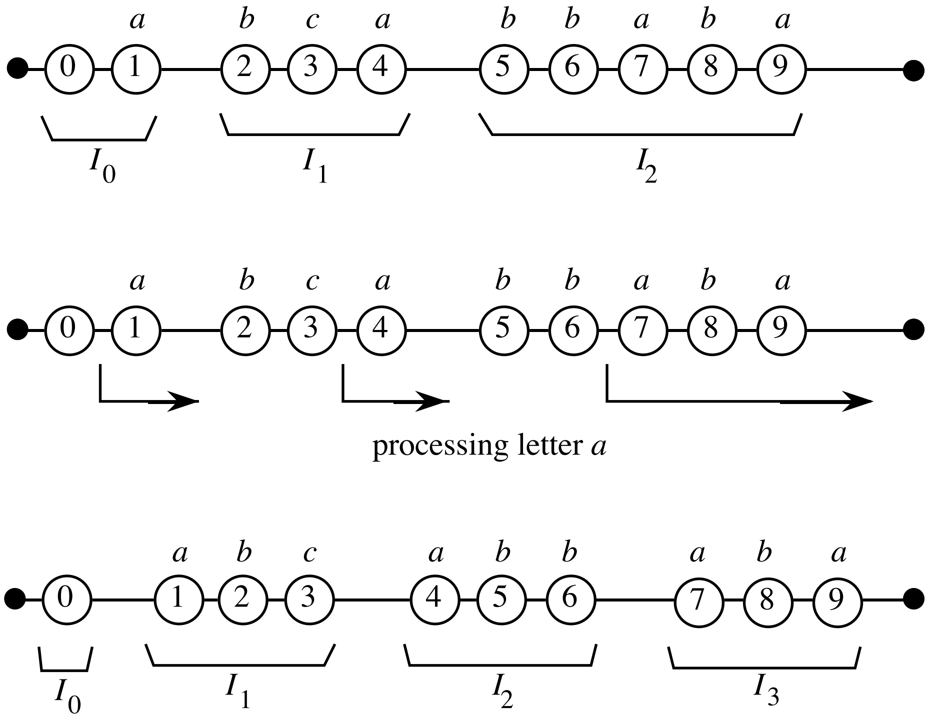


**Figure 11.5**. Hunt-Szymanski strategy: Like an abacus!
Word $y$ = *abcabbaba*. Partitions of positions just before processing
letter *a* of $x$ = *cba* (top), and just after (bottom).

```
function lcs(x, y) : integer;  { Hunt-Szymanski algorithm }
{ m = |x| and n = |y| }
begin
  I0 := {0,1,…,n}; for k := 1 to n do Ik := ∅;
  for i := 1 to m do
    for each p position of x[i] inside y in decreasing order do
    begin
      k := CLASS(p);
      if k = CLASS(p-1) then begin
        (Ik, X) := SPLIT(Ik, p);
        Ik+1 := UNION(X, Ik+1);
      end;
    end;
  return CLASS(n);
end;
```

**Theorem 11.4**

Algorithm *lcs* computes the length of a longest common subsequence of words of length $m$ and $n$ ($m \le n$) in time $O((n+r)\log n)$ time, where $r = |\{(i, j) ; x[i] = y[j]\}|$.

**Proof**

The correctness of the algorithm is left as an exercise.

The time complexity of the algorithm strongly relies on an efficient implementation of intervals $I_k$'s. With an implementation with B-trees, it can be shown that each operation *CLASS*, *SPLIT*, and *UNION* takes $O(\log n)$ time. Preprocessing lists of occurrences of letters of the word $y$ takes $O(n\log n)$ time. The rest of the algorithm takes then $O(r\log n)$ time. The result follows. ‡

According to Theorem 11.4, if $r$ is small, the computation of *lcs* by the last algorithm takes $O(n\log n)$ time, which is faster than with the dynamic programming algorithm. But, $r$ can be of order $mn$ (in the trivial case where $x = a^m$, $y = a^n$, for instance), and then the time complexity becomes $O(mn\log n)$, which is larger than with the dynamic programming algorithm.

The problem of computing lcs's can be reduced to the computation of longest increasing subsequence of a given string of elements belonging to a linearly ordered set. Let us write the coordinates of shadowed boxes (as in Figure 11.3) from the first to the last row, and from left to right within rows. Doing so, we get a string $w$. No matrix table is needed to build $w$. The words $x$ and $y$ themselves suffice. For example, for the words of Figure 11.3 we get the sequence $w = ((1,3), (2,2), (2,5), (2,6), (3,1), (3,4), (3,7), (4,2), (4,5), (4,6), (5,1), (5,4), (5,7), (6,3))$.

Define the following linear order on pairs of positions

$$(i, j) << (k, l) \text{ iff } ((i = k) \ \&\ (j > l)) \text{ or } ((i \ne k) \ \&\ (j < l)).$$

Then the longest increasing (according to <<) subsequence of the string $w$ gives the longest common subsequence of the words $x$ and $y$. There is an elegant algorithm to compute such increasing subsequences running in time $O(r\log r)$. This gives an alternative to the above algorithm.

## 11.3. String-matching with errors

String-matching with errors differs only slightly from the edit distance problem. Here, we are given pattern *pat* and text *text*, and we want to compute $\min(edit(pat, y) : y \in Fac(text))$. Simultaneously, we want to find a factor $y$ of *text* realizing the minimum, and the position of one of its occurrences in *text*. We consider the table *SE* (that stands for String-matching with Errors), of the same type as table *EDIT*:

$$SE[i, j] = \min(edit(pat[1\ldots i], y) : y \in Fac(text[1\ldots j])).$$

The computation of table *SE* can be done with dynamic programming. It is very similar to the computation of table *EDIT* (Section 11.1).

**Theorem 11.5**

The problem of string-matching with errors can be solved in $O(mn)$ time.

**Proof**

Surprisingly the algorithm is almost the same as that for computing edit distances. The only difference is that we initialize $SE[0, i]$ to 0, instead of to $i$ for *EDIT*. This is because the empty prefix of *pat* matches an empty factor of *text* (no error). The formula (*) works also for *SE*. Then, $SE[m, n]$ is the distance between *pat* and one of its best match $y$ in the text. To find an occurrence of $y$ and its position in *text*, we can use the same graph-theoretic approach as for the computation of longest common subsequences (Section 11.2). A suitable path should be recovered using the computed table *SE*. This completes the proof. ‡

One of the most interesting problems related to string-matching with errors concerns the case when the allowed number of errors is bound by a constant $k$. The number $k$ is usually understood as a small fixed constant. We show that the problem can be solved in $O(n)$ time, or more exactly in $O(kn)$ time if $k$ is not fixed. For a fixed value of the parameter $k$, this gives an algorithm having an optimal asymptotic time complexity. Recall that the string edit table *SE* is computed according to the recurrence:

$$(*) \quad SE[i, j] = \min(SE[i\text{-}1, j]+1, SE[i, j\text{-}1]+1, SE[i,j]+\partial(x[i], y[j])),$$

for words $x$ and $y$.

Suppose that we have a fixed bound $k$ on the number of errors. We have to compute only those entries of the table *SE* which contain values not exceeding $k$. The basic difficulty, in order to reduce the time complexity of the algorithm, is that the size of the table *SE* is $O(mn)$, but we require that the complexity is $O(kn)$. Only $O(kn)$ entries of the table must be considered. The basic algorithmic trick is to consider only so-called *d-nodes*, which are entries of the table *SE* satisfying special conditions. The $d$-nodes are defined in such a way that we have altogether, for $d = 0, 1, \ldots, k$, $O(kn)$ such nodes.

We consider diagonals of the table *SE*. Each diagonal is oriented top-down, left-to-right. We define a $d$-node as the last pair $(i, j)$ on a given diagonal with $SE[i, j] = d$. Note that it is possible that a diagonal has no $d$-node. The approximate string-matching problem reduces to the computation of $d$-nodes. And it is clear that there is an occurrence of the pattern with $d$ errors ending at position $j$ in *text* iff $(m, j)$ is a $d$-node.

Computation of $d$-nodes is done in the order $d = 0,1, \ldots, k$. Computation of 0-nodes is equivalent to string-matching without errors. Assume that we have already computed the $(d\text{-}1)$-nodes. We show how to compute $d$-nodes. Two auxiliary concepts are necessary: $d$-special nodes, and maximal subpaths of zero-weight on a given diagonal.

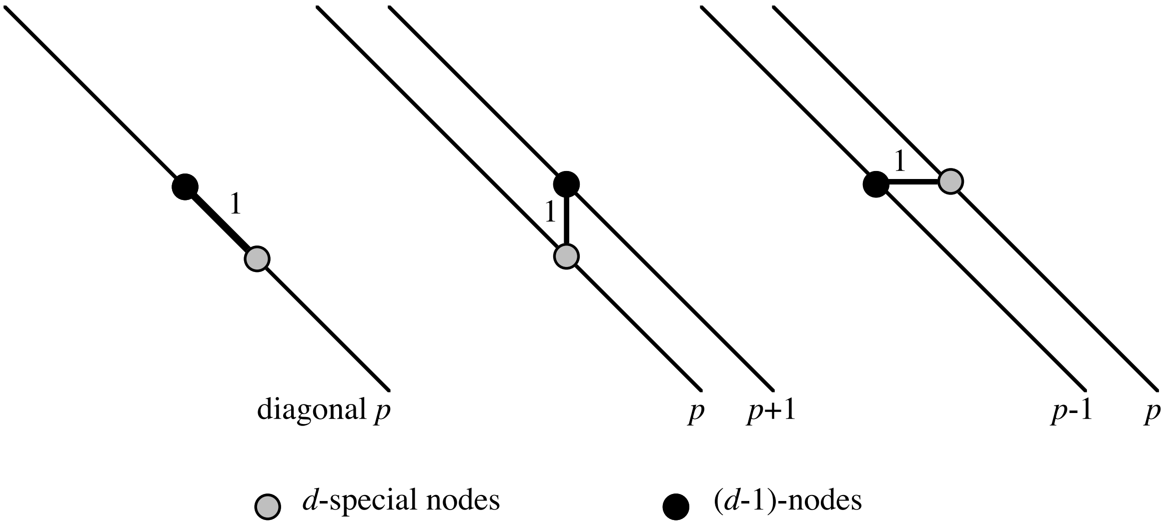


**Figure 11.6**. The computation of *d*-special nodes:
nodes reachable by one edge of weight 1 from a (*d*-1)-node.

A *d*-special node is a node reachable from a (*d*-1)-node by a single edge of weight one. The computation of *d*-special nodes is illustrated in Figure 11.6.

For a node $(i, j)$, define the node $NEXT(i, j) = (i+t, j+t)$ as a lowest node on the same diagonal as $(i, j)$ reachable from $(i, j)$ by a subpath of zero weight. The subpath can be of zero length, and, in this case, $NEXT(i, j) = (i, j)$.

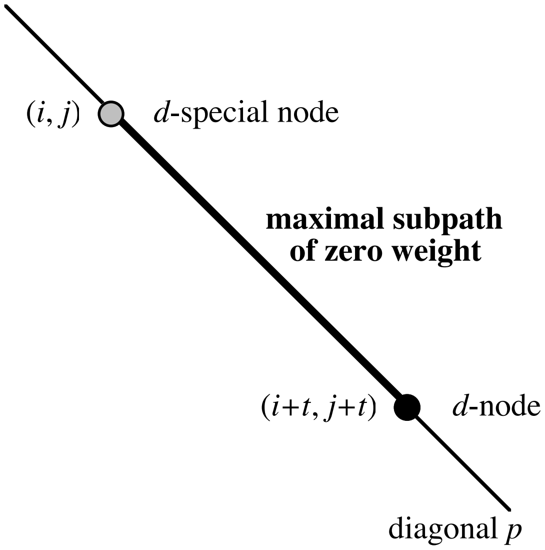


**Figure 11.7**. The computation of *d*-nodes from *d*-special nodes.

Once *d*-special nodes are computed, the *d*-nodes can be found easily, as suggested in Figure 11.7. The structure of the whole algorithm is given below.

```
Algorithm Approximate_string_matching with at most $k$ errors;
begin
  compute 0-nodes { exact string-matching }
  for $d$ = 1 to $k$ do begin
    compute $d$-special nodes; { see Figure 11.6 }
    { computation of $d$-nodes }
    $S$ := {$NEXT(i,j)$ : $(i,j)$ is a $d$-special node};
    for each diagonal $p$ do
      select, on diagonal $p$, lowest node which is in the set S;
    selected nodes form the set of $d$-nodes
  end;
end.
```

**Theorem 11.6**

Assume that the alphabet is of a constant size. Approximate string-matching with *k* errors can be done in $O(kn)$ time.

**Proof**

It is enough to prove that we can run $O(kn)$ calls of the function *NEXT* in $O(kn)$ time. We show that, after a linear-time preprocessing, each value $NEXT(i, j)$ can be computed in constant time. The equality $NEXT(i, j) = (i+t, j+t)$ means that $t$ is the size of the longest common prefix of $pat[i…m]$ and $text[j…n]$. Assume that we have computed the common suffix tree for *pat* and *text*. The computation of the longest common prefix of two suffixes is equivalent to the computation of their lowest common ancestor (LCA) in the tree. There is an algorithm (mentioned in Section 5.7) which preprocesses any tree in linear time in order to allow further LCA queries in constant time. This completes the proof. ‡

**Remark**

It can be shown that the same algorithm, implemented in the PRAM model, gives an efficient parallel algorithm for the approximate string-matching problem.

## 11.4. String-matching with don't care symbols

In this section, we assume that pattern *pat* and text *text* can contain occurrences of the symbol ø, called the *don't care symbol*. Several different don't care symbols can be considered instead of only one, but the assumption is that they are all undistinguishable from the point of view of string-matching. These symbols match any other symbol of the alphabet. We define an associated notion of *matching* on words as follows. We say that two symbols $a$, $b$ *match* if they are equal, or if one of them is a don't care symbol. We write $a \approx b$ in this case. We say that two strings $u$ and $v$ (of same length) match if $u[i] \approx v[i]$ for any position $i$. String-matching with don't care symbols is the problem of finding a factor of *text* that matches the pattern *pat* according to the present relation $\approx$.

$$\begin{array}{cccccccccccccc} a & a & a & \emptyset & b & a & b & b & \emptyset & \emptyset & a & a & b & \emptyset \\ a & \emptyset & a & b & b & \emptyset & \emptyset & b & b & a & a & a & b & a \end{array}$$

**Figure 11.8**. Matching words with the *don't care symbol* $\emptyset$.

The string-matching with don't care symbols does not use any of the techniques developed for other string-matching questions. This is because the relation $\approx$ is not transitive ($a \approx \emptyset$ and $\emptyset \approx b$ does not imply $a \approx b$). Moreover, if symbol comparisons (involving only the relation $\approx$) are the only access to input texts, then there is a quadratic lower bound for the problem, which additionally proves that the problem is quite different from other string-matching questions. The algorithm presented later is an interesting example of a reduction of a textual problem to a problem in arithmetics.

**Theorem 11.7**

If symbol comparisons are the only access to input texts, then $O(n^2)$ such comparisons are necessary to solve the string-matching with don't care symbols.

**Proof**

Consider a pattern of length $m$, and a text of length $n = 2m$, both consisting entirely of don't care symbols $\emptyset$. Occurrences of the pattern start at all positions $0\ldots m$. If the comparison "$pat[j] \approx text[i]$", for $1 \le j \le m$ and $m < i \le n$, is not done, then we can replace $pat[j]$ and $text[i]$ by two distinct symbols $a$, $b$ (that are not don't care symbols). Then the output remains unchanged, but one of the occurrences is disqualified. Hence, the algorithm is not correct. This proves that all comparisons "$pat[j] \approx text[i]$", for $1 \le j \le m$ and $m < i \le n$, must be done. This gives $m(m+1)/2 = O(n^2)$ comparisons. This completes the proof. ‡

Contrary to what is done elsewhere, we temporarily assume that positions in *pat* and *text* are numbered from zero (and not from one). We start with an algorithm which "multiplies" two words in a similar manner as two binary numbers are multiplied, but ignoring the carry. We define the product operation • as the composition of $\approx$ and the logical "and" in the following sense. If $x$, $y$ are two strings, then $z = x \bullet y$ is defined by

$$z[k] = \mathrm{AND}(x[i] \approx y[j] : i+j = k).$$

In other words, it is the logical "and" of all values $x[i] \approx y[j]$ taken over all $i$, $j$ such that both $i+j = k$ and $x[i]$, $y[j]$ are defined. We can write symbolically: $\bullet$ = ($\approx$, and).

Let $p$ to be the reverse of pattern *pat*, and consider $z = p \bullet text$. Let us examine the value of $z[k]$. We have $z[k]$ = true iff ($p[m\text{-}1] \approx text[k\text{-}m+1]$ and $p[m\text{-}2] \approx text[k\text{-}m+2]$ and ... and $p[0] \approx text[k]$). So, "$z[k]$ = true" exactly means that there is an occurrence of *pat* ending at position $k$ in *text*. Hence, the string-matching with don't care symbols reduces to the computation of products $\bullet$.

Let us define an operation on logical vectors similar to $\bullet$. If $x$, $y$ are two logical vectors, then $z = x \lozenge y$ is defined by

$$z[k] = \mathrm{OR}(x[i] \text{ and } y[j] : i+j = k).$$

For a word $x$ and a symbol $a$, denote by *logical*$(a, x)$ the logical vector whose $i$-th component is *true* iff $x[i] = a$. Define also

$$LOGICAL_{a,\,b}(x, y) = logical(a, x) \lozenge logical(b, y).$$

It is now easy to see the following fact:

> For two words $x$, $y$, the vector $x \bullet y$ equals the negation of logical OR of all vectors $LOGICAL_{a,\,b}(x, y)$ over all distinct symbols $a$, $b$ which are not don't care symbols.

A consequence of the above fact is that, for a fixed-size alphabet, the complexity of evaluating the product $\bullet$ is of the same order as that of computing the operation $\lozenge$.

Now, we show that the computation of the operation $\lozenge$ can be reduced to the computation of the ordinary product * of two integers. Let $x$, $y$ be two logical vectors of size $n$. Let $k = \log n$. Replace logical values *true* and *false* by ones and zeros, respectively. Next, insert between each two consecutive digits an additional group of $k$ zeros. We obtain two numbers $x'$, $y'$ (in binary representation). Let $z'$ be the integer, product of these numbers, $z' = x * y$. The vector $z = x \lozenge y$ can be recovered from $z'$ as follows. Take the first digit (starting at position 0), and then each $(k+1)$-th digit of $z'$; convert ones and zeros into *true* and *false*, respectively. In this way, we have proved the following statement.

**Theorem 11.8**

The string-matching problem with don't care symbols can be solved in $IM(n\log n)$ time, where $IM(r)$ denotes the complexity of multiplying two integers of size $r$.

The value $IM(r)$ depends heavily on the model of computations considered. If bit operations are counted, then the best known solution for the problem is given by the Schönhage-Strassen multiplication, which works in time only slightly larger than $O(r\log r)$. Even with the serial model of computation considered throughout the book, uniform RAM model (with logarithmic-sized integers), then, the best known complexity is at least $O(r\log r)$.

In fact, no linear-time algorithm for the problem is known. This gives an $O(n\log^2 n)$-time algorithm for the string-matching problem with don't care symbols.

String-matching with don't care symbols has a methodological interest because of its relation to arithmetics. It should be also interesting to find relations between some other typical textual problems to arithmetics.

## 11.5*. Edit distance — efficient parallel computation

The parallel computation of the edit distance can be ruled out as a shortest path problem for the corresponding grid graph $G$ (see Section 11.1). Assume for simplicity that words $x$ and $y$ are of the same length $n$. Then, $G$ has $(n+1)^2$ nodes. Let $A$ be the matrix of weights associated to edges of $G$. We can use (min, +) matrix multiplications to get the required value of the edit distance. Assume that the weight from the sink node to itself is zero. Then,

$$edit(x, y) = A^n[0, n].$$

The matrix $A^n$ can be computed by successive squarings (or an adaptation of it, if $n$ is not a power of 2):

**repeat** log$n$ **times** $A := A^2$.

Obviously, $k^3$ processors are enough to multiply two $k \times k$ matrices in $O(\log k)$ time on a CREW PRAM. In our case $k = (n+1)^2$, so, this proves that $n^6$ processors suffice to compute the edit distance. The time of computation is $O(\log^2 n)$. However, there is a more efficient algorithm, due to the special structure of the grid graph $G$. The grid graph can be decomposed into four grid graphs of the same type, see Figure 11.9. The partition of $G$ leads to a kind of parallel divide-and-conquer computation.

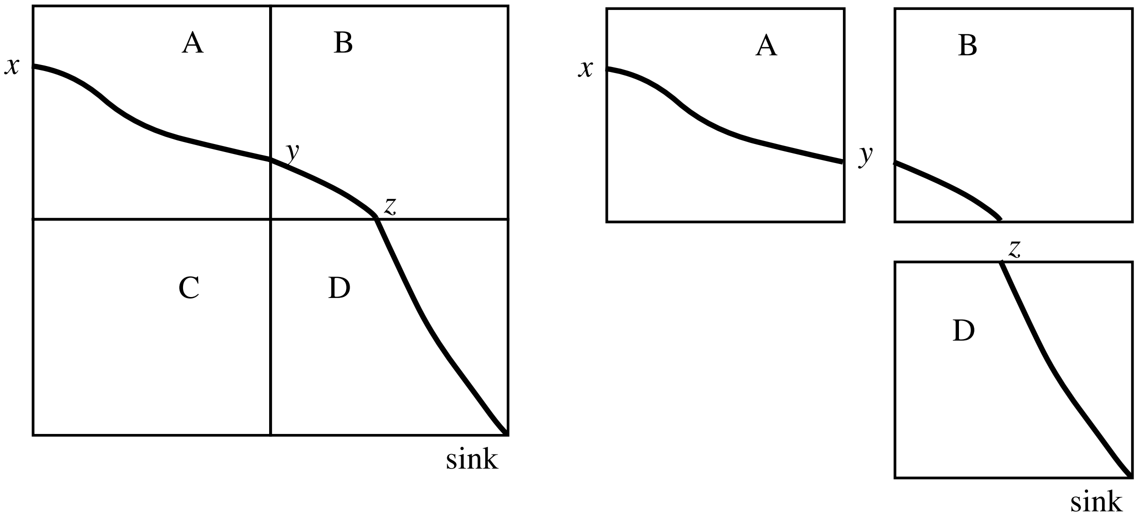


**Figure 11.9**. Decomposition of the shortest path problem into subproblems.

**Theorem 11.9**

The edit distance of two words of length $n$ can be computed in $\log^3 n$ time with $n^2$ processors.

**Proof**

The edit distance problem reduces to the computation of a shortest path from the source (left upper corner) to the sink (right lower corner) on the weighted grid graph $G$. We compute (recursively) the matrix $A$ of all costs of paths, from positions $x$ on the left or top boundary to any position $y$ on the right or bottom boundary of $G$.

Let us partition the grid into four identical subgrids, as in Figure 11.9. If we know the matrices of costs between boundary points for all subgrids, then all costs of paths between boundary positions of the whole grid can be computed with $O(M(n))$ processors in $O(\log^2 n)$ time, by a constant number of matrix multiplications. Here $M(n)$ denotes the number of processors needed to multiply, in $\log^2 n$ time, two matrices satisfying the quadrangle inequality. In chapter 8, we have seen that $M(n) = O(n^2)$. For $n/2 \times n/2$ subgrids we need $M(n/2)$ processors at one level of recursion. Altogether $M(n)$ processors suffice, since we have the inequality: $4M(n/2) \leq M(n)$ (because $M(n) = c\, n^2$). This completes the proof of the theorem. ‡

## Bibliographic notes

The edit distance computation seems to have been first published by Wagner and Fischer [WF 74]. Various applications of sequence comparisons are presented in a book edited by Sankoff and Kruskal [SK 83]. Algorithms of Sections 11.1 and 11.2 are widely used for molecular sequence comparisons, for which a large number of variants have been developed (see for instance [GG 89]). Computation of a longest common subsequence (not only its length) in linear space is from Hirschberg [Hi 75]. The last algorithm of Section 11.2 is from Hunt and Szymanski [HS 77]. It is the base of the "diff" command of Unix system. An algorithm for the longest increasing subsequence can be found in [Ma 89].

There are numerous substantial contributions to the problem, among them are those by: Hirschberg [Hi 77], Nakatsu, Kambayashi and Yajima [NKY 82], Hsu and Du [HD 84], Ukkonen [Uk 85b], Apostolico [Ap 86] and [Ap 87], Myers [My 86], Apostolico and Guerra [AG 87], Landau and Vishkin [LV 89], Apostolico, Browne and Guerra [ABG 92], Ukkonen and Wood [UW 93].

A subquadratic solution (in $O(n^2/\log n)$ time) to the computation of edit distances has been given by Masek and Paterson [MP 80] for fixed-size alphabets.

The first efficient string-matching with errors is by Landau and Vishkin [LV 86b]. A parallel algorithm is given in [GG 87b].

The computation of lower common ancestors (LCA) is discussed by Schieber and Vishkin in [SV 88] (see the bibliographic notes at the end of Chapter 5).

The best asymptotic time complexity of the string-matching with don't care symbols is achieved by the algorithm of Fischer and Paterson [FP 74].

Practical approximate string-matching is discussed by Baeza-Yates and Gonnet [BG 92], and by Wu and Manber [WM 92]. The solutions are close to each others. the second algorithm has been implemented under UNIX as command "agrep".

The parallel algorithm computing the edit distance (Section 11.5) is by Apostolico, Atallah, Larmore, and McFaddin [AALF 88]. It is also observed independently in [Ry 88] that the reduction of the edit distance problem to the shortest path problem for grid graphs leads to the use of parallel matrix multiplication. For parallel approximate string-matching the reader can also refer to [LV 89].

## Selected references

[SK 83] D. SANKOFF, J.B.KRUSKAL, *Time Warps, String Edits and Macromolecules: the Theory and Practice of Sequence Comparison*, Addison-Wesley, Reading, Mass., 1983.

[GG 87] Z. GALIL, R. GIANCARLO, Data structures and algorithms for approximate string-matching, *J. Complexity* 4 (1988) 33-72.

[LV 89] G.M. LANDAU, U. VISHKIN, Fast parallel and serial approximate string-matching, *J. Algorithms* 10 (1989) 158-169.

[Uk 85] E. UKKONEN, Algorithms for approximate string-matching, *Information and Control* 64 (1985) 100-118.

# 12. Two-dimensional pattern matching

The chapter is devoted to pattern matching in two-dimensional structures. These objects can be considered as images represented by matrices of pixels (*bit-map* images). Questions related to pattern matching in strings extend naturally to similar questions on images. However, not all algorithms have easy extensions in this sense. The two-dimensional pattern matching is interesting due to its relation to image processing. The efficiency of algorithms is even more important in the two-dimensional case because the size of the problem, number of pixels of images, is very large in practical situations.

We mainly consider rectangular images. The pattern matching problem is to locate an $m \times m'$ pattern array *PAT* inside an $n \times n'$ (text) array $T$. The position of an occurrence of *PAT* in $T$ is a pair $(i, j)$, such that $PAT = T[i+1\ldots i+m, j+1\ldots j+m']$ (see Figure 12.1).

We give two different solutions to two-dimensional pattern matching. The first reduces the problem to multi-pattern matching. The second is based on two-dimensional periodicities and the notion of duels. We then consider non-rectangular pattern in relation to approximate matching. The method of sampling is presented for two-dimensional patterns and reveals to be very powerful for almost all patterns. Finally, in the last section, we apply the naming technique to several problems concerning regularities in images.

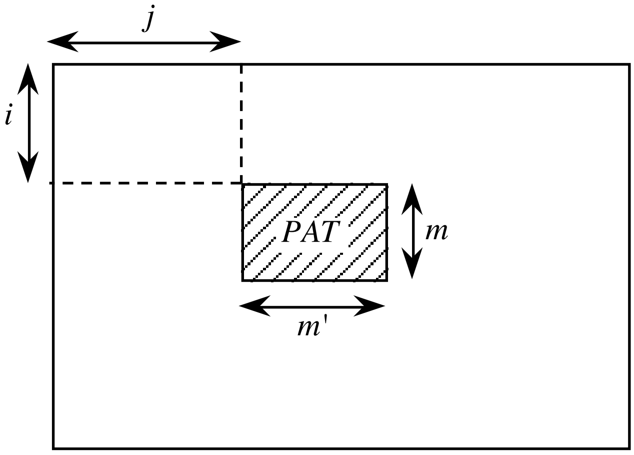


**Figure 12.1**. *PAT* occurs at position $(i, j)$ in $T$.

## 12.1. Multi-pattern approach: Baker and Bird algorithms

The first solution to 2-D pattern matching is to translate the problem into a string-matching problem. The pattern is viewed as a set of strings, its columns. To locate columns of the pattern inside columns of the text array remains to search for several patterns. Moreover, the occurrences of patterns must be found in a particular configuration inside rows: all columns of the pattern are to be found in the order specified by the pattern, and ending all on a same row of the text array. In this section, we use the Aho-Corasick approach (Section 7.1) to solve the multi-pattern matching.

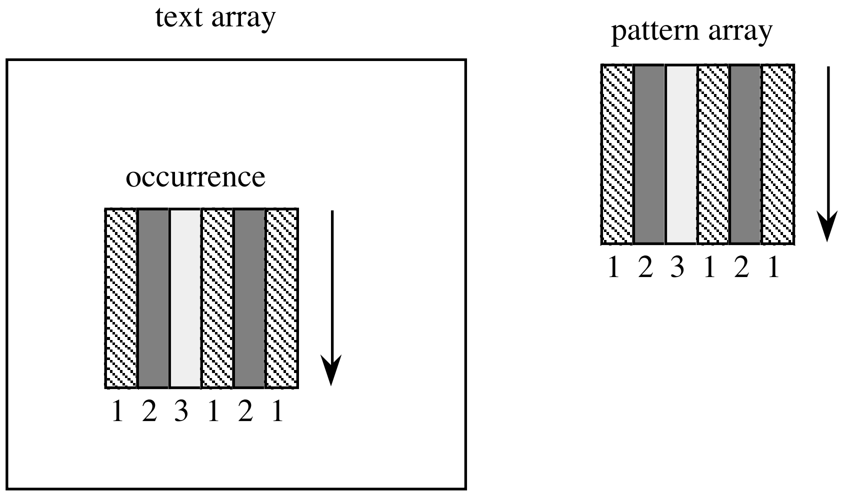


**Figure 12.2**. Two-dimensional pattern matching: searching for columns of the pattern.

The strategy to search for *PAT* in the text array *T* is the following. Let Π be the set of all (distinct) columns of *PAT* (treated as words). We first build the string-matching automaton *G* = *SMA*(Π) with terminal states (see Section 7.1). Each terminal state corresponds to a pattern of Π. So, columns of the pattern are identified with states of the SMA automaton. There can be less than *m* terminal states because of possible equalities between columns. Then, the automaton is applied to each column of *T*. We generate an array *T*' of the same size as *T*, and whose entries are states of *G*. The pattern *PAT* itself is replaced by a string *pat* over the set of states: the *i*-th symbol of *pat* is the state identified with the *i*-th column of *PAT*. The rest of the procedure consists in locating *pat* inside the lines of *T*'. The strategy is illustrated by Figures 12.3, 12.4 and 12.5. This yields the next result.

**Theorem 12.1**

The two-dimensional pattern matching can be done in $O(N\log|A|)$ time, where $N = n*n'$ is the size of the text array, and *A* is the alphabet.

**Proof**

The time to build the automaton *SMA*(Π) is $O(M\log|A|)$ where $M = m*m'$ is the size of the pattern *PAT*. The construction of the array of column numbers *T*' takes $O(N\log|A|)$ time. The final search phase, string-matching inside lines of *T*' takes $O(N)$ time. Thus, the result holds assuming that $M \leq N$. ‡

| | | |
|---|---|---|
| *a* | *a* | *a* |
| *b* | *b* | *a* |
| *a* | *a* | *b* |

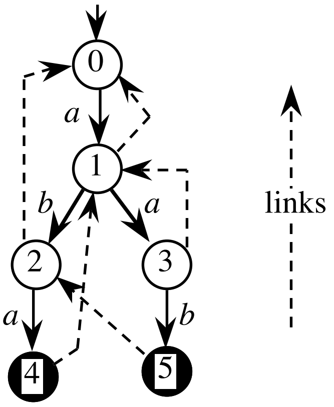
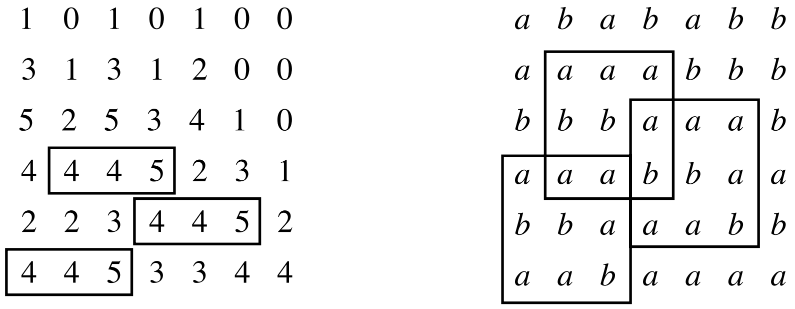


**Figure 12.3**. A pattern array, and the SMA automaton of its columns. Columns 1 and 2 are identified with state 4, column 3 with state 5.

| | | | | | | |
|---|---|---|---|---|---|---|
| *a* | *b* | *a* | *b* | *a* | *b* | *b* |
| *a* | *a* | *a* | *a* | *b* | *b* | *b* |
| *b* | *b* | *b* | *a* | *a* | *a* | *b* |
| *a* | *a* | *a* | *b* | *b* | *a* | *a* |
| *b* | *b* | *a* | *a* | *a* | *b* | *b* |
| *a* | *a* | *b* | *a* | *a* | *a* | *a* |

| | | | | | | |
|---|---|---|---|---|---|---|
| 1 | 0 | 1 | 0 | 1 | 0 | 0 |
| 3 | 1 | 3 | 1 | 2 | 0 | 0 |
| 5 | 2 | 5 | 3 | 4 | 1 | 0 |
| 4 | 4 | 4 | 5 | 2 | 3 | 1 |
| 2 | 2 | 3 | 4 | 4 | 5 | 2 |
| 4 | 4 | 5 | 3 | 3 | 4 | 4 |

**Figure 12.4**. A text array, and its associated array of states (according to the SMA automaton of Figure 12.3).



| | | | | | | |
|---|---|---|---|---|---|---|
| 1 | 0 | 1 | 0 | 1 | 0 | 0 |
| 3 | 1 | 3 | 1 | 2 | 0 | 0 |
| 5 | 2 | 5 | 3 | 4 | 1 | 0 |
| 4 | 4 | 4 | 5 | 2 | 3 | 1 |
| 2 | 2 | 3 | 4 | 4 | 5 | 2 |
| 4 | 4 | 5 | 3 | 3 | 4 | 4 |

| | | | | | | |
|---|---|---|---|---|---|---|
| *a* | *b* | *a* | *b* | *a* | *b* | *b* |
| *a* | *a* | *a* | *a* | *b* | *b* | *b* |
| *b* | *b* | *b* | *a* | *a* | *a* | *b* |
| *a* | *a* | *a* | *b* | *b* | *a* | *a* |
| *b* | *b* | *a* | *a* | *a* | *b* | *b* |
| *a* | *a* | *b* | *a* | *a* | *a* | *a* |

**Figure 12.5**. Occurrences of "445" in the array of states give occurrences of the pattern array in the original text array of Figure 12.4 Pattern "445" corresponds to the pattern array of Figure 12.3 (left).

The above algorithm seems to be inherently dependent on the alphabet. This is because of the automaton approach. The problem of existence of a linear time algorithm with a time complexity independent of the size of the alphabet (for two-dimensional pattern matching) is interesting and important from the practical point of view. We show a partial solution in the next section (alphabet-independent searching phase, but alphabet-dependent preprocessing phase).

## 12.2. Periodicity approach: Amir-Benson-Farach algorithm

The algorithm of the present section is based on the idea of *duels*. The string-matching algorithm by duels presented in Chapter 3 for "one-dimensional" strings extends to the two-dimensional case. The advantage of the approach is to produce a two-dimensional pattern matching algorithm whose search phase takes linear time, independently of the alphabet. The two-dimensional settings for duels, witnesses and consistency relation are necessary to adapt the string-matching algorithm by duels.

A period of the $m \times m'$ pattern array *PAT* is a non-null vector $p = (r, s)$ such that $-m < r < m$, $0 \leq s < m'$, and $PAT[i, j] = PAT[r+i, s+j]$ whenever both sides of the equality are defined. Note that the second component of a period is assumed to be a non-negative integer, which remains to consider that vector periods are always oriented from left to right. There are two categories of the periods, see Figures 12.7 and 12.8, according to whether $r$ is negative or not.

If there are close occurrences of the pattern in the text array, then there is an overlap of the pattern over itself, that is, a periodicity. If $x$ and $y$ are close positions of two occurrences *PAT* in the array $T$, assuming that $y$ is to the right of $x$, the vector $y$-$x$ is a period of the pattern.

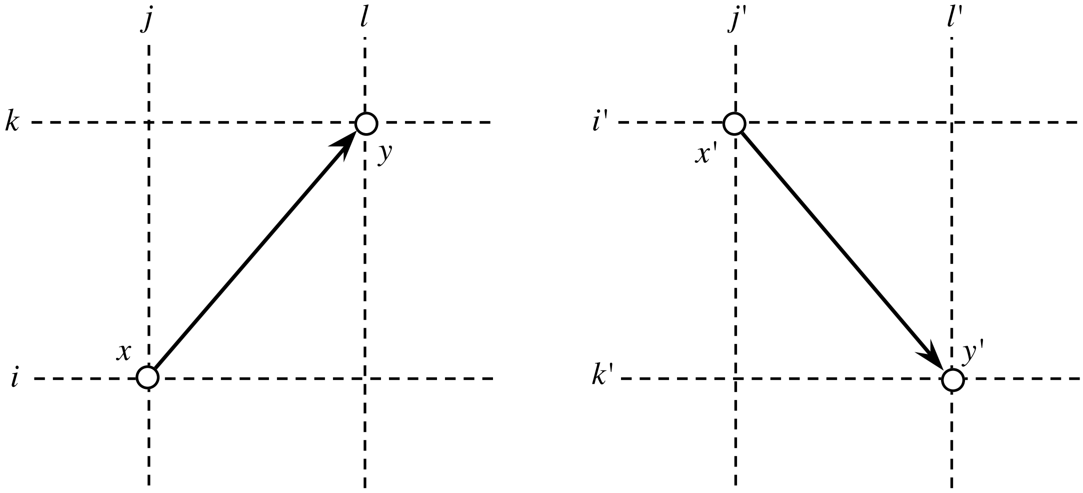


**Figure 12.6**. Orderings on positions: $x <_b y$ (left), $x' <_t y'$ (right).

Positions in arrays are numbered top-down (rows) and left-to-right (columns). We define two partial orderings $<_b$ (for bottom) and $<_t$ (for top) on positions in the array $T$:

$$(i, j) \leq_b (k, l) \text{ iff } i \geq k \text{ and } j \leq l,$$

$$(i, j) \leq_t (k, l) \text{ iff } i \leq k \text{ and } j \leq l.$$

The relation $x <_b y$ means that position $x$ is to the left and at the *bottom* of $y$. The relation $x <_t y$ means that position $x$ is to the left and at the *top* of $y$. For instance, we have $(i, j) \leq_b (k, l)$ and $(i', j') \leq_t (k', l')$ in Figure 12.6.

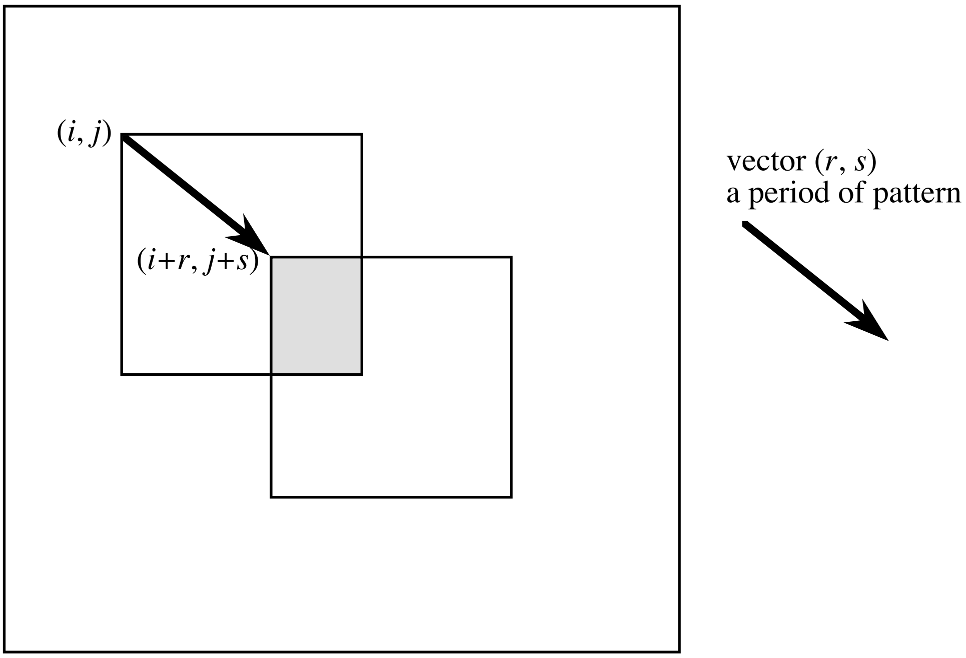


**Figure 12.7**. When $(i, j) <_t (k, l)$. If two occurrences of *PAT* overlap, *PAT* has a period $(r, s) = (k, l)$-$(i, j)$. Otherwise, a duel between $(i, j)$ and $(k, l)$ can be applied.

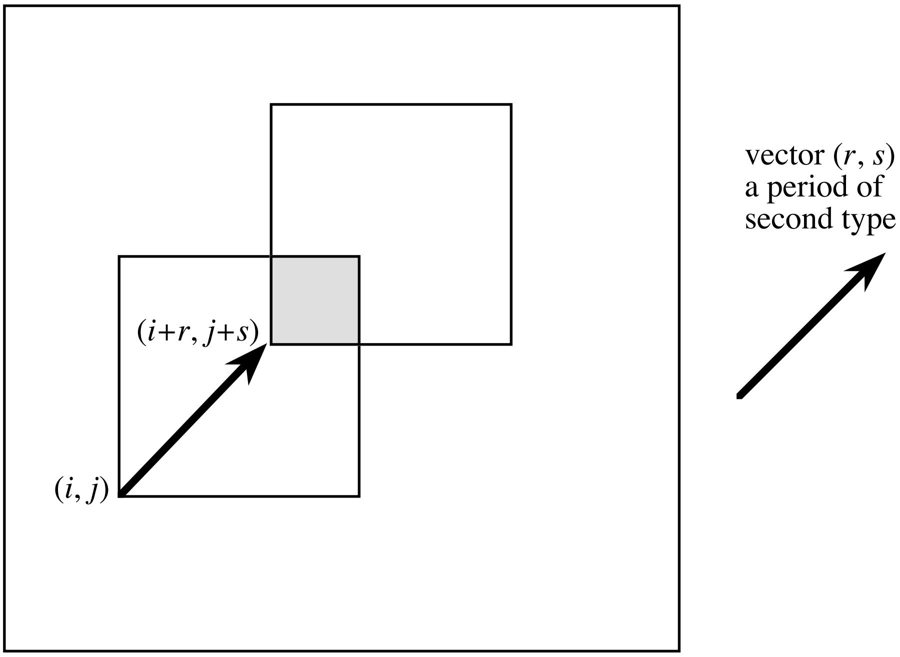


**Figure 12.8**. The second category of period, when $(i, j) <_b (k, l)$.

Making duels during the searching phase of the pattern matching algorithm suppose that we have an analogue to the *witness table* considered for strings. For arrays, the two-dimensional witness table *WIT* is defined as follows:

*WIT*[*r, s*] = *any* position (*p*, *q*) such that *PAT*[*p*, *q*] ≠ *PAT*[*r*+*p, s*+*q*],

*WIT*[*r, s*] = 0, if there is no such *(p, q)*.

The definition is illustrated in Figures 12.9 and 12.10 for the two categories of vector (*r*, *s*) (depending on whether $r \geq 0$ holds or not).

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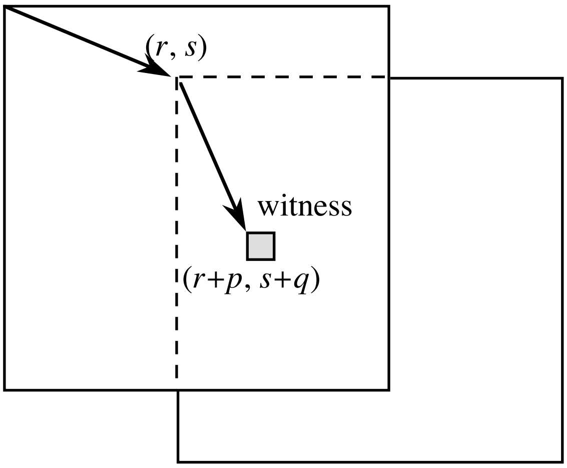

**Figure 12.9**. The first category of witnesses.
The vector (*r*, *s*) is not a period, (*p*, *q*) = *WIT*[*r*, *s*], and *PAT*[*p*, *q*] ≠ *PAT*[*r*+*p, s*+*q*].

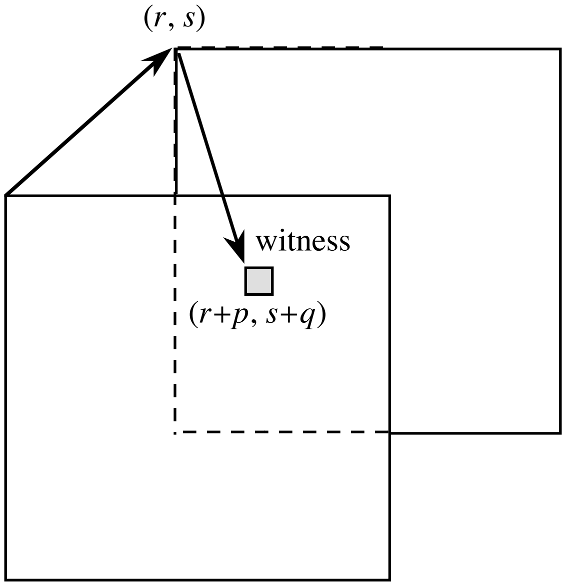

**Figure 12.10**. The second category of witnesses.
The vector (*r*, *s*) is not a period, (*p*, *q*) = *WIT*[*r*, *s*], and *PAT*[*p*, *q*] ≠ *PAT*[*r*+*p, s*+*q*].

A duel is only performed on close positions according to the following notion. A position $(k, l)$ is said to be *in the range of* the position $(i, j)$ (according to the size of *PAT*) iff $|k\text{-}i| < m$ and $|l\text{-}j| < m'$. In addition, two positions $x$ and $y$ such that $y$ is to the right of $x$, are said to be *consistent* iff $y$ is not in the range of $x$, or if $WIT[y\text{-}x] = 0$, which means that $y\text{-}x$ is a period of *PAT*.

Let us recall the notion of *duel*. If the positions $x$ and $y$ are not consistent, the pattern *PAT* cannot appear both at $x$ and at $y$ in the array $T$. In constant time, we can remove one of them as a candidate for a position of an occurrence of the pattern. Such an operation, called a *duel*, can be described as follows. Assume that positions $x$ and $y$ are not consistent, with $y$ to the right of $x$. Let $z = WIT[y\text{-}x]$. Let $a = PAT[z]$, and $b = PAT[y\text{-}x+z]$. By definition of the witness table *WIT*, symbols $a$ and $b$ are distinct. Let $c$ be the symbol $T[y+z]$. This symbol cannot be both equal to $a$ and $b$, so at least one of the positions $x$, $y$ is not a matching position for *PAT*. If $b \neq c$, the pattern cannot occur at position $x$. If $a \neq c$, the same holds for $y$. So, comparing $c$ with $a$ and $b$ permits to eliminate (at least) one of the position. Note that in some situations both positions could be eliminated, but, for simplicity of the algorithm, exactly one position is always removed at a time. This is a mere duplication of the strategy developed for "one-dimensional" string-matching. Let *duel* be defined by

$$duel(x, y) = (\text{if } b = c \text{ then } x \text{ else } y).$$

The value $duel(x, y)$ is the position which "survives" after the duel, the other position is eliminated.

We now describe the two-dimensional pattern matching algorithm based on duels. We assume the witness table of the pattern *PAT* is computed. Its precomputation is sketched at the end of the section. The first step of the searching phase reduces the problem to a two-dimensional pattern matching for unary patterns, as if all entries of *PAT* were the unique symbol $a$.

We want to eliminate from the text array $T$ a set of candidate positions in such a way that all remaining positions are pairwise consistent. Removed positions cannot be matching position of the pattern. Then, to each position $x$ on the text array we associate the value 1 iff, after duels, it corresponds to the symbol compatible with occurrences of the pattern placed at any position in the range of $x$. Otherwise we associate 0 to position $x$. Doing so, we are left with a new text array consisting only of zeros and ones. Finally, we look for occurrences of an $m{\times}m'$ array containing only 1's. So, the algorithm is essentially the same as in the one-dimensional case. But here, the relation between positions is a bit more complicated. This is why relations $<_b$ and $<_t$ have been introduced.

The following property of consistent positions is crucial for the correctness of the algorithm.

**Consistency property (transitivity):**

let $x <_t y <_t z$**,** or $x <_b y <_b z$.

If $x$, $y$ are consistent, and $y$, $z$ are consistent, then $x$, $z$ are also consistent.

According to relations $<_b$ and $<_t$, consistency refines to *bottom consistency* and *top consistency*. A set of positions is *bottom consistent* iff for any two positions $x$, $y$ of the set, such that $x <_b y$, the positions are consistent. Bottom consistent positions are defined similarly. It is clear that two elements are consistent iff they are top *and* bottom consistent. The same refers to sets of (pairwise) consistent positions.

Let $R$ be a subrectangle of the text array $T$. The set $S$ of positions in $R$ is said to be *good* with respect to $R$ if both positions in $S$ are pairwise consistent, and there is no matching position inside $R$-$S$.

Let $k$ be a column of the text array $T$. In the searching algorithm, we maintain the following invariant. A good set of consistent positions in the columns $k$, $k$+1, ..., $n'$ is known. First, we construct good sets of consistent positions in each column separately. This gives the invariant for $k = n'$. Then we satisfy the invariant for $k = n'$-1, $n'$-2, ..., 1. At the end we have a good set of consistent positions for the whole text array.

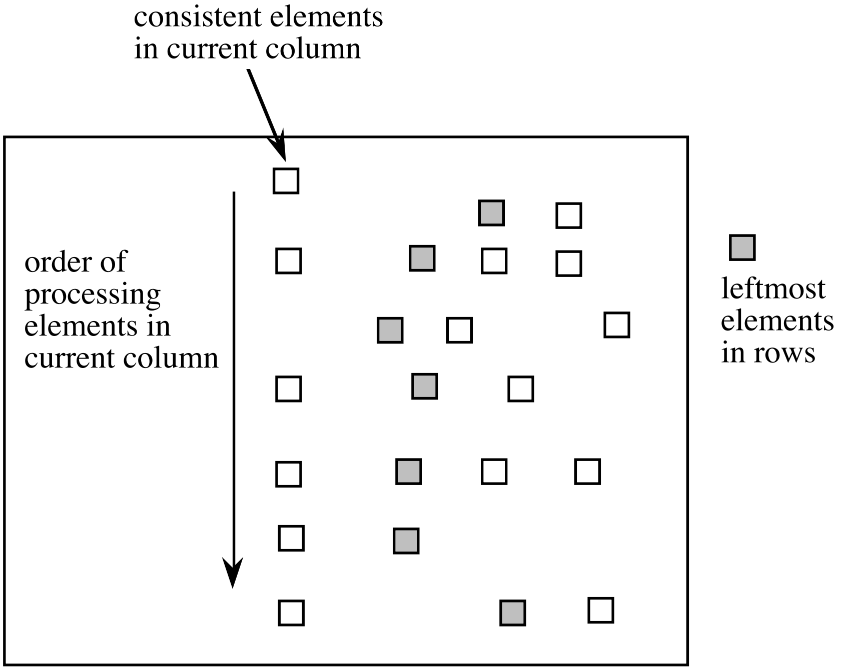
consistent elements in current column
order of processing elements in current column
leftmost elements in rows

**Figure 12.11.** The situation when processing the next column.
The current column contains positions mutually consistent inside this column.
Then, positions inconsistent with other columns are removed.

When processing the $k$-th column, we run through consistent positions of this column in a top-down fashion. We maintain the following invariant:

***inv*(*x*, *z*, *k*):**

*z* is the leftmost consistent position in its own row; let *R* be the rectangle composed of rows above *z*, and columns *k*, …, *n*'; the set *S* of all remaining positions in *R* is a good set in *R*.

Let *x*1, *x*2 be two consecutive (in the top-down order) consistent positions in the *k*-th column. Figure 12.12 illustrates how the process goes from *inv*(*x*1, *z*1, *k*) to *inv*(*x*2, *z*2, *k*).

The set of consistent positions in columns *k*+1, …, *n*' is maintained as a set of stacks. These stacks correspond to the rows. The positions in a given row, from left to right, are on their stack from top to bottom: the leftmost position in *i*-th row (in columns *k*+1, …, *n*') is at the top of the *i*-th stack. The duels of *x*1 against elements of the *i*-th row are done using the same stack procedure as in the string-matching algorithm by duels (see Chapter 3).

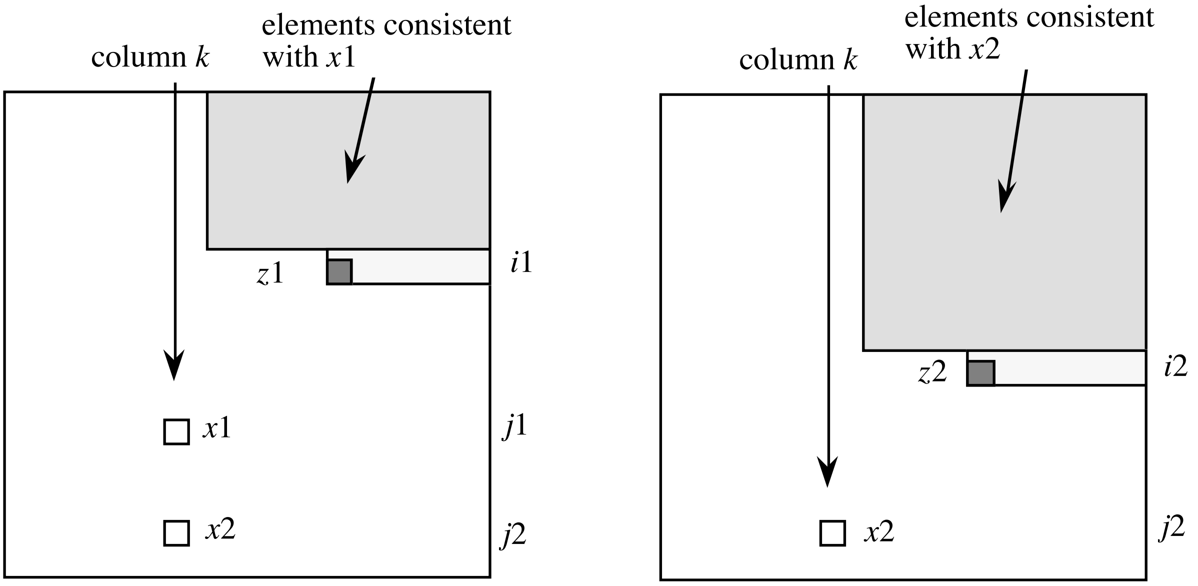

**Figure 12.12**. From *inv*(*x*1, *z*1, *k*) to *inv*(*x*2, *z*2, *k*).

Assume that *z*1 is in the *i*1-th row, and *x*1 is the *j*1-th row. Only positions in columns *k*+1, …, *n*' are considered (the duels are done between them and *x*1). We process rows in the order *i*1, *i*1+1, …; each row is processed from left to right, starting with the leftmost element. During the processing, we make duels between *x*1 and considered positions.

Assume that we start a given phase with position *x*1 in the *k*-th column, and with position *z*1 in the *i*1 row (see Figure 12.12). The rows are processed top down and left-to-right, starting with *z*1, and ending before or at the row containing *x*1. Initially *z* = *z*1. Then, assume that we consider a candidate *z* in a column to the right of *x*1. The basic operation is the duel between *x*1 and *z*. Three cases are possible:

(1) — both $x1$ and $z$ survive (they are consistent); the *crucial point* is that we know at this moment (due to transitivity of consistency) that all candidates to the right of $z$ and in the same row as $z$ are consistent with $x1$; we do not have to process them; we just go to the next row, starting with the leftmost candidate $z$ (to the right of $k$-th column) in this row;

(2) — $z$ is "killed" by $x1$ in the duel; we process the next candidate $z$ in the same row as last $z$; if there is no such candidate we just go to the next row;

(3) — $x1$ is "killed" and $z$ survives; then, the processing of $x1$ is finished; $x1$ is removed as a candidate, $z1 = z$, and we start the next phase with the next candidate $x2$ below $x1$ in the same column as $x1$; if there is no such candidate, then the processing of the whole column is finished; take $x1$ as the topmost candidate in the ($k$-1) column, and start processing column $k$-1.

Doing so, we obtain a set of consistent positions in the sense of the ordering $<_t$. If $x$, $y$ are in this order, and are in the set, then they are consistent. After that, we process again the whole text array, but in a bottom-up manner, performing essentially the same algorithm as described above for the top-down ordering. The rows are again processed from left to right. The remaining set of positions is guaranteed to be bottom consistent. Thus, the final set $S$ is a good consistent set.

The problem is reduced to "unary" pattern matching, in which the pattern consists only of one symbol, as follows. For each position $x$ in the text array, find any position $y$ in $S$ such that $x$ is in the range of $y$. Place the pattern at position $y$ on the text array, and check if the symbol at $x$ matches the corresponding symbol of the pattern. If "yes", associate "1" to position $x$. If "no", or if there is no such position $y$, associate "0" to $x$. In this way, we obtain a new array of zeros and ones. It just remains to search for a rectangular shape of size $m \times m'$ containing only 1's inside the new array. This is straightforward, and is left to the reader. The above discussion gives a proof of the next statement.

**Theorem 12.2**

If the witness table for the pattern array is computed, the search phase for the two-dimensional pattern matching can be done in linear time, independently of the size of the alphabet.

The computation of the witness table given below makes use of a suffix tree. It takes a time which depends on the size of the alphabet, though it is linear with respect to the length of the pattern. This is due to the construction of suffix trees. In the computation of the witness table the basic operation is to check the equality of two subrows of the pattern. This is done on the suffix tree for the set of rows of the pattern, and by preprocessing the tree for *LCA* queries.

**Theorem 12.3**

The witness table for an $m \times m'$ two-dimensional pattern can be computed in $O(mm'\log|A|)$ time, where $A$ is the alphabet.

**Proof**

Let us examine the situation, when the witness for the position $(r, s)$ of $PAT$ is to be computed. Let $k = m\text{-}s+1$. Assume that elements of the first, and of the $s$-th columns are names of the rows of size $k$ starting at position of these columns to the right. Denote the resulting columns by $C_1^{(k)}$ and $C_s^{(k)}$ (see Figure 12.13).

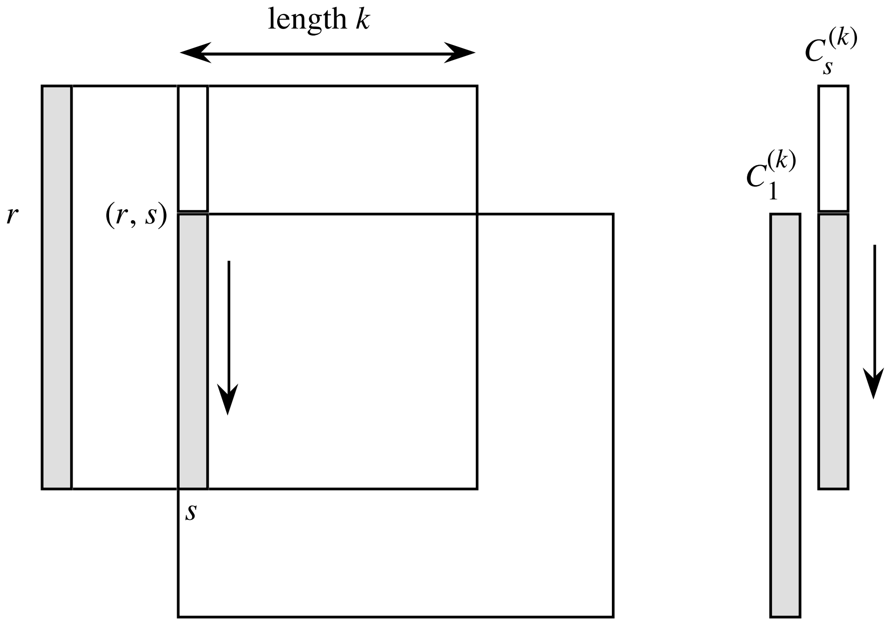

**Figure 12.13**.

Let $ST$ be the suffix tree of all rows of the pattern. It takes $O(mm'\log(|A|))$ time to build it. Preprocess the tree to be able to answer $LCA$ queries in constant time (see Section 5.7). Consider also the table $PREF$ as defined in Chapter 3.

**Claim**

The table $PREF$ of the column $C_s^{(k)}$ with respect to $C_1^{(k)}$ can be computed in $O(m)$ time, once the tree $ST$ is given.

**Proof** (of the claim)

the computation of this table essentially reduces to the computation of the table of border lengths, see Chapter 3. We don't need actually the names of entries of the columns $C_s^{(k)}$ and $C_1^{(k)}$, these names represent subrows of length $k$. It is enough to make comparisons in constant time, hence, it is enough to be able to check quickly the equality between two subrows of the same size $k$. This can be done by $LCA$ queries about the rows of the pattern array.

Assume first that $(r, s)$ is a period of the pattern. Then $PREF[r] = m\text{-}r$. Otherwise, $PREF[r]$ gives the index of the row where the witness position is. To find the witness position it is enough to find the longest common prefix of two subrows of length *k*. this can be done again by the use of *ST* and *LCA* queries. This complete the proof. ‡

## 12.3. Matching with don't care symbols, and non-rectangular patterns

Assume that the two-dimensional pattern contains a certain number of holes. Holes can be regarded as filled with a special symbol that matches any other symbol. It is the don't care symbol ∅ considered in Chapter 11 for approximate string-matching. If the pattern is not rectangular, we can also complete it , adding enough don't care symbols so that it fits into an $m \times m'$ rectangle. Doing so, both questions become similar.

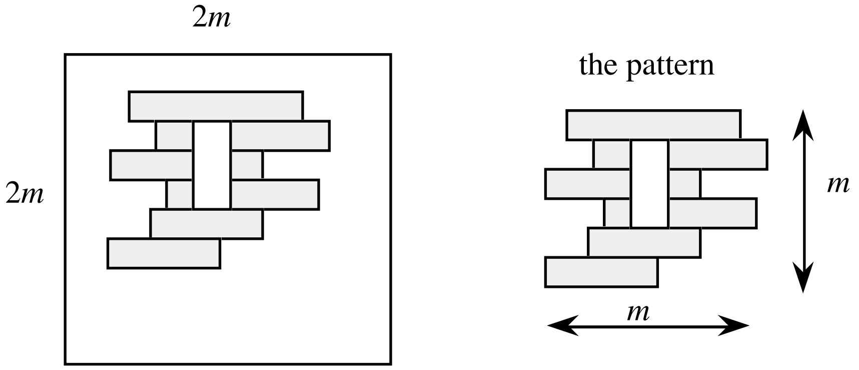

**Figure 12.14**. Searching a non-rectangular $m \times m'$ pattern inside pieces of shape $2m \times 2m'$.

**Theorem 12.4**

Two-dimensional pattern-matching with don't care symbols, and pattern-matching of non-rectangular patterns can be done in $O(N\log^2 m)$ time (with an $m \times m'$ pattern, $m \geq m'$, and an $n \times n'$ text array, $N = nn'$).

**Proof**

We linearize the problem. Let *PAT* be a non-rectangular pattern which fits into an $m \times m'$ rectangle, with $m \geq m'$. We consider windows of shape $2m \times 2m'$ on the text array. We first solve the problem as if $n = 2m$. We define *Lin*(*PAT*) as a one-dimensional version of *PAT*. It is a string with don't care symbols of size $O(m)$ constructed as follows:

— place *PAT* inside a $2m \times 2m'$ shape *S*. All positions not occupied by *PAT* are filled with the don't care symbol ∅; then, concatenate the rows of *S*, starting from the topmost row; in the string obtained in this way, remove the largest prefix, and the largest suffix containing only don't care symbols. The resulting string is *Lin*(*PAT*).

The basic property of the transformation *Lin* is:

*Lin*(*PAT*) is independent of the position where *PAT* is placed inside the shape *S*.

Let *T* be an $2m\times2m'$ text array. Let *Lin*'(*T*) be the string obtained by concatenating all rows of *T*, starting from the topmost row.

Then, searching *PAT* in *T* is equivalent to search *Lin*(*PAT*) inside *Lin*'(*T*). This can be done by methods for string-matching with don't care symbols (Section 11.4). It is proved there how to do it in time $O(n\log^2 n)$, which becomes here $O(m^2\log^2 m)$.

A text array of size greater than $2m\times2m'$ can be decomposed into such (overlapping) subarrays on which the above procedure is applied. The total time becomes then $O(N\log^2 m)$. This completes the proof. ‡

## 12.4. Matching with mismatches

The definition of a distance between two arrays is more complicated than for (one-dimensional) strings. Insertions or deletions of a symbol can result in an increase or decrease of the length of one row (column). Therefore, for simplicity, we concentrate here on the approximate pattern matching with only one edit operation: replacement of one symbol by another. This corresponds to unit-cost mismatches.

For two strings *x*, *y* denote by $MISM_k(x, y, i)$ the set of first (left-to-right) mismatch positions, up to *k*, between the substring $y[i\ldots i+|x|-1]$ and *x*. We are not interested in more than *k* mismatches.

**Lemma 12.5**

Assume we are given two strings *x* and *y*, and their suffix trees with the *LCA* preprocessing. Then, the computation of $MISM_k(x, y, i)$ can be done in time $O(k)$ for each position *i* in the text *y*.

**Proof**

First we find the longest common prefix of $y[i\ldots n]$ and *x*. This is done by an *LCA* query for the leaves corresponding to *y* and *x* in the joint suffix tree for these both texts. In this way, we obtain the first mismatch position $i_1$. Then, we look for the longest common prefix of $x[i_1-i+1\ldots m]$ and $y[i_1\ldots n]$. This is done again by asking a suitable *LCA* query about leaves related to $x[i_1-i+1\ldots m]$ and $y[i_1\ldots n]$. We obtain the next mismatch position (if it exists). We continue in this way until *k* mismatch positions are found, or (in the case there are less than *k* mismatch positions) all mismatch positions are found. The time is proportional to the number of *LCA* queries, that is $O(k)$. This completes the proof. ‡

**Theorem 12.6**

Assume the alphabet is of a constant size. The problem of pattern matching with a fixed number *k* of mismatches inside an $n\times n$ text array *T* can be solved in time $O(kn^2)$.

**Proof**

Let *PAT* be the $m \times m$ pattern, where $m \leq n$. The algorithm starts as in the exact two-dimensional pattern matching, by a multi-pattern string-matching. The Aho-Corasick automaton for all columns of the pattern is built. Then, the automaton is applied to all columns of *T* to get a state array *T*'. The pattern array is replaced by a string of states *PAT*'.

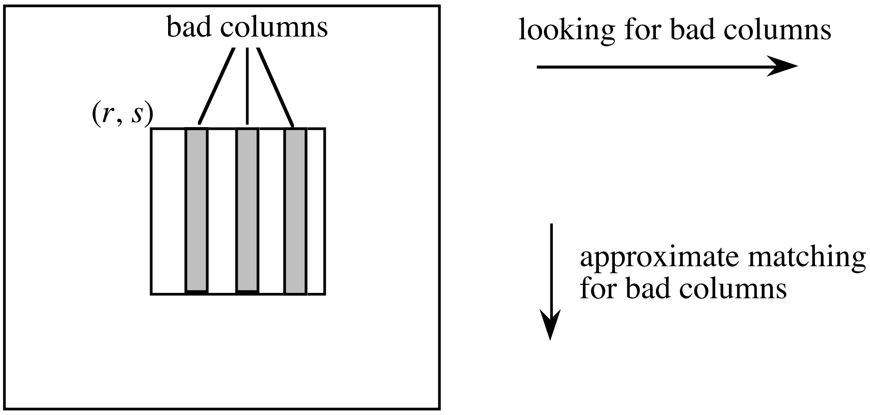

**Figure 12.15**. Approximate matching. There is at most *k* bad columns. If there is match with at most *k* mismatches, then the total number of mismatches in all bad columns cannot exceed *k*.

Figure 12.15 illustrates how we check the approximate match at position (*r*, *s*) with at most *k* mismatches. Let *y* be the *r*-th row of *T*'. We compute $MISM_k(PAT', y, s)$. This produces all columns which contain at least one mismatch with the pattern *PAT* placed at (*r*, *s*). Let us call these columns the bad columns. We compute the total number of mismatch positions in bad columns with respect to the corresponding columns of the pattern (assuming it is placed at position (*r*, *s*)). We are only interested in at most *k* mismatches in total. All mismatches are found by using the function *MISM*. The total complexity is proportional to the number of all *LCA* queries done in the algorithm. We make at most *k* such queries. Hence, for a fixed position (*r*, *s*) the complexity, after the preprocessing, is $O(k)$. Since there is a quadratic number of position, the total time complexity is as required. This completes the proof. ‡

## 12.5. Multi-pattern matching

In this section we consider a set of *k* square pattern arrays $X_1, X_2, \dots, X_k$. For a given $n \times n$ text array *T* we want to check if any of these patterns occurs in *T*. This is the multi-pattern matching in two dimensions. Assume, for simplicity, that the size of the alphabet is constant. The strategy developed for the Karp-Miller-Rosenberg algorithm (Chapter 8) yields a solution to the general multi-pattern problem which works in $O(n^2\log n)$ time. We omit the obvious proof.

**Fact**

The two-dimensional multi-pattern matching can be solved in $O(n^2\log n)$ time using the KMR algorithm.

Indeed, the above result can be improved to $O(n^2\log k)$ time, where $k$ is the number of patterns. Of course, $k$ can be of the same order as $n$, and this does not provide a substantial improvement. But we are also interested in alternative algorithms and some interesting new ideas behind them which enrich the algorithmics of two-dimensional matching.

The natural alternative algorithm considered here is based on an extension of the Aho-Corasick string-matching automaton to the two-dimensional case. By the way, this also shows the important extension of the notion of *border*, *suffix*, and *prefix* to two-dimensional arrays. This also provides another pattern matching algorithm for one pattern: it shows that searching the pattern along a fixed diagonal of the text array is reducible to the one-dimensional string-matching. Again, *LCA* preprocessing is crucial for the two-dimensional pattern matching algorithm of the section.

First consider the simple case when all the patterns are of the same shape. Assume that they are $m\times m$ arrays. The method of section 12.1 generalizes easily to this situation. This gives a linear time algorithm when all patterns of the same size.

**Theorem 12.7**

The two-dimensional multi-pattern matching can be solved in time $O(N)$ when the alphabet is fixed and all patterns are of the same size (where $N$ is the total size of the problem).

**Proof**

The algorithm works as follows. The Aho-Corasick machine is constructed for all columns of all patterns. Then, each pattern array is transformed into a string of states. We obtain a set of strings $x_1$, $x_2$, …, $x_k$. The text array $T$ is replaced by the state array $T'$ in the same way as in Section 12.1. Any multi-pattern string-matching algorithm then gives a solution. This gives a linear time algorithm for this special case (fixed alphabet). ‡

Next, we consider the general case, when the patterns are square arrays of possibly different sizes. Again, the algorithm is an extension of the Aho-Corasick multi-pattern matching.

A prefix (resp. suffix) of a square array is a square subarray containing the left top corner (resp. right bottom corner) of the array. We construct the two-dimensional version of the Aho-Corasick multi-pattern automaton $M$ as follows. Each pattern is considered as a string: its $i$-th letter is the $i$-th segment of the array. The $i$-th segment is composed of the upper part of the $i$-th column, and the left part of the $i$-th row, beginning both at the $i$-th position on the diagonal (see

Figure 12.16). The states of *M* are prefixes of all the pattern arrays. The set of states is organized in a tree whose nodes correspond to the two-dimensional prefixes of the patterns.

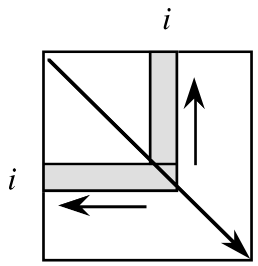

**Figure 12.16**. The *i*-th segment of a pattern array.

The edges outgoing a node at the depth *i*-1 are labeled by the names of the *i*-th segments of the patterns. We can give consistent names to *i*-th segments of all patterns in *O*(*k*log*k*) time for a given *i*, since there are at most *k* such segments, one for each pattern. The equality of two segments can be checked in constant time by an *LCPref* query (a longest common prefix query) after a suitable preprocessing of the tree whose edge labels are names of segments.

After that, the failure table *Bord* on the tree is built as in Section 7.1. The notion corresponds to borders of square arrays as illustrated in Figure 12.17. They are largest proper subarrays which are both prefix and suffix of the given array.

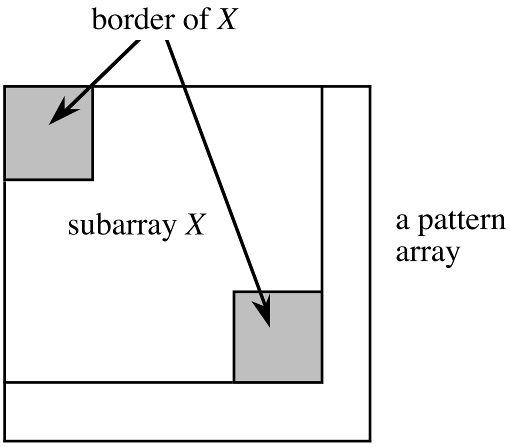

**Figure 12.17**. A border of a subarray *X* of a pattern.

We say that a segment π1 is a part of a segment π2 iff the column part of π1 is a prefix of the column part of π2 and a similar relation holds between rows of the segments. Define the following relation == between two segments. Let π1, π2 be *i*-th and *j*-th segments, respectively, with $i \le j$. Then, we write π1 == π2 iff either, both $i = j$ holds and the names of the segments are the same, or, π1 is a part of π2. The table *Bord* for the two-dimensional case is defined as for strings, except that relation == is considered instead of equality.

**Theorem 12.8**

Assume that the alphabet is fixed. Then the two-dimensional multi-pattern matching can be solved in time $O(N\log k)$ time, where $k$ is the number of patterns.

**Proof**

The two-dimensional pattern matching is essentially reduced to one-dimensional multi-pattern matching. The equality = of symbols is replaced by the relation ==, and the corresponding table *Bord* works similarly. ‡

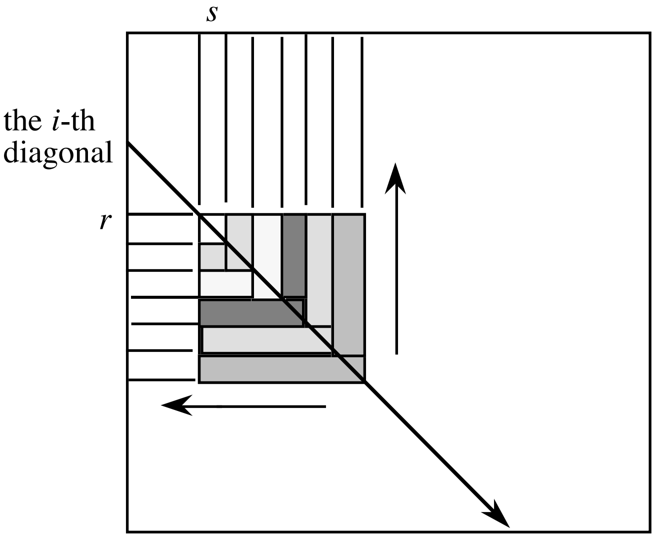

**Figure 12.18**. Checking occurrence of a pattern at position ($r$, $s$) in the text array.

## 12.6. Matching by sampling

The concept of *deterministic sample* introduced in Chapter 3 for one-dimensional patterns is very powerful. Its wide applicability appears, for instance, in the domain of parallel computations, leading to a constant-time parallel string-matching. The aim of this section is to extend and use the concept of deterministic sample to the two-dimensional case. Almost each non-periodic pattern has a deterministic sample whose properties are analogue to those for one-dimensional patterns. The use of 2D-sampling (for short) gives solutions both to sequential computation requiring only small extra space, and to constant-time parallel computation for the two-dimensional pattern matching problem.

A *deterministic sample* $S$ for $PAT$ is a set of positions in the pattern $PAT$ satisfying certain conditions. The sample $S$ occurs at position $x = (i, j)$ in the text array iff $PAT[y] = T[x+y]$ for each $y$ in $S$ (Figure 12.19).

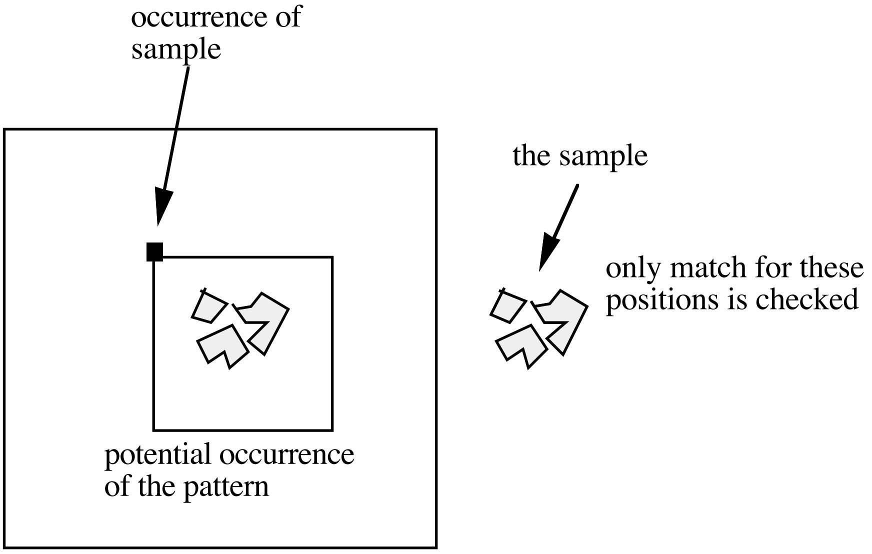
occurrence of sample
the sample
only match for these positions is checked
potential occurrence of the pattern

**Figure 12.19.** A deterministic sample *S*.

The central idea related to samples is the *field of fire* of the sample *S*. Finding an occurrence of the sample in the text assures us that there is an $m/2 \times m/2$ square in the text, called the field of fire of the occurrence of *S*, where there is only one possible matching position of the pattern. This possible matching position is $z = (k, l)$ relatively to the origin of the field of fire (see Figure 12.20). Let $x$ be a position of *S* in the text array. Denote by *fofire*($x$, *S*) the corresponding field of fire: it is the $m/2 \times m/2$ subsquare of the text array at position $x$-$z$. The field of fire should satisfy the following condition.

**Field of fire condition:**

whenever the sample *S* occurs at position $x$ in the text array, then there is no occurrence of the pattern inside the area *fofire*($x$, *S*) of the text array, except maybe at position $x$.

The size of a square *S*, denoted by $|S|$, is defined here as the length of its side. The deterministic sample *S* must be small, but effective in "killing" other positions. It must satisfy the following conditions:

(*) $|S| \leq O(\log m)$,

(**) $|fofire(x, S)| \geq m/4$.

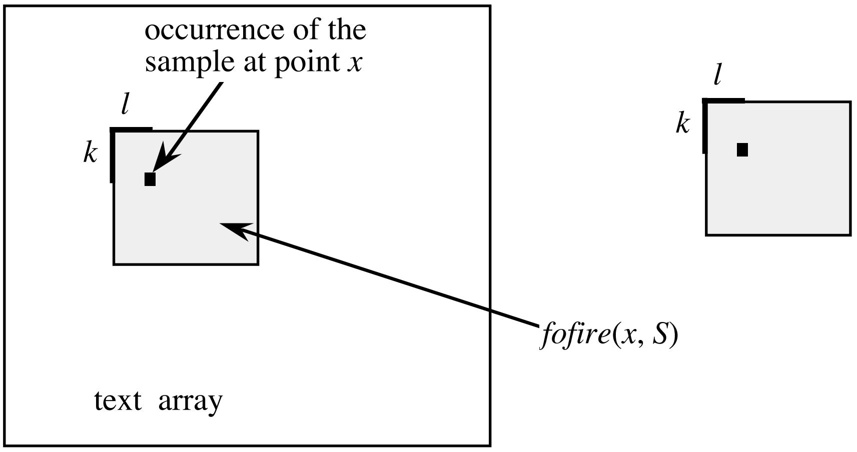

**Figure 12.20**. The field of fire of the sample $S$.

We consider only very particular samples. They are *special segments*: horizontal factor of length 4log$m$ at position ($m$/2, $m$/2) in the pattern. In other words, it is the factor of length 4log$m$ starting at position $m$/2+1 in the $m$/2+1 row of the pattern (see Figure 12.21). Moreover, we say that the pattern *PAT* is *good* if its special segment occurs only once in *PAT*. Note that any segment lying "far enough" from the boundaries of the array would work as well.

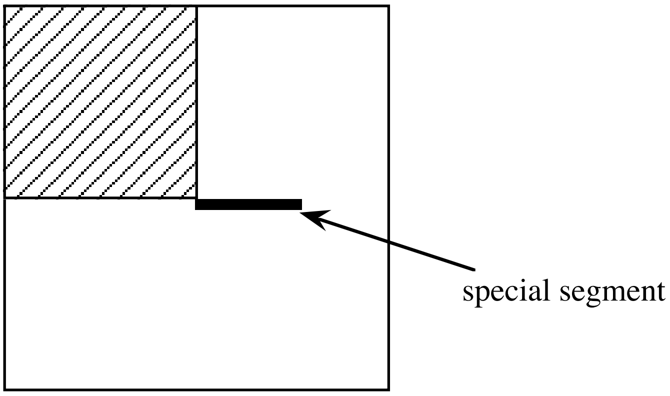

**Figure 12.21**. The special segment of *PAT*, and its field of fire.

**Theorem 12.9**

Assume that the alphabet contains at least two symbols. Then

— almost all patterns are good,

— for almost all patterns there is a logarithmic-size sample whose field of fire is an $m$/2×$m$/2 square,

— both, the sample can be found, and the goodness of the pattern can be checked either in constant extra space and linear serial time, or in constant parallel time with $O(m^2)$ processors.

**Proof**

The first point follows by simple calculations.

If the pattern is good the special segment is the sample. It is of logarithmic size. Its field of fire is the left upper $m/2 \times m/2$ quadrant of the pattern. If the sample occurs at position $x$ in the text array, then no occurrence of the pattern in the text has position $x+(k, l)$ for $0 \leq k \leq m/2$, $0 \leq l \leq m/2$, and $(k, l) \neq (0, 0)$, because then there would be two occurrences of the special segment in the pattern.

The last point follows from the fact that all occurrences of the special segment can be found within claimed complexities using algorithms for string-matching of Chapters 13 and 14.

This completes the sketch of the proof. ‡

**Theorem 12.10**

Assume that the alphabet contains at least two symbols. Then

— the two-dimensional pattern matching can be solved in constant extra space and linear serial time, for almost all patterns,

— the two-dimensional pattern matching can be solved in constant parallel time with $O(n^2)$ processors, for almost all patterns.

**Sketch of the proof**

Only good patterns are considered, so results hold only for them.

The whole text array is partitioned into $m/2 \times m/2$ windows. In each window, we search for occurrences of the special segment with a serial algorithm working with the claimed complexities. For each occurrence of the segment (sample) we check naively if it corresponds to an occurrence of the whole pattern. This is done for all windows independently, window after window.

The proof of the second point is analogue to the above argument. But now, all windows are processed simultaneously with a constant-time parallel string-matching algorithm. ‡

## 12.7. An algorithm fast on the average

A natural question related to pattern matching is to design algorithms that are fast in practice. Since the notion of "practice" is not formal, it is often considered algorithms that are fast on the average. In this section, we construct an algorithm making $O(N\log(M)/M)$ comparisons on the average for the two-dimensional pattern matching (the pattern is an $m \times m$ array, the text is an $n \times n$, $N = n^2$, and $M = m^2$). All symbols appear with the same probability independently of each others in arrays. If $M$ is of the same order as $N$, the algorithm makes only $O(\log N)$ comparisons on the average. The method described here is similar to the use of special segments in Section 12.6. We assume for simplicity that the alphabet has only two elements, and each of the two symbols of the text is chosen independently with the same probability. Let $r$ be equal to $4\log m$.

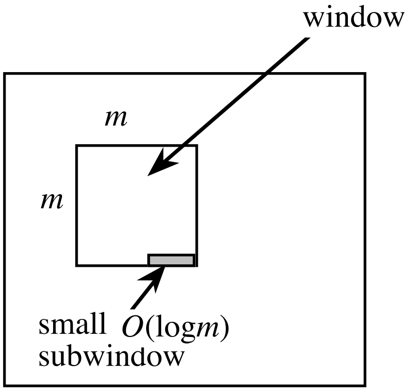

**Figure 12.22**. Searching the pattern starting in the window, first check the subwindow.

The algorithm is similar to the algorithm *fast_on_average* presented at the end of Chapter 4 as a variation of the Boyer-Moore algorithm for string-matching.

**Informal description of the algorithm**

— Partition the text array into windows of shape $m \times m$;

— the sub-window of a window consists of the last $r$ positions of the lowest row of the window;

— first check if the text contained in the sub-window is a factor of any row of the pattern;

— if so, the search for an occurrence of the pattern having its left upper corner position in the window is done by any linear time algorithm; the same procedure is applied to each window.

The suffix of length $r$ of the last row of the pattern behaves like a fingerprint. It has only logarithmic size, by definition. But it is unlikely to appear in sub-windows. The test at line 3 above can be done with the help of a suffix tree or a suffix dawg. On fixed alphabets, this takes $O(r)$ time. There are $N/M$ windows, and a simple calculation shows the following (see end of Chapter 4).

**Theorem 12.11**

The two-dimensional pattern matching can be done with $O(n^2\log(m)/m^2)$ comparisons on the average, for fixed alphabets, after preprocessing the pattern.

## 12.8. Finding regularities in parallel

We consider in this section three problems on arrays. These problems consist in finding a largest subarray which:

(1) repeats (occurs at least twice), or

(2) is a common subarray of two given arrays, or

(3) is symmetric.

The algorithmic solutions for these problems resemble the solutions for the corresponding one-dimensional problems.

Denote by $Cand1(s)$ (resp. $Cand2(s)$, $Cand3(s)$) a function whose value is any subarray of size $s$ which satisfies the condition (1) (resp. condition (2), condition (3)). If there is no such subarray then the value of the function is *nil*. The values of the function are *candidates* of size $s$. The problem is to find a non-*nil* candidate with maximum size $s$. More generally, we assume that we have a function $Cand(s)$ satisfying the following monotonicity property:

$$Cand(s+1) \neq nil \Rightarrow Cand(s) \neq nil.$$

Denote by *Maxcand* a candidate of maximal size,

$$Maxcand = \{Cand(s) : s \text{ is maximum such that } Cand(s) \neq nil\}.$$

Assume also that $Cand(0)$ is some special value.

**Lemma 12.12**

If the value $Cand(s)$ can be computed in $T(n)$ parallel time with $P(n)$ processors, then, the value of *Maxcand* can be computed in $O(T(n)\log n)$ time with the same number of processors.

**Proof**

We can assume w. l. o. g. that $n$ is a power of two, and that $Cand(n) = nil$. A variant of binary search can be applied. We look at $Cand(n/2)$. If it is *nil* then we try $Cand(n/4)$, otherwise we look at $Cand(n/2+n/4)$, and so on. In this way, after a logarithmic number of steps we get *Maxcand*. This completes the proof. ‡

The algorithm of Chapter 9 related to the computation of the dictionary of basic factors for strings has a natural counterpart for arrays. The naming technique applies as well. This is because an array of size $2k$ is composed of four (fixed finite number) subarrays of size $k$. Recall that a basic subarray has shape $k\times k$ with $k$ a power of two. Each such subarray is given a name (or a number) through $NUM_k$.

Assume that the dictionary of basic subarrays is computed for the input array. Testing the equality of two subarrays whose size is a power of two reduces to a mere comparison of their associated names. If the size of subarrays is not a power of two we can also test their equality in constant time. For that purpose, we define identifiers for subarrays whose size $s$ is not a power of two. Let $k$ be the highest power of 2 less than $s$. The identifier of the $s \times s$ subarray at position $v1$ is $Ident(v1, s) = (NUM_k(v1), NUM_k(v2), NUM_k(v3), NUM_k(v4))$, where position $v2$, $v3$, and $v4$ are as in Figure 12.23. It is clear that, if the dictionary of basic subarrays is computed, the equality of two subarrays is equivalent to the equality of their identifiers, and can be checked in constant time. The key point is that identifiers are of constant size.

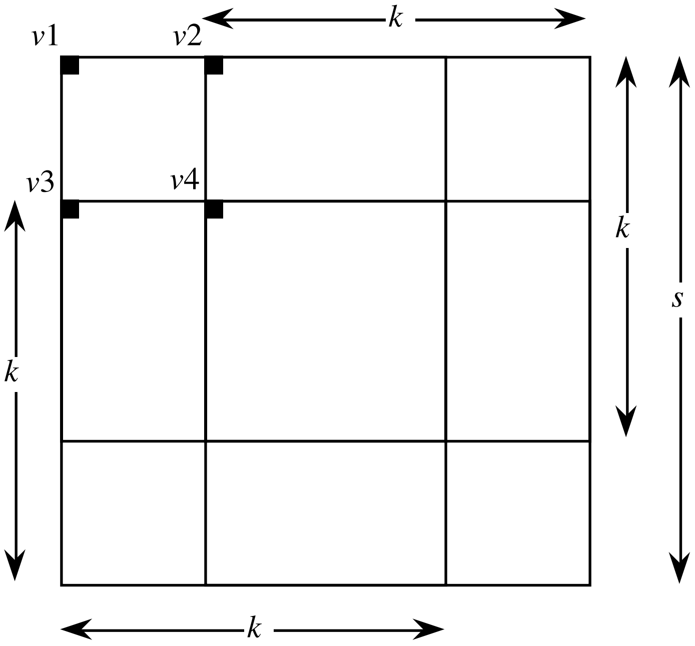

**Figure 12.23**. Identifier of a subarray of size $s$:
$Ident(v1, s) = (NUM_k(v1), NUM_k(v2), NUM_k(v3), NUM_k(v4))$
where $k$ is the highest power of 2 less than $s$.

Identifiers of subarrays can be used to search for subarrays. This gives a straightforward parallel solution to the two-dimensional pattern matching problem. The algorithm is simple but not optimal. A parallel optimal solution is presented in Chapter 14.

**Theorem 12.13**

The two-dimensional pattern matching problem can be solved with $n^2$ processors in $O(\log^2 n)$ parallel time on the exclusive-write PRAM model, and in $O(\log n)$ parallel time on the concurrent-write PRAM model.

**Proof**

Let $PAT$ be the $m \times m$ pattern array, let $T$ be the $n \times n$ text array. We create the dictionary of basic factors common to $PAT$ and $T$. The identifier $ID$ of the pattern is computed. Then we search in parallel for a subarray $P'$ of $T$ (of same size as $PAT$) whose identifier equals $ID$. The search phase takes constant time, and the computation of the dictionary relies on algorithms of Chapter 9. This completes the proof. ‡

Observe that none of the linear time sequential algorithms for two-dimensional pattern matching (Section 12.1) is easily parallelizable. We now come to the problems of the present section. We apply Lemma 12.12 successively to functions *Cand*1, *Cand*2, and *Cand*3. The complexities of algorithms for these three problems are analogue to the complexity of the pattern matching algorithm of Theorem 12.13.

**Theorem 12.14**

The largest repeated subarray of an $n \times n$ array can be computed with $n^2$ processors in $O(\log^2 n)$ parallel time on the exclusive-write PRAM model, and in $O(\log n)$ parallel time on the concurrent-write PRAM model.

**Proof**

In view of Lemma 12.12, it is enough to show how to compute *Cand*1($s$) with $n^2$ processors in $O(\log n)$ time on the exclusive-write PRAM model, and in $O(1)$ time on the concurrent-write PRAM model.

Given identifiers of all subarrays, for each position $x$ on the text array, it is an easy matter to compute in $O(\log n)$ time two positions with the same identifier. We can sort pairs (*Ident*($x$, $s$), $x$) lexicographically. Any two such consecutive pairs with the same identifier part in the sorted sequence give required positions. The model is the exclusive-write PRAM.

With concurrent writes we can use an auxiliary *bulletin board* table, and proceed similarly as in the proof of Lemma 9.4. No initialization of the bulletin board is required, and this gives $O(1)$ time. This completes the proof. ‡

**Theorem 12.15**

The largest common subarray of two $n \times n$ arrays can be computed with $n^2$ processors in $O(\log^2 n)$ parallel time on the exclusive-write PRAM model, and in $O(\log n)$ parallel time on the concurrent-write PRAM model.

**Proof**

In this case we compute, at the beginning, the common dictionary for both text arrays $S$, $T$. The rest of the proof is essentially the same as the proof of Theorem 12.14. There are small technical differences. We sort pairs (*Ident*($x$, $s$), $x$) lexicographically. Now $x$'s are positions in $S$ and $T$. We can partition the sorted sequence into segments consisting of pairs having the same first component (identifier). In these segments it is now easy to look for two positions $x$, $y$ such that $x$ is a position in $S$ and $y$ is a position in $T$. This completes the proof. ‡

**Theorem 12.16**

The largest symmetric subarray of an $n \times n$ array can be computed with $n^2$ processors in $O(\log^2 n)$ parallel time on the exclusive-write PRAM model, and in $O(\log n)$ parallel time on the concurrent-write PRAM model.

**Proof**

Let $X$ be an $n \times n$ array. In view of Lemma 12.12, it is enough to compute *Cand*3(s) with $n^2$ processors in $O(\log n)$ time on the exclusive-write PRAM model, and in $O(1)$ time on the concurrent-write PRAM model.

Let us compute the array $T$ which results by reflecting each entry of $X$ with respect to the center of the array. Denote by *Reflect*($x$, $s$) the position in $T$ of the $s \times s$ subarray $B$, reflection of the subarray $A$ occurring at position $x$ in $X$ (see Figure 12.24). Now we can compute the common dictionary of basic subarrays of arrays $X$ and $T$. The subarray $A$ of $X$ is symmetric iff $A = B$, which can be checked in constant time using $s$-identifiers at position $(i, j)$ in $X$, and at position *Reflect*(($i$, $j$), $s$) in $T$. The function *Reflect* is easily computable in constant time. Once we know which $s \times s$ subarrays are symmetric we can easily choose one of them (if there is any) as the value of *Cand*3($s$). Hence, *Cand*3($s$) can be computed within the required complexity bounds. This completes the proof. ‡

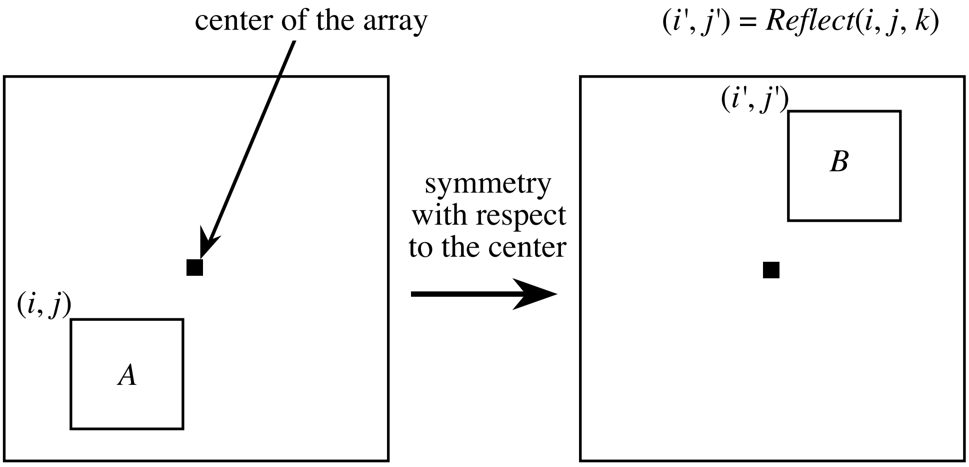
center of the array
$(i', j') = Reflect(i, j, k)$
$(i', j')$
B
symmetry with respect to the center
$(i, j)$
A

**Figure 12.24**. The $s \times s$ subarray A is symmetric iff $A = B$ iff $Ident((i, j), s) = Ident((i', j'), s)$.

## 12.9. Simple geometry of 2-dimensional periodicities.

This section prepares some theoretical tools for the Galil-Park 2d-pattern matching algorithm of Section 12.11. The proofs of several simple facts are omitted, they are left as exercises.

Let *PAT* be a two-dimensional pattern of shape $m \times m$, with its rows and columns numbered by 1, 2, ..., $m$. The vectors of *PAT* are denoted by $\pi$ and $\beta$. We consider only two-dimensional vectors with integer components. Recall that a vector $\pi$ is a *period* of *PAT* iff *PAT*[$x$] = *PAT*[$x+\pi$], whenever both sides are defined. If both sides are defined for at least one point $x$, then $\pi$ is a non-trivial period. We also write that $\pi$ is a 1d-period to emphasize its 1-dimensional status. The main difference between 1d-dimensional and 2d-dimensional pattern matching lies in different structures of periods of patterns. In two dimensions, some periods are inherently two-dimensional and are called 2d-periods.

A pair $\mu = (\pi, \beta)$ of non-colinear vectors is a *2d-period* of *PAT* iff $\pi$ and $\beta$ are non-trivial periods, and each linear combination of $\pi$ and $\beta$ is a 1d-period of *PAT*. An equivalent formulation is: *PAT* can be extended to an infinite plane in which $\pi$ and $\beta$ are periods. By a linear combination we always mean a combination with integer coefficients, i.e. a vector $i.\pi+j.\beta$, where $i, j$ are integers. Two (or more) vectors are said to be colinear iff they are in the same direction, which does not necessarily mean in this case that one is an integer combination of other (others). Let us denote by *Lattice(*$\mu$) the set of all linear combinations of $\pi$, $\beta$. The elements of *Lattice(*$\mu$) are called the lattice points. So, the pair $\mu$ is a 2d-period iff all elements of *Lattice(*$\mu$), as vectors, are periods.

A vector $\pi = (r, c)$ is said to be *small* iff its components $r$, $c$ satisfy $|r|, |c| < d.m$, where $d = 1/16$. A 2D-period is *small* iff its both components are small vectors. The pattern *PAT* is called *periodic* (*lattice-periodic or 2d-periodic* ) iff it has any *small* 1d-period (2d-period).

**Remark.** In one-dimensional string-matching a linear combination of *small* 1d-periods is always a period. But this is not generally valid in two dimensions, even for non-negative combinations of colinear vectors (as well as for non-colinear vectors, of course). If all elements of the array *PAT* are the same letter except for a small number of elements closed to one fixed corner, then there is a great number of 1d-periods, but there is no non-trivial 2d-period. The parts around the corners are responsible for irregularities.

The 2d-period $\mu = (\pi, \beta)$, is said to be *normal* iff $\pi$ is a quad-I period and $\beta$ is a quad-II period.

**Lemma 12.17 (Normalizing lemma)**

If the pattern has a small 2d-period then it has a small *normal* 2d-period.

A notion of divisibility for two 2d-periods $\mu1$, $\mu2$ is introduced as follows:

$\mu_1 \mid \mu2$ iff *Lattice*($\mu_1$) includes *Lattice*($\mu_2$).

We introduce also the notion of a *smallest* 2d-period $\mu$ = *period*(*PAT*). It is a fixed small 2d-period of *PAT* that "divides" each other small 2d-period: in other words $\mu \mid \mu'$ for each small 2d-period $\mu'$. There are several ways to precise which $\mu$ is to be chosen, but any of them is good. Assume *PAT* is 2d-periodic. We define *period*(*PAT*) as a small *normal* 2d-period ($\pi$,

$\beta$), where $\pi$ is a quad-I small period of a minimal length (in case of ties the most horizontal vector is chosen), and $\beta$ is a quad-II small period of a minimal length (in case of ties the most vertical vector is chosen). Lemma 12.17 guarantees that the definition makes sense. It can be proved that any small 1-d period corresponds to a point in *Lattice*(*PAT*). This fact toghether with Lemma 12.17 implies the following lemma.

**Lemma 12.18 (2d-periodicity lemma)**

**(a)** Assume $\mu1$, $\mu2$ are small 2d-periods of *PAT*. Then, there is a 2d-period $\mu$ such that $\mu \mid \mu1$ and $\mu \mid \mu2$.

**(b)** Assume *PAT* is lattice-periodic and $\pi$ is a small vector. Then $\pi$ is a 1d-period of *PAT* iff $\pi$ is in *Lattice*(*period*(*PAT*)). Moreover, *period(PAT)* $\mid \mu$ for all small 2d-periods $\mu$ .

**Observation.** Assume we know which points of *PAT* are small sources (see below). Then, *period(PAT)* can be computed in $O(M)$ time independently of the alphabet, if it exists.

**Lemma 12.19 (overlap lemma)**

Assume the patterns $PAT_1$ and $PAT_2$ are 2d-periodic subsquares of the same rectangle, $period(PAT_1) = \mu1$, and $period(PAT_2) = \mu2$, where $|\mu1|$ , $|\mu2| < m'/2 \leq m$. If $PAT_1$ and $PAT_2$ overlap on an $m'\times m'$ square, then $\mu1 = \mu2$.

According to their periodicities, 2d-patterns are classified into four main categories:
— *non-periodic* : no small period at all,
— *lattice-periodic* (or *2d-periodic*): at least one small 2d-period,
— *radiant-periodic* : at least two non-colinear small 1d-periods, but not lattice-periodic,
— *line-periodic*: all periods in the same direction.

We have already defined quad-I periods and quad-II periods. We recall these definitions and introduce similar categories for so-called *sources*. The pattern is divided into four $m/2\times m/2$ disjoint squares, called *quads*, and named quad I, quad II, quad III, and quad IV, according to the anticlockwise ordering, and starting with the upper left corner. So quad I corresponds to upper left square corner, and quad II corresponds to lower left square corner.

For technical reasons it is convenient that these categories are disjoint. So we assume that horizontal vectors are not quad-II vectors, and vertical vectors are not quad-I vectors. In this way, each 1d-period oriented from left to right is exactly of one type: a quad-I period or a quad-II period.

Let $Center_s(PAT) = PAT'$ be the central subarray of *PAT* which results after "peeling off" the $s$ boundary columns and rows (from top, down, right and left). The shape of such subarray is $(m\text{-}2s)\times(m\text{-}2s)$. Below we state the key lemma used to avoid the radiant-periodic case in the main algorithm. Its proof is omitted.

**Lemma 12.20 (Radiant-periodicity Lemma)**

Assume that *PAT* is radiant periodic. Then $Center_{2d.m}$(*PAT*) is not radiant-periodic.

A vector π can be identified a the point $\underline{\pi}$ of *PAT*, extremity of π when its origin is at the quad-I top left corner (point (0, 0)) or at the quad-II corner (point (*m*, 0)) of the pattern. The point $\underline{\pi}$ is called the quad-I beginning point, or the quad-II beginning point respectively, corresponding to π. If π is a period and the quad-I beginning point $\underline{\pi}$ is in *PAT* then π is called a quad-I period, and $\underline{\pi}$ is called a quad-I *source*. Quad-II periods and sources are defined analogously. Using the terminology of sources, the periodicity type of pattern *PAT* can be characterized (equivalently) as follows:

— *non-periodic* : no small source;
— *lattice-periodic* or (*2d-periodic*): at least one quad-I source and one quad-II source;
— *radiant-periodic* : not lattice-periodic and at least two non-colinear small sources;
— *line-periodic*: all sources on the same line.

Let μ = (π, β) be a 2d-vector. We say that two points *x*, *y* are μ-equivalent iff *x*-*y* is in *Lattice(*μ). A μ-path is a path consisting of edges that are vectors π, -π, β or -β. The processing of certain difficult patterns is done by exploring some simple geometry of paths on a lattice generated by two vectors π, β belonging to the same quadrant. If we have two points *x*, *y* containing distinct symbols and we have a (π, β)-path from *x*, to *y* inside the pattern, then, one of the edges of the path gives a witness of non-periodicity to one of vectors π or β. This is due to the fact that the initial and terminating positions do not match, so there should be a mismatch “on the way” from *x* to *y*. The length of the path is the number of edges it contains.

**Observation**. The basic difficulty with such approach is the length of the path. It can happen that μ is a small 2D-period, but the length of a shortest μ-path between two μ-connected points of an *m*×*m* square is quadratic. Consider, for instance, μ = ((*m*/2, 1), (1, 0)), *x* = (*m*/2, 0), and *y* = (*m*/2, *m*-1).

Despite the above observation in some situations we can find useful short paths, as shown in the next lemma. Let $Cut\_Corners_S$(A) be the part of array *A* without top-right and bottom-left corner squares of shape *s*×*s*.

**Lemma 12.21 (Linear-path Lemma)**

Assume π, β are quad-I vectors of size at most *k*. Let *S* be a subsquare of size *k*×*k* of a larger square *A*, and let *x* be the point which is the bottom-left corner or top-right corner of *S*. Assume *x* is inside $Cut\_Corners_{2k}$(*A*). Then, there is a *linear-length* μ-path inside *A* from *x* to a point *y* ≠ *x* in *S*. Such a path can be computed in *O*(*k*) time.

**Proof**

We can assume, without loss of generality that $x$ is the quad-II corner of $S$, and that $\pi$, $\beta$ are quad-I vectors of size at most $k$. Moreover, we can assume that the array $A$ is of shape $3k\times3k$, and $S$ is the square of size $k\times k$ at the top-left corner of $A$. Then, $x$ is the point of $A$ at position $(k, 0)$. Assume that $\beta$ is more a horizontal vector than $\pi$. We find a path and a point $y$ by the algorithm GREEDY below.

We prove that the algorithm GREEDY terminates successfully after a linear number of iterations and generates the required path. Consider the lines $L_0$, $L_1$, $L_2$, ..., where $L_h$ is the line parallel to $\pi$ and containing the points $x+h\beta$. So, points $x+i\beta+j\pi$ ($j$ integer) belong to the line $L_i$. If some line $L_i$ cuts the two horizontal borders of $S$, or its two vertical borders, then the segment of the line that is inside $S$ is longer than $\pi$. Thus, $x+i\beta+j\pi$ belongs to $S$ for some (negative) integer $j$. If each line $L_i$ cuts both an horizontal border of $S$ and a vertical border of it then let $i$ be such that lines $L_i$ and $L_{i+1}$ surround the diagonal segment of $S$; then it can be proved that, either there is a point $x+i\beta+j\pi$ in $S$ or a point $x+(i+1)\beta+j'\pi$ in $S$. Values of variable $y$ in the algorithm are points of a $\mu$-path inside $A$ because if "$y$-$\pi$ not in $A$", $y+\beta$ is in $A$. It remains to explain why the path has linear length, which at the same time proves that the algorithm works in $O(k)$ time. Let $\pi = (r, c)$ and $\beta = (r', c')$. The point $x+r\beta-r'\pi$ is on the same column as $x$, and can be the point $y$ if it is in $S$. It is clear that the $\mu$-path followed by the algorithm is entirely (except maybe the last edge) inside the triangle $(x, x+r\beta, x+r\beta-r'\pi)$. Thus, the length of the $\mu$-path followed by the algorithm is no longer than $r+r'$ which is $O(k)$. ‡

```
algorithm GREEDY
begin
    $y := x$;
    repeat
        if $y - \pi$ is outside the area $A$ then $y := y + \beta$
        else $y := y - \pi$;
    until $y$ is in $S$;
end.
```

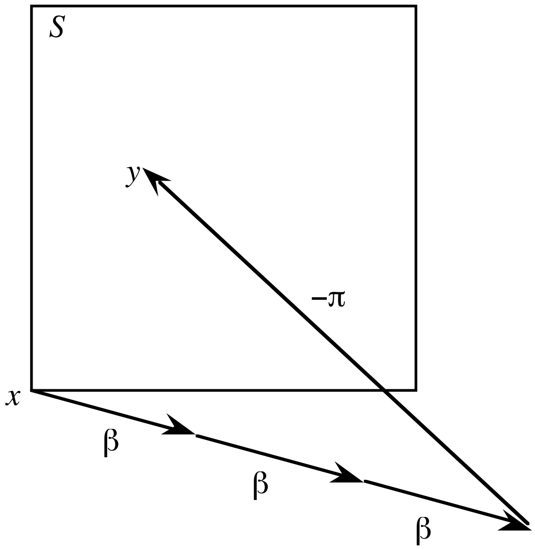

**Figure 12.25**. A short path from a given point $x$ to some other point $y$ of the square $S$.

We introduce a special type of duels called here *long-duels*. Assume we have small quad-I vectors π, β, and a point $x$ at distance at least $2k$ from quad-II and quad-IV corners. Assume also that if $y$ is any point such that $y$-$x$ is a small quad-II vector, then $PAT[x] \neq PAT[y]$. The procedure *long_duel*(π, β, $x$) "kills" one of the vectors π, β, and finds its witness. It works as follows: a (π, β)-path from a given point $x$ to some point $y$ in the pattern is found by the algorithm of the Linear-path Lemma. The path consists of a linear number of edges. Endpoints $x$ and $y$ contain distinct symbols. So one of the edges on the path gives a witness for π or β. Doing so, one of the potential small periods π or β is "eliminated" in linear time.

**Theorem 12.22 (Long-duel Theorem)**

Assume we have a set $X$ of small quad-I vectors, where $|X| = O(m)$, and we are given a position $x$ in $Cut\_Corners_{2d.m}(PAT)$. Assume also that if $y$ is any point such that $y$-$x$ is a small quad-II vector, then $PAT[x] \neq PAT[y]$. Then, we can find in linear time, using long duels, witnesses for all small quad-I vectors except maybe for a set of vectors on a same line $L$.

**Proof**

We run the following statement:

```
while X is non-empty do begin
  take any element β from X; add β to Y, and delete β from X;
  while there are two non-colinear vectors π, β in Y do
    execute long-duel(π, β, x) and delete the "looser" from Y;
end;
```

We keep in the set $Y$ the elements of $X$ that have not been eliminated so far. Initially $Y$ is empty. The invariant of the loop is: non-null witnesses for all elements not in the current sets $X$ or $Y$ are computed, and all elements of $Y$ are on the same line $L$. Altogether, the execution time is $O(m^2)$ and alphabet independent. All remaining vectors (with non-null witnesses up to now) are, at the end, on a same line $L$. This completes the proof. ‡

Let us call the algorithm of the Long-duel Theorem the *long-duel algorithm*. There is a natural analogue of the theorem for quad-II small vectors, and for quad-I, quad-III corners.

The crucial point in the processing of a difficult type of patterns (*corner* patterns) is the role played by the following suffix-testing problem: given $m$ strings $x_1$, ..., $x_m$ of total size $O(m^2)$, compute the $m \times m$ table *Suf-Test* defined as follows:

$Suf\text{-}Test[i, j] = nil$ if the $i$-th string is a suffix of the $j$-th string,

$Suf\text{-}Test[i, j]$ = position of the rightmost mismatch otherwise.

The algorithm is given below as Algorithm *Suffix-Testing*. We sketch its rough structure to show that it runs in linear-time independently of the alphabet. It is enough to compute for each pair $i, j$, the length $SUF[i, j]$ of the longest common suffix of $x_i$ and $x_j$.

The algorithm can be easily implemented to work in $O(m^2)$ time. The main point in the evaluation of the time complexity is that if a position takes part in a positive comparison (when two symbols match), then, this position is never inspected again. When we process a given $k$ and compute $SUF[k, j]$ for $j > k$, then we look first for $SUF[i, j]$, where $i = MAX[j, k\text{-}1]$, and then for $SUF[i, k]$. These data are available at this moment, due to invariant. The word $x_j$ is scanned backwards starting from position $SUF[i, j]$. The pointers go only backwards. This proves the next theorem.

```
Algorithm Suffix-Testing;
begin
  assume that strings $x_1$, …, $x_m$ are in increasing order of
  their lengths;
  { invariant($k$): for all $i$, $j$, $1 \le i \le k$, $1 \le j \le m$,
    $SUF[i, j]$ is computed, and, for each $j$, $1 \le j \le m$,
    we know $MAX[j, k] = i$, where $i$ is the index $i \le k$ which
    maximizes $SUF[i, j]$}
  make invariant(1);
  for $k$ = 2 to $m$ do
    make invariant($k$) using invariant($k$-1);
end.
```

**Theorem 12.23 (Suffix-testing Theorem)**

The suffix-testing problem for $m$ strings of total size $O(m^2)$ can be solved in $O(m^2)$ time, independently of the alphabet.

## 12.10.* Patterns with large monochromatic centers

The alphabet-independent linear-time computation of 2d-witness tables is quite technical, hence the present and next sections may be considered as optional. In this section, we present an alphabet-independent linear-time computation of witnesses for special patterns whose "large" central part is "monochromatic". The pattern *PAT* is called *mono-central* iff all symbols lying in $Center_k$ are equal to the same letter $a$ of the alphabet, and for $k < 3/8m$. Then, the central subarray of *PAT* of size at least $m/4 \times m/4$ is *monochromatic*. A position containing a letter different from letter $a$ is called a *defect*. Assume the existence of at least one defect (otherwise the preprocessing is trivial). Opposite corners of *PAT* are the corners lying on the same forward or backward diagonal of *PAT* (quad-I and quad-III, or quad-II and quad-IV corners). A *mono-central* pattern *PAT* is called *corner* if there is a pair of opposite corners $x$, $y$ of *PAT* such that each defect can be reached by at most two small vectors from $x$ or $y$. The *corner* patterns are the hardest with respect to their witness computation, and this is because they can be radiant-periodic. The non-corner patterns are simpler to deal with, due to the following observation.

**Observation**

If *PAT* is a periodic *non-corner mono-central* pattern, then *PAT* is non-periodic or line-periodic (so, *PAT* is *not* radiant-periodic).

The applicability of the *long-duel* algorithm follows from the next lemma.

**Lemma 12.24 (Subsquare Lemma)**

Let us assume that *PAT* is mono-central, and that there is a defect inside the area $A$ = $Cut\_corners_{2k}(PAT)$. Then there is a defect position $x$ inside $A$ satisfying one of the following conditions:

**(1)** $x$ is a quad-I or quad-III corner of a $k{\times}k$ subsquare $S$ containing no defect position strictly inside $S$;

**(2)** $x$ is a quad-II or quad-IV corner of a $k{\times}k$ subsquare $S$ containing no defect position at all, except $x$.

**Proof**

Take a defect point in $A$ closest to the center of *PAT*. ‡

**Theorem 12.25 (Non-corner Theorem)**

The witness table for all small vectors of a mono-central non-corner pattern *PAT* can be computed in $O(m^2)$ time.

**Proof**

Consider the defect $z$ closest to the center of *PAT*. Assume without loss of generality that $z$ is in quadrant II. The position $z$ is the witness (of non-periodicity) for all small quad-II vectors, except maybe vertical vectors. The case of vertical and horizontal periodicities is very easy to process, so, we assume that all witnesses for vertical and horizontal vectors are computed and *PAT* is not vertically nor horizontally periodic. The set of potential small quad-I periods is sparsified using vertical duels in columns. Afterwards, in quadrant I we have only a linear number of candidates for small periods. Denote by $X$ the set of these candidates. To compute witnesses for quad-I small vectors it is enough to find a point $x$ satisfying the assumptions of the Long-duel Theorem. Take the defect $x$ implied by the Subsquare Lemma. If condition (1) of this lemma holds, then $x$ is itself the witness for all quad-I vectors which are not vertical nor horizontal vectors. Otherwise, $x$ is “good” to apply the *long-duel* Theorem. The case of horizontally or vertically periodic pattern can be easily processed. This completes the proof. ‡

**Theorem 12.26 (Corner Theorem)**

Consider an $m{\times}m$ array *PAT* that is a mono-central corner pattern. Then, witnesses for all vectors of size at most $m/8$ can be computed in $O(m^2)$ time.

**Proof**

Assume that opposite corners from the definition of corner patterns are quad-II and quad-IV corners. So, all defects are closed to quad-II and quad-IV corners. These corners are separated by a large area of non-defects. So, we can compute periods and witnesses with respect to each corner separately. Hence, without loss of generality, we can assume that all defects are close to the quad-II corner, and, in particular, that there is no defect that contains the same symbol *a* in quadrants I, III and IV. Assume *PAT* contains at least one defect in quadrant II. *PAT* has obviously no small quad-II periods, since the rightmost defect gives witnesses against all quad-II vectors. We show how to compute witnesses for small quad-I vectors.

Let *PAT*1 be the following transformation of the pattern. Replace in each row all symbols by *a*, except the rightmost non-*a* symbol of each row. Replace these rightmost non-*a* symbols by a special symbol $. Let *X* be the set of positions containing the symbol $; call them *special* positions.

For *x* in *X* denote by *string*(*x*) the word in *PAT* consisting of the part of the row containing *x* from the left side up to *x* (including *x*). Let π be a vector of size at most *m*/4. Then, it is easy to see the following:

π is not a period iff

**(1)** π is not a period in *PAT*1, or

**(2)** for two positions *x*, *y* in X we have *y*-*x* = π and *string*(*x*) is not a suffix of *string*(*y*) (then, a witness for π is given by a mismatch between *string*(*x*) and *string*(*y*)).

The computation of all witnesses for vectors of size at most *k* in *PAT*1 is rather easy. Only quad-I vectors are to be processed. Assume there is no small vertical period. Then, the set of potential small quad-I periods is sparsified using duels in columns. Afterwards a linear number of candidates remain. Each of them is checked against all (linear number) symbols at special positions in a naive way. The witnesses arising from condition (2) are computed using directly the *Suffix-testing* Algorithm. This completes the proof. ‡

We extend the definition of *defects*. Assume a mono-central pattern *PAT* has a lattice-periodic central subarray *C* of size at least *m*/4. We say that *x* is a *lattice-defect* iff *x* does not agree with (contains a symbol different from) any point *y* in *C* that is lattice-equivalent to *x*. Let *Mono*(*PAT*) be the pattern in which all positions which are not *lattice-defects* are replaced by the same special symbol. We omit the proof of the following simple lemma.

**Lemma 12.27** (**Mono Lemma**)

If a small vector π is in the lattice generated by the smallest period of *C*, then, π is a period of *PAT* iff π is a period of *Mono*(*PAT*).

## 12.11.* A version of the Galil-Park algorithm

Recall that the periodicity type of a subarray depends on its size. When we say that the witnesses for a given array or subarray are computed we mean the witnesses, if there are any, for all vectors small according to the size of the presently considered array.

**Lemma 12.28 (Line Lemma)**

Assume we have a set $S$ of points in a fixed quadrant of $PAT$, such that all of them are on the same line $L$. Then, we can check which of them correspond to periods and compute witnesses, wherever they are, in $O(m^2)$ time independently of the alphabet.

**Proof**

The proof reduces to the computation of witness tables for $m$ one-dimensional strings of size $2m$ each. Let $L_i$ be all lines parallel to $L$; take $m$ pairs of lines $(L_i, K_i)$, where $K_i$ is parallel to $L_i$ and the distance between $K_i$ and $L_i$ equals the distance between the point (0, 0) and $L$. Each line is taken as a string of symbols. For each $i$, lines $L_i$ and $K_i$ are concatenated, and witnesses for these strings are computed by a one-dimensional classical algorithm. ‡

Assume $C$ is a central subarray of shape $s{\times}s$, where $s \leq m$. Denote $Large\_Extend(C) = D$, where $D$ is a central subarray of shape $2s{\times}2s$. If ever $2s > m$, we define $Large\_Extend(C) = PAT$. Observe that a small period with respect to $Large\_Extend(C)$, in case $Large\_Extend(C) \neq PAT$, means a vector of size at most $2d.s$ ($d = 1/16$, see Section 12.9). $Large\_Extend(C)$ is twice larger than $C$ except maybe at the last iteration of the algorithm. The reason for such irregularity is that while making duels for small vectors in $D$ we use mismatches in $C$ and we should guarantee that $D$ is enough large with respect to $C$ and that vectors (taking part in a duel) starting in $C$ do not go outside the pattern $PAT$. Define also $Small\_Extend(C)$ as a central subarray of shape $3/2s{\times}3/2s$.

Due to Lemma 12.20, if $Large\_Extend(C) \neq PAT$ and if it is radiant-periodic then $Small\_Extend(C)$ is not radiant periodic. This saves one case (radiant-periodic) in the algorithm: $C$ is never radiant-periodic.

Before each iteration in GP algorithm the witnesses and periods are already known for a central subarray $C$ whose shape is $s{\times}s$. The witnesses for a larger central subarray $D$ are computed, where $D = Large\_Extend(C)$, or $D = Small\_Extend(C)$ in the case $Large\_Extend(C)$ is radiant-periodic and $Large\_Extend(C) \neq PAT$. In the latter case, $D$ is of shape $3/2s{\times}3/2s$, and Lemma 12.20 guarantees that $D$ is not radiant-periodic. Then $C$ is set to $D$ and the next iteration starts.

```
Algorithm GP;{ modified Galil-Park algorithm; computes witnesses for all small vectors
}
begin
  C := an initial constant-sized non radiant-periodic central
      subarray of PAT;
  compute the witness table of C in O(1) time;
  D := Large_Extend(C);
  while $C \neq PAT$ do begin {main iteration, C has $s \times s$ shape}
    if C is non-periodic then begin
      the witness table of C is used to make duels between
      candidates for small periods in D;
      after duelling, only a constant number of candidates
      remains;
      the witnesses for them are computed in a naive way;
    end else if C is line-periodic then begin
      consider the areas Q1, Q2 of candidates of small
      (with respect to D) periods in respectively quad I and
      quad II of D; divide each area into $d.s \times d.s$ subsquares;
      in each smaller subsquare do begin
        make duels between candidates using witnesses from C;
        only candidates on the same line survive,
        apply the algorithm from the Line Lemma;
      end;
    end else {C is lattice-periodic} begin
      let $\mu$ = period(C);
      for each small candidate period $\pi \notin Lattice(\mu)$ do
        {use Lemma 1}
        find a $\mu$-equivalent point y in C in quad I or quad II,
        then the witness corresponding to y gives easily a
        witness for x;
      for each small candidate period $\pi \in Lattice(\mu)$ do
        compute witness of $\pi$ in Mono(PAT); {Mono Lemma}
        {use algorithms from Non-corner or Corner Theorems}
    end;
    if $D \neq PAT$ and D is radiant-periodic then
      D := Small_Extend(C)
    else begin C := D; D := Large_Extend(C) end;
  end; {main iteration}
```

```
end.
```

Three disjoint cases are considered in the algorithm depending on whether $C$ is non-periodic, lattice-periodic, or line-periodic. The first case (non-periodic) is very simple. At each iteration we spend $O(r^2)$, where $r$ is the size of the actual array $D$; this size grows at least by a factor 3/2 at each iteration. Altogether, the time is linear with respect to the total size of the pattern, as the sum of a geometric progression.

When the witness table is eventually computed, the Amir-Benson-Farach searching phase of Section 12.2 can be applied. Altoghether we have proved the following result.

**Theorem 12.29**

There is a 2d-pattern matching algorithm whose time complexity is linear and independent of the alphabet (including the preprocessing).

## Bibliographic notes

The simple linear time (on fixed alphabets) two-dimensional pattern matching algorithm of Section 12.1 has been found independently by Bird [Bi 77] and Baker [Ba 78].

The linear-time searching algorithm of Section 12.2 is from Amir, Benson, and Farach [ABF 92]. It is quite surprising that this is the first alphabet-independent linear-time algorithm, because in the case of strings the first algorithm satisfying the same requirements is the algorithm of Morris and Pratt [MP 70]. The gap is more than twenty years! Furthermore, the preprocessing phase of the algorithm in [ABF 92] is not alphabet-independent. Galil and Park have recently designed a global alphabet-independent linear-time algorithm for two-dimensional pattern matching [GP 92b]. The question of periodicity of two-dimensional patterns is discussed in several papers, especially in [AB 92], [GP 92], and [RR 93].

The algorithm to search for non-rectangular patterns is from Amir and Farach [AF 91].

The powerful concept of deterministic sample was introduced by Vishkin in [Vi 91] for strings. The wide applicability of this concept was recently shown by Galil [Ga 92] who designed a constant parallel time string-matching (with linear number of processors). The sampling method of Section 12.6 is from Crochemore, Gasieniec, and Rytter [CGR 92].

The algorithm "fast on the average" is a simple application of a similar algorithm described in Chapter 4. The idea comes from [KMP 77].

Almost optimal parallel algorithms of Section 12.8 are from Crochemore and Rytter [CR 91c].

A notion of suffix tree on arrays is discussed by Giancarlo in [Gi 93]. Arrays are transformed into linear structures as in Section 12.5. The tree used in this section is essentially the suffix tree of Chapter 5.

The basic source for the classification of 2-dimensional periodicities (Section 12.9) is the article of Amir and Benson [AB92]. The rest of the chapter is an adaptation of the result of Galil and Park in [GP 92b].

## Selected references

[AB 92] A. AMIR, G. BENSON, Two-dimensional periodicity and its application, in: (*Proc. Symp. On Discrete Algorithms*, 1992) 440-452.

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[Ba 78] T.P. BAKER, A technique for extending rapid exact-match string-matching to arrays of more than one dimension, *SIAM J.Comput.* 7 (1978) 533-541.

[Bi 77] R.S. BIRD, Two-dimensional pattern-matching, *Inf. Process. Lett.* 6 (1977) 168-170.

[CC 93] R. COLE, M. CROCHEMORE, Z. GALIL, L. GASIENIEC, R. HARIHARAN, S. MUTHUKRISHNAN, K. PARK, W. RYTTER, Optimally fast parallel algorithms for preprocessing and pattern matching in one and two dimensions, in: (*FOCS'93*, 1993).

[GP 92b] Z. GALIL, K. PARK, Truly alphabet-independent two-dimensional matching, in: (*Proc. 33rd Annual IEEE Symposium on the Foundations of Computer Science*, 1992) 247-256.

# 13. Time-space optimal string-matching

In the chapter, we discuss the optimality of the string-matching problem according to both time and space complexities.

String-matching algorithms of Chapter 3 make a heavy use of the failure function *Bord*. This function gives the lengths of borders of pattern prefixes. This is equivalent to memorizing all the periods of pattern prefixes. A more useful information to deal with shifts in KMP algorithm would be the periods of words *ua*, for all prefixes *u* of *pat* and all possible letters of the alphabet *A* of the searched text. Indeed, this is realized by the minimal deterministic automaton recognizing the set of words ending with the pattern *pat*: the SMA automaton of Chapter 7. But the memory space needed to implement the automaton, in a straightforward way, is $O(|A|.|pat|)$, quantity which depends on the size of the alphabet. This chapter presents three different solutions to string-matching that all lead to algorithms running in linear time and using simultaneously only bounded space in addition to the text and the pattern. These algorithms are thus time-space optimal.

The first two presented solutions to time-space optimal string-matching are GS and CP algorithms. These algorithms, called *factorized string-matching*, may be considered as intermediate between KMP and BM algorithms. Like them, they run in linear time (including the preprocessing phase), but require only a bounded memory space compared to space linear in the size of the pattern for KMP and BM. The general scheme, common to GS and CP algorithms, is given in the next section.

The last section presents another more recent solution to optimal string-matching. The algorithm uses a left-to-right scan of the pattern, as KMP does. It is based on a memoryless lazy computation of periods. The great theoretical interest in scanning the pattern from left to right is that the algorithm naturally finds all "overhanging" occurrences of the pattern in the text. And this yields a time-space optimal algorithm to compute the periods of a word.

## 13.1. Prelude to factorized string-matching

CP and GS algorithms have a common feature. Scans depend on a factorization *uv* of the pattern *pat*. The scan for a position of the window is conceptually divided into two successive phases. The first phase (right scan) consists in matching *v* only against *text*. The letters of *v* are scanned from left to right. When a mismatch is found during the first phase (right mismatch), there is no second phase and the pattern is shifted to the right. Otherwise, if no mismatch happens during the first phase, that is, when an occurrence of *v* is found in *text*, the second phase starts (left scan). The left part *u* of the pattern is matched against the text. The word *u* can be scanned from right to left as in the Boyer and Moore approach, but the direction of this scan is not important. If a mismatch occurs at the second phase (left mismatch), the pattern is shifted to the right according to a rule different from the rule used in the case of right mismatch. After a shift the same process repeats until an occurrence of *pat* is eventually found, or the end of *text* is reached.

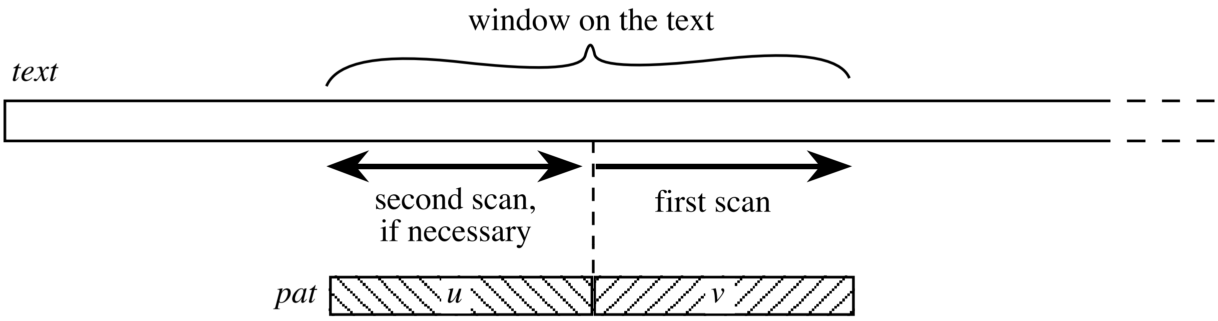


**Figure 13.1**. Scheme for factorized string-matching.

An important property of GS and CP algorithms is that shifts they perform are computable in constant time and constant space. The scheme for factorized string-matching is shown below.

```
Algorithm time-space-optimal-string-matching(text, pat);
{ n = |text|; m = |pat|; }
begin
  (u, v) := factorize(pat);
  pos := 0;  i := |u|;
  while pos ≤ n-m do begin
    { right scan }
    while i < m and pat[i+1] = text[pos+i+1] do i := i+1;
    if i=m then begin
      { left scan }
      if text[pos+1, …, pos+|u|] = u then return true;
    end;
    (pos, i) := shift(pos, i);
  end;
  return false;
end.
```

The preprocessing of the pattern consists in splitting it into two parts *u* and *v* (*pat* = *uv*). GS and CP algorithms greatly differ in the way they decompose the pattern, and also in the way they shift the pattern. We explain informally what are the main features of these algorithms.

The decomposition of the pattern used in GS algorithm is called a *perfect factorization*. It gives a position inside the pattern from which at most one highly periodic factor starts (to the right). For the shifts, the algorithm distinguishes between two cases according to whether a highly periodic prefix of the right part of the factorization is found or not in the text.

CP algorithm uses a decomposition of the pattern called a *critical factorization*. This factorization gives a position inside the pattern where the local period coincides with the global period of the pattern. The rule for shifts takes into account the period of the entire pattern, which is a great advantage from the point of view of practical time complexity.

The precise description of these algorithms is given in following sections. However, the next lines summarize the rules applied by the algorithms to shift the pattern along the text.

**Shift in GS:**

*shift*(*pos*, *i*) = **if** $v[1\ldots i\text{-}|u|]$ not highly periodic **then** $(pos+(i\text{-}|u|)/3+1), |u|)$
**else** $(pos+p, i\text{-}p)$, where $p$ is the unique small period of prefixes of $v$.

**Shift in CP:**

*shift*(*pos*, *i*) = **if** $i<m$ **then** $(pos+i\text{-}|u|, |u|)$ **else** $(pos+p, \max(|u|, i\text{-}p))$,
where $p$ is *period*(*pat*), the smallest period of the pattern.

The main conclusion of the present chapter is summarized in the next statement.

**Theorem 13.1**

The string-matching problem can be solved in $O(|text|+|pat|)$ time using constant space in addition to the pattern and the text. The constants involved in '$O$' notation are independent of the size of the alphabet.

## 13.2. GS algorithm : search phase

This section is devoted only to the search phase of first time-space optimal string-matching algorithm of the chapter, GS algorithm. The preprocessing phase is treated in the next section.

GS algorithm can be regarded as a space efficient implementation of KMP algorithm (Chapter 3). Its space efficiency is based on properties of repeated factors inside the pattern *pat*. While CP algorithm deals with squares (repetitions) from their center, GS algorithm treats repetitions (of higher order) from their left end. In the context of KMP algorithm, the idea to save on space is to avoid storing all the periods of prefixes of the pattern. Only small periods are memorized, where "small" is relative to the length of the prefix. Approximations of other periods are computed when needed during the search phase.

In this section we consider an integer $k > 1$. It is a parameter of the method we are discussing, and typically we shall consider $k = 3$. Let $x$ be a non-empty word. A primitive word $w$ is called a *k-highly repeating prefix* of $x$ (a *k-hrp* of $x$, in short) if $w^k$ is a prefix of $x$. Recall that a word $w$ is said to be *primitive* if it is not a (proper) power of another word. Primitive words are non empty, so are $k$-hrp's.

**Example**

Consider the word *abaababaabab*. It has two 2-hrp's, namely *aba* and *abaab*. The periods of its prefixes are shown in the next array.

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | *a* | *b* | *a* | *a* | *b* | *a* | *b* | *a* | *a* | *b* | *a* | *b* |
| Prefix lengths : | 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
| Periods : | - | 1 | 2 | 2 | 3 | 3 | 3 | 5 | 5 | 5 | 5 | 5 | 5 |
| Exponents : | - | 1 | 1 | 1.5 | 1.3 | 1.7 | 2 | 1.4 | 1.6 | 1.8 | 2 | 2.2 | 2.4 |

Only 4 prefixes have an exponent greater than or equal to 2. The shortest of them, *abaaba*, is the square of the first 2-hrp. The three other prefixes are "under the influence" of the second 2-hrp *abaab*. ‡

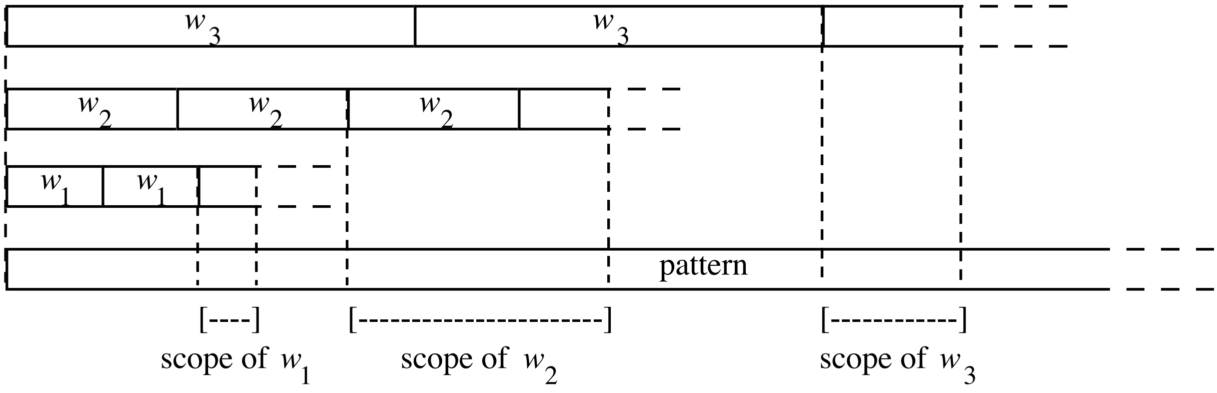


**Figure 13.2**. Scopes of three highly repeating prefixes ($w_1$, $w_2$, $w_3$).

When $w$ is a $k$-hrp of $x$, $period(w^2) = |w|$. Thus, we can consider the longest prefix $z$ of $x$ that has period $|w|$. We define *the scope of w* as the interval of integers $[|w^2|, |z|]$. Note that, by definition, any prefix of $x$ whose length falls inside the scope of $w$ has period $|w|$. Some shorter prefixes may also have the same period, but we do not deal with them. Figure 13.2 shows the structure of scopes of $k$-hrp's of a word $x$. It happens that scopes are disjoint (see proof of Lemma 13.3.

**Example** (continued)

Inside the word *abaababaabab*, the scope of *aba* is [6, 6], and the scope of *abaab* is [10, 12]. ‡

We first present a simple string-matching algorithm based on the notion of scopes of *k*-hrp's. The algorithm is a version of KMP algorithm. During a run of the algorithm, lengths of shifts are computed with the help of scopes of *k*-hrp's. We assume that these intervals have been computed previously.

```
Algorithm Simple-Search;
{ An O(r)-space version of KMP, where r is the number     }
{ of k-highly repeating prefixes of pat and               }
{ ([$L_j$, $R_j$] / j=1,…,r) is their sequence of scopes        }
begin
  pos := 0;  i := 0;
  while pos ≤ n-m do begin
    while i < m and pat[i+1] = text[pos+i+1] do i := i+1;
    if i = m then report match at position pos;
    if i belongs to some [$L_j$, $R_j$] then begin
      pos := pos+$L_j$/2;  i := i-$L_j$/2;
    end else begin
      pos := pos+$\lfloor i/k \rfloor$+1;  i := 0;
    end;
  end;
end.
```

Inside algorithm *Simple-Search*, the test "*i* belongs to some [$L_j$, $R_j$]" can be implemented in a straightforward way so that it needs $O(1)$ space, and that its time does not affect the asymptotic time complexity of the whole algorithm.

**Lemma 13.2**

If the pattern *pat* has *r* *k*-hrp's, algorithm *Simple-Search* runs in time $O(|text|)$ using $O(r)$ space. It makes less than $k.|text|$ symbol comparisons.

**Proof**

To evaluate the time performance of the algorithm it can be shown that the value of expression $k.pos+i$ is strictly increased after each symbol comparison. ‡

The correctness of algorithm *Simple-Search* is a direct consequence of the following lemma. It essentially gives a lower bound on periods of prefixes whose length does not belong to any scope of a highly repeating prefix.

**Lemma 13.3**

Let $([L_j, R_j] \,/\, j=1,\ldots,r)$ be the sequence of scopes of all $k$-hrp's of a word $x$. Then any non-empty prefix $u$ of $x$ satisfies :

— $period(u) = L_j/2$ if $|u| \in [L_j,R_j]$ for some $j$,

— $period(u) > |u|/k$ otherwise.

**Proof**

We first prove that two different scopes $[L_1, R_1]$ and $[L_2, R_2]$ are disjoint. Let $w_1$ and $w_2$ be their corresponding $k$-hrp's, and assume that, for instance, $|w_1| < |w_2|$. We show that $R_1 < L_2$. Let $z$ be the prefix of length $R_1$ of $x$. If $L_2 \leq R_1$, the square $w_2{}^2$ is a prefix of $z$. Therefore the periodicity lemma applies to periods $|w_1|$ and $|w_2|$ of $w_2{}^2$. It implies that $\gcd(|w_1|, |w_2|)$ is a period of this prefix. But, since $|w_1| < |w_2|$, $\gcd(|w_1|, |w_2|) < |w_2|$, and we get a contradiction with the primitivity of $w_2$.

Let $u$ be a non-empty prefix of $x$. If $|u|$ does not belong to any scope of $k$-highly repeating prefix, then obviously $period(u) > |u|/k$.

Assume that $|u|$ belongs to some $[L_j,R_j]$. It is then a prefix of some power $w_j{}^e$ $(e \geq k > 1)$ of the $k$-highly repeating prefix $w_j$. The quantity $|w_j| = \mathrm{L}_j/2$ is a period of $u$. Moreover, it is the smallest period of $u$, because otherwise $|u|$ would belong to another scope, a contradiction. Then $period(u) = L_j/2$. ‡

The preprocessing phase required by algorithm *Simple-Search* is presented below. Its correctness is left to the reader. It is an adaptation of algorithm *Simple-Search*, and it works as if the pattern is being searched for inside itself. It also runs in linear time.

Algorithms *Simple-Search* and *Scopes* require $O(r)$ extra space to work. This space is used to store the $r$ scopes of $k$-hrp's of the pattern *pat*. A simple application of the periodicity lemma shows that, for $k \geq 3$, any word $x$ has no more than $\log_{k\text{-}1}|x|$ $k$-hrp's. This relies on the following fact : if $u$ and $v$ are two $k$-hrp's of $x$ and $|u| < |v|$, then the even stronger inequality holds: $(k\text{-}1)|u| < |v|$. For $k = 2$, the same kind of logarithmic bound also holds (see next examples). So, algorithms *Simple-Search* and *Scopes* together solve the string-matching problem in linear time with logarithmic extra space.

```
Algorithm Scopes
{ Compute the list of scopes of all k-hrp's of pat }
begin
  SCOPE := empty list;
  pos := 1; i := 0;
  while pos+i < m do begin
    while pos+i < m and pat[i+1] = pat[pos+i+1] do i := i+1;
    if pos ≤ (pos+i)/k then add [2*pos, pos+i] to end of SCOPE;
    if i belongs to some [L_j, R_j] in SCOPE then begin
      pos := pos+L_j/2; i := i-L_j/2;
    end else begin
      pos := pos+⌊i/k⌋+1; i := 0;
    end;
  end;
  return the list SCOPE;
end.
```

**Example**

Let $k = 2$, and consider the Fibonacci word $Fib_9$ displayed in Figure 13.3 (recall that the sequence of Fibonacci words is defined by $Fib_1 = b$, $Fib_2 = a$, and $Fib_i = Fib_{i-1}Fib_{i-2}$ for $i > 2$). Figure 13.3 shows the scopes of its 2-hrp's. It can be proved that the number of 2-hrp's of a Fibonacci word $F$ is $\Theta(\log|F|)$ (see next example). ‡

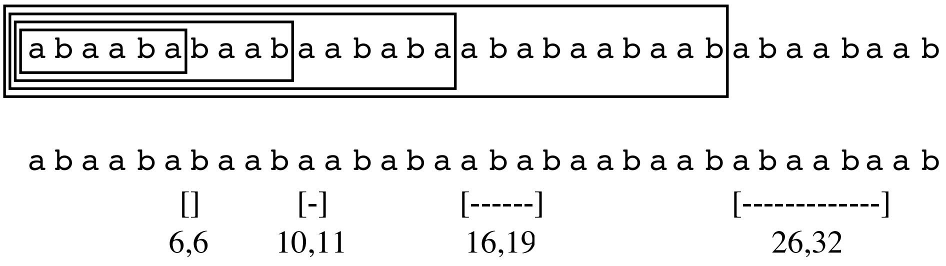

a b a a b a b a a b a a b a b a a b a b a a b a a b a b a a b a a b
a b a a b a b a a b a a b a b a a b a b a a b a a b a b a a b a a b
[]
[-]
[------]
[-------------]
6,6
10,11
16,19
26,32

**Figure 13.3**. Four scopes in a Fibonacci word.
Fibonacci words have a logarithmic number of 2-hrp's.

**Example**

We give words having the maximum number of square prefixes (indeed, maximum number of 2-hrp's). They are the squares of words $h_i$, $i \geq 1$, defined inductively by

$$h_1 = a,\ h_2 = aab,\ h_3 = aabaaba, \text{ and}$$
$$h_i = h_{i-1}\, h_{i-2}, \text{ for } i > 3.$$

For instance, $h_5^2$ = *aabaabaaabaabaaba.aabaabaaabaabaaba*. Its square prefixes are $h_1^2$, $h_2^2$, $h_3^2$, $h_4^2$, and $h_5^2$ itself. In other terms, its 2-hrp's are $h_1$, $h_2$, $h_3$, $h_4$, and $h_5$. Note that $h_5^2$ has the same length as the Fibonacci word $Fib_9$ (see previous example). But, this latter word has only four 2-hrp's.
It can be proved that words shorter than $h_i^2$ start with less than $i$ squares (of primitive words), or, equivalently, with less than $i$ 2-hrp's. Moreover, for all $i \geq 4$, word $h_i$ is the unique word starting with $i$ 2-hrp's. ‡

We are now ready to present GS algorithm. Let $k = 3$. The idea is to scan the pattern from a position where at most one $k$-hrp starts. Fortunately, such a position always exists because words satisfy a remarkable combinatorial property stated in the next theorem and proved in Section 13.3.

**Theorem** (*perfect factorization theorem*)

Any non-empty word $x$ can be factorized into $uv$ such that

— $|u| < 2.period(v)$, and

— $v$ has at most one 3-hrp.

The example of pattern *aaa…a* shows that we cannot require that the right part $v$ of the factorization has no 3-hrp. A factorization $uv$ of $x$ that satisfies the conclusion of the theorem is called a *perfect factorization*. After a preprocessing phase aimed at computing a perfect factorization, GS algorithm presented below follows the scheme introduced in Section 13.1, and uses the algorithm *Simple-Search*.

```
Algorithm GS; { informal description }
{ search for pat in text }
begin
  (u, v) := perfect factorization of pat;
  find all occurrences of v in text with Simple-Search;
  for each position q of an occurrence of v in text do
    if u ends at q then report the match at position q-|u|;
end.
```

The following theorem shows that GS algorithm is time-space optimal.

**Theorem 13.4**

GS algorithm computes all positions of occurrences of *pat* inside *text*.

The algorithm runs in time $O(|pat|+|text|)$, and uses a bounded memory space.

The number of letter comparisons made during the search phase is less than $5|text|$.

**Proof**

The correctness mainly comes from that of algorithm *Simple-Search*.

We assume that the first statement of GS algorithm runs in time $O(|pat|)$. This assumption is satisfied by the preprocessing algorithm of Section 13.3.

By Lemma 13.2 the search for *v* in *text* uses at most $3.|text|$ symbol comparisons. The distance between two consecutive occurrences of *v* in *text* is not less than *period*(*v*). Thus, the condition $|u| < 2.period(v)$ implies that a given letter of *text* is matched against a letter of *u* (during the test "*u* ends at *q* ?") at most twice, which globally gives at most $2.|text|$ more symbol comparisons. ‡

## 13.3. Preprocessing the pattern : perfect factorization

This section is devoted to the preprocessing phase of GS algorithm presented in the previous section. The preprocessing consists in computing a perfect factorization of the pattern. The method relies on a constructive proof of the perfect factorization theorem. We first prove that such a factorization exits, and then, we analyze the complexity of the factorization algorithm. The parameter *k* of Section 13.2 is set to 3 all along the present section. So, the hrp's (highly repeating prefixes) that are considered should be understood as 3-hrp's, but all the results are also valid for *k*-hrp's with $k > 3$. We are thus interested in cubes occurring in the pattern. If the pattern is cube-free, no preprocessing for GS algorithm is even needed.

In the following, we denote by hrp1($x$) and hrp2($x$) respectively, the shortest and the second shortest hrp of a given non-empty word $x$, when they are defined.

The structure of the factorization algorithm is based on a sequence $W(x)$ of hrp1's. The elements of the sequence $W(x) = (w_1, w_2,\ldots, w_r)$ are called *the working factors of x*, and are defined as follows. The first element $w_1$ is hrp1($x$) if $x$ starts with a cube, and is $x$ itself otherwise. Let $x = w_1x'$, and assume that $x'$ is a non-empty word. Then $w_2$ is defined in the same manner on $x'$, and so on, until there is no hrp. The last element of the sequence is a suffix of $x$ that does not start with a cube. In particular, the sequence is reduced to $x$ itself if it does not start with a cube.

We shall see that there is a perfect factorization $uv$ of $x$ of the form $u = w_1w_2\ldots w_j$, $v = w_{j+1}\ldots w_r$. So, a natural procedure to factorize $x$ would be to compute the positions of working factors, and test, at each position, whether there are two hrp's starting there. The procedure would stop as soon as at most one hrp is found starting at the current position. Unfortunately, this could cost a quadratic number of comparisons. In order to keep the time complexity linear, the test is done only at some specific positions, called *testing points*. The first testing point on $x$ is the position 0. When $x$ has no second hrp, there is no more testing point, and the factor $u$ of the perfect factorization of $x$ is empty. Assume now that $x$ has a second hrp, $z$ = hrp2($x$). Then, the second testing point is the last position of a working factor inside $z$. In other terms, the second testing point is $|w_1w_2...w_j|$, where $j$ is the largest integer such that $|w_1w_2...w_j| < |z|$. The rest of the sequence of testing point is defined in the same way on the rest of the word $x$ (i.e. on $w_{j+1}...w_r$).

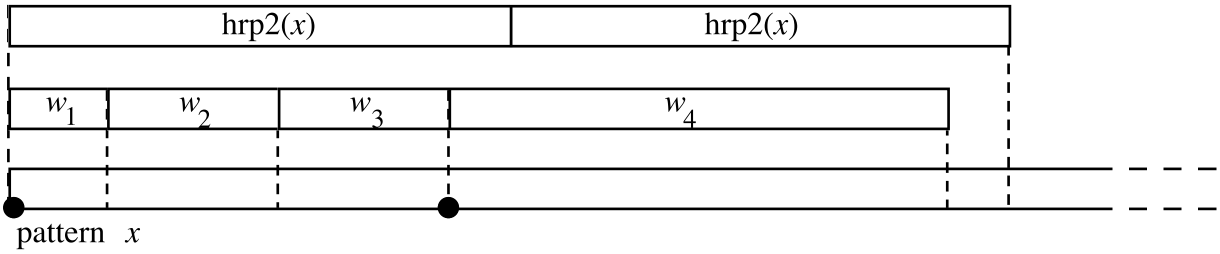


**Figure 13.4**. The first two testing points ●.
The working factor *w4* as the same length as hrp2($x$).

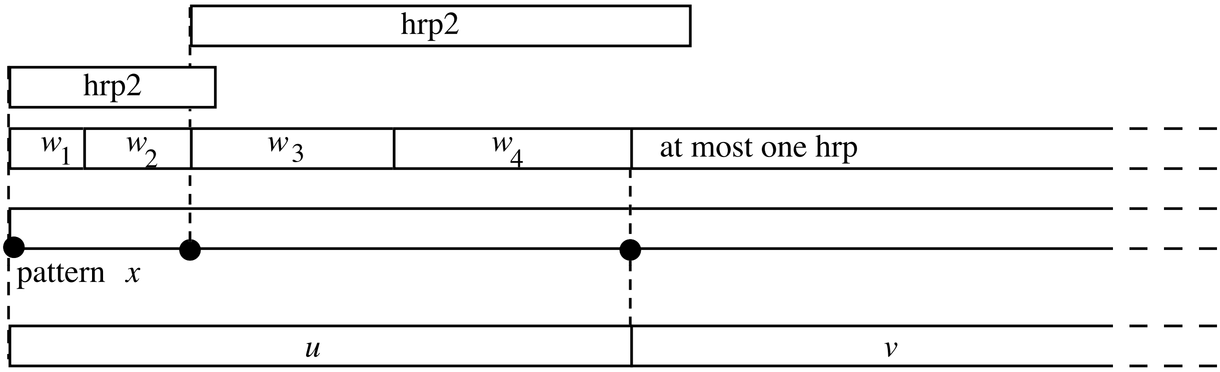


**Figure 13.5**. The sequence of working factors $w_1$, $w_2$,... leads to testing points ●, and eventually to a perfect factorization $uv$ of $x$.

The preprocessing phase of GS algorithm, which reduces to the computation of a perfect factorization of the pattern, is shown below. It computes the sequence of positions $i$ of working factors from left to right, and checks at each testing point whether a second hrp (or cube) starts.

```
Algorithm Perfect_fact;
{ preprocessing pat for GS algorithm;  m = |pat|  }
{ computes a perfect factorization of pattern pat }
begin
  i := 0;  h1 := |hrp1(pat)|;  h2 := |hrp2(pat)|;
  while h1 and h2 exist do begin
    i := i+h1;  h1 := |hrp1(pat[i+1…m])|;
    if h1 ≥ h2 then h2 := |hrp2(pat[i+1…m])|;
  end;
  return factorization (pat[1…i], pat[i+1…m]) of pat;
end.
```

**Theorem 13.5**

Algorithm *Perfect_fact* computes a perfect factorization of the pattern *pat*. It runs in time $O(|pat|)$ and requires constant extra space.

**Proof**

The proof strongly relies on Lemma 13.6 below.

**Correctness**. A straightforward verification shows that variable *i* runs through the positions of working factors of *pat*, $w_1, w_2,\ldots, w_r$. At the end of the execution of the algorithm, the value of *i* is the last testing point on *pat*, $|w_1w_2\ldots w_{r-1}|$. The output is the factorization *uv* defined by $u = w_1w_2\ldots w_{r-1}$ and $v = w_r$. By construction, *v* starts with at most one hrp. Thus, it remains to prove that the condition on lengths is also satisfied, $|pat[1\ldots i]| < 2.period(pat[i+1\ldots|pat|])$, or, equivalently, to prove the inequality $|w_1w_2\ldots w_{r-1}| < 2.period(w_r)$.

The property is obviously true if the sequence $(w_1, w_2,\ldots, w_r)$ is reduced to *pat* itself, because in this situation *u* is the empty word. Thus, we assume $r > 1$, which implies that the sequence of hrp2's computed by the algorithm is not empty. Let it be $(z_1, z_2,\ldots, z_t)$ (note that $0 < t < r$). We certainly have $|u| < |z_1|+|z_2|+\ldots+|z_t|$. We also have $|z_t| \leq period(v)$ because the contrary would contradict part (c) of Lemma 13.6. Furthermore, by part (d) of Lemma 13.6, we get $|z_j| < |z_t|/2^{t-j}$. The conclusion comes :

$$|u| < |z_1|+|z_2|+\ldots+|z_t| < 2.|z_t| \leq 2.period(v),$$

This ends the proof of correctness of the algorithm.

**Complexity**. First note that algorithm *Scopes* of Section 13.2 can be used to compute hrp1's (resp. hrp2's). The trick is simply to stop the execution of the algorithm the first time it discovers the first hrp (resp. the second hrp). Doing so, the computation of hrp1(*y*) for a given a word *y*, takes time $O(|\text{hrp1}(y)|)$ if hrp1(*y*) exists, and $O(|y|)$ otherwise. The same is true for hrp2's. The extra space needed to compute these values is constant because the list *SCOPE* used in algorithm *Scopes* contains at most one element. Thus, the global algorithm also needs only constant extra space.

The time complexity of the algorithm may be analyzed as follows. The total cost of computation of hrp1's, by the above argument, is proportional to the total length of working factors (including the last one that may have no hrp), which is exactly $|pat|$. The same argument also shows that the total cost of computation of hrp2's is proportional to their total length, plus the length of $v$ (last test): $|z_1|+|z_2|+\ldots+|z_t|+|v|$. We have already seen above that $|z_1|+|z_2|+\ldots+|z_t| < 2.|z_t|$, and, since $2.|z_t| < |pat|$ (indeed $3.|z_t| \leq |pat|$), the previous sum is less than $2.|pat|$.
The time complexity of the algorithm is thus linear as expected. ‡

The following lemma may be regarded as a constructive version of the perfect factorization theorem. Part (d), which roughly says that each hrp2 is at least twice longer than the preceding one, is the key point used both in the correctness and in the time analysis of algorithm *Perfect_fact* (proof of Theorem 13.5).

**Lemma 13.6**

Let $W(x) = (w_1, w_2,\ldots, w_r)$ be the sequence of working factors for $x$.

(a) — If $j < k$, then $w_j$ is a prefix of $w_k$; lengths of $w_i$'s are in non decreasing order.

Assume that both hrp2($x$) exists, and $x$ has a second testing point $i = |w_1w_2\ldots w_j|$.

(b) — hrp2($x$) is at least twice longer than $w_1$, $|\text{hrp2}(x)| > 2.|w_1|$.

(c) — If $j < r$, the next working factor is not shorter than hrp2($x$), $|w_{j+1}| \geq |\text{hrp2}(x)|$.

(d) — If hrp2($x[i+1\ldots|x|]$) exists, it is at least twice longer than hrp2($x$).

**Proof**

Parts (a) and (b) are mere applications of the periodicity lemma (see Chapter 2). Part (d) is a consequence of (b) and (c) together. So, it only remains to prove part (c).

Let $h$ be hrp2($x$). We want to show that $w_{j+1}$ cannot be shorter than $h$. The assumptions imply that $w_{j+1}$ overlaps the boundary between the first two occurrences of $h$, as shown in Figures 13.6 and 13.7. Assume that $|w_{j+1}| < |h|$ holds. Let $y$ and $y'$ be the non-empty words defined by the equalities $h = w_1w_2\ldots \mathrm{w}_jy'$, and $w_{j+1} = y'y$. Because we assume that $w_{j+1}$ is shorter than $h$, $y$ is a prefix of $h$, so that we can consider the word $z$ defined by $h = yz$. We now focus our attention on the occurrence of the word $g = zy$, rotation of $h$, occurring at position $|y|$ in $x$.

**Case 1** (Figure 13.6). We first consider the situation when the beginning of $g$ inside $h$ falls properly inside some $w_k$. Integer $k$ is less that $j$+1 because $|w_{j+1}| < |g|$. Since $h = \text{hrp2}(x)$, $h^3$ is a prefix of $x$. Therefore, another occurrence of $g$ follows immediately the occurrence we consider. Because $w_{j+1}$ is an hrp1, $w_{j+1}$ is a prefix of $g$. Part (a) implies that $w_k$ is a prefix of both $w_{k+1}$ and $w_{j+1}$, and then is also a prefix of $g$. This eventually implies that $w_k$ is an internal factor of $w_kw_k$, a contradiction with the primitivity of $w_k$ (consequence of the weak periodicity lemma).

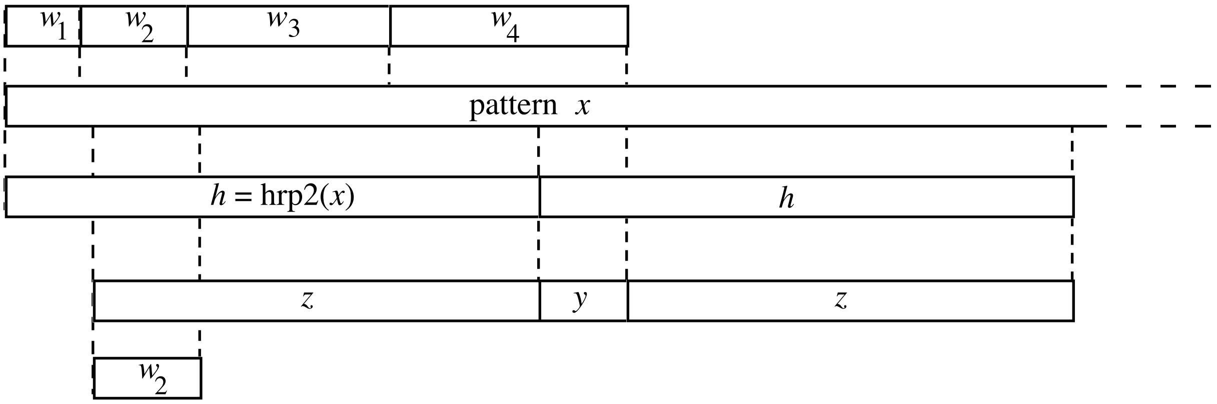


**Figure 13.6**. Proving (c), i.e. on the figure $|w_4| \geq |h|$.
Case 1: impossible because *w2* is primitive.

**Case 2** ( Figure 13.7). The second situation is when $g$ (= $zy$) = $w_k...w_jw_{j+1}$. Again, hypothesis $|w_{j+1}| < |h|$ leads to $k < j+1$. This implies $2|w_k| \leq |h|$, and then, the word $w_k$ is an hrp of $zyz$. Thus, just after the occurrence of $g$ that is considered, $w_k$ is still an hrp1. This proves, through part (a), that $w_{j+1} = w_k$. But then, $g$ is a non-trivial power of $w_k$, and its rotation $h$ = hrp2($x$) is not primitive, a contradiction.
This completes the proof of Lemma 3.14. ‡

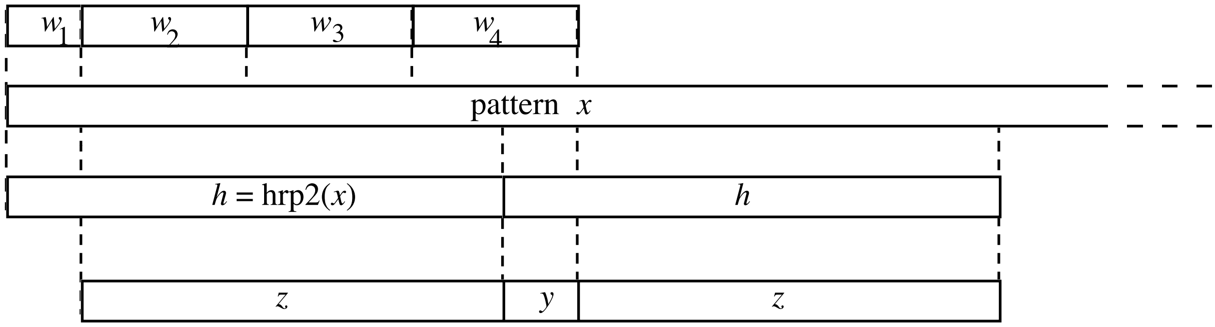


**Figure 13.7**. Proving (c), i.e. on the figure $|w_4| \geq |h|$.
Case 2: $|w_2| = |w_3| = |w_4|$, impossible because $h$ = hrp2($x$) is primitive.

## Note

We can also consider perfect factorizations with the parameter $k$ = 2. But then, not all words have a perfect factorization. A counterexample is given by the word $x = (aabaabab)^4$. The longest suffix of $x$ having only one 2-hrp (or one square prefix) is $v$ = *baababaabaabab* of period 8. The corresponding prefix $u = (aabaabab)^2aa$ has length 18. With exponent $e$ instead of 4, we can make the ratio $|u|/period(v)$ as big as required, provided $e$ is chosen large enough. So, there is no statement equivalent to the perfect factorization theorem for squares.

## 13.4. CP algorithm : search phase

This section deals with the search phase of the second time-space optimal string-matching algorithm of the chapter, CP algorithm. The preprocessing phase of the whole algorithm, and the proof of the combinatorial theorem on which CP algorithm is based, are given in the next section. We first introduce the notions on words related to the design of CP algorithm, and afterwards, we present its search phase.

Let $x$ be a non-empty word, and let $uv$ be a factorization of $x$. Denote by $l$ the length of $u$ ($0 \le l \le |x|$). A non-empty word $w$ is called a *repetition for the factorization uv*, or a *repetition at position l* in $x$, if the two following conditions are satisfied :

— $w$ is a suffix of $u$, or $u$ is a suffix of $w$,

— $w$ is a prefix of $v$, or $v$ is a prefix of $w$.

The generic situation for a repetition is when the cut between factors $u$ and $v$ of $x$ is the center of a square occurring in $x$ (see Figure 13.8). The other cases correspond to a cut close to the ends of $x$, or equivalently to an overflow of $w$. Note that the word $w = vu$ is a repetition for $uv$, so that any factorization of $x$ has a repetition.

The length $r$ of a repetition for the factorization $uv$ is called a *local period for uv*, or a *local period of x* at position $l$. The smallest possible value of $r$ is called *the local period for uv*, and denoted by $r(u, v)$. It is convenient to reformulate the definition of a local period as follows. A positive integer $r$ is a local period of $x$ at position $l$ if $x[i] = x[i+r]$ for all indices $i$ such that $l-r+1 \le i \le l$, and such that both sides of the equality are defined (see Figure 13.8). The word $w$ of the previous definition, repetition at position $l$, is then defined by

$$w[i] = x[l+i] \text{ or } w[i] = x[l-r+i]$$

(for $1 \le i \le r$) according to which expression is defined on the right-hand side.

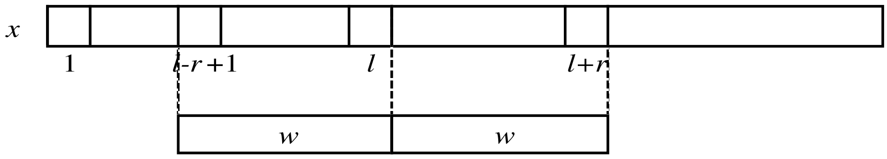


**Figure 13.8**. A local period $r$, and repetition $w$ at position $l$ in $x$.

**Example**

Consider the word $x = abaabaa$. Its local period at position 3 is $r(aba, abaa) = 1$, which corresponds to the repetition $w = a$. At position 2, $r(ab, aabaa) = 3$, and the shortest repetition is $w = aab$.

The local period of the word $x = aababab$ at position 6 is $r(aababa, b) = 2$ with repetition $w = ba$. Finally, the shortest repetition at position 2 is $r(aa, babab) = 7$, corresponding to $w = bababaa$. ‡

It is an easy consequence of the definitions that, when $x = uv$,

$$1 \leq r(u, v) \leq period(x).$$

A factorization $uv$ of $x$ that satisfies $r(u, v) = period(x)$ is called a *critical factorization*, and the position $l = |u|$ is called a *critical position* of $x$. At a critical position, the local period coincides with the smallest period of the whole word. The string-matching algorithm of this section relies on the combinatorial property of words stated in the following theorem. Its proof is given in Section 13.5.

**Theorem** (*critical factorization theorem*)

Any word $x$ has at least one critical factorization $uv$ (i.e. $r(u, v) = period(x)$). Moreover, $u$ can be chosen such that $|u| < period(x)$.

**Example**

The (smallest) period of the word *aabababaab* is 7. Its local periods are given in the next array.

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | *a* | *a* | *b* | *a* | *b* | *a* | *b* | *a* | *a* | *b* | |
| Positions : | 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
| Local periods : | 1 | 1 | 7 | 2 | 2 | 2 | 2 | 7 | 1 | 3 | 1 |

This shows that factorizations (*aa*, *bababaab*) and (*aababab*, *aab*) are critical. ‡

CP algorithm is designed according to the scheme of Section 13.1. In the following, it is assumed that $uv$ is a critical factorization of $pat$ that satisfies $|u| < period(pat)$. The rules that guide shifts in CP algorithm are relatively simple. In case of a mismatch during the right scan, the shift pushes the cut of the critical factorization to the right of the letter of the text that caused the mismatch. Otherwise, the length of the shift is the period of $pat$ (see Figure 13.9).

The searching algorithm has an additional feature : prefix memorization. This trick has already been used in Chapter 4 to improve on the worst-case time complexity of BM algorithm. It is used here with the same purpose.

The first instance of CP algorithm is presented below as CP1 algorithm. It assumes that both the period $period(pat)$, and a critical factorization $uv$ with $|u| < period(pat)$ have been computed previously. Precomputations are discussed in the next section.

```
Algorithm CP1; { informal description, see Figure 13.9 }
{ uv is a critical factorization of pat }
begin
  align left end of pat and text;
  while not end of text do begin
    { right scan } scan v from left to right against text;
    if mismatch then shift pat of the length of the scan
    else begin
      { left scan } scan u against text,
      and report possible match;
      shift pat of length period(pat);
    end;
  end;
end.
```

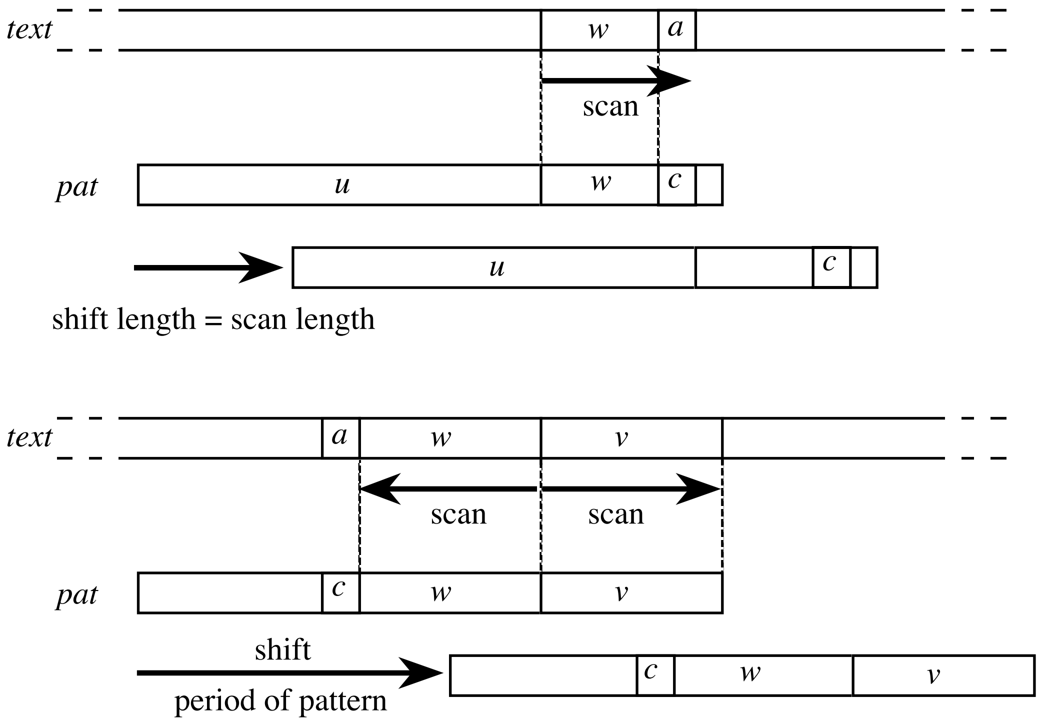


**Figure 13.9**. CP string-matching : shift after a mismatch on the right (top), and after a mismatch on the left (bottom).

```
Algorithm CP1;
{ search for pat in text; m = |pat|; n = |text| }
{ p = period(pat) }
{ uv is a critical factorization of pat such that |u| < p }
begin
  pos := 0; s := 0;
  while (pos+m ≤ n) do begin
    i := max(|u|, s)+1;
    { right scan }
    while (i ≤ m and pat[i] = text[pos+i]) do i := i + 1;
    if (i ≤ |pat|) then begin
      pos := pos+i-|u|; s := 0;
    end else begin
      j := |u|;
      { left scan }
      while (j > s and pat[j] = text[pos+j]) do j := j - 1;
      if (j ≤ s) then report match at position pos;
      pos := pos + p; s := m - p;
    end;
  end;
end.
```

The algorithm uses four local variables *i*, *j*, *s* and *pos*. The variables *i* and *j* are used as cursors on the pattern to perform the scan on each side of the critical position respectively (see Figure 13.10). The variable *s* is used to memorize a prefix of the pattern that matches the text at the current position, given by the variable *pos* (see Figure 13.11). Variable *s* is updated at every mismatch. It can be set to a non-zero value only in the case of a mismatch occurring during the scan of the left part of the pattern.

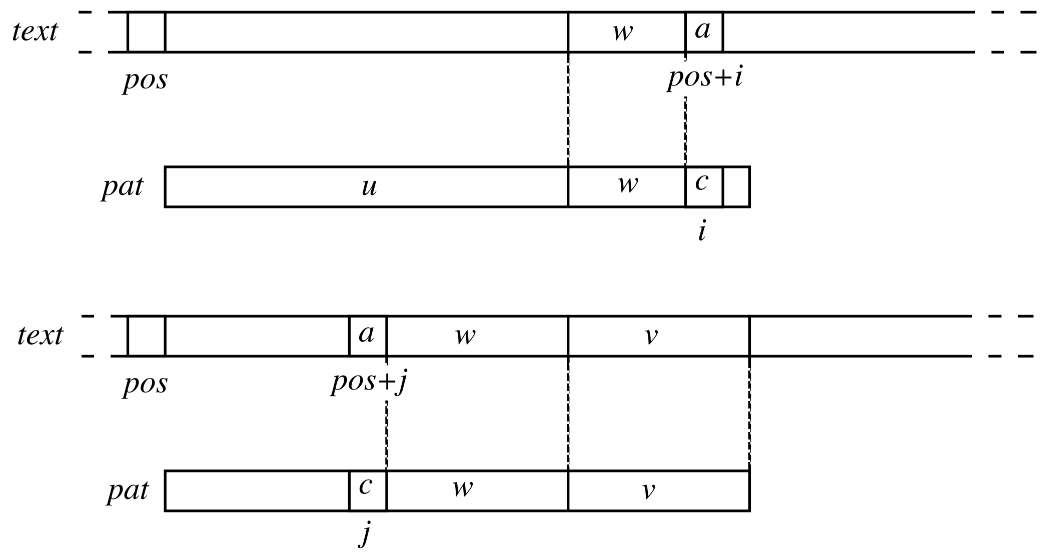


**Figure 13.10**. The role of variables *pos*, *i*, *j*.

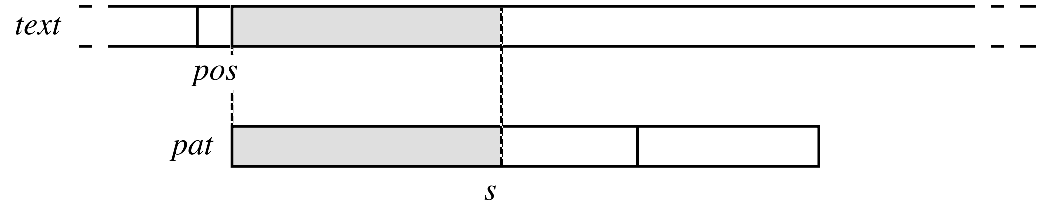


**Figure 13.11**. The role of variable *s* : prefix memorization.

Before proving the correctness of the algorithm, we first give a property of a critical factorization of a word.

**Lemma 13.7**

Let *uv* be a critical factorization of a non-empty word *x*. If *w* is both a suffix of *u* and a prefix of *v*, then $|w|$ is a multiple of *period*(*x*).

**Proof**

The property trivially holds if *w* is the empty word. Otherwise, since *period*(*x*) is also a period of *w*, this word can be written $(yz)^e y$ with $|yz| = period(x)$, *z* non-empty, and $e > 0$. If *y* is non-empty, it is a repetition for *uv*. But $|y| < period(x)$ contradicts the fact that *uv* is a critical factorization (see Figure 13.12). Hence, $|w| = e.period(x)$ as expected. ‡

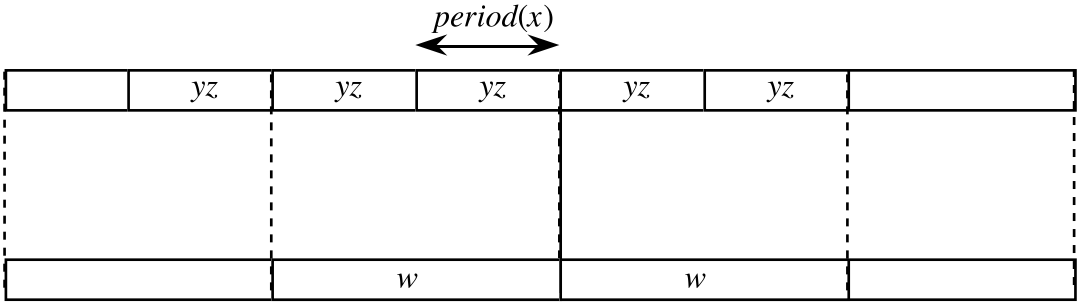


**Figure 13.12**. A repetition *w* for a critical factorization.

**Lemma 13.8** (correctness of CP1)

CP1 algorithm computes the positions of all occurrences of *pat* inside *text*.

**Proof**

Let $q_1, q_2,\ldots, q_K$ be the successive values of the variable *pos* during a run of CP1 on inputs *pat* and *text*. It is clear that the algorithm reports position $q_k$ if and only if it is a position of an occurrence of *pat* in *text*. So, it remains to show that no matching position is missed:

(*) any position of an occurrence of *pat* in *text* is some $q_k$.

Before coming to the proof of (*), the reader may note that the following property is an invariant of the main "while" loop:

$$pat[s'] = text[pos+s'],\ 1 \leq s' \leq s,$$

i.e. the prefix of *pat* of length *s* occurs in *text* at position *pos*.

**Proof of (*)**. We prove that no position *q* strictly between two consecutive values of *pos* can be a matching position. Let *q* be a matching position such that $q_k < q$. Consider the step of the main "while" loop where the initial value of *pos* is $q_k$. Let *i*' be the value assigned to the variable *i* by the right scan, and let *s*' be the value of *s* at the beginning of the step. We now consider two cases according to a mismatch occurring in the right part or in the left part of the pattern. In both cases, we use the following argument : if, after a mismatch, the shift is too small, then its length is a multiple of the period of the pattern, which implies that the same mismatch recurs.

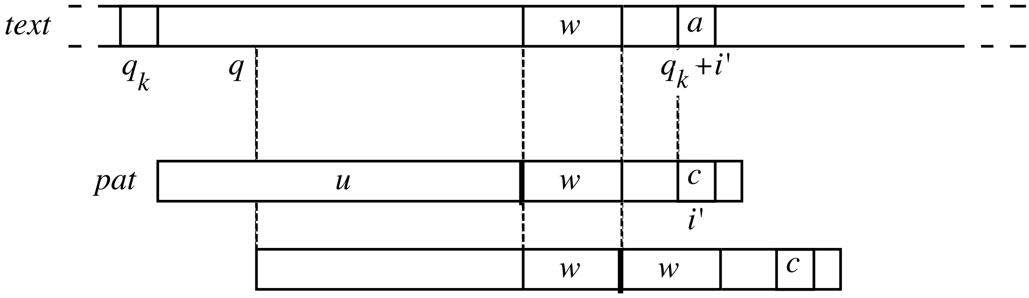


**Figure 13.13**. Case of right mismatch.

**Case 1** (Figure 13.13). If $i' \le |pat|$ a mismatch has occurred during the right scan, and we have :

$$pat[l+1\ldots i'-1] = text[q_k+|u|+1\ldots q_k+i'-1], \text{ and } pat[i'] \neq text[q_k+i'].$$

Let $w$ be the word $text[q_k+|u|+1\ldots q+l]$.

If $q < q_k + i' - |u|$, the above equality implies

$$pat[l+1\ldots l+q-q_k] = w.$$

Since $q \in Pos(pat, text)$ the suffixes of length $\max(1, |u|+1-q+q_k)$ of $w$ and of $pat[l+1-q+q_k\ldots l]$ coincide. The quantity $q-q_k$ is then a local period at the critical position $|u|$ and, by Lemma 13.7, $q-q_k$ is a multiple of $period(pat)$. So, $pat[i'] = pat[i'-q+q_k]$. But, since $q$ is a matching position, we have $pat[i'-q+q_k] = text[q+i'-q+q_k]$ which gives a contradiction with the mismatch $pat[i'] \neq text[q_k+i']$. This proves $q \ge q_k + i' - |x_l|$.

So far, we have proved that, if a mismatch occurs during the right scan, $q$ is greater than or equal to $q_k+i-|u|$, quantity which is exactly $q_{k+1}$.

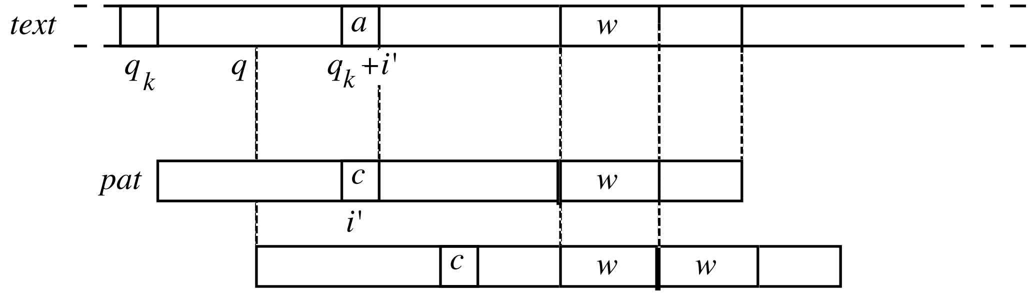


**Figure 13.14**. Case of left mismatch.

**Case 2** (Figure 13.14). If no mismatch is met during the right scan, the right part $v$ of $pat$ occurs at position $q_k+|u|$ in $text$. The word $w = text[q_k+|u|+1\ldots q+l]$ then occurs in $pat$ at position $|u|$. Since $q$ is a matching position, $w$ also occurs at the left of position $|u|$. Thus, $|w|$ is a

local period at the critical position $|u|$, and $|w| \geq$ *period*(*pat*). We get $q\text{-}q_k \geq$ *period*(*pat*). Since $q_{k+1} = q_k$+*period*(*pat*), in this second case again the inequality $q \geq q_{k+1}$ holds.
This proves assertion (*), and ends the proof of the theorem. ‡

The time complexity of CP1 algorithm is proportional to the number of comparisons between letters of *pat* and *text*. This number is bounded by 2.|*text*| as shown by the following lemma.

**Lemma 13.9**

The execution of CP1 algorithm uses less than 2.|*text*| symbol comparisons.

**Proof**

Each comparison done during the right scan strictly increases the value of *pos*+*i*. Hence, their number is at most |*text*| - |*u*|, because expression *pos*+*i* has initial value |*u*|+1 and terminal value |*text*| in the worst case.
During the left scan, comparisons are done on letters of the left part of the pattern. After the left scan, the length of the shift is *period*(*pat*). Since, by assumption, the length of *u* is less than *period*(*pat*), two different comparisons performed during left scans are done on letters of *text* occurring at different positions inside *text*. Then, at most |*text*| letter comparisons are done during all left scans.
This gives the upper bound 2.|*text*| to the number of letter comparisons. ‡

CP1 algorithm uses the period of the pattern. A previous computation of this period is possible with KMP algorithm. But since we want an algorithm that is globally linear in time with constant extra space, it is desirable to improve on the precomputation of the period of the pattern. There are two ways to achieve that goal. One way is a direct computation of the period by an algorithm working in linear time and constant space. Such an algorithm is described in Section 13.6. The approach described here is different. It avoids the use of the period of the pattern in some situations. A variant CP2 is designed for that purpose. The key point is that the period of the pattern is actually needed only when it is small, which roughly means that the period is less than half the length of the pattern. So, CP2 algorithm is intended to be used when the period of the pattern is large. This approach has the additional advantage to keep the maximal number of comparisons spent by the algorithm relatively small.

CP2 algorithm is described below. It differs from CP1 in two points. First, the "prefix memorization" is no longer used. Second, it treats differently mismatches occurring during left scans (left mismatches). In this situation, instead of shifting the pattern *period*(*pat*) places to the right, it is only shifted $q$ places to the right with $q \leq$ *period*(*pat*). Since $q$ can be less than *period*(*pat*), prefix memorization is indeed impossible.

The correctness of CP2 algorithm is straightforward from that of CP1. Note that, if we choose $q = 1$, we get a kind of naive algorithm absolutely inefficient! In fact, CP2 is to be applied with an integer $q$ satisfying the additional condition $q > \max(|u|, |v|)$ (recall that $uv$ is a critical factorization of *pat*). With this assumption, the maximal number of symbol comparisons used by CP2 is less than $2.|text|$, as it is for CP1.

```
Algorithm CP2;
{ search for pat in text; m = |pat|; n = |text| }
{ search phase without p = period(pat) }
{ q satisfies 0 < q ≤ p }
{ uv is a critical factorization of pat such that |u| < p }
begin
  pos := 0;
  while (pos+m ≤ n) do begin
    i := |u|+1;
    { right scan }
    while (i ≤ m and pat[i] = text[pos+i]) do i := i + 1;
    if (i ≤ m) then
      pos := pos + i-|u|;
    else begin
      j := |u|;
      { left scan }
      while (j > 0 and pat[j] = text[pos+j]) do j := j - 1;
      if (j = 0) then report match at position pos;
      pos := pos + q;
    end;
  end;
end.
```

**Lemma 13.10**

CP2 algorithm computes the positions of all occurrences of *pat* inside *text*.

Furthermore, if the parameter $q$ of the algorithm satisfies $q > \max(|u|, |v|)$, the number of letter comparisons used by CP2 is less than $2.|text|$.

**Proof**

One can get the first assertion by reproducing a simplified version of the proof of correctness of CP1 (Lemma 13.8).

We first prove that the total number of comparisons performed during right scans is bounded by $|text|$. Consider two consecutive values $k$ and $k'$ of the sum $pos+i$. If these values are obtained during the same scan, then $k' = k+1$ because $i$ is increased by one unit. Otherwise, *pos* is increased either by instruction "$pos := pos + i\text{-}|u|$" or by instruction "$pos := pos + q$". In the first case, $k' = k-|u|+|u|+1 = k+1$ again. In the second case, $k' \geq k+q-|u|$, and the assumption $q > \max(|u|, |v|)$ implies $k' \geq k+1$. Since comparisons during right scans strictly increase the value of *pos*+*i*, which has initial value $|u|+1$ and final value at most $|text|+1$, the claim is proved.

We show that the number of comparisons performed during left scans is also bounded by $|text|$. Consider two values $k$ and $k'$ of the sum *pos*+*j* respectively obtained during two consecutive left scans. Let $p$ be the value *pos* has, during the first of these two scans. Then $k \leq p+l$, and $k' \geq p' = p+q$. The assumption $q > \max(|u|, |v|)$ implies $k' \geq k+1$. Thus, no two letter comparisons made during left scans are done on a same letter of *text*, which proves the claim.

The total number of comparisons is thus bounded by $2.|text|$. ‡

The complete CP string-matching algorithm is shown below. It calls a procedure to compute a critical factorization *uv* of the pattern, suitable for CP1 and CP2 algorithms. Moreover, as we shall see in Section 13.5, the procedure computes the period of the right part *v* without any additional cost. After this preprocessing phase, a simple test allows to decide which version of the search phase is to be run, CP1 or CP2.

```
Algorithm CP { search for pat in text }
begin
  (u, v) := critical factorization of pat
            such that |u| < period(pat);
  p := period(v);
  if (u is a suffix of v[1…p]) then
    { p = period(pat) }
    run CP1 algorithm on text using u, v, and period p
  else begin
    q := max(|u|, |v|) + 1;
    run CP2 algorithm on text using u, v, and parameter q;
  end;
end.
```

**Theorem 13.11**

CP algorithm computes the positions of all occurrences of *pat* inside *text*.

The algorithm runs in time $O(|pat|+|text|)$, and uses a bounded memory space.

The number of letter comparisons made during the search phase is less than $2.|text|$.

**Proof**

We assume that the first instruction of CP algorithm runs in time $O(|pat|)$ with bounded extra space. An algorithm satisfying this condition is presented in Section 13.5.

We have to prove that, after the first statement, and the succeeding test, conditions are met to realize the search phase either with CP1 or with CP2 algorithms.

Assume first that $u$ is a suffix of $v[1...p]$. Then, obviously, the integer $p$ is also a period of *pat* itself. Thus, CP works correctly because CP1 does (see Lemma 13.8).

Assume now that $u$ is a not a suffix of $v[1...p]$. In this situation the correctness of CP depends on that of CP2. The conclusion comes from Lemma 13.10, if we prove that $q = \max(|u|, |v|)+1$ satisfies $q \leq period(pat)$. And, since $|u| < period(|pat|)$ by assumption, it remains to show that $|v| < period(|pat|)$. Equivalently, because $uv$ is a critical factorization, we show that $v$ is shorter than the local period for $uv$.

We prove that there is no non-empty word $w$ such that $wu$ is a prefix of *pat*. Assume, the contrary, that is, $wu$ is prefix of *pat*. If $w$ is non-empty its length is a local period for $uv$, and then, $|w| \geq period(pat) \geq period(v)$. We cannot have $|w| = period(v)$ because $u$ is not a suffix of $v[1...p]$. We cannot either have $|w| > period(v)$ because this would lead to a local period for $uv$ strictly less than $period(v)$, a contradiction. This proves the assertion, and ends the correctness of CP algorithm.

The conclusions on the running time of CP algorithm, and on the maximum number of comparisons executed by CP algorithm readily come from Lemmas 13.9 and 13.10, and from the assumption made at the beginning of the proof on the first instruction. ‡

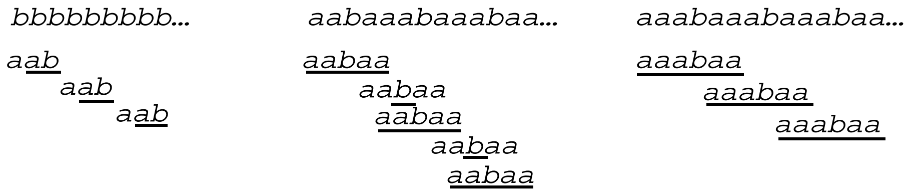
**Note**

We shall see that the first instruction of CP algorithm uses less than $4.|pat|$ symbol comparisons of the kind "<, =, >". Since the test "$u$ is a suffix of $v[1...p]$ ?" takes at most $|pat|/2$ comparisons, the preprocessing phase globally uses $4.5.|pat|$ comparisons. ‡

We end this section by giving examples of the behavior of CP algorithm. The examples are presented in Figure 13.15 where the letters of the pattern scanned during the search phase of the algorithm are underlined.

On pattern $pat = a^nb$ the algorithm finds its unique critical factorization $(a^n, b)$. The search for *pat* inside the text $text = b^m$ uses $2|text|/|pat|$ comparisons, and so does BM algorithm. Both algorithms attempt to match the last two letters of *pat* against the letters of *text*, and shift *pat* $n$+1 places to the right as shown in Figure 13.15 (i).

The pattern $pat = a^nba^n$ has period $n$+1. Its critical factorization computed by CP algorithm is $(a^n, ba^n)$. CP algorithm behaves like CP1, and uses $2|text|-2e-2$ comparisons to match *pat* in $text = (a^nba)^ea^{n-1}$ (see Figure 13.15 (ii)). The same number of comparisons is reached when searching for $pat = a^nba^{n-1}$ inside $text = (a^nb)^ea^{n-1}$, but, in this latter case, the algorithm behaves like CP2 (see Figure 13.15 (iii)).



(i) (ii) (iii)

**Figure 13.15**. Behavior of the search phase of CP algorithm.

## 13.5.* Preprocessing the pattern : critical factorization

In this section we are interested in the computation of critical factorizations, which is the central part of the preprocessing of CP algorithm. Among the existing proofs of the critical factorization theorem for *x*, one relies on the property that if $x = ayb$ (*a*, *b* are letters), then a critical factorization of *x* either comes from a critical factorization of *ay*, or from a critical factorization of *yb*. This leads to a quadratic algorithm. Another proof relies on the notion of a Lyndon factorization. It leads, via the use of a linear time string-matching algorithm to a linear time algorithm for computing a critical factorization. This method is not suitable for our purpose, because the aim is to incorporate the algorithm in a string-matching algorithm.

The proof of the critical factorization theorem presented here gives a method both practically and algorithmically simple to compute a critical position, and which, in addition, uses only constant additional memory space. The method relies on a computation of maximal suffixes that is presented afterwards.

**Remark**

A weak version of the critical factorization theorem occurs if one makes the additional assumption that the inequality $3.period(x) \leq |x|$ holds. Indeed, in this case, one may write $x = l.w.w.r$ where $|w| = period(x)$, and *w* is chosen alphabetically minimal among its cyclic shifts. This means, by definition, that *w* is a Lyndon word (see Chapter 15). One can prove that a Lyndon word is unbordered. Consequently the factorization (*lw*, *wr*) is critical. ‡

The present proof of the theorem (in the general case) requires two orderings on words that are recalled first. Each ordering ≤ on the alphabet *A* extends to an *alphabetical ordering* on the set $A^*$. It is defined as usual by $x \leq y$ if either

— *x* is a prefix of *y*, or

— *x* is *strongly less* than *y*, denoted by $x << y$ (i.e. $x = w.a.x'$ , $y = w.b.y'$ with *w*, *x*', *y*' words of $A^*$ and *a*, *b* two letters such that $a < b$).

The following theorem shows the existence of critical factorizations adapted to CP algorithm. The statement involves two alphabetical orderings on words. The first one is $\leq$ induced by a given ordering $\leq$ on the alphabet. The second ordering on $A^*$, called the *reverse ordering* and denoted by $\subseteq$, is obtained by reversing the order $\leq$ on $A$.

**Remark**

The ordering $\subseteq$ is not the inverse of $\leq$. For instance, on $A = \{a, b\}$ with $a < b$, we have both $abb \leq abbaa$ and $abb \subseteq abbaa$.

In fact, it is easy to see that the intersection of the orderings $\leq$ and $\subseteq$ is exactly the prefix ordering. Which means that, for any words $x$ and $y$, inequalities $x \leq y$ and $x \subseteq y$ are equivalent to $x$ is a prefix of $y$. ‡

**Theorem 13.12**

Let $x$ be a non-empty word on $A$. Let $x = uv = u'v'$, where $v$ (resp. $v'$) is the alphabetically maximal suffix of $x$ according to the ordering $\leq$ (resp. $\subseteq$).

If $|v| \leq |v'|$ then $uv$ is a critical factorization of $x$. Otherwise, $u'v'$ is a critical factorization of $x$. Moreover, $|u|, |u'| < period(x)$.

**Proof**

We first rule out the case where the word $x$ has period 1, that is to say, when $x$ is a power of a single letter. In this case any factorization of $x$ is critical.

We now suppose that $|v| \leq |v'|$ and prove that $uv$ is a critical factorization. The other case ($|v'| < |v|$) is symmetrical. Indeed, $|v| < |v'|$ because $x$ contains at least two different letters. Let us prove first that $u \neq \varepsilon$. Let indeed $x = ay$ with $a$ in $A$. If $u = \varepsilon$, then $x = v = v'$, and both inequalities $y \leq x$ and $y \subseteq x$ are satisfied by definitions of $v$ and $v'$. Thus, $y$ is a prefix of $x$ whence $period(x) = 1$ contrary to the hypothesis.

Let $w$ be the shortest repetition for $uv$ ($|w| = r(u, v)$). We distinguish four cases according to whether $w$ is a suffix of $u$ or vice-versa, and to whether $w$ is a prefix of $v$ or vice-versa.

**Case 1** : $w$ is both a suffix of $u$, and a prefix of $v$.

The word $v$ can be written $wz$ ($z \in A^*$). Since $wv$ and $z$ are suffixes of $x$, by the definition of $v$ we have $wv \leq v$ and $z \leq v$. The first inequality can be rewritten $wwz \leq wz$ and implies $wz \leq z$. The second inequality gives $z \leq wz$. We then obtain $z = wz$, whence $w = \varepsilon$, a contradiction.

**Case 2** : $w$ is a suffix of $u$, and $v$ is a prefix of $w$.

The word $w$ can be written $vz$ ($z \in A^*$). But then, $vzv$ is a suffix of $x$ strictly greater than $v$, a contradiction with the definition of $v$.

**Case 3** (Figure 13.16): $u$ is a suffix of $w$, and $v$ is a prefix of $w$.

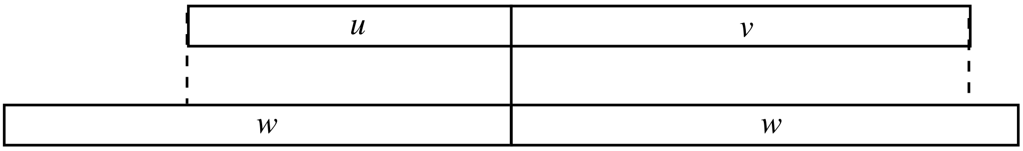


**Figure 13.16**. Case 3.

The integer $|w|$ is a period of $x$ because $x$ is a factor of $ww$. The period of $x$ cannot be shorter than $|w|$ because this quantity is the local period for $uv$. Hence $period(x) = |w|$, which proves that the factorization $uv$ is critical.

**Case 4** (Figure 13.17): $u$ is a suffix of $w$ and $w$ is a prefix of $v$.

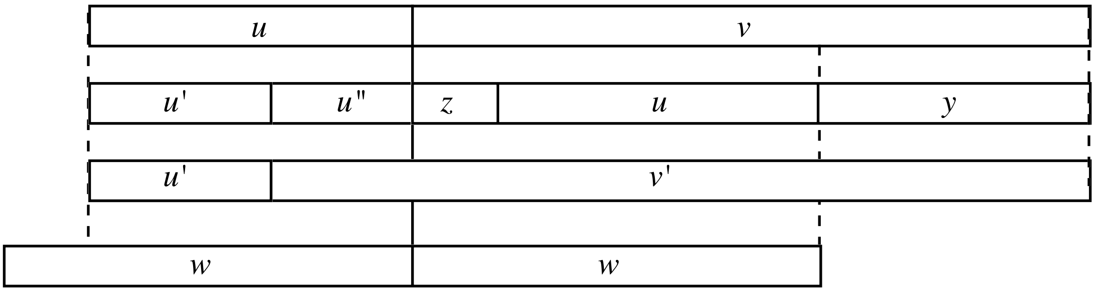


**Figure 13.17**. Case 4.

Let $w = zu$ and $v = wy$ ($z, y \in A*$). Since $|w|$ is the local period for $uv$, as in the previous case we only need to prove that $|w|$ is a period of $x$.

Let $u''$ be the non-empty word such that $u = u'u''$ (recall that hypothesis $|v| < |v'|$ implies that $u'$ is a proper prefix of $u$). Since $u''y$ is a suffix of $x$, by the definition of $v'$, we get $u''y \subseteq v' = u''v$, hence $y \subseteq v$. By the definition of v, we also have $y \leq v$. By the remark above, these two inequalities imply that $y$ is a prefix of $v$. Hence, $y$ is a border of $v$, and $v$ is thus a prefix of $w^e$ for some integer $e > 0$. Then, $x$ is a factor of $w^{e+1}$, which shows that $|w|$ is a period of $x$ as expected. This ends Case 4.

The proof shows that cases 1 and 2 are impossible. As a consequence, $|u|$ is less than the local period. We then get $|u| < period(x)$ because the factorization $uv$ is critical. We also get $|u'| < period(x)$ when $|u'| < |u|$. The same argument holds symmetrically under the assumption $|v'| < |v|$. This completes the whole proof. ‡

According to Theorem 13.12, the computation of a critical factorization reduces to that of maximal suffixes. More accurately, it requires the computation of two maximal suffixes corresponding to reversed orderings of the alphabet.

The rest of the section is devoted to the preprocessing part of CP algorithm. It is given below. The design of this phase of CP algorithm is a direct consequence of Theorem 13.12.

The algorithm calls the procedure *MS* that essentially computes the maximal suffix of a word. For a word $x$, it returns both $(u, v)$ such that $x = uv$ and $v$ is the maximal suffix of $x$, and $p = period(v)$. The next algorithm runs in linear time and uses only a bounded memory space because, as we shall see afterwards, algorithm *MS* has the same performance.

```
Algorithm { preprocessing of pat for CP algorithm }
{ compute a critical factorization of pat }
begin
  (u, v, p) := MS(pat) according to ≤;
  (u', v', p') := MS(pat) according to ⊆;
  if (|v| < |v'|) then
    return (u, v) and p the period of v;
  else
    return (u', v') and p' the period of v';
end.
```

**Example**

Consider the word *abaabaa* of period 3. Its maximal suffix for the usual ordering on letters is *baabaa*. The factorization (*a*, *baabaa*) is not critical because its local period is 2 (repetition *ba*). According to the reverse ordering, the maximal suffix becomes *aabaa*. The factorization (*ab*, *aabaa*) is critical.

The word *ababaabbababa* has period 8. Its maximal suffixes for usual and reverse orderings are respectively *bbababa* and *aabbababa*. Their associated factorizations (*ababaa*, *bbababa*) and (*abab*, *aabbababa*) are both critical. ‡

We end the section with a brief description of algorithm *MS*. The algorithm below is strongly related to the Lyndon factorization of a word presented in Chapter 15. The reader should refer to this chapter to develop a proof of correctness of the algorithm.

```
Algorithm MS(x) { computes Maxsuf(x) and its period }
{ operates in linear and constant space }
begin
  ms := 0;  j := 1;  k :=1;  p := 1;
  while (j + k ≤ n) do begin
    a' := x[ms+k];  a := x[j+k];
    if (a < a') then begin
      j := j+k; k := 1; p := j-ms;
    end if (a = a') then
      if (k ≠ p) then
        k := k+1
      else begin
        j := j+p; k := 1;
      end
    else { a > a' } begin
      ms := j; j := ms+1; k := 1; p := 1;
    end;
  end;
  return (x[1…ms], x[ms+1…|x|], p);
end.
```

Let *Maxsuf*($x$) be the suffix of $x$ which is maximal for alphabetic ordering. We consider the words $f$, $g$, and the integer $e > 0$ such that *Maxsuf*($x$) $= f^e g$ with $|f| =$ *period*(*Maxsuf*($x$)), and $g$ is a proper prefix of $f$. We define *Per* and *Rest* by *Per*($x$) $= f$, *Rest*($x$) $= g$. Note that *Rest*($x$) is a border of *Maxsuf*($x$), and that *Border*(*Maxsuf*($x$)) $= f^{e-1}g$, even when $e = 1$.

The interpretation of the variables *ms*, *j*, *k* occurring in the algorithm *MS* is indicated on Figure 13.18. The integer $p$ is the period of *Maxsuf*($x$), that is also the length of *Per*($x$). The integer *ms* is the position of *Maxsuf*($x$) in $x$, and $j$ is the position of the last occurrence of *Rest*($x$) in *Maxsuf*($x$).

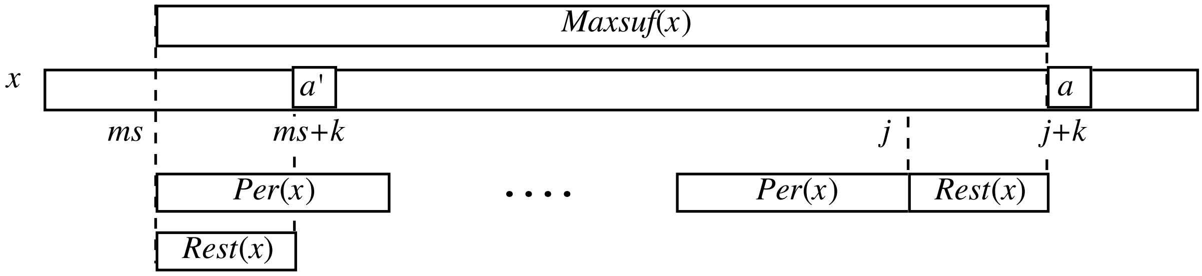


**Figure 13.18**. Variables in *MS* algorithm.

**Example**

Let $x = abcbcbacbcbacbc$. Then, for the usual ordering, $Maxsuf(x) = cbcbacbcbacbc$, which is also $(cbcba)^2cbc$.

The maximal suffix of $xa$ is $cbcbacbcbacbca = Maxsuf(x)a$, which is a border-free word.

The maximal suffix of $xb$ is $cbcbacbcbacbcb = Maxsuf(x)b$. This word has the same period as $Maxsuf(x)$.

Finally, the maximal suffix of $xc$ is $cc$. ‡

The correctness of *MS* algorithm essentially relies on Lemma 13.13 (see Chapter 15 for a proof of a similar result). Its time complexity is stated in Lemma 13.14.

**Lemma 13.13**

Let $x$ be a word and $a$ be a letter. Let $a'$ be the letter such that $Rest(x)a'$ is a prefix of $Maxsuf(x)$. Then the triple $(Maxsuf(xa), Per(xa), Rest(xa))$ is equal to

$(Maxsuf(x)a, Maxsuf(x)a, \varepsilon)$ if $a < a'$,

$(Maxsuf(x)a, Per(x), Rest(x)a)$ or $(Maxsuf(x)a, Per(x), \varepsilon)$ if $a = a'$,

$(Maxsuf(Rest(x)a), Per(Rest(x)a), Rest(Rest(x)a))$ if $a > a'$.

**Lemma 13.14**

*MS* algorithm runs in time $O(|x|)$ with constant additional memory space. It makes less than $2.|x|$ letter comparisons.

**Proof**

The value of expression $ms + j + k$ is increased by at least one unit after each symbol comparison. The result then comes from inequalities $2 \le ms + j + k \le 2.|x| + 1$. ‡

## 13.6. Optimal computation of periods

In this section we develop yet another time-space optimal string-matching algorithm, which naturally extends to the computation of periods of word with the same performance.

GS and CP algorithms factorize the pattern *pat* into *uv* according to some property of the periodicities existing inside the pattern. The search phase is thereafter guided by the search for the right part *v* of the pattern. Both algorithms tend to avoid some periodicities of the pattern to make the search faster. This contrasts with both KMP algorithm and MPS algorithm whose first phase amounts to compute periods of the pattern. The present algorithm adopts the same strategy as the latter. It computes periods to realize shifts. This is done "on the fly" during the search phase using maximal suffix computations, and periods are not stored. Moreover, no preprocessing is needed.

When a shift is to be done, the strategy is to compute the period of the scanned segment of the text (including the mismatch letter). The algorithm does not always find the exact period of this segment, but in any case it computes an approximation of it. The approximation is good enough to produce an overall linear-time algorithm, and the computation requires only a bounded extra memory space.

```
Algorithm { preliminary version of algorithm P }
{ search for pat in text; no preprocessing needed  }
begin
  pos := 0;  i := 0;
  while (pos ≤ n-m) do begin
    while i < m and text[pos+i+1] = pat[i+1] do i := i+1;
    if i = m then report match at position pos;
    (u, v, p) := MS(pat[1…i]text[pos+i+1]);
    if (u suffix of v[1…p]) then begin
      pos := pos+p;  i := i-p;
    end else begin
      pos := pos+max(|u|,⌊(i+1)/2⌋)+1;  i := 0;
    end
  end;
end.
```

The algorithm above resembles KMP algorithm. It makes use of a left-to-right scan of the pattern against the text. When, during the execution, a mismatch is encountered, or an occurrence of the pattern is discovered, the algorithm shifts the pattern to the right. The shift is computed as follows. Let *y* be the longest prefix of the pattern found at the current position in the text. Let also $b$ be the letter in the text that follows immediately the occurrence of $y$. Then, the algorithm tries to make a shift of length as close as possible to *period*($yb$) (in the above algorithm, $yb$ is *pat*[1…*i*]*text*[*pos*+*i*+1]). This quantity corresponds to the best possible shift in such a situation. The computation of an approximation of *period*($yb$) is done after the computation of the maximal suffix of $yb$. This is an analogue to what is done at the preprocessing phase of CP algorithm in Section 13.5.

The correctness of the algorithm amounts to prove that the length of the shift is not larger than the period of $x = yb$. But, this is a direct consequence of Lemma 13.16 below that relates the factorization of $x$ to its maximal suffix, and to the period of this suffix. To state it we need to introduce the notion of MS-factorization of a non-empty word $x$.

Let $v$ be the maximal suffix of $x$ (according to the alphabetical ordering). Let $u$ be such that $x = uv$. Considering its (smallest) period, the word $v$ can be written $w^e w'$ where $e \geq 1$, $|w| =$ *period*($v$), and $w'$ is a proper prefix of $w$. Recall that the pattern $x$ is non-empty so that words $u$, $v$, $w$ and $w'$ are well defined. The sequence ($u$, $w$, $e$, $w'$) is called the *MS-factorization of x* (MS stands for maximal suffix).

The MS-factorization of $x$ into $uw^e w'$ gives a rather precise information on the period of $x$. Among interesting properties it is worth noting that $w$ is border-free (it has no smaller period than its length). The inequality *period*($x$) > $|u|$ is a rather intuitive property of the maximal suffix, saying that this suffix must start inside the first period of the word (see Theorem 13.12).

**Lemma 13.15**

Let $uw^e w'$ be the MS-factorization of a non-empty word $x$, and $v = w^e w'$ be the maximal suffix of $x$. Then, the five properties hold:

(1) — the word $w$ is border-free.

(2) — if $u$ is a suffix of $w$, *period*($x$) = *period*($v$),

(3) — *period*($x$) > $|u|$,

(4) — if $|u| \geq |w|$, *period*($x$) > $|v| = |x|-|u|$,

(5) — if $u$ is not suffix of $w$, and $|u| < |w|$, *period*($x$) > min($|v|$, $|uw^e|$).

**Proof**

(1) Assume that $w = zz' = z''z$ for three non-empty words $z$, $z'$ and $z''$. The word $zw^{e-1}w'$ is a suffix of $x$ distinct from $v$, so, it is greater than $v$ according to the alphabetical ordering. The inequality $zw^{e-1}w' < v$ rewrites as $zw^{e-1}w' < zz'w^{e-1}w'$, and implies $w^{e-1}w' < z'w^{e-1}w'$. Moreover, $zw^{e-1}w'$ is not a prefix of $v$ because otherwise the smallest period of $v$ would be $|z''|$, less than $|w|$, contrary to the definition of $w$. Since then $w^{e-1}w'$ is not a prefix of $z'w^{e-1}w'$, there is a word $y$, and letters $a$ and $b$ such that simultaneously $ya$ is a prefix of $w^{e-1}w'$, $yb$ is a prefix of $z'w^{e-1}w'$, and $a < b$. Since $ya$ is also a prefix of $v$, we get $v < z'w^{e-1}w'$, a contradiction with the definition of $v$.

Thus, $w$ cannot be properly written simultaneously as $zz'$ and $z''z$. This means that $w$ is borderfree, or, equivalently, *period*($w$) = $|w|$.

(2) When $u$ is a suffix of $w$, $|w|$ is obviously a period of the whole word $x$. The smallest period of $x$ cannot be less than the smallest period of its suffix $v$. Since this period is precisely $|w|$, we get the conclusion $period(x) = period(v) = |w|$.

(3) We prove that $period(x) > |u|$. Otherwise, if $period(x) \leq |u|$, there is an occurrence of $v$ in $x$ distinct from its occurrence as suffix. In other words, $x$ can be written $u'vv'$ with $|u'| < |u|$, and $|v'| > 0$. But the suffix $vv'$ is then alphabetically greater than $v$, a contradiction with the definition of $v$.

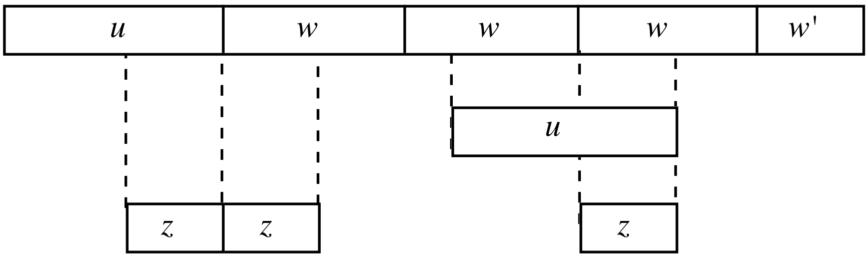


**Figure 13.19**. Impossible : no suffix of $u$ can be a prefix of $w$.

(4) (Figure 13.19) Assume that $|u| \geq |w|$. We prove that $period(x) > |v|$ (= $|x|$-$|u|$). If the contrary holds, there is an occurrence of $u$ in $x$ distinct from the prefix occurrence. This occurrence overlaps $v$. Then, taking into account that $|u| \geq |w|$, there is a non-empty word $z$ that is both a prefix of $w$ and a suffix of $u$. The former property shows that $v$ can be written $zz'$ (for some word $z'$), and the latter property shows that $zv$ is a suffix of $x$. The maximality of $v$ implies $v > zv$, that is $zz' > zv$. But this yields $z' > v$, a contradiction with the definition of $v$.

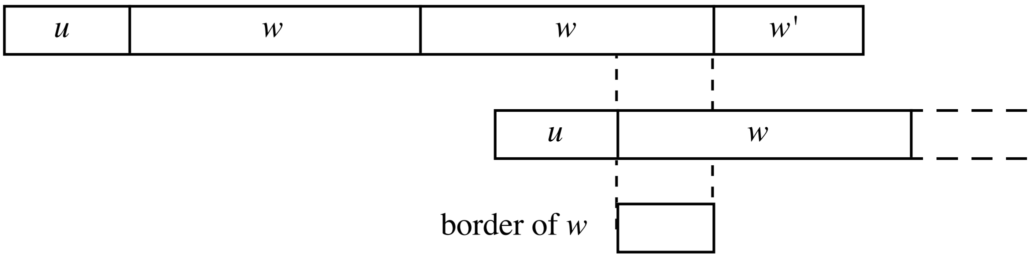


**Figure 13.20**. Impossible because $w$ is border-free.

(5) (Figure 13.20) Assume that $u$ is not a suffix of $w$, and that $|u| < |w|$. Assume also, ab absurdo, that $period(x) \leq \min(|v|, |uw^e|)$. Let $z$ be the prefix of $x$ of length $period(x)$. The word $x$ itself is then a prefix of $zx$. From $period(x) \leq |v|$ we deduce that the word $zu$ is a common prefix to $x$ and $zx$. And from $period(x) \leq |uw^e|$ we know that $u$ overlaps $w^e$. If $u$ overlaps the boundary between two $w$'s, or the boundary between the last $w$ and $w'$, the same argument as in case (4) applies and leads to a contradiction. The remaining situation is when $u$ is a factor of $w$, as shown in Figure 13.20. The last occurrence of $w$ in the prefix $zuw$ of $zx$ overlaps an

occurrence of $w$ in the prefix $uw^e$ of $x$. Note that these occurrences of $w$ cannot be equal or adjacent because $u$ is not suffix of $w$. This gives a contradiction with the border-freeness of $w$ stated in (i).
This completes the proof of the lemma. ‡

**Note**
One may note that, in case (4), $u$ cannot be a suffix of $w$, because this would imply $u = w$ which is impossible by (3). ‡

An immediate consequence of Lemma 13.15 is that condition (2) is certainly true for words having a small period, id est, having a period not greater than half their length ($period(x) \leq |x|/2$). The computation of the smallest period of these words can then be deduced from a computation of their maximal suffixes (and MS-factorization), together with a test "is $u$ a suffix of $w$ ?". This fact is used in CP algorithm (Section 13.4) to approximate smallest periods of patterns. The following lemma amounts to the correctness of algorithm $P$. It provides an accurate approximation of the smallest period of the word $x$.

**Lemma 13.16**

Let $uw^ew'$ be the MS-factorization of a non-empty word $x$, and let $v$ (= $w^ew'$) be the maximal suffix of $x$.
— If $u$ is a suffix of $w$, $period(x) = period(v) = |w|$.
— Otherwise, $period(x) > \max(|u|, \min(|v|, |uw^e|)) \geq |x|/2$.

**Proof**
This is mainly a corollary of Lemma 13.15.
When $u$ is not a suffix of $w$, statements (3), (4), and (5) of Lemma 13.15 show that the inequality $period(x) > \max(|u|, \min(|v|, |uw^e|))$ holds. It remains to prove that the last quantity is greater than $|x|/2$.
The inequality is trivially satisfied if $|u| \geq |x|/2$. Otherwise, quantity $|v|$, which is equal to $|x|-|u|$ is greater than $|x|/2$. And $|uw^e|$, equal to $|x|-|w'|$, is also greater than $|x|/2$ because $|w'| < |w|$. Then, $\min(|v|, |uw^e|) > |x|/2$, which ends the proof. ‡

**Examples**
Bounds on the smallest period given in Lemma 13.15 are sharp. We list few examples of patterns that give evidence of this fact. We consider words on the alphabet $\{a, b, c\}$ with the usual ordering ($a < b < c$).
Let $x$ be $aaaaba$. The maximal suffix of $x$ is $v=ba$ whose smallest period is 2. In the MS-factorization $uw^ew'$ of $x$, $u = aaaa$, $w = ba$, and $w'$ is empty. Then, $period(x) = 5 = |u|+1$. As stated in Lemma 13.15 case (3), $period(x)$ is greater than $|u|$, but only by one unit.

The word $x$ = *aababa* meets case (4) of Lemma 13.15. Here $u$ = *aa*, $w$ = *ba*, and $w$' is empty. The smallest period of $x$, 5, is exactly one unit more than the length of the maximal suffix *baba*.

We exhibit two examples for case (5) of Lemma 13.15. The first example is $x$ = *acabca*. We have $u$ = *a*, $w$ = *cab*, and $w$' = *ca*. Then, the quantity min(|$v$|, |$uw^e$|) is |$uw^e$| = 4. The smallest period of $x$ is *period*($x$) = 5. The word satisfies *period*($x$) = |$uw^e$|+1 = |$v$|. The second example is $x$ = *ababbbab*. For it, $u$ = *aba*, $w$ = *bbba*, and $w$' = *b*. This is a reverse situation where min(|$v$|, |$uw^e$|) = |$v$| = 5. The smallest period of $x$ is now 6, and we have *period*($x$) = |$v$|+1 < |$uw^e$|. ‡

Algorithm *MS* may be implemented to run in linear time (see Section 13.5). But even with this assumption, algorithm *P* does not always run in linear time. Quadratic complexity is due to computations of maximal suffixes. For instance, if the pattern is $a^{m-1}b$ and the text is a long repetition of the only letter $a$, at each position in the text, the maximal suffix of $a^m$ is re-computed from scratch, leading to an $O$(|*pat*|.|*text*|) time complexity.

Indeed, quadratic behavior of the algorithm is only reached with highly periodic patterns (or, more precisely, with patterns having a highly periodic prefix). But, with such kind of pattern, entire re-computations of maximal suffixes are not necessary. So, the trick to reduce the running time is to save as much as possible of the work done to compute the maximal suffix. We introduce a new algorithm for that purpose. It is called *Next_MS*, and shown below. It is a mere transformation of algorithm *MS* of Section 13.5. The tuple of variables of *MS*, (*ms*, *j*, *k*, *p*), is made accessible to the string-matching algorithm, so that it can control its values. The tuple (*ms*, *j*, *k*, *p*) is called the *MS-tuple of x*. It is related to the MS-factorization ($u$, $w$, $e$, $w$') of $x$ by the equalities :

$$ms = |u|, j = |uw^e|, k = |w'|+1, p = |w| = period(v).$$

Figure 13.21 displays the situation. The value of *ms* is the position in $x$ of its maximal suffix $v$, and $j$ is the position of the rest $w$'. The period of $v$, that is also the length of $w$, is given by $p$.

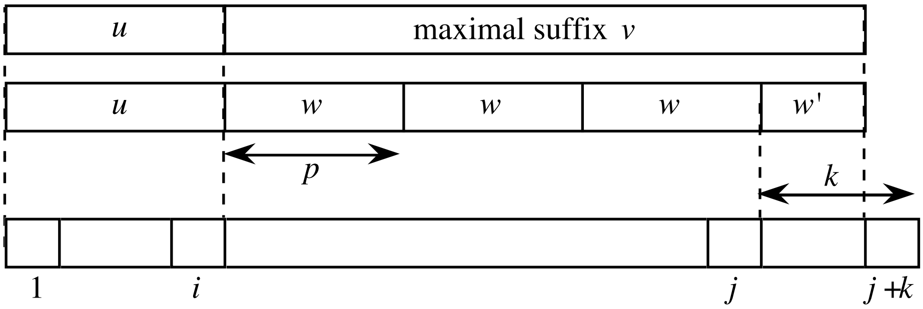


**Figure 13.21**. The MS-tuple (*ms*, *j*, *k*, *p*) of the pattern.

The string-matching algorithm is shown below as algorithm *P* (for Periods). The difference with the preliminary version lies in the computation of the MS-tuple (*ms*, *j*, *k*, *p*). In this version, the MS-tuple is still initialized, as in the preliminary version, at the beginning of a run of the algorithm and after each shift, except in one situation met with highly periodic pattern. In this case the variable *j* of the MS-tuple is just decreased by the period *p*, length of the shift. Algorithm *P* contains another modification: it computes all *overhanging occurrences* of the pattern *pat* inside the text *text* (when *text* is prefix of *z.pat*). This is realized by a change on the test of the main 'while' loop, and by the technical instruction "`if pos+i = n then i := i-1`" whose purpose is to avoid considering symbols beyond the end of the text.

```
Algorithm P;
{ search for pat in text }
{ time-space optimal; no preprocessing needed }
begin
  pos := 0;  i := 0;  (ms,j,k,p) := (0,1,1,1);
  while (pos ≤ n) do begin
    while pos+i+1 ≤ n and i+1 ≤ m and text[pos+i+1] = pat[i+1]
    do i := i+1;
    if pos+i = n or i = m then report match at position pos;
    if pos+i = n then i := i-1;
    let scanned be pat[1…i]text[pos+i+1];
    (ms,j,k,p) := Next_MS(pat[1…i]text[pos+i+1],(ms,j,k,p));
    if pat[1…ms] suffix of
        the prefix of length p of pat[ms+1…i]text[pos+i+1] then
      if j-ms > p then begin { shift = period in an hrp }
        pos := pos+p;  i := i-p;  j := j-p;
      end else begin { shift = period outside an hrp }
        pos := pos+p;  i := i-p;  (ms,j,k,p) := (0,1,1,1);
      end
    else begin { shift close to period }
      pos := pos+max(ms, min(i-ms,j))+1;  i := 0;
      (ms,j,k,p) := (0,1,1,1);
    end;
  end;
end.
```

Provided algorithm *Next_MS* is proved correct, the correctness of algorithm *P* relies on Lemma 13.16 (as the correctness of the preliminary version does), and on Lemma 13.17 below. Before proving it, we first explain the main idea on an example.

**Example**

Consider the pattern *pat* = *babbbabbbab*. Its maximal suffix is $v$ = *bbbabbbab*. Both words have smallest period 4. With the notation of MS-factorizations, we have $u$ = *ba*, $w$ = *bbba*, and $w$' = *b*. The exponent of $w$ in $v$ is $e = 2$. If the last four letters of *pat* are deleted, corresponding for instance to a shift of 4 positions to the right, we are left with the word $x_1$ = *babbbab*. Its MS-factorization is $u_1$ = *ba*, $v_1$ = *bbbab*, $w_1$ = *bbba* and $w_1$' = *b*. Note that the second factorization is produced from the first one by pruning one occurrence of $w$. Indeed, this generalizes to any word for which the exponent $e$ of the MS-factorization is greater than 1 (see Figure 13.22). The above result does not necessarily hold when $e = 1$. Let, for instance, *pat* be *bbabbbabb*. It has period 4, like its maximal suffix $v$ = *bbbabb*. Deletion of the last four letters yields $x_1$ = *bbabb*, which is its own maximal suffix and has period 3. This situation is quite far from the previous one. ‡

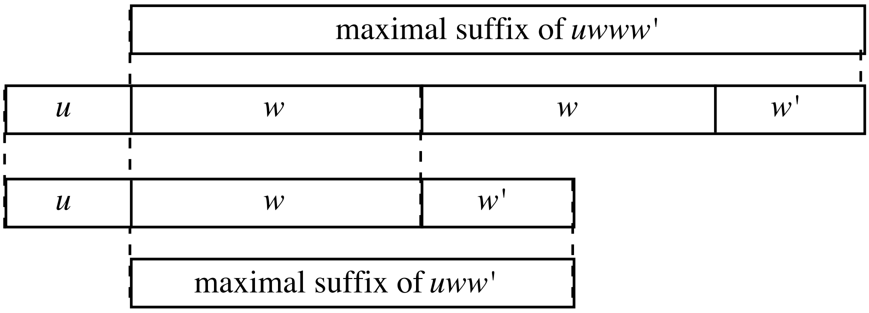


**Figure 13.22**. Highly periodic pattern.

**Lemma 13.17**

Let ($u$, $w$, $e$, $w$') be the MS-factorization of a non-empty word $x$ ($w^e w$' is the maximal suffix of $x = uw^e w$'). If $u$ is a suffix of $w$ and $e > 1$, then ($u$, $w$, $e$-1, $w$') is the MS-factorization of $x' = uw^{e-1}w$'. In particular, the word $w^{e-1}w$' is the maximal suffix of $x$'.

**Proof**

Let $v = w^e w$' be the maximal suffix of $x$. Any proper suffix of $v$ of the form $zw^{e-1}w$' (with $z \neq \varepsilon$) is less than $v$ itself by definition. But, since $w$ is border-free (Lemma 13.15), the longest common prefix of $w$ and $z$ is shorter than $z$. This leads to $w > z$ and proves that $w$ is greater than all its proper suffixes. This further proves that $w^{e-1}w$' is its own maximal suffix. And, since hypothesis *period*($x$) = |$w$| is equivalent to "$u$ is a suffix of $w$", this also proves that $w^{e-1}w$' is the maximal suffix of $uw^{e-1}w$'.

The equality *period*($w^{e-1}w$') = |$w$| is another consequence of the border-freeness of $w$ stated in Lemma 13.15. Thus, ($u$, $w$, $e$-1, $w$') is the MS-factorization of $x$' as announced. ‡

A pattern $x$ which satisfies hypothesis of Lemma 13.17 has a rather small period, and may be considered as highly periodic. Its smallest period is not greater than half its length.

Conversely, if the smallest period of $x$ is not greater than $|x|/3$, the conclusion of Lemma 13.17 applies.

We now explain how Lemma 13.17 is used to improve on the complexity of the preliminary version of the string-matching algorithm. When a shift done according to a period leaves a match between the text and the pattern of the form $uw^{e-1}w'$, we avoid computing the next maximal suffix from scratch. We better exploit the known factorization of the match. Inside algorithm *P* the test "$j$-$ms > p$" is equivalent to condition "$e > 1$" of Lemma 13.17. Doing so, we get a linear time algorithm. Below is the modification of Algorithm *MS* used in algorithm *P*.

```
Algorithm Next_MS (x[1…m], (ms,j,k,p));
begin
  while ($j + k \le n$) do begin
    if ($x[i+k] = x[j+k]$) then begin
      if ($k = p$) then begin
        $j := j+p$; $k := 1$;
      end else $k := k+1$;
    end else if ($x[i+k] > x[j+k]$) then end
      $j := j+k$; $k := 1$; $p := j-ms$;
    end else begin
      $ms := j$; $j := ms+1$; $k := 1$; $p := 1$;
    end;
  end;
  return (ms, j, k, p);
end.
```

**Lemma 13.18**

The number of letter comparisons executed during a run of algorithm *P* on words *pat* and *text* is less than $6.|text|+5$. This includes comparisons done during *Next_MS* calls.

**Proof**

First consider the test for prefix condition in algorithm *P* (third "if"). The comparisons executed on the prefix $pat[1\ldots i]$ of the pattern can be charged to $text[pos+1\ldots pos+i]$. Whichever shift follows the test, the value of *pos* increases by more then *ms*. Thus, never again, the comparisons are charged to the factor $text[pos+1\ldots pos+i]$ of the text. The total number of these comparisons is thus bounded by $|text|$.

We next prove that each other letter comparison executed during a run of algorithm *P* (including comparisons done during calls of *Next_MS*) leads to a strict increment of the value of expression 5*pos*+*i*+*ms*+*j*+*k*. Since its initial value is 3, and its final value is 5|*text*|+8, this proves the claim.

Whatever is the result of the letter comparison inside algorithm *Next_MS*, the value of *ms*+*j*+*k* increases by 1, and even by more than 1 when the last line of the algorithm is executed. It is worth to note that the inequality $k \le j\text{-}ms$ always holds.

Successful comparisons at the first instruction of algorithm *P* trivially increase *i*, and consequently expression 5*pos*+*i*+*ms*+*j*+*k*. At the same line, there is at most one unsuccessful comparison. This comparison is eventually followed by a shift. We examine successively the three possible shifts in the order they appear in algorithm *P*.

The effect of the first shift is to replace 5*pos*+*i*+*ms*+*j*+*k* by 5(*pos*+*p*)+(*i*-*p*+1)+*ms*+(*j*-*p*)+*k*. The expression is thus increased by 3*p*+1, which is greater than 1.

The second shift is executed when $j\text{-}ms > p$ does not hold. This means indeed that $j\text{-}ms = p$ (*j*-*ms* is always a multiple of *p*). We also know that $ms < p$ (see Lemma 13.15 case (2)). One can observe on algorithm *Next_MS* that $k \le p$. Now, immediately after the shift, *i* is decreased by *p*-1, *ms* and *k* are decreased by less than *p*, and $j = ms+p$ is decreased by less than 2.*p*. Since *pos* is replaced by *pos*+*p* the value of 5*pos*+*i*+*ms*+*j*+*k* is increased by more than 1.

Finally, consider the effect of the third shift on the expression. If *s* is the value of max(*ms*, min(*i*-*ms*, *j*))+1, the increment of expression 5*pos*+*i*+*ms*+*j*+*k* is $I = 5s\text{-}(i\text{-}1)\text{-}ms\text{-}(j\text{-}1)\text{-}(k\text{-}1) = 5s\text{-}i\text{-}ms\text{-}j\text{-}k+3$, that is, 5*s*-2*i*-*ms*+2, because $j+k = i+1$. The value *s* is greater than or equal to both *ms* and *i*/2. So $I \ge 2$, which proves that the third shift increases the value of 5*pos*+*i*+*ms*+*j*+*k* by more than 1.

The effect of the second "if" in algorithm *P*, that can decrease *i* by one unit, is of no importance in the preceding analysis. ‡

Since algorithm *P* computes all overhanging occurrences of the pattern inside the text, it can be used, in a natural way, to compute all periods of a word. Each (overhanging) position of *x* inside *x* itself (except position 0) is a period of word *x*. We give below a straightforward adaptation of algorithm *P* that computes the smallest period of a word. It can easily be extended to compute all periods of its input. As a consequence of Lemma 13.18, we get the following result.

**Theorem 13.19**

The periods of a word *x* can be computed in time *O*(|*x*|) with a constant amount of space in addition to *x*.

```
function Per(x);
{ time-space optimal computation of period(x) }
begin
  per := 1; i := 0; (ms,j,k,p) := (0,1,1,1);
  while per+i+1 ≤ |x| do begin
    if x[per+i+1] = x[i+1] then i := i+1
    else begin
      (ms,j,k,p) := Next_MS(x[1…i]x[per+i+1],(ms,j,k,p));
      if (x[1…ms] suffix of
          the prefix of length p of x[ms+1…i]x[per+i+1]) then
        if (j-ms > p) then begin
          per := per+p; i := i-p+; j := j-p;
        end else end
          per := per+p; i := i-p+; (ms,j,k,p) := (0,1,1,1);
        end
      else begin
        per := per+max(ms, min(i-ms,j))+1; i := 0;
        (ms,j,k,p) := (0,1,1,1);
      end;
    end;
  end;
  return(per);
end.
```

## Bibliographic notes.

The first time-space optimal string-matching algorithm is from Galil and Seiferas [GS 83]. The same authors have designed other string-matching algorithm requiring only a small memory space [GS 80], [GS 81]. In the original article [GS 83], the perfect factorization theorem is proved for the parameter $k \geq 4$. The present proof, also valid for $k = 3$, and the exposition of Sections 13.2 and 13.3 is from [CR 93].

Algorithm CP of Sections 13.4 and 13.5 is from Crochemore and Perrin [CP 91]. The present proof of the critical factorization theorem is also from [CP 91]. The theorem is originally from Cesari, Duval, and Vincent (see [Lo 83]). The algorithm to compute the maximal suffix of a string is adapted from an algorithm of Duval [Du 83] (see also Chapter 15).

The time-space optimal computation of periods of a string given in Section 13.6 is from [Cr 92]. The result is announced in [GS 83]. Although the proof contains a small flaw, the idea leads to another time-space optimal computation of periods (see [CR 93]).

## Selected references

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# 14. Time-processors optimal string-matching

There are two types of optimal parallel algorithms for the string-matching problem. The first type uses in an essential way the combinatorics of periods in texts. In the second type, no special combinatorics of texts is necessary. In this chapter, we first follow the approach of Vishkin's algorithm. Then, the Galil's sieve method is shown. It produces a constant-time optimal algorithm. These algorithms are of the first type. Next, we present the suffix-prefix algorithm of Kedem, Landau and Palem (KLP). This algorithm is of the second type. It is essential for the optimality of this algorithm that we use the model of parallel machine with concurrent writes (CRCW PRAM). KLP algorithm can be viewed as a further application of the dictionary of basic factors (Chapter 9). The suffix-prefix string-matching introduced there is extended to the case of two-dimensional patterns at the end of the section.

## 14.1. Vishkin's parallel string-matching by duels and by sampling

Historically, the first optimal parallel algorithm for string-matching used the notion of expensive duels, see Chapter 3. Moreover, it was optimal only for fixed alphabets. The notion has been strengthened to the more powerful operation of *duel* that leads to an optimal parallel string-matching. Unfortunately, preprocessing the table of witnesses required by the method is rather complicated. So, we just state the result, but omit the proof and refer the reader to references at the end of the chapter.

**Theorem 14.1**

The smallest period and the witness table of a pattern of length $m$, can be computed in $O(\log m)$ time with $m/\log m$ processors of a CRCW PRAM, or in $O(\log^2 m)$ time with $m/\log^2 m$ processors of a CREW PRAM.

Suppose that $v$ is the shortest prefix of the pattern which is a period of the pattern. If the pattern is periodic ($vv$ is a prefix of the pattern) then $vv^-$ is called the non-periodic part of the pattern ($v^-$ denotes the word $v$ with the last symbol removed). We omit the proof of the following fact, which justifies the name "non-periodic part" of the pattern:

**Lemma 14.2**

If the pattern is periodic (it is twice longer than its period) then its non-periodic part is non-periodic.

The witness table is relevant only for the non-periodic pattern. So, it is easier to deal with non-periodic patterns. We prove that such assumption can be done without loss of generality, by ruling out the case of periodic patterns.

**Lemma 14.3**

Assume that the pattern is periodic, and that all occurrences (in the text) of its non-periodic part are known. Then, we can find all occurrences of the whole pattern in the text

(i) — in $O(1)$ time with $n$ processors in the CRCW PRAM model,

(ii) — in $O(\log m)$ time with $n/\log m$ processors in the CREW PRAM model.

**Proof**

We reduce the general problem to unary string-matching. Let $w = vv^{-}$ be the non-periodic part of the pattern. Assume that $w$ starts at position $i$ in the text. By a segment containing position $i$ we mean the largest segment of the text containing position $i$ and having a period of size $|v|$. We assign a processor to each position. All these processors simultaneously write 1 into their positions if the symbol at distance $|v|$ to the left contains the same symbol. The last position containing 1 to the right of $i$ (all positions between them also contain ones) is the end of the segment containing $i$. Similarly, we can compute the first position of the segment containing $i$. It is easy to compute it optimally for all positions $i$ in $O(\log m)$ time by a parallel prefix computation (see Chapter 9). The constant time computation on a CRCW PRAM is more advanced, we refer the reader to [BG 90]. Some tricks are used by applying the power of concurrent writes. This completes the proof. ‡

Now we can assume that the pattern is non-periodic. We use the witness table used in Chapter 3 in two sequential string-matching algorithms: by duels and by sampling. The parallel counterparts of these algorithms are presented.

Recall that a position $l$ on the text is said to be *in the range of* a position $k$ iff $k < l < k+m$. We say that two positions $k < l$ on the text are *consistent* iff $l$ is not in the range of $k$, or if $WIT[l\text{-}k] = 0$. If the positions are not consistent, then, in constant time we can remove one of them as a candidate for a starting position of the pattern using the operation *duel*, see Chapter 3.

Let us partition the input text into *windows* of size $m/2$. Then, the duel between two positions in the same window eliminates at least one of them. The position which "survives" is the value of the duel. Define the operation $\otimes$ by $i \otimes j = duel(i, j)$. The operation $\otimes$ is "practically" associative. This means that the value of $i_1 \otimes i_2 \otimes i_3 \otimes \ldots \otimes i_{m/2}$ depends on the order of multiplications, but all values (for all possible orders) are equivalent for our purpose. We need any of the possible values.

Once the witness table is computed, the string-matching problem reduces to instances of the parallel prefix computation problem. We have the following algorithm.

```
algorithm Vishkin_string_matching_by_duels;
begin
  consider windows of size $m/2$ on text;
  /* sieve phase */
  for each window do in parallel
    /* ⊗ can be treated as if it were associative */
    compute the surviving position $i_1 \otimes i_2 \otimes i_3 \otimes .. \otimes i_{m/2}$,
    where $i_1, i_2, i_3, ..., i_{m/2}$ are consecutive positions
    in the window;
  /* naive phase */
  for each surviving position $i$ do in parallel
    check naively an occurrence of pat at position $i$
    using $m$ processors;
end.
```

**Theorem 14.4**

Assume we know the witness table and the period of the pattern. Then, the string-matching problem can be solved optimally in $O(\log m)$ time with $O(n/\log m)$ processors of a CREW PRAM.

**Proof**

Let $i_1, i_2, i_3, \ldots, i_{m/2}$ be the sequence of positions in a given window. We can compute $i_1 \otimes i_2 \otimes \ i_3 \otimes \ldots \otimes \ i_{m/2}$ using an optimal parallel algorithm for the parallel prefix computation, see Chapter 9. Then, in a given window, only one position survives; this position is the value of $i_1 \otimes \ i_2 \otimes \ i_3 \otimes \ldots \otimes \ i_{m/2}$. This operation can be done simultaneously for all windows of size $m/2$. For all windows, this takes time $O(\log m)$ with $O(n/\log m)$ processors of a CREW PRAM. Afterwards, we have $O(n/m)$ surviving positions altogether. For each of them we can check the match using $m/\log m$ processors. Again, a parallel prefix computation is used to collect the result, that is, to compute conjunction of $m$ boolean values (match or mismatch, for a given position). This takes again $O(\log m)$ time with $O(n/\log m)$ processors.

Finally, we collect $O(n/m)$ boolean values by a similar process. It gives an optimal parallel algorithms working with the announced complexities. This completes the proof. ‡

The consequence of Lemma 14.1 and Theorem 14.4 altogether is the basic result of this section stated as the following corollary.

**Corollary 14.5**

There is an $O(\log^2 n)$ time parallel algorithm that solves the string matching problem (including preprocessing) with $O(n/\log^2 n)$ processors of a CREW PRAM.

The idea of deterministic sampling was originally developed for parallel string-matching. In Chapter 3, a sequential use of sampling is shown. Recall the definition of the good sample. A sample $S$ is a set of positions in the pattern. A sample $S$ occurs at position $i$ in the text iff $pat[j] = text[i+j]$ for each $j$ in $S$. A sample $S$ is called a *deterministic sample* iff it is small ($|S| = O(\log m)$), and it has a big field of fire — a segment $[i\text{-}k\ldots i+m/2\text{-}k]$. If the sample occurs at $i$ in the text, then positions in the field of fire of $i$, except $i$, cannot be matching positions. The important property of samples is that if we have two positions of occurrences of the sample in a window of size $m/2$, then one "kills" the other: only one can possibly be a matching position.

```
algorithm Vishkin-string-matching-by-sampling;
begin
  consider windows of size $m/2$ on text;
  /* sieve phase */
  for each window do in parallel begin
    for each position $i$ in the window do in parallel
      kill $i$ if the sample does not occur at $i$;
    kill all surviving positions in the window,
      except the first and the last;
    eliminate one of them in the field of fire of the other;
  end;
  /* naive phase */
  for each surviving position $i$ do in parallel
    check naively an occurrence of pat starting at $i$
    using $m$ processors;
end.
```

In the sieve phase, we use $n\log m$ processors to check a sample match at each position. In the naive phase, we have $O(n/m)$ windows, and, in each window, $m$ processors are used. This proves the following.

**Theorem 14.6**

Assume we know the deterministic sample and the period of the pattern. Then, the string-matching problem can be solved in $O(1)$ time with $O(n\log m)$ processors in the CRCW PRAM model.

The deterministic sample can be computed in $O(\log^2 m)$ time with $n$ processors by a direct parallel implementation of the sequential construction of deterministic samples presented in Chapter 3. But faster sampling methods are possible (see bibliographic notes).

## 14.2.* Galil's sieve

The constant time parallel sampling algorithm of the last section is not optimal but only by a logarithmic factor ($\log m$). In order to produce an optimal searching phase, we apply a method to eliminate all but $O(n/\log m)$ candidate positions in constant time with $n$ processors. We call it the Galil's sieve. After applying the sieve with the sampling algorithm of the last section, only $O(n/\log m)$ positions have to be checked as sample matches. Hence, we can do the search phase of the string-matching in constant time with an optimal number of processors (linear number of processors). This is stated in the next theorem.

**Theorem 14.7**

There is a preprocessing of the pattern in $O(\log^2 m)$ time with $m$ processors such that the search phase on any given text can be done in constant time with linear number of processors.

The proof of Theorem 14.7 relies on the next lemmas of the section. The present proof consists in the description of Galil's sieve. It is based on a simple combinatorial fact described below. Let $T$ be an $r$×$r$ zero-one array. We say that a $j$-th column hits a $i$-th row iff $T[i, j] = 1$. A set of columns hits a given row if at least one of its columns hits this row, see Figure 14.1.

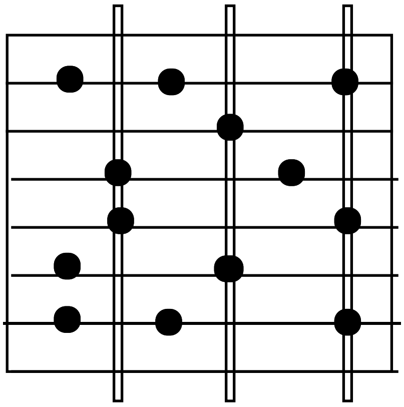


**Figure 14.1**. A hitting set of columns: the three columns hit all rows.

**Lemma 14.8** (hitting set lemma)

Assume we have $r \times r$ zero-one array $T$ such that each row contains at least $s$ ones. Then, there is a set $H$ of $O(r/s \log r)$ columns that hits all the rows of $T$.

**Proof**

The required set $H$ is constructed by the following algorithm.

```
algorithm Hitting-set;
begin
  H := empty set; R := set of all rows of the array;
  while R non-empty do begin
    choose a column j hitting the largest number of rows of R;
    delete from R the rows hit by the j-th column;
    add the j-th column to H;
  end;
  return H;
end.
```

It is enough to prove the following:

the number of iterations of the algorithm "Hitting-set" is $O(r/s \log r)$.

Let *total* be the total number of ones in all rows of $R$. Since there are $r$ columns (containing altogether all ones), the selected $j$-th column contains *at least total*/*r* ones. We remove at least *total*/r rows, each containing at least $s$ ones. This implies that we remove at least $s.total/r$ ones. Doing so, the total number of ones decreases at each iteration by a factor at least $(1\text{-}s/r)$. It is easy to calculate that there is a number $k = O(r/s \log r)$, such that $(1\text{-}s/r)^k < 1/r^2$. Initially, we have globally at most $r^2$ ones. Hence, after $k$ iterations there is no one, and $R$ is empty. This completes the proof. ‡

Let us consider occurrences of the pattern which start in a "window" of size $m/4$ on the text, see Figure 14.2. It is enough to remove all but $O(m/\log m)$ candidate positions in such a window. Let us fix one such window. Let us partition the pattern into four quarters. The window corresponds to the first quarter of the pattern. Let us call the two middle quarters the *essential part of the pattern*. Let $z$ be a factor of size $\log m/4$ of the essential part, and which has the highest number of occurrences inside this part. The segment of length $m/2$ of the text immediately following the window is called the *essential part of the text*.

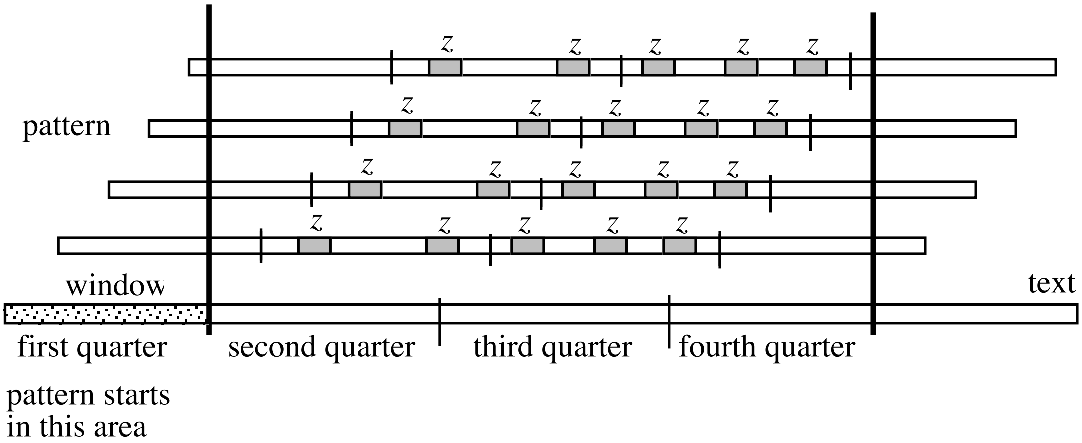


**Figure 14.2**. The factor $z$ in the essential part of the pattern.

We assume for simplicity that the alphabet is binary. If the alphabet is unbounded, it has no more than $n$ letters, and the sieve method is considered for small subwords of length doubly logarithmic.

**Lemma 14.9**

If an occurrence of the pattern starts in the window, then we can find one occurrence of $z$ inside the essential part of the text in constant time with $m$ processors.

**Proof**

There are at least $s = m^{0.5}$ occurrences of $z$ inside the essential part of the pattern, since there are $m/2$ occurrences and at most $2^{\log m/4}$ possible subwords of length $\log m/4$. Let us consider all possible occurrences of the pattern starting in the window and the relative occurrences of $z$ in the essential part. Consider $m/4$ shifts of the pattern, and, in each of them, put 1 at starting positions of $z$. We have $m/4$ rows, each of them with $\sqrt{m}$ ones. According to the hitting-set lemma there is a set $H$ of positions (corresponding to columns in the "hitting set" lemma) in the essential part of the text such that, if there is any occurrence of the pattern starting in the window, then there is an occurrence of $z$ in the essential part of text starting at a position in $H$. The set $H$ is small, $|H| = O(m/\log m)$, in fact it is even of lower order, due to the hitting-set lemma. So, it is enough to check for an occurrence at positions in the hitting set. This can be done on a CRCW PRAM in constant time with $|z|$ processors for each position in $H$. Altogether a linear number of processors is enough. This completes the proof. ‡

We introduce the idea of *segments* related to the factor $z$ (in text or in pattern). A *segment* of an occurrence of $z$ in a given word $w$ is the maximal factor of $w$ containing $z$, and having the same period as $z$. We leave the proof of the following technical fact to the reader.

**Lemma 14.10**

Assume we are given the period of $z$ and an occurrence of $z$ in a given text. Then the segment of the occurrence of $z$ can be found in constant time with $n$ processors of a CRCW PRAM.

**Lemma 14.11** (Galil's sieve lemma)

Assume that the pattern is non-periodic, and both the subword $z$ and its hitting set $H$ of size $m/\log m$ are constructed. Then, we can eliminate all but $O(m/\log m)$ candidate positions for matching positions in a given window in constant time with $m$ processors.

**Proof**

We have to remove all but $O(m/\log m)$ candidates from the window. First, we find one occurrence of $z$ in the essential part of the text. This can done optimally according to Lemma 14.9. If there is no occurrence then all positions in the window can be eliminated. Therefore, we assume that there is an occurrence, and we find one. Now there are two cases according to whether $z$ is periodic or non-periodic.

**Case 1 (z is non-periodic)**

This is the simpler case. Let $k_1$, $k_2$, ..., $k_p$ be the sequence of positions of occurrences of $z$ in the pattern, see Figure 14.3. There are at most $O(m/|z|)$ occurrences due to the non-periodicity of $z$. This number is $O(m/\log m)$ because $|z| = \log m$.

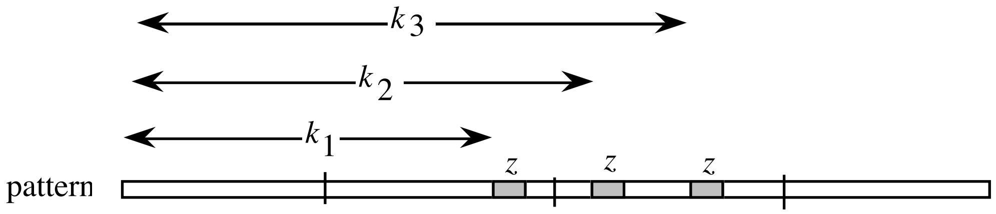


**Figure 14.3**. Positions of $z$ in the pattern.

Now, if we found an occurrence of $z$ at position $i$ in the essential part of the text, then the possible candidates for matching positions of the pattern in the window are only $i$-$k_1$, $i$-$k_2$, ..., $i$-$k_p$, see Figure 14.4. All positions in the window which do not appear in this sequence are eliminated. This completes the proof in the non-periodic case.

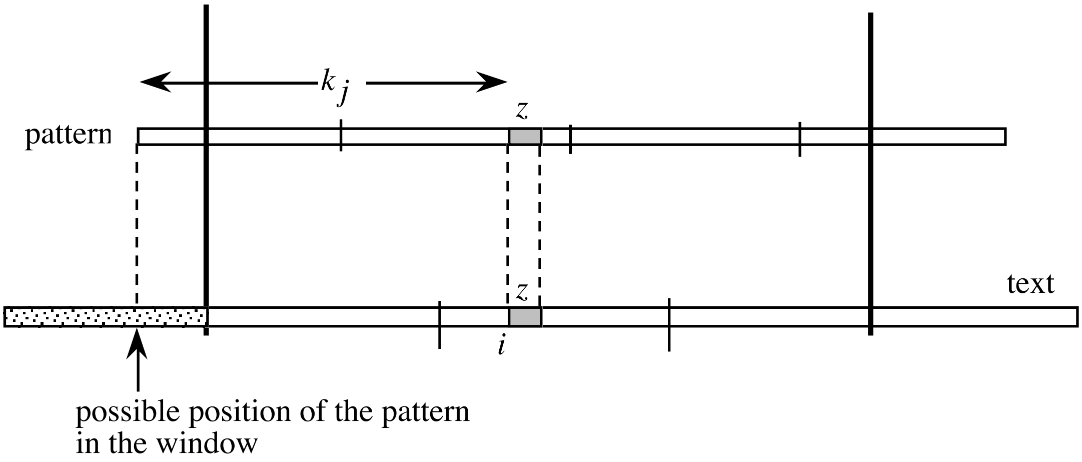


**Figure 14.4**. Possible matching position $i$-$k_j$.

**Case 2 (z is periodic)**

Now we cannot apply directly the same argument when $z$ is periodic, because the number of occurrences of $z$ can be larger than $O(m/\log m)$. However, we shall deal with extended occurrences of $z$: the segments of $z$. Let us fix $z$. It is easy to see that two segments cannot overlap more than at $|z|/2$ positions. Hence, the number of segments in the pattern is $O(m/\log m)$. For a given $z$ found in the essential part of the text we compute its segment. Then the end of this segment corresponds to an end of some segment in the pattern, or the beginning of the segment corresponds to the beginning of some segment in the pattern. We use the same argument as in the first case. This completes the proof. ‡

The conclusion of the section, corollary of the previous lemma, gives a constant-time string-matching algorithm.

**Theorem 14.12**

The search of a preprocessed pattern in a text of length $n$ can be done in constant time with $O(n)$ processors in the CRCW PRAM model.

## 14.3. The suffix-prefix matching of Kedem, Landau and Palem

The method discussed in the present section is based on the naming (or numbering) technique, which is intensively used by KMR algorithm (see Chapters 8 and 9). The crucial point in the optimal parallel string-matching algorithm presented here is to give consistent names to some segments of the pattern. The basic tool is the dictionary of basic factors (DBF, in short). However, the main drawback of the DBF is its size: it contains names for $n\log n$ objects. The solution proposed by KLP algorithm is to use a weak form of the DBF. It contains only names for all subwords of length $2^k$ that start at a position in the text divisible by $2^k$ (for each integer $k$ = 0, 1, …, log$n$). We call this structure the *weak dictionary of basic factors* (weak DBF, for short).

**Lemma 14.13**

The weak DBF contains the names of $O(n)$ objects. It can be constructed in $O(\log n)$ time with $O(n/\log n)$ processors of a CRCW PRAM.

**Proof**

The construction of the weak DBF can be carried out essentially in the same way as that of the DBF. But then the total work is linear, due to the fact that the total number of objects is linear. Hence $O(n/\log n)$ processors are enough. ‡

KLP algorithm reduces the string-matching problem to the suffix-prefix problem (below). That is, we have to give names only to (some) suffixes and prefixes of two strings. The number of objects is linear, and due to this fact, an algorithm with linear total work is possible. The problem consists essentially in building a dictionary for prefixes and suffixes. This is why the dictionary of basic factors is useful.

Let $p$ and $s$ be words of length $n$. The suffix-prefix (SP, for short) problem for words $p$ and $s$ of the same length is defined as follows.

**SP problem:**

name consistently all prefixes of $p$ and all suffixes of $s$ together.

A linear time sequential computation is straightforward: the SP problem for two words of length $n$ can be solved sequentially in $O(n)$ time. This is a simple application of Knuth-Morris-Pratt algorithm, and of the notion of failure function (see Chapter 3).

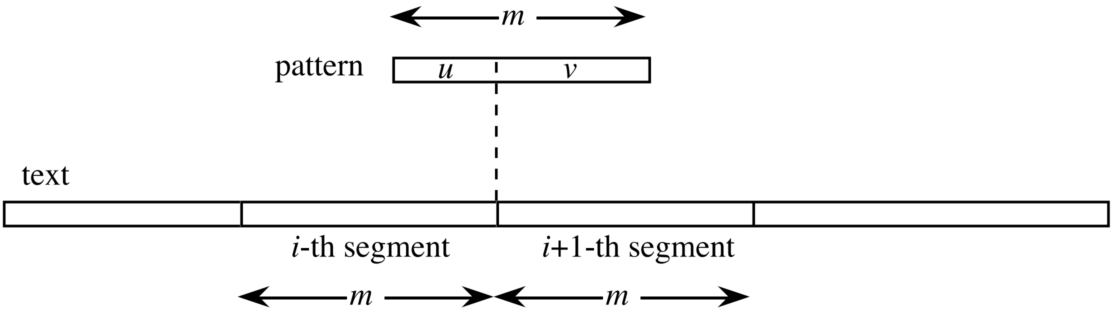
The SP problem can be solved by an optimal parallel algorithm, but this requires a non-trivial construction. It is postponed after the application to string-matching presented in the next theorem. The theorem shows the significance of the SP problem. It is also presented here to acquaint the reader with the problem, before constructing an optimal parallel algorithm.

**Theorem 14.14**

Assume that the SP problem for two strings can be solved by an optimal parallel algorithm. Then, the string-matching problem can also be solved by an optimal parallel algorithm.

**Proof**

Let us factorize the text into (disjoint) segments of size $m$ (length of the pattern). Then the string-matching is reduced to $2n/m$ SP problems of size $m$. If the pattern overlaps the border between the $i$-th and $(i+1)$-th segment then some prefix $u$ of the pattern should be a suffix of the $i$-th segment, and the associated suffix $v$ of the pattern should be a prefix of the ($i$+1)-th segment (see Figure 14.5).



.

**Figure 14.5**. Suffix-prefix matching.

We have $O(n/m)$ SP problems of size $m$. They can be computed independently, each with $O(m)$ work. Altogether the algorithm works in logarithmic time ($O(\log m)$, with a total work of $O(n)$. This completes the proof. ‡

One of the basic parts of KLP algorithm is the reduction of the number of objects. This reduction is possible due to encoding of segments of length $\log n$ by their names of $O(1)$ size (small integers). The main tool to do that is the string-matching automaton for several patterns. In what follows we assume that the input alphabet is of a constant size. This assumption is only used in the proof of Lemma 14.15 below. In fact, the lemma also holds for unbounded alphabet, but the proof is more complicated (see bibliographic notes). Hence the whole suffix-prefix algorithm works essentially with the same complexity even if the assumption on the size of alphabet is dropped.

**Lemma 14.15**

Assume we have $r$ patterns of the same length $k$. Then in time $O(k)$ on a CRCW PRAM

(a) — we can construct the string-matching automaton $G$ of the patterns with work $O(kr)$;

(b) — if $G$ is computed, then we can find all occurrences of the patterns in a given text of length $n$ with $O(n)$ work.

**Proof**

The proof of point (a) is essentially the parallel implementation of the sequential algorithm for the multi-pattern machine (see Chapter 7). The structure of this machine is based on the tree $T$ of the prefixes of all patterns. The states of the automaton correspond to prefixes. The tree grows in a breadth-first-search order. We use the algorithm for the construction of the multi-pattern automaton without use of the failure table. The transitions from a node at a given level are computed in a constant time, while transitions for all states at higher levels are computed, see Chapter 7. The bfs order is well suited to parallel construction level-by-level. At a given level we process all nodes simultaneously with $rk$ processors. As a side effect, we have consistent names for all patterns: two patterns are equal iff they have the same names. There is a special name corresponding to all words of length $k$ which are not equal to any of the $k$ patterns.

The proof of the point (b) is rather tricky. The constructed automaton can be used to scan the text. For each segment composed of the last $k$ symbols read so far, write the name of the pattern equal to that segment, or the special value if no pattern matches. One automaton can process sequentially a factor of length $2k$ of the text, and give names to the last $k$ positions (occurrences or non-occurrences of patterns) in that portion of the text. We can activate a copy of the automaton $G$ at each position divisible by $k$ (one can assume that $k$ divides $n$). The $n/k$ automata work simultaneously for $2k$ steps. After that all segments of length $k$ got their names. All automata traverse the same (quite big) graph representing the automaton $G$. The total time is $O(2k)$, and the total work is $O(n)$. ‡

For technical reasons we need to consider the following extended SP problem.

**ESP problem:**

Given strings $s$ and $p_1, p_2, \ldots, p_r$ of the same length $k$,

name consistently all prefixes of $p_1, p_2, \ldots, p_r$ and all suffixes of $s$.

A striking fact about the ESP problem is that there is an algorithm that processes prefixes and suffixes in a non symmetric fashion. In the lemma below we privilege prefixes, though one can make a reverse construction.

**Lemma 14.16 (key lemma)**

The ESP problem for strings $s$ and $p_1, p_2, \ldots, p_r$ of the same length $k$ can be solved in time $O(\log k)$, and work $O(kr + k\log k)$.

**Proof**

Assume for simplicity that $k$ is a power of two. Let us look for a computation on both $s$ and one of the $p_i$'s, which is denoted by $p$. The same processing applies to all $p_i$'s simultaneously. Compute the complete DBF for $s$ and the weak DBF for $p$ together. In the weak DBF names are given only to words of size $2^h$ starting at positions divisible by $2^h$, for any $h \geq 0$. The weak DBF is of $O(k)$ size, while the complete DBF is of $O(k\log k)$ size. For all patterns, there are $r$ weak DBF's, so the work spent on them is now $O(kr)$.

The algorithm proceeds in $\log k$ stages. Let us call an $h$-word any word whose length is divisible by $2^h$. An $h$-word is maximal if it cannot be extended to the right into a different $h$-word. The end of the maximal $h$-word starting at position $j$ is denoted by $end_h(j)$. The basic property of $end_h(j)$ is that the difference $end_h(j) - end_{h+1}(j)$ is either 0 or $2^h$.

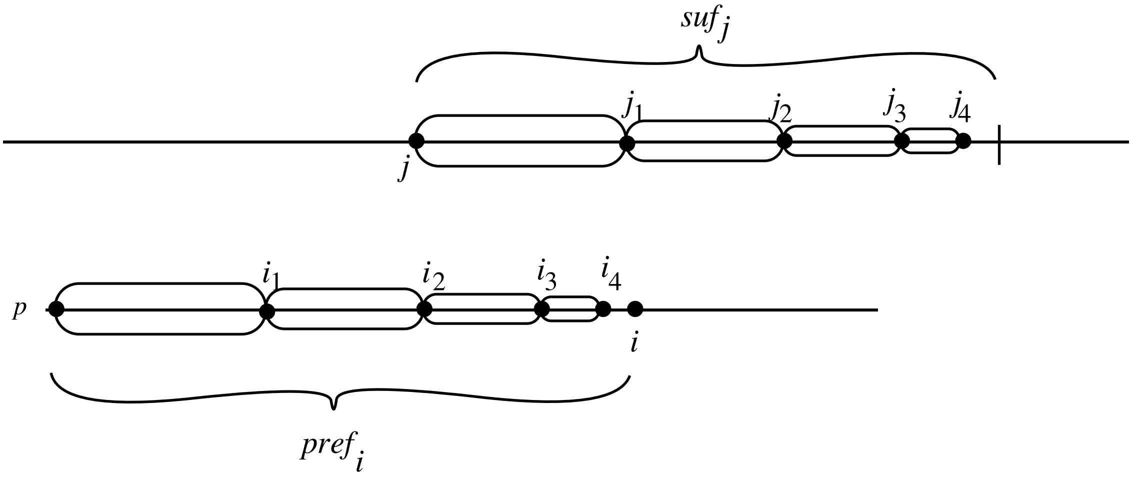


**Figure 14.6**.

In the algorithm we maintain the following invariant.

*INV*($h$): all maximal $h$-words of $s$, and all $h$-prefixes of $p$ have consistent names.

After computing the DBF for $s$, and the weak DBF for $p$, this invariant holds for $h = \log k$. In fact, the computation of the ESP problem reduces to satisfying *INV*(0). We describe how to efficiently preserve the invariant from $h$+1 to $h$.

```
procedure STAGE(h);
{ INV(h+1) holds }
begin
  for each position j in s do in parallel begin
    if $end_{h+1}(j) \neq end_h(j)$ then
      combine names of subwords
      $s[j..end_{h+1}(j)]$ and $s[end_{h+1}(j)..end_h(j)]$;
    for each (h+1)-prefix p[1..i] of p do in parallel
      combine names of p[1..j] and $p[j..j+2^h]$
      to get names for $p[1..j+2^h]$;
  end;
{ INV(h) holds }
end.
```

The procedure can be simply extended to handle all patterns $p_i$ simultaneously. Then, the whole algorithm has the following structure:

```
    for h := logn-1 downto 0 do STAGE(h).
```

$O(k)$ processors are obviously enough to process $s$, one processor per each position $j$. Hence, $O(k\log k)$ work is spent on $s$. But for a given $p_i$ of length $k$ we spend only $O(k)$ work, since at stage $h$ we process only ($h$+1)-prefixes. The total number of all $h$-prefixes, for $h$ running from 0 to log$n$, is linear. Hence, the total work spent on a single $p_i$ is $O(k)$, and it is $O(rk)$ on all $p_i$'s. This complete the proof. ‡

**Theorem 14.17**

The SP problem for two words $p$, $s$ of same length $n$ can be solved on a CRCW PRAM in logarithmic time with linear work.

**Proof**

Assume for simplicity that $n$ is divisible by log$n$. Consider the subwords $p_1$, $p_2$, …, $p_{\log n}$ of $p$ of length $n$-log$n$ starting inside the prefix of length log$n$ of $p$, see Figure 14.7.

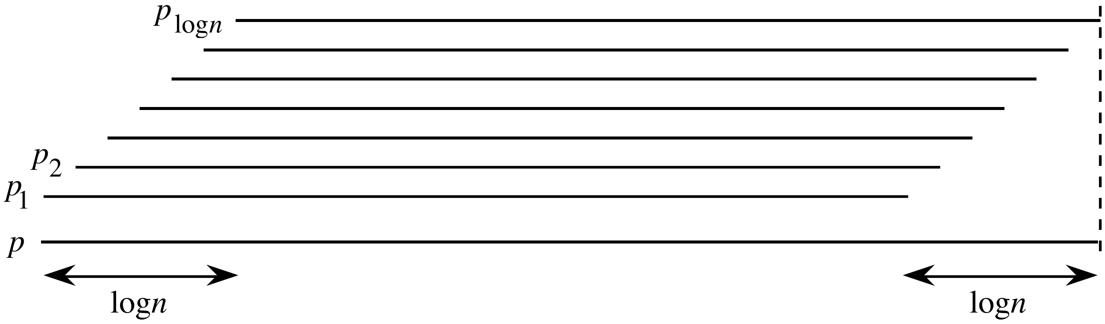


**Figure 14.7**.

Factorize the text $s$ into segments of length log$n$, and call them small patterns. We can find all occurrences of the small patterns in $p$ with $O(n)$ work, due to Lemma 14.15. The name of the small segment starting at position $j$ in $p$ is consistent with the name of a small pattern starting at that position.

Now we can factorize each $p_i$ into segments of length log$n$. We name the segment consistently with names of small patterns. The name of a small segment starting at a given position of $p$ can be found in $O(1)$ time after finding all occurrences of small patterns. Doing so, we compress $s$ into a text $s$', and each pattern $p_i$ into a text $p_i$' of length $n$/log$n$.

We solve the ESP problem for $s$' and $p_1$', $p_2$', $p_3$', …, $p_{\log n}$'. The time is logarithmic and the total work is linear due to Lemma 14.16. This proves the following:

**Claim 1**

We can compute, in logarithmic time with linear work, consistent names for all suffixes of $s$ and all prefixes of subpatterns $p_i$'s whose length is divisible by log$n$.

Consider now the prefix $\underline{p}$ of length log$n$ of $p$, and all log$n$-segments $\underline{s}_i$ of $s$. Assign one processor to each segment $\underline{s}_i$. This processor computes the SP problem for $\underline{p}$ and $\underline{s}_i$

sequentially in log$n$ time, due to Lemma 14.16. There are $n$/log$n$ processors, hence the total work is linear. In this way we have proved:

**Claim 2**

We can compute optimally consistent names for all prefixes of $\underline{p}$ and all suffixes of logarithmic-size segments $\underline{s}_i$.

Now we are ready to solve the original SP problem for $p$ and $s$. Take the prefix of $p$ of a given size $i$, and the suffix of $s$ of same size $i$. We have enough information to check in constant time if the equality $p[1\ldots i] = s[n\text{-}i\text{+}1\ldots n]$ holds. We can write $i$ as $i = i1\text{+}i2$, where $i1 \leq \log n$ and $i2$ is divisible by log$n$.

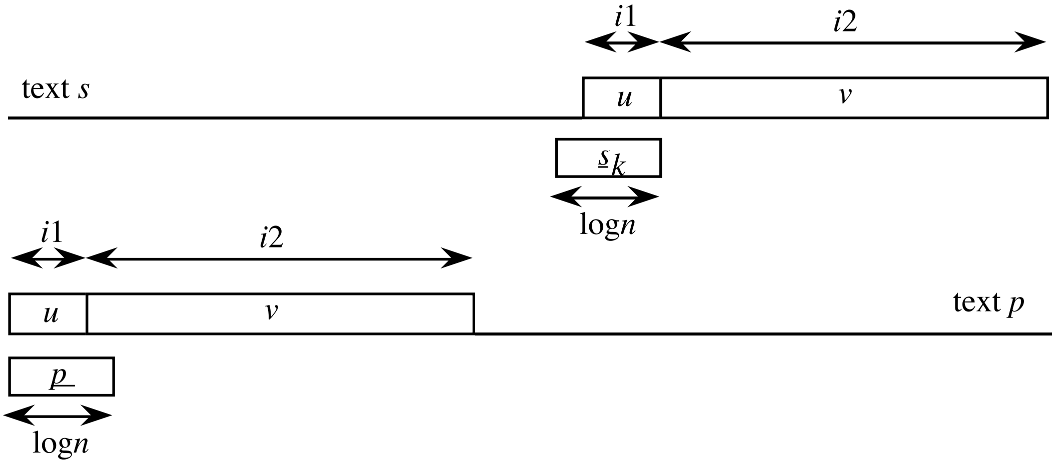


**Figure 14.8**.

Now it is enough to check names of the suffix of $s$ of length $i2$, and prefix of $p_{i1}$ of length $i2$, see Figure 14.8. This can be done in constant time, due to Claim 1, since $i2$ is divisible by log$n$. Next, we check the names of the (small) prefix of $p$ of length $i1$ and the suffix $s[ni\text{+}1\ldots n\text{-}i2]$ of a logarithmic segment $\underline{s}_k$ of $s$. This can be done in constant time due to Claim 2. We perform this operation simultaneously for all $i$. This completes the proof. ‡

## 14.4. A variation of KLP algorithm

In this section we present a variation of the KLP algorithm. Its aim is to provide a version the KLP algorithm that extends easily to the two-dimensional case. The basic parts of KLP algorithm and the dictionary algorithm (parallel version of KMR algorithm) are constructions of dictionaries which enable to check in a constant time whether some factors of text or pattern match.

Recall that factors whose length is a power of two are said to be *basic factors*. One can also assume that the size of the pattern is a power of two. If not, then we can search for two subpatterns which are prefix and suffix of the pattern, and whose common size is the largest possible power of two. A basic factor $f$ of the pattern is called a *regular basic factor* iff an occurrence of it starts in the pattern at a position divisible by the size of $f$. The basic property of regular factors is that a pattern of size $n$ has $O(n)$ regular basic factors. This fact implies the key lemma, which has already been proved in Chapter 9.

**Lemma 14.17 (key lemma )**

Consider $t$ patterns, each of size $M$. There is an algorithm to locate all of them in a one-dimensional string or a two-dimensional image of size $N$ in time $O(\log M)$ with total work $O(N\log M+tM)$.

**Proof**

The algorithm is derived form the parallel version of KMR algorithm. If we look closer at the pattern matching algorithm derived from KMR algorithm, then it is easy to see that the total work of the algorithm is proportional to the number of considered factors. We can assume w.l.o.g. that the size $M$ of patterns is a power of two. So, in patterns, only regular factors need to be processed. Hence, the work spent on one pattern is $O(M)$. Similarly, for the $t$ patterns of size $M$, the work is $O(tM)$. This completes the proof. ‡

Let us fix the integer $k$ as a parameter of order $\log m$. Lengths of texts are assumed to be multiples of $k$. The factors of length $k$ of texts and patterns are called *small factors*. The small factors which have an occurrence at a position divisible by their size are called *regular small factor*. Let $x$ be a string of length $n$, and let $small(x, i)$ be the small factor of $x$ starting at position $i$ ($1 < i \leq n$). The string $small(x, i)$ is well defined if x is padded with $k$-1 special endmarkers at the end. Define the string $\underline{x} = \underline{x}_1\underline{x}_2\ldots\underline{x}_n$ by

$$\underline{x}_i = name(small(x, i)), \text{ for } 1 < i \leq n,$$

where $name(f)$ is the name of the regular small factor equal to $f$. Names are assumed to be consistent: if $small(x, i) = small(x, j)$ then $\underline{x}_i = \underline{x}_j$.

The string $\underline{x}$ is called here the *dictionary of small factors* of $x$. A simple way to compute such dictionary is to use the parallel version of the Karp-Miller-Rosenberg algorithm. This gives $n\log\log n$ total work, very close to optimal. the optimality can be achieved, if the alphabet is of constant size, using a kind of the "four Russian trick", as explained below.

In this paragraph, we consider for simplicity that the alphabet is binary, and that $k = \log m/4$. There are potentially only $m^{1/2}$ binary strings of length $2k$. For each of them, we can precompute the names of all their small factors of length $k$. These names can be the integers having the corresponding factors as binary representations. We have enough processors for all the $m^{1/2}$ binary strings of length $2k$ to do that, since the total number of processors must be $O(n/\log m)$. Then, to produce $\underline{x}$ the dictionary of small factors of a string $x$ of length $n$ ($\geq m$), it is first factorized into segments of length $2k$. Independently and at the same time each segment is treated. One processor can encode it into a binary number in $O(\log m)$ time, looking at the precomputed table of names of its small factors, and writing down $k$ consecutive entries of the string $\underline{x}$ in time $O(k) = O(\log m)$. Thus, the overall procedure works in time $O(\log m)$ with $O(n/\log m)$ processors. This proves the next lemma on fixed alphabets.

The breakthrough for this approach is done by KLP algorithm: the assumption on fixed-size alphabet can be dropped. This is because only names corresponding to regular small factors have to be considered in the naming procedure for all factors (two factors whose names are not equal to any regular small factor can have the same name, even if they are equal). The total length of all small regular factors is linear, and each of them has logarithmic size. The Aho-Corasick pattern machine for all regular basic factors can be constructed by an optimal algorithm, due to the linearity of their total length. But, such an approach does not work if we want to make a pattern matching machine for all small factors.

**Lemma 14.19**

The dictionary of small factors can be computed in $O(\log m)$ time with linear work.

The description of the string-matching algorithm of the section is written in a way suitable for the two-dimensional extension of Section 14.5. The algorithm for two dimensions is conceptually a natural extension of the one-dimensional case. The basic parts of one-dimensional and two-dimensional pattern-matching algorithms are similar:

— computation of the dictionary of small factors,

— compression of strings by encoding disjoint $\log m$-size blocks by their names, and

— application of the algorithm of Lemma 14.18.

Two auxiliary functions are necessary: *shift* and *compress*. Let $k = \log m$. We assume that $n$ (length of *text*) and $m$ (length of *pat*) are multiples of $k$. For $0 \leq r \leq k$-1, let us denote by *shift*(*pat*, *r*) (see Figure 14.9) the string defined by

$$shift(pat, r) = pat[1+r\ldots m\text{-}k+r].$$

For a string $z$ let us denote by *compress*($z$) the string defined by

$$compress(z) = \underline{z}_1\ \underline{z}_k\ \underline{z}_{2k}\ \ldots \underline{z}_{(h-1)k},$$

where $h = |z|/k$. The string *compress*($z$) contains the same information as $z$, but is shorter by a logarithmic reduction factor. Each letter of the new string encodes a logarithmic size block of $z$. Intuitively speaking *compress*($z$) is a concatenation of names of consecutive small factors, which compose the string $z$. Small factors (strings of length $\log m$) are replaced by one symbol. The compression ratio is $\log m$. In the following, $\underline{p}_i$ is the name of the small factor of *pat* starting at position $i$ in *pat*, and $\underline{t}_i$ is the name of the small factor of *text* starting at position $i$ in *text*.

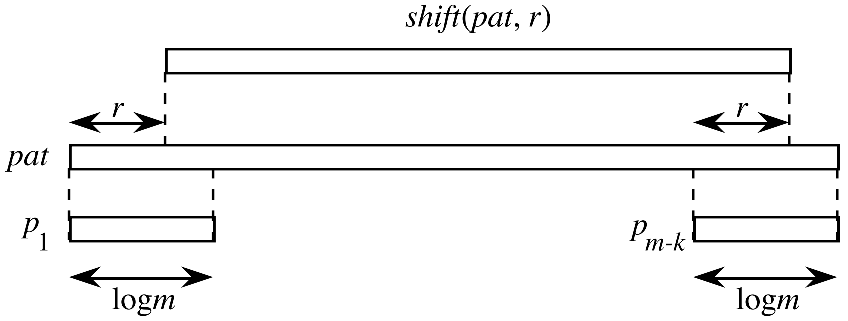


**Figure 14.9**. Operation shift. To test a match it is enough to identify the part *shift*(*pat*, *r*), and the first and last full small factors of the pattern, $p_1$ and $p_{m\text{-}k}$.
The identification of *shift*(*pat*, *r*) is done by searching for its compressed version.

The correctness of the algorithm below is based on the following obvious observation: an occurrence of *pat* occurs at position *i* in *text* iff the following conditions are satisfied

(*) *compress*(*shift*(*pat*, *k*-(*i* mod *k*))) starts in *compress*(*text*) at position (*i* div *k*),
$\underline{p}_1 = \underline{t}_{i+1}$, and $\underline{p}_{m\text{-}k} = \underline{t}_{i+m\text{-}k}$.

The condition (*) is illustrated by Figure 14.10 (see also Figure 14.9). The structure of the algorithm based on condition (*) is given below.

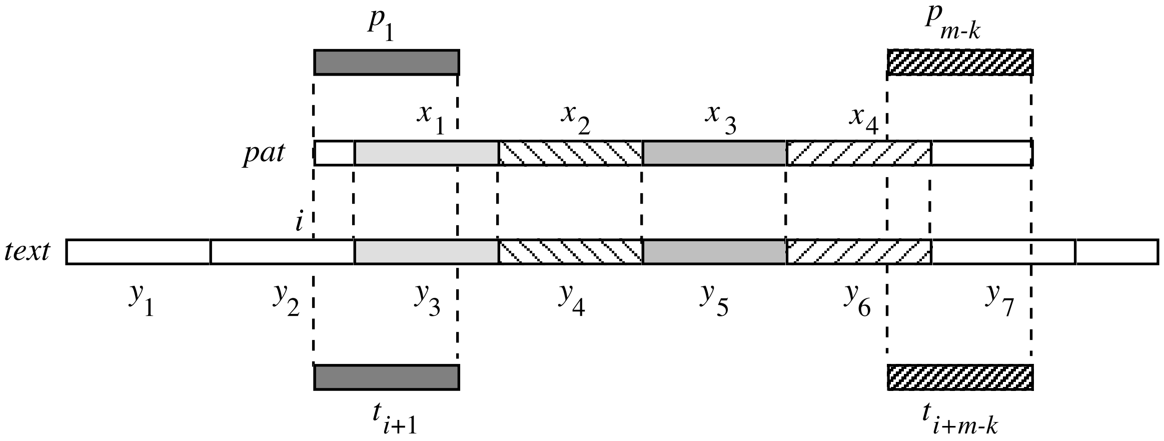


**Figure 14.10**. Test at position *i* in *text*. $x_1x_2x_3x_4$ = *compress*(*shift*(*pat*, *k*-(*i* mod *k*)+1)), *compress*(*text*) = $y_1y_2y_3y_4y_5y_6y_7$; *pat* occurs at position *i* in *text* iff $x_1x_2x_3x_4$ starts at the 3rd position of $y_1y_2y_3y_4y_5y_6y_7$, $\underline{p}_1 = \underline{t}_{i+1}$, and $\underline{p}_{m\text{-}k} = \underline{t}_{i+m\text{-}k}$.

```
Algorithm { parallel optimal string-matching }
begin
  build the common dictionary of small factors of pat and text;
  construct tables $\underline{p}$ and $\underline{t}$;
  localize all patterns compress(shift(pat,0)),
    compress(shift(pat,1)),.., compress(shift(pat,k-1))
    in compress(text) by the algorithm of Lemma 14.18;
  for each position i do in parallel
    { in constant time by one processor
      due to previous localizations }
    if condition (*) holds for i then
      report the match at position i;
end.
```

**Theorem 14.20**

The above algorithm solves optimally the string-matching problem on a CRCW PRAM. It runs in $O(\log m)$ time with $O(n/\log m)$ processors (the total work is linear).

**Proof**

The compressed text has size $n/\log m$. There are $\log m$ compressed patterns, each of size $m/\log m$. Hence, according to Lemma 14.18, the total work, when applying the algorithm of this lemma, is $O((n/\log m)\log m + \log m(m/\log m)) = O(n)$. This completes the proof. ‡

## 14.5. Optimal two-dimensional pattern matching

In this section, we show how the algorithm of the previous section generalizes to two-dimensional arrays, and leads to an optimal two-dimensional pattern matching algorithm. We assume w.l.o.g. that the pattern and the text are squares: *PAT* is an $m\times m$ array, $T$ is an $n\times n$ array. The general case of rectangular arrays can be handled in the same way. But then the shorter side of the pattern must be is at least $\log m$ long, that is, the pattern must not be thin. Otherwise, the algorithm of section 14.4 can be adapted to this specific problem.

Recall that subarrays whose length is a power of two are said to be *basic subarrays*. We assume that $m$ is a power of two. If not, then we can search for four (possibly overlapping) subpattern whose length is a power of two. We say that a basic subarray of shape $s\times s'$ is *regular* iff it starts at a position whose horizontal and vertical coordinates are, respectively, multiples of $s$ and $s'$. The *size* of the two-dimensional image is its area.

There is a fifth type of subarrays in addition to regular and/or basic subarrays: *thin subarrays*. It is a natural generalization of small factors of the previous section to the two-dimensional case. Thin factors are $m$×log$m$ subarrays of the pattern, and $n$×log$m$ subarrays of text. They arise if we cut the two-dimensional pattern by $m$/log$m$-1 lines at distance log$m$ from each others (see Figure 14.11).

The algorithm below provides an optimal two-dimensional matching. It is based on the fact that the key lemma of Section 14.4 (Lemma 14.18) works similarly for two-dimensional images. The compression realized with the help of small factors in the case of strings, is done by thin subarrays in the case of two-dimensional. The text array as well as the pattern are cut into thin pieces on which the main part of the search is done. We assume, for the simplicity of presentation, that we deal with images whose sides have lengths divisible by $m$. Formally, the cut-lines are columns log$m$, 2log$m$, …, $n$-log$m$ of the text array, see Figure 14.11. There are $n$/log$m$-1 cut lines.

Let us denote by $P_j$ the $j$-th column of $PAT$. For $0 \leq r \leq k$-1 denote by $SHIFT(PAT, r)$ the rectangle composed of columns $P_{1+r}$, …, $P_{m\text{-}k+r}$. For a rectangle $Z$ denote by $COMPRESS(Z)$ the array $\underline{Z}_1\underline{Z}_k\underline{Z}_{2k} \ldots \underline{Z}_{(h\text{-}1)k}$, where $h = |Z|/k$, and $\underline{Z}_i$ is the column of names of log$m$-size rows of the thin subarray $Z_i$. The rectangle $COMPRESS(Z)$ contains the same information as $Z$, but in smaller form. Each column of the new rectangle encodes a thin subarray. Two-dimensional (thin) objects are reduced to one-dimensional objects. The compression ratio on sizes of arrays is log$m$. We denote by $\underline{P}_i$ the compressed thin subarrays of $PAT$ starting at column $i$, and by $\underline{T}$ the array of names of log$m$-size factors of rows of $T$. The algorithm of the section implements the same idea as in the former section. The correctness of the algorithm is based on the following obvious observation (see Figure 14.11). An occurrence of $PAT$ occurs at ($i$, $j$) in the image $T$ iff the following condition is satisfied:

(**) $COMPRESS(SHIFT(PAT, k\text{-}(j \bmod k)))$ occurs in $COMPRESS(T)$ at position ($i$, $j$ div $k$), $\underline{P}_1$ occurs at position ($i$, $j$) in $\underline{T}$ , and $\underline{P}_{m\text{-}k}$ occurs at position ($i$, $j$+$m$-$k$) in $\underline{T}$.

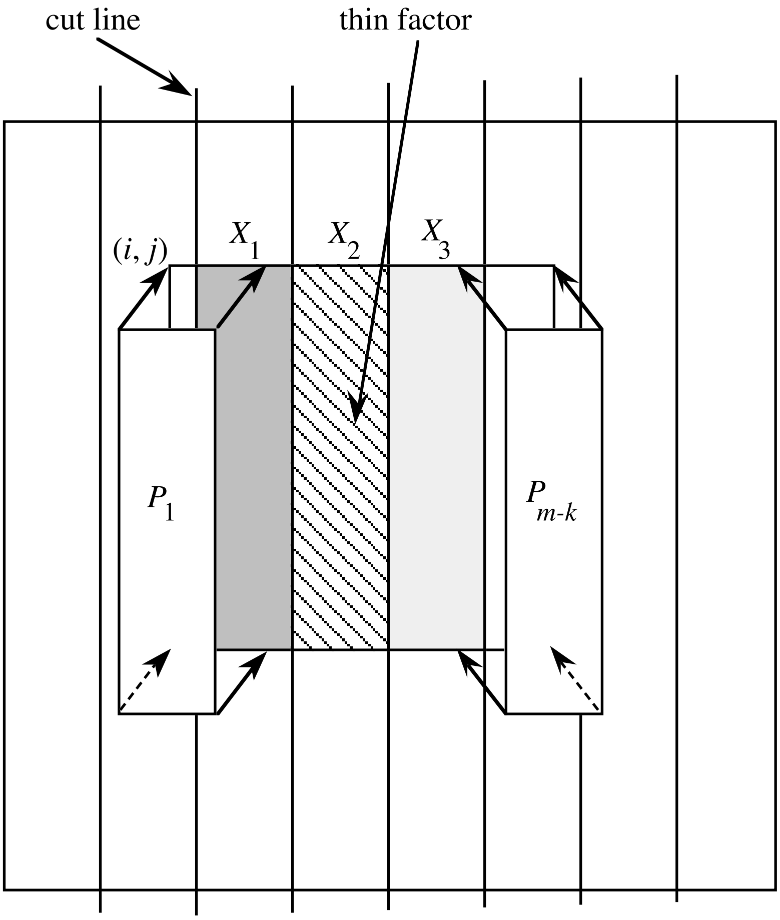


**Figure 14.11**. Partitioning of the pattern and the text arrays by cut-lines.We search for the compressed part of pattern image $\underline{X_1}\underline{X_2}\underline{X_3}$ in the compressed text array, and then search for the first and last thin subarrays of *PAT*, $P_1$ and $P_{m\text{-}k}$.

The structure of the two-dimensional algorithm is essentially the same as the algorithm of section 14.4. It yields the following result.

**Theorem 14.21**

Under the CRCW PRAM model, the algorithm below solves optimally the two-dimensional pattern matching problem in time $O(\log m)$ and linear work.

**Proof**

The proof is similar to that of Theorem 14.20. It is a simple application of Lemma 14.18. Here the size of the compressed text array is $N/\log m$ ($N = n^2$). The number of shifted patterns is still $\log m$. So, the total work is $(N/\log m)\log m + \log m(M/\log m) = O(N)$. ‡

```
Algorithm { optimal two-dimensional pattern matching }
begin
  compute the dictionary of small subarrays together
    for rows of $PAT$ and $T$;
  construct tables of names $\underline{P}$ and $\underline{T}$;
  localize patterns $COMPRESS(SHIFT(PAT,0))$,
    $COMPRESS(SHIFT(PAT,1))$,.., $COMPRESS(SHIFT(PAT,k-1))$
    in the image $COMPRESS(T)$ by the algorithm of Lemma 14.18;
  for each $j$ do in parallel
    find all occurrences of the first and last columns of $\underline{P}$
    in the $j$-th column of $\underline{T}$ ;
    { of the first and last thin factors of pattern,
      one-text/one-pattern algorithm }
  for each position $(i,j)$ of $T$ do in parallel
    { in constant time by one processor for each $(i,j)$
      due to the information already computed }
    if condition (**) holds for $(i,j)$ then
      report a match at position $(i,j)$;
end.
```

## 14.6. Recent approach to optimal parallel computation of witness tables: the splitting technique.

Quite recently a new approach was discovered to compute the witness table *WIT* of the pattern. It uses what is called the *splitting technique*. We sketch here only the basic ideas of the technique. Several open problems have been cracked by this approach. We list the four most interesting problems that are so solved positively:

**1** — existence of a deterministic optimal string-matching algorithm working in $O(\log m)$ time on a CREW PRAM,

**2** — existence of a randomized string-matching algorithm working in constant time with a linear number of processors on a CRCW PRAM,

**3** — existence of an $O(\log n)$ time string-matching algorithm working on a *hypercube* computer with a linear number of processors,

**4** — existence of an $O(n^{1/2})$ time string-mtching algorithm on a *mesh-connected* array of processors.

**Theroem 14.22**

There exist algorithms for each of the four points listed above.

The technique also provides a new optimal deterministic string-matching algorithm working in $O(\log\log n)$ time on a CRCW PRAM.

Recall that the CRCW PRAM is the weakest model of the PRAM with concurrent writes (whenever such writes happen the same value is written by each processor), and the CREW PRAM is the PRAM without concurrent writes. Vishkin's algorithm (see Section 14.1) works in $O(\log^2 n)$ time if implemented on a CREW PRAM. An optimal $O(\log n \log\log n)$ time algorithm for the CREW PRAM model was given before by Breslauer and Galil.

The power of the splitting technique is related to the following recurrence relations:

$$(*)\ \ time(n) = O(\log n) + time(n^{1/2}),$$

$$(**)\ \ time(n) = O(1) + time(n^{1/2}).$$

**Claim 1:**

The solutions to recurrence relations (*) and (**) satisfy, respectively:

$$time(n) = O(\log n) \text{ and } time(n) = O(\log\log n).$$

Let $P$ be a pattern of length $m$. The witness table $WIT$ is computed only for the positions inside the interval $FirstHalf = [1...m/2]$. We say that a set $S$ of positions is *k-regularly sparse* iff $S$ is the set of positions $i$ inside *FirstHalf* such that $i$ mod $k = 1$. If $S$ is regularly sparse then let *sparsity(S)* be the minimal $k$ for which $S$ is $k$-regularly sparse. Let us notee

$$P^{(q)} = P(q)P(k+q)P(2k+q)P(3k+q)...,$$

for $1 \le q \le k$. Denote by *SPLIT(P, k)* the set of strings $P^{(q)}$, $1 \le q \le k$.

**Example**

*SPLIT*(*abacbdabadaa*, 3) = {*acad*, *bbba*, *adaa*}. ‡

Assume $S$ is a $k$-regularly sparse set of positions. Denote by *COLLECT*($P$, $k$) the procedure which computes values of the witness table for all positions in $S$, assuming that the witness tables for all strings in *SPLIT*($P$, $k$) are known.

**Claim 2:**

Assume the witness tables for all strings in *SPLIT*($P$, $k$) are known. Then *COLLECT*($P$, $k$) can be implemented by an optimal parallel algorithm in $O(\log m)$ time on a CREW PRAM, and in $O(1)$ on a CRCW PRAM.

The next fact is more technical. Denote by *SPARSIFY*($P$) the function which computes the witness table at all positions in *FirstHalf* except at a set $S$ that is $k$-regularly sparse. The value returned by the function is the sparsity of $S$; when $k > m/2$, $S$ is empty. In fact, the main role of the function is the sparsification of non-computed entries of the witness table.

**Claim 3:**

*SPARSIFY*($P$) can be computed by an optimal parallel algorithm in $O(\log m)$ time on a CREW PRAM, and in $O(1)$ on a CRCW PRAM.

The value $k$ of *SPARSIFY*($P$) satisfies $k \geq m^{1/2}$.

The basic component of the function *SPARSIFY* is the function *FINDSUB*($P$) that finds a non-periodic subword $z$ of $P$ of size $m^{1/2}$, or reports that there is no such subword. A similar construction is used in the sieve algorithm of Section 14.2. It is easy to check whether the prefix $z'$ of size $m^{1/2}$ is non-periodic or not (we have a quadratic number of processors with respect to $m^{1/2}$); if $z'$ is periodic we find the continuation of the periodicity and take the last subword of size $m^{1/2}$. The computed segment $z$ can be preprocessed (its witness table is computed). Then, all occurrences of $z$ are found, and based of them the sparsification is performed.

We present only how to compute witness tables in $O(\log m)$ time using $O(m\log m)$ processors. The number of processors can be further reduced by a logarithmic factor, which makes the algorithm optimal. The algorithm is shown below as procedure *Compute_by_Splitting*.

According to the recurrence relation (*), the time for computing the witness table using the procedure *Compute_by_Splitting* is $O(\log m)$ on a CREW PRAM, and $O(\log\log m)$ on a CRCW PRAM. Implementations of the subprocedures *SPARSIFY* and *COLLECT* on an hypercube and on a mesh-connected computer give the results stated in points 3 and 4 above.

```
procedure Compute_by_Splitting($P$);
begin
  $k$ := 1;
  while $k \leq m/2$ do begin
    $k$ := SPARSIFY($P$);
    ($P^{(1)}$, $P^{(2)}$,.., $P^{(k)}$) := SPLIT($P$, $k$);
    for each $q$, $1 \leq q \leq k$ do in parallel
      Compute_by_Splitting($P^{(q)}$);
    COLLECT($P$, $k$);
  end;
end;
```

The constant-time randomized algorithm (point 2) is much more complicated to design. After achieving a large sparsification, the algorithm stops further calls, and starts a special randomized iteration. Indeed, it is more convenient to consider an iterative algorithm. The definition of *SPARSIFY*(*P*) needs to be slightly changed: the new version sparsifies the set *S* of non-computed entries of the witness table assuming that *S* is already sparse. The basic point is that the sparsity grows according to the inequality:

$$k' \geq k.(m/k)^{1/2},$$

where *k* is the old sparsity, and *k*' is the new sparsity of the set *S* of non-computed entries. The randomization starts when *sparsity* ≥ $m^{7/8}$. This is achieved after at most three deterministic iterations.

The constant-time string-matching requires also a quite technical (though very interesting) construction of several deterministic samples in constant time. But this is outside the scope of the book. We refer the reader to bibliographic notes for details.

## Bibliographic notes

The first optimal parallel algorithm for string-matching was given by Galil in [Ga 85]. The algorithm is optimal only for alphabets of constant size. Vishkin improved on the notion of slow duels of Galil, and described the more powerful concept of (fast) duels that leads to an optimal algorithm independently of the size of the alphabet [Vi 85]. The optimal parallel string-matching algorithm working in $O(\log^2 n)$ time on a CREW PRAM is also from Vishkin [Vi 85].

The idea of witnesses and duels was later used by Vishkin in [Vi 91] in the string-matching by sampling. The concept of deterministic sampling is very powerful. It has been used by Galil to design a constant-time optimal parallel searching algorithm (the preprocessing is not included). This result was an improvement upon the $\log^* n$ result of Vishkin, though practically $\log^* n$ can be also treated as a constant.

If preprocessing is included, the lower bound for the parallel time of string-matching is loglog*n*. It has been proved by Breslauer and Galil [BG 90], who also gave an optimal loglog*n* time algorithm. The algorithm uses a scheme similar to an optimal algorithm for finding the maximum of *n* integers by Shiloach and Vishkin [SV 81]. Recently it has been shown that it is possible to combine a loglog*n* time preprocessing with the constant-time optimal parallel search of Galil, see [C-R 93b].

Section 14.3 is adapted from the suffix-prefix approach of Kedem, Landau, and Palem [KLP 89]. The counterpart to the relative simplicity of their algorithm is the use of a large auxiliary space (though space $n^{1+\varepsilon}$ is enough, for any $\varepsilon>0$, with the help of some arithmetic tricks). Algorithms of Galil and Vishkin require only linear space, but their algorithms are much more sophisticated. The assumption on the size of alphabet in Section 14.3 can be dropped (see [KLP 89]). We do not know how to convert the KLP suffix-prefix algorithm into an optimal fast parallel string-matching algorithm working on a CREW PRAM. Such an algorithm working in $O(\log^2 n)$ time was given by Vishkin, see [Vi 85].

The "four Russian trick" of encoding small segments by numbers is a classical method. It is used in particular in [Ga 85], and in [ML 85] for string problems.

The optimal $O(\log n)$ time parallel two-dimensional pattern matching is from [CR 92]. An optimal searching algorithm running in $O(\log\log n)$ time is presented in [ABF 92b]. The splitting technique of Section 14.6 is adapted from [C-R 93c]. Consequences of the technique can also be found in this paper.

## Selected references

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# 15. Miscellaneous.

The chapter presents several interesting questions on strings that are not already considered in previous chapters. They are: *string-matching by hashing* and its extension to two-dimensional pattern matching, *tree-pattern matching* as an example of pattern matching questions on trees, *shortest common superstrings*, *cyclic equality of words* and *Lyndon factorization of words*, *unique decipherability* problem of codes, *equality of words over partially commutative alphabets*, and breaking paragraphs into lines. The treatment of problems is not always done in full details.

## 15.1. String matching by hashing: Karp-Rabin algorithm

The concept of hashing and fingerprinting is very successful from the practical point of view. When we have to compare two objects $x$ and $y$ we can look at their "fingerprints" given by $hash(x)$, $hash(y)$. If the fingerprints of two objects are equal, there is a strong suspicion that they are really the same object, and we can apply then a more deeper test of equality (if necessary). The two basic properties of fingerprints are:

— efficiently computable,

— highly discriminating: it is unlikely to have both $x \neq y$ and $hash(x) = hash(y)$.

The idea of hashing is used in the Karp-Rabin string-matching algorithm. The fingerprint $FP$ of the pattern (of length $m$) is computed first. Then, for each position $i$ on the text, the fingerprint $FT$ of $text[i+1...i+m]$ is computed. If ever $FT = FP$, we check directly if the equality $pat = text[i+1...i+m]$ really holds.

Going from a position $i$ on the text to the next position $i$+1 efficiently, requires another property of hashing functions for this specific problem (see Figure 15.1):

— $hash(text[i+1...i+m])$ should be easily computable from $hash(text[i...i+m-1])$.

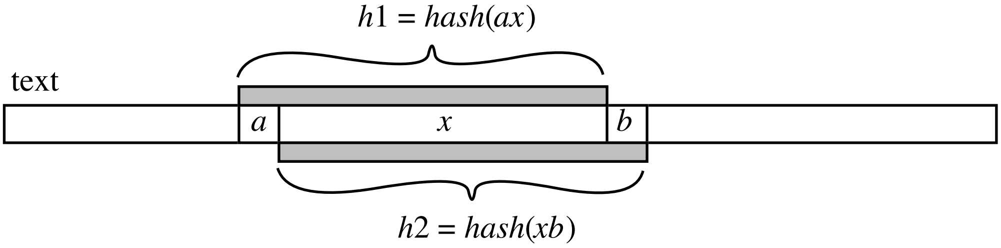

**Figure 15.1**. $h2$ should be easily computable from $h1$;
$h2 = f(a, b, h1)$, where $f$ is easy to compute.

Assume for simplicity that the alphabet is {0,1}. Then each string $x$ of length $m$ can be treated as a binary integer. If $m$ is large, the number becomes too large to fit into a unique memory cell. It is convenient then to take as fingerprint the value "$x$ mod $Q$", where $Q$ is a prime number as large as possible (for example the largest prime number which fits into a memory cell). The fingerprint function is then

$$hash(x) = [x]_2 \bmod Q,$$

where $[u]_2$ is the number whose binary representation is the string $u$ of length $m$. All strings arguments of *hash* are of length $m$. Let $g = 2^{m-1} \bmod Q$. Then, the function $f$ (see Figure 15.1) can be computed by the formula:

$$f(a, b, h) = 2(h\text{-}ag)+b.$$

Proceeding that way, the third basic property of fingerprints is satisfied: $f$ is easily computable. This is implemented in the algorithm below.

```
Algorithm Karp-Rabin; { string-matching by hashing }
begin
  $FP$ := [$pat$[1..$m$]]$_2$ mod $Q$;   $g$ := $2^{m-1}$ mod $Q$;
  $FT$ := [$text$[1..$m$]]$_2$ mod $Q$;
  for $i$ := 0 to $n$-$m$ do begin
    if $FT$ = $FP$ { small probability } then
      check equality $pat$ = $text$[$i$+1..$i$+$m$]
      applying symbol by symbol comparisons, { cost = $O(m)$ }
      and report a possible match;
    $FT$ := $f$($text$[$i$+1], $text$[$i$+$m$+1], $FT$);
  end;
end.
```

The worst case complexity of the algorithm is quadratic. But it could be difficult to find interesting input data causing the algorithm to make a quadratic number of comparisons (the non-interesting example is when *pat* and *text* consist only of repetitions of the same symbol). On the average, the algorithm is fast, but the best time complexity is still linear. This is to be compared with the lower bound of string-matching on the average (which is $O(n\log m/m)$), and the best time complexity of Boyer-Moore type of algorithms (which is $O(n/m)$). String-matching by hashing produces a straightforward $O(\log n)$ randomized optimal parallel algorithm because the process is reduced to prefix computations.

One can also apply other hashing functions satisfying the three basic properties above. The original Karp-Rabin algorithm chooses the prime number randomly.

Essentially, the idea of hashing can also be used to the problem of finding repetitions in strings and arrays (looking for repetitions of fingerprints). The algorithm below is an extension of Karp-Rabin algorithm to two-dimensional pattern matching. Let *m* be the number of rows of the pattern array. Fingerprints are computed for columns of the pattern, and for factors of length *m* of columns of the text array. The problem then reduces to ordinary string-matching on the alphabet of fingerprints. Since this alphabet is large, an algorithm whose performance is independent of the alphabet is actually required.

```
Algorithm two-dimensional pattern matching by hashing;
{ $PAT$ is an $m \times m'$ array, $T$ is an $n \times n'$ array }
begin
  $pat$ := $hash(P_1)…hash(P_{m'})$, where $P_j$ is the $j$-th column of $PAT$;
  $text$ := $hash(T_1)…hash(T_{n'})$, where $T_j$ is the prefix of length $m$
                               of the $j$-th column of $T$;
  for $i$ := 0 to $n-m$ do begin
    if $pat$ occurs in $text$ at position $j$ then
      check if $PAT$ occurs in $T$ at position $(i, j)$
      applying symbol by symbol comparisons, { cost = $O(mm')$ }
      and report a possible match;
    if $i \neq n-m$ then { shift one row down }
      for $j$ := 1 to $n'$ do
        $text[j]$ := $f(T[i+1, j], T[i+m+1, j], text[j])$;
  end;
end.
```

## 15.2. Efficient tree-pattern matching

The pattern matching problem for trees consists in finding all occurrences of the pattern tree *P* in the host tree *T*. The sizes (number of nodes) of *P* and *T* are, respectively, *m* and *n*. An example of occurrence of a pattern *P* in a tree *T* is shown in Figure 15.2.

We consider rooted trees whose edges are labelled by symbols. We assume that the edges leading to the sons of the same node have distinct labels. If the tree is ordered (the sons of each node are linearly ordered) then this assumption can be dropped, because then the number of a son is an implicit part of the label.

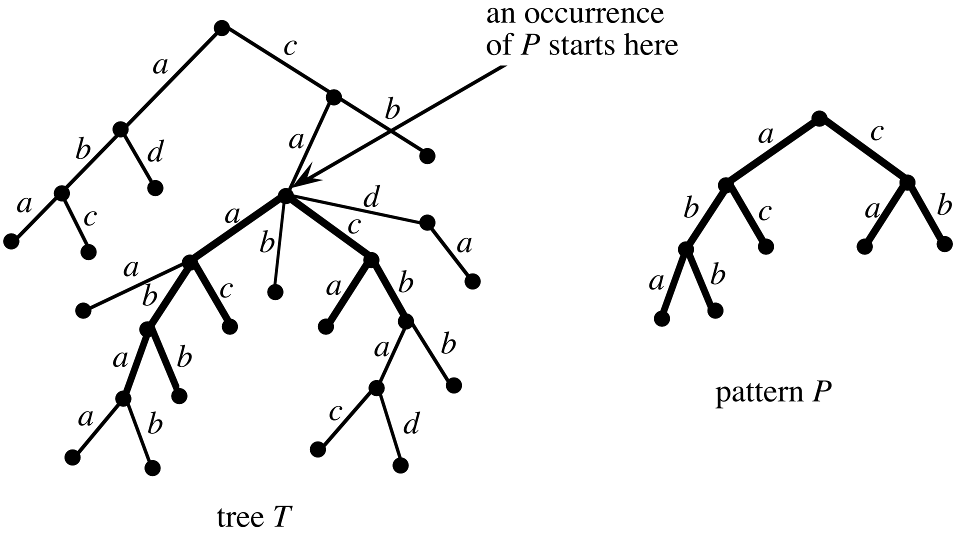

**Figure 15.2**. An occurrence of pattern *P* in the tree *T*.

Let *p*(*v*) be the path from the root of *P* to the node *v* in *P*. The previous assumption allows to identify this path with its label (the string of labels of edges along the path). The paths *p*(*v*)'s are called here node-paths. We say that a path (string) *p* occurs at node *w* if there is a path down the tree starting at *w* and labelled by *p*. Then, we say that pattern *P* occurs at node *w* in *T* iff paths *p*(*v*) occur at *w*, for all leaves *v* of *P*. The usual string-matching problem for a single pattern is a special case of the tree-pattern matching problem. In this case *P* and *T* are single paths. If the pattern is a single path and *T* is an arbitrary tree, then, the problem is also easy to carry out. Just build the KMP string-matching automaton *G* for *P*, and traverse the tree *T* in a DFS or BFS order computing the occurrences of *P* along the paths. The total time is linear. In fact, the same procedure can be applied if the set of all *p*(*v*)'s is suffix-free (a set of strings is suffix-free if no string is a suffix of another one in the set).

**Lemma 15.1** (easy tree-pattern matching)

If the set of all node-paths corresponding to leaves of *P* is suffix-free, then we can find all occurrences of *P* in *T* in linear time.

**Proof**

Construct the multi-pattern string-matching automaton *G*, where the set of string-patterns is given by all *p*(*v*)'s. Then, traverse *T* using *G*, and, for each node *w* where ends an occurrence of *p*(*v*) for some leaf *v*, record it in the ancestor *u* of *w* at distance $height_P(v)$ from *w*. There is a linear number of such recordings due to the fact that no *p*(*v*) can end on a same node. Afterwards, we check for each node *u* if it has the record for each leaf *v* of *P*. If yes, then *u* is the beginning of an occurrence of *P* in *T*. Altogether this takes linear time. ‡

We say that a pattern is a simple *caterpillar* if it consists of one path, called the *backbone*, and edges leading from a backbone to leaves (see Figure 15.3). The edges of the backbone are labelled by $a$, and all other edges are labelled by $b$.

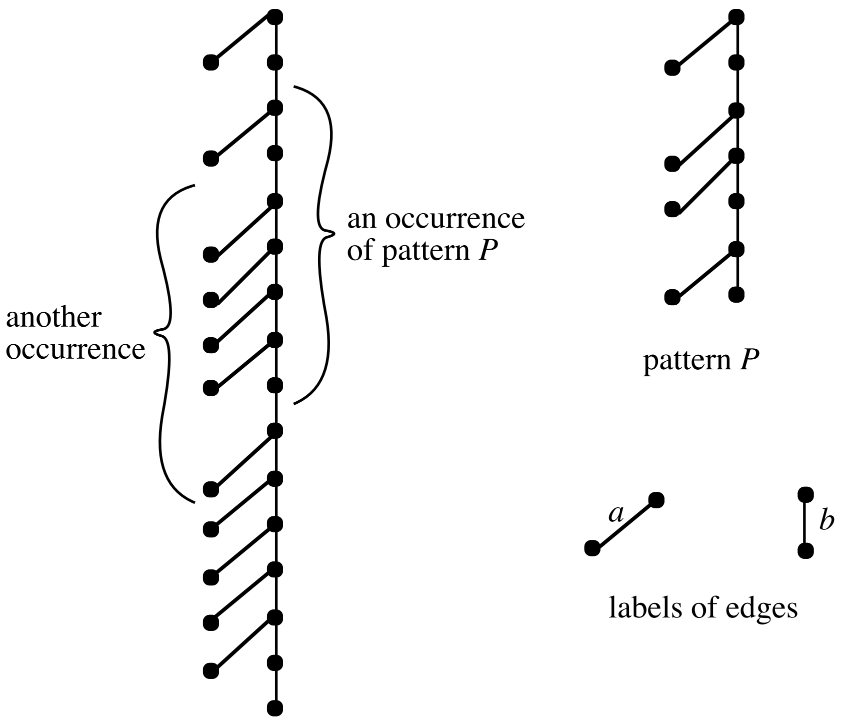

**Figure 15.3**. The tree-pattern matching corresponds here to string-matching with don't cares, where *text* = 1010111101111100, and *pat* = 1Ø11Ø1Ø.

**Lemma 15.2** (easy tree-pattern matching)

Let $P$ and $T$ be simple caterpillars. All occurrences of $P$ in $T$ can found in time $O(n\log^2 n)$.

**Proof**

The problem reduces to the string-matching with don't care symbols, which has the required complexity (in fact even slightly smaller), see Chapter 11. We place 1 on a given node of the backbone if there is a $b$-edge outgoing that node, otherwise we place 0. The pattern is processed similarly, except that instead of zeros we put don't care symbols Ø, see Figure 15.3. This symbol matches any other symbol. In this way, $P$ and $T$ are substituted by two strings. The string-matching with don't care symbols is then applied. This completes the proof. ‡

**Lemma 15.3** (easy tree-pattern matching)

Assume that the pattern tree $P$ contains a suffix-free set $S$ of size $k$ of node-paths. Then, all occurrences of $P$ in $T$ can be found in time $O(nm/k + m\log m)$.

**Proof**

First we show how to find such a set $S$, when it is known to exists. $S$ is found by constructing the suffix tree for the set of all reversed node-paths with added endmarker #. Afterwards, edges labelled with # are removed. This guarantees that there is a node for each reversed node-path. This suffix tree can be constructed in $O(m\log m)$ time adapting the construction of suffix trees for a single string. The path $p(v)$ is not a suffix of $p(v')$ if the node corresponding to $p(v)^R$ in the constructed suffix tree is not an ancestor of node corresponding to $p(v')^R$. The assumption of the lemma implies that there are at least $k$ leaves in the suffix tree. Choose any $k$ leaves. They correspond to a suffix-free set $S$ of node-paths of $P$. In this way, $S$ is built.

Then, identify $S$ with the sample sub-pattern of $P$ consisting only of the node-paths of $P$ which are in $S$. We can find all occurrences of the sample $S$ in linear time, due to Lemma 15.1. It can be checked that there are at most $n/k$ occurrences of $S$ in $T$. For each of the occurrences of the sample, we check by a "naive" $O(m)$-time algorithm a possible occurrence of the whole pattern $P$. This takes $O(nm/k)$ time. Globally, the matching takes $O(nm/k + m\log m)$ time as announced in the statement. ‡

**Lemma 15.4** (easy tree-pattern matching)

Assume $P$ is of height $h$. Then, all occurrences of $P$ in $T$ can found in time $O(nh)$.

**Proof**

The naive algorithm actually works in that time. The proof is left to the reader. ‡

The aim is to design an algorithm working in time $O(nm^{0.5})$. Let $l = m^{0.5}$. If we have $k \geq l$ in Lemma 15.3, or $h < 3l$ in Lemma 15.4, then we have an algorithm with the required complexity. In any case, the sub-pattern consisting of node-paths of length at most $3l$ can be matched separately, using Lemma 15.4. Therefore, we are left with hard patterns, which do not satisfy assumptions of Lemmas 15.3 or 15.4. The pattern $P$ is said to be *hard* iff it satisfies:

(*) — in each set of at least $l$ node-paths there are two strings such that one is the suffix of the other,

(**) — the depth of all leaves is at least $3l$.

The key to the efficient algorithm is the high periodicity of node-paths of a hard pattern tree. For a leaf $v$ of $P$, consider the bottom $l+1$ ancestors of $v$. Then, there are two distinct ancestors $u$, $w$ such that $p(u)$ is a proper suffix of $p(w)$. The segment $p$ of size $|p(w)|-|p(u)|$ is a period of $p(w)$, and the latter word results by cutting off the path $t$ from $v$ to $w$. This path $t$ is called the tail.

Let us take the lowest nodes $u$, $w$. Then $p$ is primitive. The pair $(t, p)$ is uniquely determined by $v$. It is called the tail-period of $p(v)$ and of $v$. We leave to the reader the proof that there are at most $l$ distinct tail-period pairs, and that they can be found all in time $O(ml)$ (by a version of KMP algorithm). This proves the following lemma.

**Lemma 15.5**

Assume that $P$ is hard. Then each node-path of $P$ has a period $p \leq l$ $(= m^{0.5})$, after cutting off a part $t$ of size at most $l$ at the bottom. The word $p$ is primitive. There are $O(p)$ distinct tail-period pairs $(t, p)$, and they can be found all in time $O(ml)$.

The main result of the section stated below gives an upper bound to the tree-pattern matching problem.

**Theorem 15.6**

The tree-pattern matching problem can be solved in time $O(nm^{0.5}\log^2 n)$.

**Proof**

Let $P' = P(t, p)$ be the part of pattern $P$ formed by all node-paths with a given characteristics $(t, p)$. It is enough to show how to find all occurrences of $P'$ in $T$ in linear time. There are at most

$|p|$ leaves of $P'$, hence it is enough to prove that all occurrences of each node-path of $P$ in $T$ can be found in time $O(n/|p|)$. This looks impossible, because $n/|p|$ is much smaller than n, but the whole tree $T$ of size $n$ is to be searched. However, the key point is that we can make a suitable preprocessing which takes linear time, and which can be used later for all node-paths of $P'$. After the preprocessing, the tree $T$ is compressed into a smaller structure of size $O(n/|p|)$. We have to look carefully at the structure of node-paths of $P'$ of periodicity $p$, together with the tails $t$ outgoing; they have all the same characteristic $(t, p)$.

The tree $P'$ consists of a small top tree, and a set of branches which results by cutting off that tree. These branches are called main branches. Each such branch starts with the full occurrence of the period $p$. At some points, where an occurrence of $p$ ends, an occurrence of the tail $t$ can start, see Figure 15.4. There are at most $p$ main branches. All path-nodes of the small tree are proper suffixes of the period $p$. We leave to the reader as an exercise to find all occurrences in $T$ of the top tree in time $O(n)$. It is enough now to find occurrences of all branches in time $O(n)$.

First we preprocess the tree $T$. We find all occurrences of the period $p$, and of the tail $t$ in $T$ in linear time due to Lemma 15.1. Each subpath of $T$ from a node $v$ to some node $w$ corresponding to an occurrence of $p$ is replaced by a special edge $(v, w)$ labelled $a$. After that, we remove isolated special edges (one-edge biconnected components), as each main branch contains at least two $p$'s. Then, for each node $w$, if an occurrence of the tail $t$ starts at $w$, we add a special edge $(w, w')$ labelled $b$, where $w'$ is a newly created leaf. Let us consider the graph $T'$ consisting of such special edges. The constructed graph is a forest, since the tail is not a continuation of $p$ ($p$ is primitive).

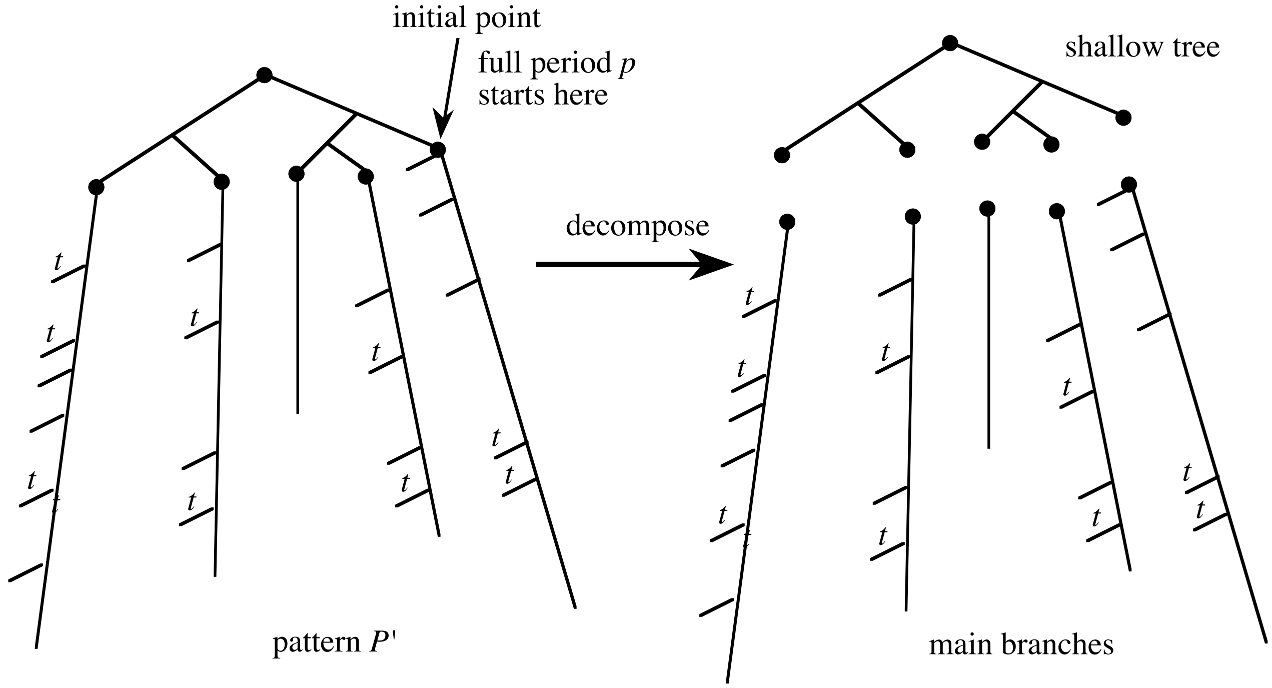

**Figure 15.4**. The structure of the tree $P' = P(t, p)$, and its decomposition.

The forest $T'$ consists of disjoint caterpillars. We leave as an exercise to show that the total size of $T'$ is $O(n/p)$.

Let us compress each main branch of $P'$ in a similar way as we transformed $T$ into $T'$, see Figure 15.5. The basic point is that after compression each main branch becomes a simple caterpillar! It is easy to see that it is enough to find all occurrences of such caterpillars in $T'$.

Now we can use Lemma 15.2. Each compressed main branch (a simple caterpillar) can be matched against the set $T'$ of compressed caterpillars in time $O(n/p.\log^2 n)$, due to Lemma 15.2. There are $O(p)$ branches. Hence, the total time is $O(n)$ for finding all occurrences of $P(t, p)$. But there are only $O(m^{0.5})$ such trees. Therefore, the total time needed for the tree-pattern matching is $O(nm^{0.5})$. This completes the proof. ‡

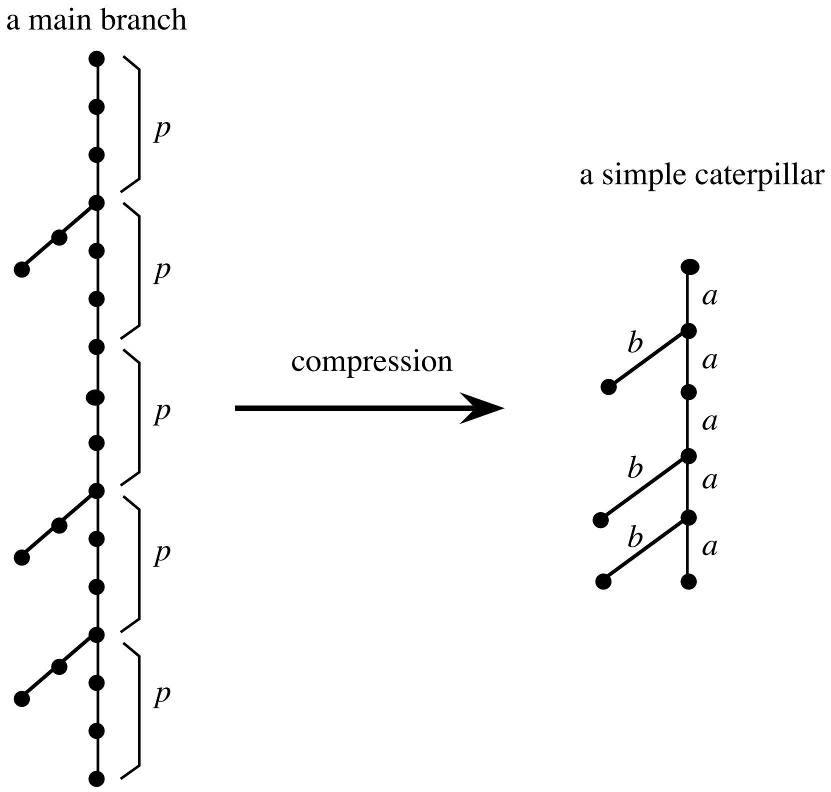

**Figure 15.5**. The compression of a main branch into a simple caterpillar.

## 15.3. Shortest common superstrings: Gallant algorithm

The shortest common superstring problem is defined as follows: given a finite set of strings $R$ find a shortest text $w$ such that $Fac(w) \supseteq R$. The size of the problem is the total size of all words in $R$.

The problem is known to be NP-complete. So the natural question is to find a polynomial approximation of the exact algorithm. The method of Gallant consists in computing an approximate solution.

Without loss of generality, we assume (throughout this section) that $R$ is a factor-free set, this means that no word in $R$ is a factor of another word in $R$. Otherwise, if $u$ is a factor of $v$ ($u$, $v \in R$), a solution for $R$-$\{u\}$ is a solution for $R$. For two words $x$, $y$ define $Overlap(x, y)$ as the maximal prefix of $y$ which is a suffix of $x$. If $v = Overlap(x, y)$, then $x$, $y$ are of the form

$$x = u_1v, y = vu_2.$$

Let us define $x$ © $y$ as the word $u_1vu_2$ ( $= u_1y = xu_2$). Observe that the shortest superstring of two words $u$, $v$ is $u$ © $v$, or $v$ © $u$. Since the set $R$ is factor-free, the operation © has the following properties:

(*) — operation © is associative (on *R*),

(**) — the minimal shortest superstring for *R* is of the form $x_1 \copyright x_2 \copyright x_3 \copyright \ldots \copyright x_k$ where $x_1, x_2, x_3, \ldots, x_k$ is a permutation of all words of the set *R*.

```
function Gallant(R); { greedy approach to SCS }
begin
  if R consists of one word w then
    return w
  else begin
    find two words x, y such that Overlap(x,y) is maximal;
    S := R - {x, y} ∪ {x © y};
    return Gallant(S);
  end;
end;
```

The above algorithm is quite effective in the sense of compression. The superstring represents (in a certain sense) all subwords of *R*. Let *n* be the sum of lengths of all words in *R*. Let $w_{min}$ be a shortest common superstring, and let $w_{Gal}$ be the output of Gallant algorithm. Note that $w_{min} \le w_{Gal} \le n$. The difference $n - |w_{min}|$ is the size of compression. The better is the compression the smaller is the shortest superstring. The following lemma states that the compression reached by Gallant algorithm is at least half the optimal value (see bibliographic references).

**Lemma 15.7**

$n - |w_{Gal}| \ge (n - |w_{min})/2$.

**Example**

Take the following example set $R = \{w_1, w_2, w_3, w_4, w_5\}$, where

$w_1 = egiakh$, $w_2 = fbdiac$, $w_3 = hbgegi$, $w_4 = iacbd$, $w_5 = bdiach$.

Then, the shortest superstring has length 15. However, Gallant algorithm produces the following result

$$\begin{aligned} w_{Gal} &= \text{Gallant}(w_1, w_2 \copyright w_5, w_3, w_4) \\ &= \text{Gallant}(w_3 \copyright w_1, w_2 \copyright w_5, w_4) \\ &= \text{Gallant}(w_3 \copyright w_1 \copyright w_2 \copyright w_5, w_4) \\ &= w_3 \copyright w_1 \copyright w_2 \copyright w_5 \copyright w_4. \end{aligned}$$

Its size is

$$\begin{aligned} & n - Overlap(w_3, w_1) - Overlap(w_1, w_2) - Overlap(w_2, w_5) - Overlap(w_5, w_4) \\ &\quad = 29 - 3 - 0 - 5 - 0 = 21. \end{aligned}$$

In this case, $n$ - $|w_{Gal}|$ = 8, and $n$ - $|w_{min}|$ = 14. ‡

An alternative approach to Gallant algorithm is to find a permutation $x_1$, $x_2$, $x_3$, …, $x_k$ of all words of $R$, such that $x_1©x_2©x_3©…©x_k$ is of minimal size. But, this produces exactly a shortest superstring (property **). Translated into graph notation (with nodes $x_i$'s, linked by edges weighted by lengths of overlaps) the problem reduces to the Travelling salesman problem, which is also NP-complete. Heuristics for this latter problem can be used for the shortest superstring problem.

The complexity of Gallant algorithm depends on the implementation. Obviously the basic operation is computing overlaps. It is easy to see that for two given strings $u$, $v$ the overlap is the size of the border of the word $v\#u$. Hence, methods from Chapter 3 can be used here. This leads to an $O(nk)$ implementation of Gallant method. Best known implementations of the method work in time $O(n\log n)$, using sophisticated data structures.

## 15.4. Cyclic equality of words, and Lyndon factorization

A *conjugate* or *rotation* of a word $u$ of length $n$ is any word of the form $u[k+1…n]u[1…k]$, denoted by $u^{(k)}$ (note that $u^{(0)} = u^{(n)} = u$).

Let $u$, $w$ be two words of the same length $n$. They are said to be *cyclic-equivalent* (or conjugate) iff $u^{(i)} = w^{(j)}$ for some $i$, $j$. In other terms, words $u$ and $w$ have the same set of conjugates. If words $u$ and $w$ are written as circles, they are cyclic-equivalent if the circles coincide after appropriate rotations.

There are several linear time algorithms for testing the cyclic-equivalence of two words. The simplest one is to apply any string-matching to pattern *pat* = $u$ and text *text* = $ww$ (words $u$ and $w$ are conjugate iff *pat* occurs in *text*). Another algorithm is to find maximal suffixes of $uu$ and $ww$. Let $u'$ (resp. $w'$) be the prefix of length $n$ of the maximal suffix of $u$ (resp. $w$). Denote $u'$ = *maxconj*($u$), $w'$ = *maxconj*($w$). The word $u'$ (resp. $w'$) is a maximal conjugate of $u$ (resp. $w$). Then, it is enough to check if *maxconj*($u$) = *maxconj*($w$).

We have chosen this problem because there is a simpler interesting algorithm, working in linear time and constant space simultaneously, which deserves presentation.

```
Algorithm { checks cyclic equality of u, w of common length n }
begin
  x := ww, y := uu ;
  i := 0; j := 0;
  while (i < n) and (j < n) do begin
    k := 1;
    while x[i+k] = y[j+k] do k := k+1;
    if k > n then return true;
    if x[i+k] > y[j+k] then i := i+k else j := j+k;
    { invariant }
  end;
  return false;
end.
```

Let $D(w)$ and $D(u)$ be defined by

$$D(w) = \{k : 1 \le k \le n \text{ and } w^{(k)} > u^{(j)} \text{ for some } j\},$$
$$D(u) = \{k : 1 \le k \le n \text{ and } u^{(k)} > w^{(j)} \text{ for some } j\}.$$

We use the following simple fact:

if $D(w) = [1\ldots n]$, or $D(u) = [1\ldots n]$ then words $u$, $w$ are not cyclic equivalent.

Now the correctness of the algorithm follows from preserving the invariant:

$$D(w) \supseteq [1\ldots i], \text{ and } D(u) \supseteq [1\ldots j].$$

The number of symbol comparisons is linear. We leave to the reader the estimation of this number. The largest number of comparisons is for words $u$ = 111..1201 and $w$ = 1111...120.

There is strong connection between the preceding problem and the Lyndon factorization of words that is considered for the rest of the section. The factorization is related to Lyndon words defined according to a lexicographic ordering on words on a fixed alphabet $A$.

Let $u$ and $v$ be two words from $A^*$. We say that $u$ is *strongly smaller* than $v$, denoted by $u << v$, if $u$ and $v$ can be written $wau'$ and $wbv'$ respectively, with $w$, $u'$, $v'$ words, and $a$, $b$ letters such that $a < b$. The lexicographic ordering induced on $A^*$ by the ordering of letters is also denoted by $\le$, and is defined by

$$u \le v \text{ iff } (u << v \text{ or } u \text{ prefix of } v).$$

A Lyndon word is a non-empty word $u$ such that $u < u^{(k)}$ for $0 < k < |u|$. So, a Lyndon word is smaller than its conjugates (in a non-trivial sense). It is equivalent to say (but not entirely straightforward) that the non-empty word $u$ is smaller than (according to the lexicographic ordering) its proper non-empty suffixes. This is the reason why the algorithm below is also closely related to the computation of the maximum suffix of a word (see algorithm *Maxsuf* in Chapter 13). It is useful to notice that a Lyndon word $u$ is border-free, which means that $period(u) = |u|$.

A Lyndon factorization of a word $x$ is a sequence of Lyndon words $(u_1, u_2, \ldots, u_k)$, for $k \geq 0$, such that both $x = u_1u_2\ldots u_k$, and $u_1 \geq u_2 \geq \ldots \geq u_k$. In fact, there is a unique Lyndon factorization of a given word, as stated by the next theorem. Since letters are Lyndon words, any non-empty word is a composition of Lyndon words. Regarding Lemma 15.9, the Lyndon factorization is such a factorization having the minimum number of elements.

**Theorem 15.8**

Any word has a unique Lyndon factorization.

```
Algorithm Lyndon_Fact(x);
{ computes the Lyndon factorization of x of length n }
{ operates in linear time and constant space }
begin
  x[n+1] := '#'; { # is smaller than all other letters }
  ms := 0;  j := 1;  k := 1;  p := 1;
  while (j + k ≤ n+1) do begin
    a' := x[ms+k];  a := x[j+k];
    if (a' < a) then begin
      j := j+k; k := 1; p := j-ms;
    end else if (a' = a) then
      if (k ≠ p) then
        k := k+1
      else begin
        j := j+p; k := 1;
      end
    else {a' > a} begin
      repeat
        writeln(x[ms+1..ms+p]); ms := ms+p;
      until ms = j;
      j := ms+1; k := 1; p := 1;
    end;
  end;
end.
```

**Example**

Let $A$ be $\{a, b\}$ with the usual ordering ($a < b$). The set of Lyndon words on $A$ contains

*b*, *a*, *ab*, *aab*, *abb*, *aaab*, *aabb*, *abbb*, ….

It also contains the words *aababbababbb*, or *aababbaabbabab*, for instance.
The Lyndon factorization of *bababababbabaababaabaa* is

(*b*, *abababb*, *ab*, *aabab*, *aab*, *a*, *a*). ‡

The algorithm *Lyndon_Fact* above produces the Lyndon factorization of its input string. We do not prove formally its correctness, but indicate how the algorithm works, and what are the main properties useful to prove it.

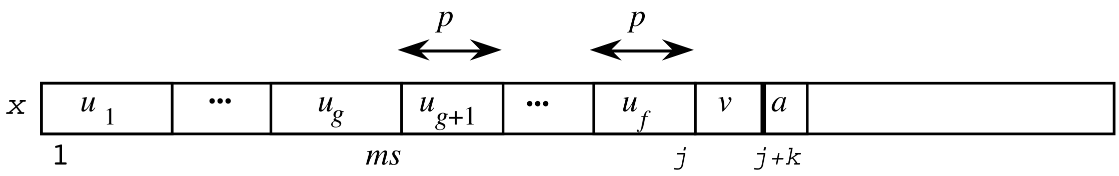

**Figure 15.6**. Variables in *Lyndon_Fact* algorithm.

Figure 15.6 shows the variables used in the algorithm. The invariant of the main loop is the following. The prefix $x[1\ldots j+k-1]$ of $x$ is factorized as $u_1u_2\ldots u_gu_{g+1}\ldots u_fv$, with

— $u_1, u_2, \ldots, u_g, u_{g+1}, \ldots, u_f$ are Lyndon words,

— $u_1 \geq u_2 \geq \ldots \geq u_g > u_{g+1} = \ldots = u_f$,

— $v$ is a proper prefix of $u_f$ (possibly empty),

— $u_g >> u_{g+1}\ldots u_fv$.

The variable $ms$ is such that $x[1\ldots ms] = u_1u_2\ldots u_g$. In other terms, $ms$ is the position of the factor $u_{g+1}$ in $x$. The Lyndon factorization of prefix $x[1\ldots ms]$ of $x$ is already computed when $ms$ has this value. Moreover, $u_1, u_2, \ldots, u_g$ are the $g$ first elements of the Lyndon factorization of the whole word $x$. The variable $j$ stores the position of $v$ in $x$, that is, is such that $x[1\ldots j] = u_1u_2\ldots u_f$. The value of variable $p$ is the common length of $u_{g+1}, \ldots, u_f$. It is also the period of $u_{g+1}\ldots u_fv$. Finally, $k = |v|+1$.

At the current step of the algorithm, the next letter $a$ of $x$ is compared with the corresponding letter $a'$ in $u_{g+1}$ (letter following the prefix $v$ of $u_{g+1}$). Three cases come from the comparison of letters. If they coincide, then the same periodicity (as that of $u_{g+1}\ldots u_fv$) continues, and the algorithm has essentially to maintain the third property. If $a$ is smaller than $a'$, $u_{g+1}, \ldots, u_f$ become elements of the Lyndon factorization of $x$, and the whole factorization process restarts at the beginning of $v$. In the third situation, $a'$ is smaller than $a$. The very surprising fact is that all properties implies then that the word $u_{g+1}\ldots u_fva$ is a Lyndon word. Since $va'$ is a prefix of the Lyndon word $u_f$, and $a' < a$, by Lemma 15.10, $va$ is a Lyndon word. Moreover, we have $u_f < va$ (and even $u_f << va$). Thus, applying Lemma 15.9 successively, we get that $u_fva$, $u_{f\text{-}1}u_fva$, …, and finally $u_{g+1}\ldots u_{f\text{-}1}u_fva$ are Lyndon words (all greater than $u_{g+1}$). So, the proof of correctness, is essentially a consequence of the two next lemmas. The first one provides an important property of Lyndon words, which can be used to generate them in lexicographic order.

**Lemma 15.9**

If $u$ and $v$ are Lyndon words such that $u < v$, then $uv$ is a Lyndon word and $u < uv < v$.

**Proof**

We prove that proper non-empty suffixes $z$ of $uv$ are greater than $uv$ itself.

First, consider the case $z = v$. We have to prove $uv < v$. This is obvious when $u << v$. Otherwise, $u$ is a proper prefix of $v$, that is, $v = uw$ for a non-empty word $w$. Since $v$ is a Lyndon word, we have $v < w$, which implies $uv < uw$ as required.

If $z$ is a proper suffix of $v$, we have $uv < v < z$, because $v$ is a Lyndon word, and by the above result.

Finally, let $z$ be a suffix of $uv$ of the form $wv$, with $w$ a proper non-empty suffix of $u$. Since $u$ is a Lyndon word, we have $u < w$, and even $u << w$ because $u$ cannot be a prefix of $w$. Thus, $uv < wv$. ‡

**Lemma 15.10**

If $vb$ is a prefix of a Lyndon word, and $b < c$ ($b$, $c$ letters), then $vc$ is a Lyndon word.

**Proof**

Let $u$ be the Lyndon word having prefix $vb$.

We prove that proper non-empty suffixes of $vc$ are greater than $vc$ itself. These suffixes are of the form $zc$. For some word $w$, $zbw$ is a suffix of $u$. Since $u$ is a Lyndon word, $u < zbw$.

If $zb$ is not a prefix of $u$, we have indeed $u << zb$, and thus also $v << zb$, because $v$ is a prefix of $u$ not shorter than $zb$. Therefore $vc < zb < zc$.

If $zb$ is a prefix of $u$, it is also a prefix of $v$, and we have directly $v < zc$. ‡

## 15.5. Unique decipherability problem

A set of words $H$ is said to be a *uniquely-decipherable code* if words that are compositions of words of $H$ have only one factorization according to $H$. The unique decipherability problem is to test whether a set of words satisfies the condition. The size of the problem when $H$ is a finite set, $n$, is the total length of all elements of $H$; in particular, the cardinality of $H$ is also bounded by $n$. Note that we can consider that $\varepsilon \notin H$, because otherwise $H$ is not uniquely decipherable and the problem is solved

Another way to set up the problem is to consider a *coding function* $h$, or substitution, from $B^*$ to $A^*$ ($B$, and $A$ two finite alphabets). The function is a morphism (i.e. it satisfies both properties: $h(\varepsilon) = \varepsilon$, $h(uv) = h(u)h(v)$ for all $u$, $v$), and the set $H$, called the code, is $\{h(a) : a \in B\}$. The elements of $H$ are called *code-words*. Then, asking whether $h$ is a one-to-one function is equivalent to the unique decipherability for $H$, provided all $h(a)$'s are pairwise distinct. Coding functions related to data compression algorithms are considered in Chapter 10. We can assume that all code-words $h(a)$ are non-empty and pairwise distinct. If not, then obviously the function is not one-to-one and the problem is solved.

We translate the unique decipherability condition for $H$ into a problem on a graph $G$ that is defined now. The nodes of $G$ are suffixes of the code-words (including the empty word). There is an edge in $G$ from $u$ to $v$ iff $v = u//x$ or $v = x//u$ for some code-word $x$. The operation $y//z$ is defined only if $z$ is a prefix of $y$, that is, if $y = zw$ for some word $w$, and the result is precisely this word $w$.

In the graph $G$, is defined the set of initial nodes, *Init*. Initial nodes are those of the form $x//y$ where $x$, $y$ are two (distinct) code-words. Let us call the empty word the *sink*. Then, it is easy to prove the following fact:

> the code $H$ is uniquely decipherable iff there is no path in $G$ from an initial node to the sink.

**Example**

Let $H = \{ab, abba, baaabad, aa, badcc, cc, dccbad, badba\}$. The corresponding graph $G$ is presented in Figure 15.7.

This code is not uniquely decipherable because there is a path from *ba* to the sink. The word *ba* is an initial node because $ba = abba//ab$. The path is:

$$ba \rightarrow aabad \rightarrow bad \rightarrow cc \rightarrow \varepsilon.$$

We have $baaabad//ba = aabad$; $aabad//aa = bad$; $badcc//bad = cc$; $cc//cc = \varepsilon$. The path corresponds to two factorizations of the word *baaabadcc*:

*baaabad.cc* and *ba.aa.badcc*. ‡

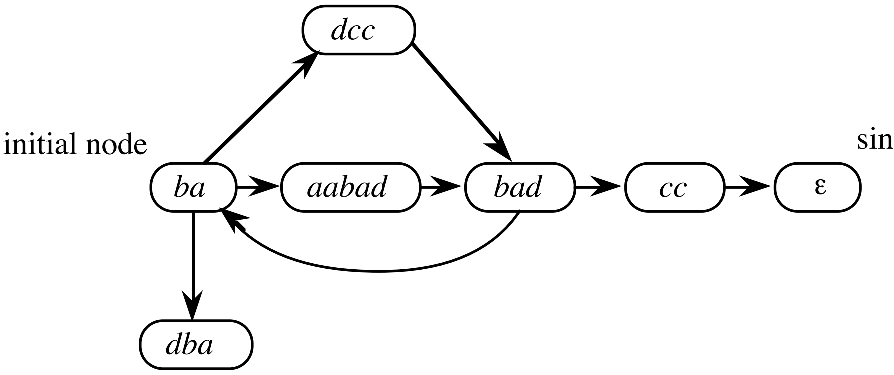

**Figure 15.7**. Graph $G$ for the example code.

The size of graph $G$ is $O(n^2)$, and we can search a path from an initial node to the sink in time proportional to the size of the graph by any standard algorithm. We show that the construction of $G$ can also be accomplished within the same time bound. If we can answer questions like "is $x//y$ defined?" and "is $y//x$ defined" in constant time, then, there is at most a quadratic number of such questions, and we are done. The question "is $y//x$ defined" is equivalent to "does the pattern $x$ start in the text $y$ at position $|y|-|x|$?", so it is related to string matching. Hence, it is enough for each code word $y$ treated as a text to make string-matchings with respect to all other code-words $x$ treated as patterns. For a fixed code-word $y$ (as a text) this takes $O(n+|y|)$ time, since $n$ is the total size of all code-words. Altogether this takes $O(n^2)$ time if we sum over all $y$'s. This proves the following.

**Theorem 15.11**

The unique decipherability problem can be solved in time $O(n^2)$.

A more precise estimation of the same algorithm shows that it works in time $O(nk)$, where $k$ is the number of codewords. By applying some data structures, the space complexity can also be improved for some instances of the problem. The close relationship between the unique decipherability problem and accessibility problem in graphs is quite inherent, especially if space complexity is considered. Indeed, the problems are mutually reducible using additional constant memory of a random access machine (or log$n$ deterministic space of a Turing machine).

## 15.6.* Equality of words over partially commutative alphabets

Assume that we have a symmetric binary relation $C$ over the alphabet $A$. The relation is called the *commutativity relation*. Relation $C$ induces an equivalence on $A^*$. Two words $x$ and $y$ over $A$ are said to be equivalent, denoted by $x \approx y$, iff one of them can be obtained from the other by commuting certain symbols in the word several times. Formally, we define $ubav \approx uabv$ when $(a, b) \in C$ (symbols $a$, $b$ commute), and we get an equivalence relation by closing this relation under reflexivity and transitivity. We consider the complexity of the following problem: check the equivalence of two strings $x$, $y$ of the same length $n$.

At first glance, the problem looks like an NP-complete problem. The straightforward algorithm is to generate all strings equivalent to $x$ and check if one of them is $y$. But the equivalence class of $x$ can contain an exponential number of words (for example when symbols $a$, $b$ commute and $x = a^m b^m$), leading to an exponential-time algorithm. Fortunately, there is a very simple algorithm with linear time complexity in the case of fixed size alphabets. This is due to a specific combinatorial property of words over partially commutative alphabets.

Denote by $h_{a,b}$ the morphism which erases from its input word all symbols except occurrences of $a$ and $b$. Let $\#_a(x)$ be the number of occurrences of symbol $a$ in $x$.

**Lemma 15.12**

Words $x$ and $y$ are equivalent, $x \approx y$, iff the following two conditions hold:
(1) — $\#_a(x) = \#_a(y)$ for each symbol $a$ of the alphabet,
(2) — $h_{a,b}(x) = h_{a,b}(y)$ for each pair of distinct non-commuting symbols $a$, $b$.

As a simple corollary we have the following theorem.

**Theorem 15.13**

The equality of two words over a partially commutative alphabet of fixed size can checked in linear time.

We shortly discuss what happens when the size $k$ of the alphabet is not treated as a constant. The lemma implies an $O(k^2n)$ algorithm, because the number of distinct pairs of letters is quadratic. However, instead of taking morphisms leaving only two symbols in texts (erasing all others) we can consider morphisms leaving a set of mutually non-commuting symbols. Denote by $h_X$ the morphism which erases in the text all symbols except symbols in set $X$. Let $\prod$ be a family of subsets of the alphabet such that each two symbols contained in the same set do not commute, and each two non-commuting symbols are contained together in some set from $\prod$. Then condition (2) of Lemma 15.12 is equivalent to: $h_X(x) = h_X(y)$ for each $X$ in $\prod$. The cardinality of $\prod$ can be much smaller than the number of all non-commuting pairs. For example, consider the following relation $C$ over alphabet $\{1, 2, 3, 4, 5, 6\}$:

$$(i, j) \in C \text{ iff } |i\text{-}j] = 1.$$

There are 10 pairs of non-commuting symbols, while we can take $\prod$ of cardinality 5,

$$\prod = \{\{a, c, e\}, \{b, d, f\}, \{c, f\}, \{d, a, f\}, \{e, b\}\}.$$

Hence, we have only to check equality of 5 pairs of words instead 20.

But there are cases when this approach does not help. Take the alphabet $\{1, 2, \ldots, 2r\}$ with commutativity relation:

$$(i, j) \in C \text{ iff } i, j \leq r \text{ or } i, j > r.$$

The size of the alphabet is here $k = 2r$. The graph of $C$ consists of two disjoint cliques, each of size $r$. There is a quadratic number of non-commuting pairs, and no set $\prod$ helps because for each three distinct symbols two of them commute. This suggests that the algorithm should have complexity of order $k^2n$. However, there is a simple $O(kn)$-time algorithm to check $x \approx y$ in this case. Let $\#_1(z)$ be a vector of size $r$ whose $i$-th component is the number of occurrences of the $i$-th symbol in $z$, and let $\#_2(z)$ be a vector of size $r$ whose $i$-th component is the number of occurrences of the $(r+i)$-th symbol in $z$. For each word $x$, let $H(x)$ be the string obtained from $x$ by replacing each factor $z$ between two consecutive symbols from $\{1, 2, \ldots, r\}$ by

$\#_2(z)$. Then, each word $z$ (over $\{1, 2, \ldots, r\}$) between two consecutive vectors newly inserted is replaced by $\#_1(z)$. $H(x)$ can be computed in $O(nk)$ time. Finally, it is easy to see that $x \approx y$ iff $H(x) = H(y)$.

It is typical for problems related to partially commutative alphabets that their complexity depends on the structure of the commutativity relation graph.

For many textual problems the introduction of partial commutativity of the alphabet changes their complexity dramatically. The typical example is the unique decipherability problem. For partially commutative alphabets with three letters, the problem has still an efficient (polynomial time) solution. However, for partially commutative alphabets with four letters there does not exist any algorithm for this problem at all. In other terms, the problem is undecidable.

We prove shortly that for three-letter alphabets the unique decipherability problem is still algorithmically tractable. This can be seen as follows. The unique decipherability problem is easily reducible to the disjointness problem of two languages $L_1$, $L_2$ accepted by finite automata $A_1$, $A_2$. Consider the following two commutativity relations on the alphabet $\{a, b, c\}$ presented graphically by

$$R1{:}\quad a \qquad b—c,$$
$$R2{:}\quad a—c—b.$$

Let $Cl(L)$ be the closure of language $L$ with respect to the relation $\approx$.

$$Cl(L) = \{x : x \approx y \text{ for some } y \text{ in } L\}.$$

Take the following morphism $h$ defined by $h(a) = a$, $h(b) = b$, $h(c) = \varepsilon$. The only action of the morphism is to erase all letters $c$ in its input text. Now, it can be proved easily, in the case of relations $R_1$ and $R_2$, that, knowing automata $A_1$, $A_2$, we can construct a non-deterministic pushdown automaton $A$ accepting the language

$$L = h(Cl(L_1) \cap Cl(L_2)).$$

So, the languages $L_1$, $L_2$ are disjoint iff $L = \emptyset$. Finally, the emptiness problem for non-deterministic pushdown automata is solvable in polynomial time.

We describe briefly the construction of automaton $A$ for the commutativity relation $R_2$. The pushdown store of $A$ acts as a counter (guessed number of occurrences of symbol $c$). We can view $A$ as a composition of $A_1$ and $A_2$. Whenever $A$ reads the symbol $a$ or $b$, then $A_1$ and $A_2$ go to next states, and their next states form a pair which is a next state of $A$. At any time, $A$ can non-deterministically assume in an ε-move the input symbol $c$ for one of the machines $A_1$, $A_2$ (without advancing its input head); then, the simulated machine makes a move as if the reading symbol were $c$. If the machine $A_1$ is chosen, the counter is incremented by one; on the contrary, if $A_2$ is chosen, the counter is decremented by one. The machine $A$ accepts, if there is a computation which ends in accepting states (for both $A_1$ and $A_2$), and if the final value of the counter is zero. Using the description of $A_1$, $A_2$ the construction of $A$ can be done efficiently.

The case of the relation is $R_1$ is similar. Other possible relations for three-letter alphabets are easy to deal with. It is interesting to note that if we take a relation $R$ on four letters similar to

$R_2$ then the problem becomes more complex. Let the commutativity relation $R$ be defined by: $a—b—c—d$. The decidability (or undecidability) of the unique decipherability problem with relation $R$ is still an open problem. But, if we add to the relation $R$ the pair $a—d$, then, it is known that the unique decipherability problem becomes undecidable.

## 15.7. Hirschberg-Larmore algorithm for breaking paragraphs into lines

In this section, we describe an application of text manipulation to text editing. It is the problem of breaking a paragraph into lines optimally. The algorithm may be seen as another application of the notion of the failure function, introduced in Chapter 3 for KMP string-matching algorithm.

The problem of breaking a paragraph is defined as follows. We are given a *paragraph* (a sequence) of $n$ words (in the usual sense) $x_1, \ldots, x_n$, and bounds *lmin*, *lmax* on lengths of lines. The $i$-th word of the paragraph has length $w_i$. A *line* is an interval $[i\ldots j]$ of consecutive words $x_k$'s ($i \le k \le j$). The length of line $[i\ldots j]$, denoted by $line(i, j)$, is the total length of its words, that is, $w_i + w_{i+1} + \ldots + w_j$. Bounds *lmin* and *lmax* are related to smallest and largest length of lines respectively. The optimal length of a line is *lmax*. Moreover, the length of the line $[i\ldots j]$ is said to be *legal* iff $lmin \le line(i, j) \le lmax$. Let us denote the corresponding predicate by $legal(i, j)$.

For a legal line, its penalty is defined as $penalty(i, j) = C.(lmax\text{-}line(i, j))$, for some constant $C$. The problem of breaking a paragraph consists in finding a sequence of integers $i_1$ (=1), $i_2, i_3, \ldots, i_k$ (=$n$) such that both lines $[i_1, i_2]$, $[i_2+1, i_3]$, …, $[i_{k-1}+1, i_k]$ have legal lengths, and the total penalty (sum of penalties of lines) is minimum. Integers $i_1, i_2, i_3, \ldots, i_k$ are called the *breaking-points* of the paragraph.

We assume that there is no penalty (or zero penalty) for the first line, if its length does not exceed *lmax*. It is as if we treated the paragraph from the end. In the usual definition of the problem the last line is not penalized for being too short. Reversing the order of words in paragraphs leads to an algorithm that is even more similar to KMP algorithm, since indices are processed from left to right.

Let $break[i]$ be the rightmost breaking-point preceding $i$ in an optimal breaking of the subparagraph $[1\ldots i]$. When $break[i]$ is computed for all values of $i$ (from 1 to $n$), the problem is solved: the sequence of breaking-point can be recovered by iterating *break* from $n$.

We first design a brute-force breaking algorithm that uses quadratic time. The informal scheme of such a naive algorithm is given below. It uses the table $f$ : $f[i]$ is the total penalty of breaking into lines the subparagraph $[1\ldots i]$. The scheme assumes that $f[i]$ is initialized to 0 for all integers $i$ such that $line[1, i] \le lmax$, and $f[i]$ is initialized to infinity for all other values of $i$.

```
for i := 1 to n do begin
  j := an integer which minimizes f[j]+penalty(j+1, i);
  break[i] := j;
  f[i] := f[j]+penalty(j+1, i);
end;
```

The value of *j* is computed by scanning the interval [*first*[*i*], …, *last*[*i*]], where *first*[*i*] is the smallest integer *k* for which *legal*(*k*, *i*) holds, and where, similarly, *last*[*i*] is the largest such *k* less than *i*. The interval [*first*[*i*], …, *last*[*i*]] is called the *legal interval* of *i*. All values *first*[*i*], *last*[*i*], *line*(1, *i*) can be precomputed. So, the above scheme yields an $O(n^2)$ time algorithm. The next theorem shows that this can be improved considerably.

**Theorem 15.14**

The problem of breaking optimally a paragraph can be solved in $O(n)$ time.

**Proof**

Define the function $g[j] = f[j] + C.line(j, n)$. The crucial point is the following property:

> a value of *j* which minimizes *f*[*j*]+*penalty*(*j*+1, *i*) also minimizes *g*[*j*] in the legal interval for *j*.

It can be checked by simple arithmetics that the difference between expressions depends only on *i*. Another important property is the monotonicity of breaking-points:

> $i' < i$ implies $break[i'] \leq break[i]$.

Hence, the value of *j* is to be found in the interval [max(*first*[*i*], *break*[*i*-1]), *last*[*i*]]. Define *Next*[*j*] to be the first position $k \leq i$ to the right of *j* such that $g[k] \leq g[j]$. When looking for the minimal value of *g*[*j*] in a legal interval we can initialize *j* to the beginning of the interval, and compute successive positions by iterating *Next*

$$j_1 = Next[j], j_2 = Next[j_1], \ldots,$$

until the value is undefined, or it goes outside the interval. In this way, *Next* works as the failure table of KMP algorithm. This produces the following algorithm.

```
Algorithm HL; { breaking a paragraph of $n$ words into lines }
begin
  precompute values first[i], last[i], line(1, i) for all $i \le n$;
  let k be the maximal index such that $line[1, k] \le lmax$;
  initialize f[i] to 0, break[i] to 0 for all $i \le k$,
    and compute corresponding values g[i] and Next[i] for $j \le k$;
  j := 0;
  for i := k+1 to n do begin
    { invariant:  $break[i] < i$, $first[i] < last[i] < i$ }
    { legal interval is [first[i],…,last[i]] }
    if $j < first[i]$ then j := first[i];
    while Next[j] defined and $Next[j] \le last[i]$ do
    { j is not rightmost minimal }  j := Next[j];
    break[i] := j; f[i] := f[j]+penalty(j+1, i);
    g[i] := f[i]+C.line(1, i);
    Update_table_next;
  end;
  return table break, which gives optimal breaking;
end.
```

The algorithm works in linear time by a similar argument as that used in the analysis of the KMP algorithm, if the total cost of updating the table *Next* is linear. Let $j_1$, $j_2$, …, $j_r$ be the increasing sequence of indices $j$ for which *Next*[$j$] is not defined at a given stage of the algorithm. Then the values of $g[j]$ are strictly increasing for this sequence. We keep the sequence $j_1, j_2, \ldots, j_r$ on a stack $S$, the last element at the top. The next procedure is applied.

```
procedure Update_table_next;
begin
  repeat
    pop the top indices j of the stack S;
    Next[j] := i;
  until $g[j] < g[i]$;
  push i onto S;
end;
```

The total complexity of computing table *Next* is linear, since each position is popped from $S$ at most once. This completes the proof of the theorem. ‡

We refer the reader to [HL 87a] for more details on the algorithm, and for extensions to more sophisticated penalty functions. For example, we can assume that optimal lengths of lines are properly inside the interval [*lmin*, *lmax*], and that penalty of a line is a linear function of the distance from optimal length. The penalty can also be a nonlinear function. The linear time complexity works as far as the penalty function is concave.

## Bibliographic notes

String-matching by hashing has been first considered by Harrison [Ha 71]. A complete analysis is presented by Karp and Rabin in [KR 87]. The same idea (using hashing) is applied for finding repetitions in [Ra 85]. An adaptation of Karp-Rabin algorithm to two-dimensional pattern matching has been designed by Feng and Takaoka [FT 89].

The contents of Section 15.2 is adapted from the tree-pattern matching algorithm of Dubiner, Galil, and Magen [DGM 90].

The approximation of the SCS problem by Gallant may be found in [Ga 82]. An efficient implementation has been designed by Tarhio and Ukkonen [TU 88]. Stronger methods are developed in [Tu 89], providing an $O(n\log n)$-time algorithm, but requiring quite complicated data structures.

The book of Lothaire [Lo 83] contains motivations for factorization problems from the point of view of combinatorics on texts. The Lyndon factorization algorithm of Section 15.4 in from Duval [Du 83]. An algorithm for the canonization of circular strings (computing the smallest conjugate) based on KMP string-matching algorithm is given by Booth in [Bo 80]. The fastest known algorithm is by Shiloach [Sh 81]. The relation between Lyndon factorization and smallest conjugate of a word in considered by Apostolico and Crochemore in [AC 91].

The algorithm for testing unique decipherability of a code is usually attributed to Sardinas and Paterson (see [Lo 83]). By using specific data structures, Apostolico and Giancarlo have improved on the space complexity of the algorithm [AG 84]. The literature on unique decipherability problem is quite rich (see for instance [BP 85]). The problem is complete in the class of non-deterministic $\log n$-space computations (see [Ry 86]).

An interesting exposition on algorithmic problems related to partially commutative alphabets is by Perrin in [Pe 85]. The algorithmic properties of the unique decipherability problem for partially commutative alphabets were considered by Chrobak and Rytter in [CR 87b]. For the emptiness problem for non-deterministic pushdown automata in polynomial time the reader can refer to [HU 79]. String-matching over partially commutative alphabets is solved by Hashiguchi and Yamada in [HY 92].

The application of failure functions to the problem of breaking a paragraph into lines is from Hirschberg and Larmore [HL 87a].

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