An Introduction to the Fundamentals & Functionality of the R Programming Language

— Part I: An Overview —

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Table of Contents

1 Some Language Essentials **2**
Starting R . . . 3
Entering expressions . . . 3
Incomplete expressions . . . 4
Recall/correction of previous expressions . . . 4
Quitting R . . . 4
Assignment . . . 5
Functions . . . 6
Finding help . . . 8
Packages . . . 9
Data types and structures . . . 11

2 Data Import and Prep **15**
Microsoft Excel Files . . . 15
Some good programming practices . . . 16
The `read.table()` function . . . 17
Attributes of a read-in data set . . . 18
Factors . . . 19
Customizing data sets after input . . . 22
A thought to end with: R code files . . . 26

3 Generating Descriptive Statistics **28**
Accessing variables in your data frame . . . 28
Tables of categorical variables . . . 30
Univariate summary statistics of continuous variables . . . 32
More on missing values . . . 34
Group-wise summary statistics of continuous variables . . . 34
Automatic summaries of both categorical and continuous variables . . . 39
Diverting screen output to a file . . . 45
A though to end with: Object-oriented programming . . . 46

4 R Graphics **50**
Traditional graphics . . . 50
Trellis graphics . . . 50
Building plots in layers . . . 50
Arguments of plotting functions . . . 53
The `par()` function . . . 53
Temporary/persistent alterations of graphical parameters . . . 54
Histograms, stripcharts, and boxplots . . . 55
Scatterplots, barplots, and dotplots . . . 58
Graphical output . . . 66

Preface

I have been using R since the summer of 2000 and have been trying to teach it to others for almost as long. When I was learning R (on my own) I got very frustrated with most of the existing R documentation. In particular, a lot of the documentation was written as a companion manuscript to an introductory statistics course. These and others covered the 'fundamentals of R' in a chapter or two and then spent the rest of their time demonstrating how to perform various statistical analyses using R. I felt they introduced you to some of the fundamentals, but very few discussed them extensively. I have also found over the years that, even as a full-time Biostatistician, 99% of my time is spent dealing with these fundamentals, not statistical analyses. Therefore, the purpose of this document and its companion is to introduce you to the fundamentals and functionality of the R programming language. The only statistics that will be covered is how to generate descriptive statistics and some statistics related graphics.

This document and its companion are by no means an 'original' piece of work. I have merely assembled much of the existing documentation into my own set of documents. However, I have tried to present the topics in a slightly different order than what is usually done. Specifically, the first document ('An Overview') covers some of the fundamentals, but then gets you right into the functionality – we read in a data set, make modifications to it, summarize it with descriptive statistics, and generate various graphical depictions of it. The goal is that you will be very comfortable interacting with R by the end of the first document. The second document ('The Nuts & Bolts') returns to the fundamentals, covering various topics in more depth. The second document also includes a catalog of various R functions and an R graphics reference. Throughout both documents, I have also tried to include as much of my practical experience with R that I could.

I hope you find my group of documents helpful and hope they allow you to start using R confidently. YOu can find this document, it's companion and other supporting files at `http://biostat.mc.vanderbilt.edu/TheresaScott` under *Current Teaching Material*. Feel free to contact me at `theresa.scott@vanderbilt.edu` with any questions and/or comments. I also welcome any suggestions and (constructive) criticism.

Lastly, the following is a crude list of the references I have used to compile this document and its companion:

- Contributed documents, manuals, frequently asked questions, and newsletters available via the Other, Manuals, FAQs, and Newsletter links under the Documentation header at the R website.
- Several books including[1]
  - *'An Introduction to R'* by WN Venables, et al.
  - *'Introductory Statistics with R'* by Peter Dalgaard.
  - *'R Graphics'* by Paul Murrell.
  - *'Using R for Introductory Statistics'* by John Verzani.
  - *'Statistics: An Introduction Using R* by Michael J Crawley.
  - *'A Handbook of Statistical Analyses using R'* by Brian Everitt and Torsten Hothorn.
  - *'An R and S-Plus Companion to Applied Regression'* by John Fox.
  - *'Data Analysis and Graphics Using R'* by John Maindonald and John Braun.

[1]Note, a comprehensive list is available via the Books link under the same Documentation header at the R website.

Chapter 1

Some Language Essentials

Learning objective
To understand how to use R interactively and the language essentials of assignment, functions, and data structures.

The goal of this document is to *briefly* introduce you to the very powerful facilities that the R programming language provides. We cannot do this, however, without briefly covering some of the essentials of the R language.

R is a *free interactive programming language and environment*, created as an integrated suite of software facilities for data manipulation, simulation, calculation, and graphical display. Even though R is mainly used as a statistical analysis package, R is in no way limited to just statistics. As a side, R is an independent, open-source implementation of the S language. The commercial product S-PLUS is also based on S, and R and S-PLUS are essentially identical.

The benefits of using R include:

- Its availability as *free* software – 'free' in terms of price, and (more importantly) in terms of freedom to run, copy, distribute, study, change, and improve the software.
- Its ability to run on Windows, MacOS, and Linux and UNIX platforms.
- The ability to completely reproduce your analysis and results, if properly documented, since the language is code driven. This is not always true with menu driven analysis packages; they are often much harder to document.
- Its extendability – hundreds of libraries of functions to use, as well as the ability to write your own functions.
- Its flexibility – unlike some classical software programs (e.g., SAS and SPSS), which display all the results of an analysis, R allows you to assign any results to a (symbolic) variable, so that an analysis can be done with minimal or no output, and the parts of the results of interest can be extracted and used in subsequent analyses.
- Its excellent graphing capabilities, including the ease with which well-designed publication-quality plots can be produced.

For this course, you should have already installed R onto your laptop/computer – these notes were compiled using R version 2.8.1 (2008-12-22). In general, both the complete instructions and the necessary accompanying files needed to install R are distributed by the *Comprehensive R Archive Network* (CRAN) on their website `http://www.cran.r-project.org`. See any of the following Documentation for detailed instructions: the 'R Installation and Administration' document under the Manuals link; the FAQ link (both general and Windows and Mac specific); and/or the 'Installing R under Windows' article in the June 2001 edition (Vol. 1/2; pages 11-14) Newsletter. ***NOTE:*** You will also need to have administrative rights to your laptop/computer in order to successfully install a *package*, which we will cover via a practice exercise.

Before going further, it is helpful to interact with R on the simplest level – that is, using it as a calculator. The following session is intended to introduce you to some of the features of the R environment by using them.

STARTING R: When using the Windows or Mac versions of R, launch R by double-clicking the R icon on the desktop, or by finding the R program under the `start` menu. This will start R in a new *console window* with a *command line subwindow.* On the other hand, when using the Linux/Unix version of R, launch R by typing '`R`' at the shell command prompt (i.e., '`$ R`' if we assume that the shell prompt is '`$`') of a terminal window. This will cause R to start up as an interactive program in the current terminal window.

→ *Practice Exercise:* Go ahead and start R using one of the mentioned methods that is appropriate for your type of laptop/computer.

ENTERING EXPRESSIONS: There are several ways to interact with R, but the simplest way is to type *expressions* at the cursor following the *command line prompt*, which is denoted by the greater than symbol, `>`. To evaluate the expression, we simply press the ENTER key. The simplest expressions to enter at the command line are arithmetic expressions involving numbers and algebraic operators. R includes the usual arithmetic operators: `+` (addition), `-` (subtraction), `*` (multiplication), `/` (division), and `^` (exponentiation). Note, unlike most arithmetic operators, the exponentiation operator, `^`, works from the right to the left – `2^2^3` = 2^8 not 4^3. The set of arithmetic operators also includes `%%` (modulo) and `%/%` (integer division). In addition, (1) instead of using a newline, (short) expressions can be separated by a semi-colon (`;`); and (2) parentheses can be used to *group expressions*, altering the order in which expression are evaluated.

→ *Practice Exercise:* Type any of the following arithmetic expression at the command line and press ENTER or try any of your own.

```
> 2 * 10

[1] 20

> 10 + 13 - 21

[1] 2

> 2^3

[1] 8

> 1 - 2 * 3

[1] -5

> (1 - 2) * 3

[1] -3
```

As we see, the output of each evaluated expression is printed (*and lost*). In addition, the printed output may appear odd. The `[1]` in front of the output is part of R's way of printing intrinsic *data structures* to the screen. More specifically, when printed output consists of many values spread over several lines, each line begins with the index (number) of the first element of the line. You also probably noticed the additional spaces around some of the arithmetic operators. Although spaces are not required to separate elements of an arithmetic expression (i.e., are ignored), judicious use of spaces can help to clarify the meaning of the expression.

EXPRESSION EVALUATION: R evaluates expressions using a type of *question-and-answer model*. Specifically, when you type an expression at the command line prompt and press ENTER, the command is first transformed by R into an internal representation. If the expression is syntactically complete, the transformed expression is then executed and R returns (prints) the result value of the expression to the screen. Once executed, R then asks for more input by printing the command line prompt and cursor. In future sections, we will see that not all expressions return (print) a result value.

INCOMPLETE EXPRESSIONS: If an expression is not syntactically complete when ENTER is pressed, R will print the *continuation prompt*, `+`, at the beginning of the second and subsequent lines and continue to read input until the expression is syntactically complete.

→ *Practice Exercise:* To demonstrate how R reacts to incomplete expressions, type in the mathematical expression `2 + 3 + 5 - 2` at the command line by hitting the `ENTER` key after each arithmetic operator:

```
> 2 +
+ 3 +
+ 5 -
+ 2
[1] 8
```

The other main reasons why an expression may be incomplete are because of unmatched parentheses and/or quotation marks. In the Windows/Mac versions of R, use the Esc key to cancel an incomplete expression, which will print a new command line prompt and cursor. In the Unix/Linux version of R, use Ctrl-C.

RECALL/CORRECTION OF PREVIOUS EXPRESSIONS: Using the command line in R can involve a fair amount of typing. However, there are ways to reduce the amount of necessary typing. Specifically, the R console keeps a history of the expressions entered, which is known as the *command history*. Individually, the expressions can be accessed using the up- and down-*arrow keys*. Repeatedly pushing the up-arrow will scroll backwards through the command history. With the up- and down-arrow keys we can access the desired previous expression and then edit it as desired using keys like the left- and right-arrow keys, the Home and End keys (or Ctrl-a and Ctrl-e, respectively), and the Backspace and Delete keys. Another useful keyboard shortcut to use in conjunction with the Home key/Ctrl-a is Ctrl-k, which 'kills' (deletes) the current line (if the cursor is at the beginning of the line).

→ *Practice Exercise:* Using the up-arrow key, recall one of your previous arithmetic expressions, and use the left- and right-arrow keys, the Home and End keys, and the Backspace and Delete keys to modify and re-evaluate the expression.

QUITTING R: Lastly, to quit R, type `q()` at the command line prompt – you must include the parentheses ('`()`'). You will then be asked `Save workspace image?`. Answer "No" by clicking the `No` button or typing `n`. Don't worry if this doesn't make a lot of sense right now; we'll be discuss it more in the 'Object Management' section of the second document. ***NOTE:*** When we type `q()` and hit ENTER, we are actually executing the quit *function*. We will be discussing *functions* in more detail soon.

THE GRAMMAR OF EXPRESSIONS: Up to this point, all of the expressions we have entered at the command line have been simple mathematical expressions involving only numbers and arithmetic operators. Also, up to this point, the result of each evaluated expression has been printed and then discarded. Obviously, we need to be able to use R as more than just a calculator. Specifically, we need to be able to (among other things): (1) retain the results of specific evaluated expressions; (2) use data that consists of more than one number; and (3) possess the tools to carry out a variety of desired tasks. The solution to these desires will involve evaluating expressions that include (1) *assignment*, (2) *functions*, and/or (3) *data structures*.

***TERMINOLOGY* – 'object':** We will use the term *object* quite often in future sections. You can think of an object as anything in R that is returned (printed) by an evaluated expression, anything that you define via assignment, or anything that is already defined by R (i.e., functions).

ASSIGNMENT: R allows values to be assigned a (symbolic) *name*, which allows the name to be used to represent that value in subsequent expressions. The simplest example would be to assign the value of 5 to the name '`x`' using the *assignment operator* (`<-`):

```
> x <- 5
```

The expression `x <- 5` can be read as "the name `x` is assigned the value `5`." The assignment operator `<-` consists of a less than sign (`<`) followed by a minus sign (`-`) *without any spaces between them.* The less than sign 'points' to the name receiving the value. In general, no result is printed when a name is assigned to a value. In order to print the value of the evaluated expression, we must enter the name of the value at the command line.

```
> x

[1] 5
```

A way to evaluate the assignment and to print the evaluated result is to wrap the assignment expression with a set of parentheses. For example,

```
> (x <- 5)

[1] 5
```

As mentioned, once a value has been assigned to a name, that name can be used to represent the value in subsequent expressions:

```
> 10 * x + 2

[1] 52
```

A name can also be '*re-assigned*' at any time, and the old value is overwritten with the new:

```
> x

[1] 5

> x <- 2
> x

[1] 2
```

As we saw with our arithmetic expressions, spacing around operators is generally disregarded by R, but notice that adding a space in the middle of an assignment operator `<-` changes the meaning to 'less than' followed by 'minus' (conversely, omitting the space when comparing a variable to a negative number has unexpected consequences). As an example,

```
> x < -5

[1] FALSE
```

→ *Practice Exercise:* At the command line, work through a similar example by assigning the value 10 to the name '`y`', evaluating the expression `y^2 + 20`, and re-assigning the name '`y`' to the value 8.

IMPORTANT: The value we assign to a name is not limited to a single value. In general, the evaluated value of any expression, which is commonly referred to as an object, can be assigned to a name. For example, in future sections, we will assign a name to our read-in data set, which will allow us to refer to our data set by name in all subsequent expressions. Another example would be to assign a name to the output of a regression model in order to use certain portions of the model output in subsequent expressions. In the same sense, an expression is allowed to be on the target side (left side) of an assignment, not just a (symbolic) name. For example, we can replace (re-assign) the missing values of a variable with a value of zero.

NAMING OBJECTS: There are some limitations as to what can be used to name an object. Specifically, object names (1) may consist of letters (`A-Z` and `a-z`), digits (`0-9`), periods (‘`.`’), and the underscore (‘`_`’); and (2) must not start with a digit nor underscore, nor with a period followed by a digit. Mathematical operators, such as `+`, `-`, $*$, and `/`, in addition to other special characters are also not allowed to be used in object names. And ***DON'T FORGET***, R is case sensitive – so, `x` and `X` are two distinct objects.

FUNCTIONS: Almost everything in R is done by invoking *functions*. Functions in R can do three things: (1) have values passed to them; (2) return a value; and/or (3) generate *side effects*, which are anything that is not the returning of a value. Examples of functions that generate side effects are printing and plotting functions. Every function in R, whether intrinsic to the language or user-written, is defined using the same basic statement: `FUNname <- function( arglist ) { body }`, where `FUNname` is the name of the function; *`arglist`* is a *comma* separated list of zero or more arguments that can be passed to the function; and *`body`* contains the expressions that perform the actions of the function. In turn, the format to invoke a function is to type its name followed by a set of parentheses containing zero or more arguments. In other words, we can think of calculus with its mathematical functions like `f(x)` or `g(x, y)`. As John Verzani put it in his book, ‘functions are like pets’ – they don't come (aren't invoked) unless we call them by name (case-sensitive and spelled properly); they have a mouth (the parentheses) that likes to be fed (the arguments to the function), and they will complain if they are not fed properly (the output of warnings and/or errors). ***BE AWARE:***

1. Because R is case sensitive, so are the names of functions. So, for example, the `reshape()` and `reShape()` functions are two distinct functions.
2. In R, in order to be executed, a function *always* needs to be invoked with parentheses, even if there are no arguments explicitly specified between them. As with any other assigned object, typing the name of an object at the command line and pressing ENTER causes the assigned value of the object to be printed. In the case of a function, typing only the name of the function (and not including the parentheses) prints the body of the function.

   → *Practice Exercise:* At the command line, compare the result of evaluating `date` (without parentheses) and `date()` (including the parentheses). Similarly, see what happens when you try to quit R by evaluating only `q` (without the parentheses).

   ```
   > date
   function ()
   .Internal(date())
   <environment: namespace:base>
   > date()
   [1] "Mon Jun 22 09:12:23 2009"
   ```

You will notice in this document that we typeset all of the function names with the parentheses in order to remind us of this.

SPECIFYING FUNCTION ARGUMENTS: A function's arguments are how values are passed to the function when it is invoked. The arguments of a function can be an `ARGname` or an `ARGname = VALUE` construct. The argument list can also contain a special type of argument: `...` (‘dot dot dot’). An `ARGname` argument is often the first argument in a function's argument list and often represents the main data object being passed to the function. For example, we can define a function `ourFUN` that has one formal argument, `x=`.

```
> ourFUN <- function(x) {
+     x + 5
+ }
> ourFUN(x = 2)
```

```
[1] 7
```

Note, the value of an `ARGname` argument *always* has to be specified. Otherwise, you will receive an error. For example, if we tried to invoke the `ourFUN()` function without specifying a value for `x=` (i.e., executing `ourFUN()`), we receive the following error: `Error in ourFUN(): argument "x" is missing with no default`.

The `ARGname = VALUE` construct is used to specify a default value for an argument. If you do not specify a value for that argument when the function is invoked, the default value will be used and evaluated in the body of the function, as if you passed `ARGname = VALUE` in the function invocation. However, if you do specify a value for that argument, the specified value will be used instead of the default value. For example,

```
> anotherFUN <- function(x, y = 5) {
+     x + y
+ }
> anotherFUN(x = 2)

[1] 7

> anotherFUN(x = 2, y = 7)

[1] 9
```

Lastly, the `...` argument can hold a variable number of arguments, and is mostly used for passing arguments to other functions invoked in the body of the outer function. For example,

```
> lastFUN <- function(z, ...) {
+     ourFUN(z) - anotherFUN(z, ...)
+ }
> lastFUN(z = 2)

[1] 0

> lastFUN(z = 2, y = 10)

[1] -5
```

In `lastFUN(z = 2)`, no additional arguments are passed from the `lastFUN()` function to the `anotherFUN()` function through the `...` argument. Therefore, the default value of `y=` in the `anotherFUN()` function is used. In `lastFUN(z = 2, y = 10)`, the `y = 10` argument is passed to the `anotherFUN()` function in the body of the `lastFUN()` function.

When invoking a function, arguments may be specified by name using their `ARGname` tag (e.g., `y = 10`), or they may be specified by their *position* in the order of the list of arguments, which is determined by using the commas separating the arguments as placeholders. However, specifying arguments by their position can be dangerous, especially if you reference the order of the arguments incorrectly. It also makes your code harder to read. A much safer alternative is to specify the first argument by its position and specify all other arguments using their `ARGname` tag. The advantage of specifying arguments by their name is that named arguments may be specified in any order. In addition, specifying arguments by their name makes your code more easily readable – both for yourself and others. And remember, if you are not changing the default value, arguments with default values can be omitted from the invocation.

To illustrate how a function's arguments can be specified, let's consider the case where I want to use the `read.table()` function to read in a data file, `samplefile.csv`, which is a comma-delimited file with missing values represented by a question mark (`?`). Let's first look at the `read.table()` function's arguments using the `args()` function, which displays the names and corresponding default values (if any) of a function:

```
> args(read.table)

function (file, header = FALSE, sep = "", quote = "\"'", dec = ".",
    row.names, col.names, as.is = !stringsAsFactors, na.strings = "NA",
    colClasses = NA, nrows = -1, skip = 0, check.names = TRUE,
    fill = !blank.lines.skip, strip.white = FALSE, blank.lines.skip = TRUE,
    comment.char = "#", allowEscapes = FALSE, flush = FALSE,
    stringsAsFactors = default.stringsAsFactors(), encoding = "unknown")
NULL
```

As you can see, the `read.table()` function has many arguments (20 to be exact) and many argument defaults – for example, the default field separator character is white space (`sep = ""`). In this case, I could invoke the `read.table()` function using the following code: `read.table("samplefile.csv", sep = ",", na.strings = "?")`. In this example, I specified the `file=` argument by position (the first argument) and the `sep=` and `na.strings=` arguments by name. I didn't have to specify any other arguments because I did not need to change any of their default values. On the other hand, if I wanted to specify all three arguments using their position (the first, 3rd, and 9th arguments) I would have to use the following code, which is really difficult to understand: `read.table("samplefile.csv", , ",", , , , , , "?")`.

LOGICAL ARGUMENTS: As shown by the default value of the `read.table()` function's `header=` argument, arguments are often specified using a *logical value* of `TRUE` or `FALSE` (all capitals and no quotes). Often, you will see `TRUE` and `FALSE` abbreviated to `T` and `F`, and in fact `T` and `F` are objects which are set to `TRUE` and `FALSE` by default. However, `T` and `F` are not *reserved* objects, which means their default `TRUE` and `FALSE` values can be overwritten (i.e., re-assigned). For example,

```
> T

[1] TRUE

> T <- 2
> T

[1] 2
```

This fact can cause a lot of problems when you specify logical arguments with just `T` or `F`. Just imagine assigning `T` or `F` to some other value in your code and then, later on, trying to specify a logical argument of a function with the re-assigned `T` or `F`. You may receive a warning or an error, or even worse, you may not receive a warning or error, in which case the result of the function has probably been grossly affected. Therefore, I highly suggest that you always use `TRUE` and `FALSE` when specifying logical arguments.

NESTED FUNCTIONS: As mentioned, most functions, when invoked, return an evaluated value. This means that the expression invoking a function can be passed as an argument to yet another function invocation. This is the concept of *nested functions*. An example would be to calculate the arithmetic mean of a random sample of ages ranging from 10 to 60 years. To do this, we can use the `seq()` (sequence) function to generate the possible ages from 10 to 60 years, the `sample()` function to generate a random sample of the possible ages, and the `mean()` function to calculate the arithmetic mean of the random sample:

```
> mean(sample(seq(from = 10, to = 60), size = 100, replace = TRUE))

[1] 36.51
```

FINDING HELP: In general, the `args()` function is very helpful when you need to verify the argument name and/or default value of an argument before invoking a function, but it does not give you any further details regarding each argument. Luckily, R has a built-in help system that allows you to access individual help files of functions and other language specifics. The `help()` function will access the help file of a specific topic, like the `mean()` function, but you need to know the exact topic name on which the help documentation is sought. The `help()` function can be called in several ways, which are all equivalent: `help(mean)`;

`?mean`; `?"mean"`; or `help("mean")`. To use the `help()` function to access the help files on a topic specified by *special* or *non-conventional* characters, for example ∗ or `[[`, the argument must be enclosed in double or single quotes, making it a character string (i.e., `help("*")`). By default, the `help()` function only searches in the *packages* which have been *loaded* in memory using the `library()` function – see the **PACKAGES** section for more details. If the `help()` function's `try.all.packages=` argument is specified as `TRUE`, then the `help()` function will search in all (installed) packages. In turn, you can display the help file from a package not loaded in memory using the `help()` function's `package=` argument. For example, `help("bs", package = "splines")`. Details regarding each argument is given in the `Arguments` and `Details` sections of a function's *help file*. Other useful sections of most help files are the `See also` and `Examples` sections, which list the topic names of other help files similar to the present one and contains some example code using the present function, respectively.

In the Windows/Mac versions on R, the help pages can also be accessed via the Help drop-down menu. In addition, help is available in HTML format on most R installations by calling the `help.start()` function, which will launch a Web browser that allows the help pages to be browsed with hyperlinks. The Search Engine and Keywords link in the page loaded by `help.start()` is particularly useful as it contains a high-level concept list which searches through available functions. It can be a great way to get your bearings quickly and to understand the breadth of what R has to offer.

An alternative to the `help()` and `help.start()` functions is the `apropos()` function, which returns a list containing all the objects (functions or assigned variables) whose name contains the character string specified. Only the packages loaded in memory are searched. An example would be to search all the objects for the character string "mean":

```
> apropos("mean")

 [1] "colMeans"        "kmeans"          "mean"            "mean.data.frame"
 [5] "mean.Date"       "mean.default"    "mean.difftime"   "mean.POSIXct"
 [9] "mean.POSIXlt"    "rowMeans"        "weighted.mean"
```

→ *Practice Exercise:* Let's look at the `read.table()` function's help file – `?read.table` or `help(read.table)`.

PACKAGES: R functions are organized into and stored in *packages*. The contents of a package (i.e., its functions) are available only when the package is *loaded* in memory. Thus, it is possible to load only the packages containing the functions that are needed, which makes R run faster and uses less memory. It is also very easy to make use of functions that other people have written and compiled into a package. Currently, over 500 of these 'contributed' packages are available on the CRAN website via the Packages link under the Software section. The packages are listed in alphabetical order, but there is also a CRANTaskViews link, which allows you to browse through some of the packages by topic and provides tools to automatically install all packages for special areas of interest. As you can imagine, the packages cover a wide variety of applications, both statistical and otherwise. The site for each package contains a brief description, the source files, an index of contents, and a downloadable reference manual.

When you install a released version of R, a specific subset of *base* packages are automatically installed. The *base* packages are considered part of the R source code, contain basic functions that allow R to work, and are briefly described in the following table.

Package	Description
`base`	Base functions
`datasets`	Built-in datasets
`grDevices`	Graphics devices for base and grid graphics
`graphics`	Base graphics functions
`grid`	A rewrite of the graphics layout capabilities, plus some support for interaction
`methods`	Formally defined methods and classes for R objects, plus other programming tools

`splines`	Regression spline functions and classes
`stats`	Statistical functions
`stats4`	Statistical Functions using ‘S4 Classes’
`tools`	Tools for package development and administration
`utils`	Utility functions

In addition to these *base* packages, several *recommended* packages are also automatically installed when you install R. The packages are ‘recommended’ since they cover statistical methods often used in data analysis. They are briefly described in the following table.

Package	**Description**
`boot`	Resampling and bootstrapping methods
`class`	Classification methods
`cluster`	Clustering methods
`foreign`	Read data stored in various formats including Stata, SAS, SPSS, & Epi Info
`KernSmooth`	Methods for kernel smoothing and density estimation (including bivariate kernels)
`lattice`	Lattice (Trellis) graphics
`MASS`	Contains many functions, tools and data sets from the libraries of ‘Modern Applied Statistics with S’ by Venables & Ripley
`mgcv`	Generalized additive models
`nlme`	Linear and non-linear mixed-effects models
`nnet`	Neural networks and multinomial log-linear models
`rcompgen`	Completion generator for R
`rpart`	Recursive partitioning
`spatial`	Spatial analyses (‘kriging’, spatial covariance, etc)
`survival`	Survival analyses

The location where these base and recommended packages are installed is known as the *main library*, which is the directory `R_HOME/library`, where `R_HOME` denotes the path to your version of R. On a Linux, Unix, or Mac machine, `R_HOME` is `/usr/lib/R` or `/usr/local/lib/R`. On a Windows machine `R_HOME` is `C:\Program Files\R\R-version`, where `version` is the R version number (e.g., `2.5.1`). By default, further packages will be installed into `R_HOME/library`, as well. It is also possible to have more than one library, so think of a ‘library’ as just a directory containing installed packages.

Packages can be downloaded and installed from within R using the `install.packages()` function. If you are connected to the Internet, you can download and install a package directly from CRAN using `install.packages("pkg)"`, where *`pkg`* is the name of the desired package. R will then ask you to select a *CRAN mirror* from which to install the desired package(s) – CRAN is a collection of sites which carry identical materials and were created as mirror sites to lessen the load on any one server. Personally, I normally select one of the USA mirrors, such as CA1. If you are not connected to the Internet, you can download and save a package's source or binary file from CRAN Packages link and then specify the path to file when you invoke the `install.packages()` function. In either case, if the package is installed correctly, R will return a new command line prompt. In the Windows/Mac versions of R, you will also find a menu called Packages that provides an interface to install packages. Specifically, if you are connected to the Internet, select Install package(s)... from the Packages drop-menu. Next select a CRAN mirror from which to install the desired package(s) and click OK. Next, from the list of packages, select the one(s) you wish to install and click OK – you can select more than one package by holding down the Ctrl key. As with the `intstall.packages()` function, if the package is installed correctly, R will return a new command line prompt. In addition, you can use the Packages drop-menu to install a package if you are not connected to the Internet – Install package(s) from local zip files.... ***IMPORTANT:*** You need to have administrative rights to your laptop (computer) in order to successfully install a package.

When invoked with no arguments specified, the `library()` function returns the list of packages that are installed, which includes the above-mentioned base and recommended packages. The `library()` function is also used to *load* a specific package – `library(pkg)`, where *pkg* is the *installed* package. You need to install a package only once, but, as mentioned, a package's contents are available only when it is *loaded* in memory. It is important to realize that packages must be loaded during every R session you wish to use them in. Luckily, a subset of the *base* packages that are automatically installed are also automatically *loaded* when you start R: `base` (obviously), `datasets`, `grDevices`, `graphics`, `methods`, `stats`, and `utils`. You can also use the `search()` function to see which packages are currently loaded (whether automatically or explicitly loaded with the `library()` function). Each package name is preceded with `package:`.

```
> search()

 [1] ".GlobalEnv"        "package:tools"     "package:stats"     "package:graphics"
 [5] "package:grDevices" "package:utils"     "package:datasets"  "package:methods"
 [9] "Autoloads"         "package:base"
```

Regardless of whether the package has been loaded (but it has to be installed), you can use `library(help = pkg)` or `help(package = pkg)` to list the functions (help topics) it contains. You can also read a brief description of the package by typing `packageDescription("pkg")`.

It is recommended that you either reinstall your packages or *update* the existing packages each time the newest version of R is released, or when a newer version of the package(s) is/are released. Luckily, even if you are unaware of any updates in the package versions, and you are connected to the Internet, the `update.packages()` function can be used to update a single package (`update.packages("pkg")`), or to update all of your installed packages (`update.packages()` – no arguments specified). When invoked with no arguments, the `update.packages()` function downloads the list of available packages and their current version, compares it with those installed and offers to fetch and install any that have later version on CRAN. If you are using the Windows or Mac version of R, there will be a Update packages... selection under the Packages drop-menu.

You can *unload* a specific loaded package using the `detach()` function – `detach("package:pkg")`. And installed packages can be removed (i.e., *uninstalled*) using the `remove.packages()` function – `remove.packages(c("pkg1", "pkg2"))`, where *pkg1* and *pkg2* are the package you want to uninstall.

More information regarding packages can be found in the 'Add-on packages' chapter of the 'Installation and Administration' manual on the R website (`www.r-project.org`; click on the Manuals link under the `Documentation` heading). The FAQs link on the R website also contains some information. And, the 'R Help Desk' column in the December 2003 edition (Vol. 3/3; pages 37-39) Newsletter discusses 'Package Management'.

→ *Practice Exercise:* Let's install and then load the `Hmisc` package, which we will use in both this document and the next. As a side, the `Hmisc` package (i.e. 'Harrell Miscellaneous'), which was developed by Frank Harrell, PhD, contains many functions useful for analyzing data, producing high-level graphics, performing utility operations, importing data sets, making advanced tables, recoding variables, and much more. For this practice exercise, select the Hmisc package and then click OK if using the `Packages` drop-menu, or specify `install.packages("Hmisc")` if using the command line. If the package is installed correctly, R will return a new command line prompt. Now, to *load* the `Hmisc` package, type `library(Hmisc)` at the command line and hit Enter. ***NOTE***, these notes were compiled using `Hmisc` version 3.4-4.

Before we can do anything else with any functions and assignment, we need to learn more about the types and structures of data that R assumes and uses.

DATA TYPES & STRUCTURES: As we have seen, R recognizes a number when we type one. This also includes negative numbers (e.g., `-2`). To specify a piece of text (also called a *character string*), type it within either single or double quotes, such as `'cat'` or `"Drug X"`. R also recognizes *logical values* (also called boolean values), which are typed as `TRUE` and `FALSE` (all capitals and no quotes). And there is a special value, `NA`, which represents a missing or unknown value (again, no quotes). There are also three other special constants: (1) `NULL`, which is used to indicate an empty object; (2) `Inf`, which denotes infinity; and (3) `NaN` ('not a number'), which is produced by numerical computations whose results is undefined (e.g., `1/0`, `0/0`, or `Inf - Inf`).

In addition to these basic types of data, R provides a number of *data structures* that allow multiple values to be specified as a single object. The data structures are *vectors*, *matrices*, *arrays*, *data frames*, and *lists*. In this document, we will work with vectors, data frames, and lists (briefly). We will discuss all of the data structures in more detail in the next document.

VECTORS: The *vector* is the simplest data structure in R. For example, a single value in R (i.e., the logical value `TRUE` or the numeric value `2`) is actually just a vector of length 1. Vectors are one dimensional (i.e., have only a length attribute) and consist of an ordered collection of elements. All elements of a vector must be the same data type – i.e., all numeric, all character (text strings), or all logical – but can also include missing elements designated with the `NA` value. There are a number of functions (and an operator) that can be used to easily construct *vectors* of any length, including the `c()` (concatenate) function and the `seq()` (sequence) function (and colon, `:`, operator). The `c()` (concatenate) function constructs a vector by joining the supplied elements end-to-end. The elements supplied can be single numeric, character, logical, and/or missing values. The elements can also be vectors themselves. The only stipulation is that all the supplied elements must be of the same data type. To use the `c()` function we merely separate the elements by commas:

```
> c(2, 3, 5, 2, 7, 1)

[1] 2 3 5 2 7 1

> c(TRUE, FALSE, FALSE, TRUE)

[1]  TRUE FALSE FALSE  TRUE

> c("cat", "dog", "bird", "horse")

[1] "cat"   "dog"   "bird"  "horse"

> x <- c(2, NA, 5, NA, NA, 7)
> y <- c(10, 15, 12)
> c(y, x)

[1] 10 15 12  2 NA  5 NA NA  7
```

If different types of elements are mixed, all will be coerced into a common type, which is usually character. For example,

```
> c(1:3, "cat")

[1] "1"   "2"   "3"   "cat"
```

The `seq()` (sequence) function is a general tool for generating equidistant series of numbers. The `seq()` function has five formal arguments, but only some of them may be specified in any one function invocation. This causes the `seq()` function to be invoked in one of four ways:

1. `seq(value)`, where `value` is an integer. If `value` is a positive integer, `seq(value)` generates the sequence `1, 2, ..., value`. If `value` is a negative integer, `seq(value)` generates the sequence `1, 0, ..., -value`. For example,

```
> seq(5)

[1] 1 2 3 4 5

> seq(-5)

[1]  1  0 -1 -2 -3 -4 -5
```

2. `seq(from, to)`, where `from` and `to` specify the beginning and end of the sequence, respectively. This form generates the sequence `from`, `from+1`, `(from+1)+1`, `...`, `to` if `to` > `from`, or the sequence `from`, `from-1`, `(from-1)-1`, `...`, `to` if `to` < `from`. The same sequences can be generated using the colon (`:`) operator. In the following examples, the first two invocations and the second two invocations are equivalent. For example,

   ```
   > seq(from = 2, to = 10)

   [1]  2  3  4  5  6  7  8  9 10

   > 2:10

   [1]  2  3  4  5  6  7  8  9 10

   > seq(from = 10, to = 3)

   [1] 10  9  8  7  6  5  4  3

   > 10:3

   [1] 10  9  8  7  6  5  4  3
   ```

   `from` and `to` need not be integers. In this case, the sequence increments by 1 up to the sequence value less than or equal to `to` if `to` > `from`, or the sequence decrements by 1 down to the sequence value greater than or equal to `from` if `to` < `from`. For example,

   ```
   > 5.7:20.2

    [1]  5.7  6.7  7.7  8.7  9.7 10.7 11.7 12.7 13.7 14.7 15.7 16.7 17.7 18.7 19.7

   > 10.5:3.25

   [1] 10.5  9.5  8.5  7.5  6.5  5.5  4.5  3.5
   ```

3. `seq(from, to, by)`, where `from` and `to` are the same as before, and `by` specifies the increment of the sequence (default, `by = 1`). This form generates the sequence `from`, `from+by`, `(from+by)+by`, `...`, up to the sequence value less than or equal to `to` if `to` > `from` and `by` is positive, or the sequence `from`, `from-by`, `(from-by)-by`, `...`, down to the sequence value greater than or equal to `from` if `to` < `from` and `by` is negative. For example,

   ```
   > seq(from = -1, to = 1, by = 0.2)

    [1] -1.0 -0.8 -0.6 -0.4 -0.2  0.0  0.2  0.4  0.6  0.8  1.0

   > seq(from = 9, to = 1, by = -2)

   [1] 9 7 5 3 1

   > seq(from = 5.7, to = 11.2, by = 0.4)

    [1]  5.7  6.1  6.5  6.9  7.3  7.7  8.1  8.5  8.9  9.3  9.7 10.1 10.5 10.9
   ```

4. `seq(from, to, length)`, where `from` and `to` are the same as before, and `length` specifies the desired length of the sequence. This form generates the sequence of `length` equally spaced values from `from` to `to`. As we saw in the second form `seq(from, to)`, if `length` is not specified, the default `by = 1` is used. For example,

   ```
   > seq(from = 2, to = 15, length = 7)

   [1]  2.000000  4.166667  6.333333  8.500000 10.666667 12.833333 15.000000
   ```

NOTE: Assignment can be appropriately incorporated into any of the previous demonstrations of the `c()` (concatenate) and `seq()` functions.

DATA FRAMES: A *data frame* in R corresponds to what other statistical packages call a 'data matrix' or a 'data set' – the (2-dimensional) data structure used to store a complete set of data, which consists of a set of variables (columns) observed on a number of cases (rows). The different columns of a data frame may be of different data types, but all the elements of any one column must be of the same data type. As with vectors, the elements of any one column can also include missing elements designated with the `NA` value. Most types of data you will want to read into R and analyze are best described by data frames. The `data.frame()` function can be used to construct a data frame from scratch. Often, the data arguments you supply to the `data.frame()` function will be individual vectors, which will construct the columns of the data frame. These data arguments can be specified with or without a corresponding column name – either in the form `value` or the form `COLname = value`. For example, we can use the `sample()` function to generate a random data frame.

```
> ourdf <- data.frame(id = 101:110, sex = sample(c("M", "F"), size = 10,
+     replace = TRUE), age = sample(20:50, size = 10, replace = TRUE),
+     tx = sample(c("Drug", "Placebo"), size = 10, replace = TRUE),
+     diabetes = sample(c(TRUE, FALSE)))
> ourdf

    id sex age      tx diabetes
1  101   M  49 Placebo    FALSE
2  102   M  50 Placebo     TRUE
3  103   M  20 Placebo    FALSE
4  104   M  38    Drug     TRUE
5  105   F  40 Placebo    FALSE
6  106   M  45 Placebo     TRUE
7  107   F  26 Placebo    FALSE
8  108   F  22 Placebo     TRUE
9  109   M  40 Placebo    FALSE
10 110   M  39 Placebo     TRUE
```

With the `data.frame()` function, character vectors are automatically coerced into *factors*, which we will discuss in the next chapter. Also, all invalid characters in column names (e.g., spaces, dashes, or question marks) are converted to periods (`.`). We will cover how to construct a data frame by reading in a data file in the next chapter – the much more convenient way to generate a data frame.

A THOUGHT TO END WITH: Like learning any new programming language, R has a steep learning curve, in part due to a number of fine points and common pitfalls which may surprise the user at first. However, taking the time to really learn R will be well worth it in the end – DON'T QUIT!

Chapter 2

Data Import and Prep

Learning objectives
To understand how to import a delimited text file, obtain the various attributes of a read-in data set, and customize a data set after input.

Now that we have discussed some of the essentials of the R language, our next logical step would be to perform some analysis on an actual data set. Based on our knowledge from the first lecture, we could use the `c()` ('concatenate') and `data.frame()` functions to construct our data set by typing in the values of each variable and assigning each vector its corresponding variable name. However, in general, this plan of attack is quite impractical depending on the size of the desired data set. It also provides a perfect opportunity for errors to creep into the data set. If the data is already recorded in some format, it's better to be able to read it in. The way this is done depends on how the data is stored, as data sets may be found on web pages, as formatted text files, as spreadsheets, or in many other formats.

MOTIVATING DATA SET: The rest of this document will center around an example data set – a random subset of the well known *Primary Biliary Cirrhosis* data set. The full data set contains the data from the Mayo Clinic trial in primary biliary cirrhosis (PBC) of the liver conducted between 1974 and 1984. Specifically, the trial was a randomized placebo controlled trial of the drug D-penicillamine. The random subset of the PBC data set that we will be using has been saved as a Microsoft Excel file (`pbc.xls`). The file contains N = 100 records (rows) and the following variables (columns):

Variable Name	**Variable Description**
`ID`	Case number
`FUDays`	Number of days between registration and the earlier of death, transplantion, or study analysis time in July, 1986
`Status`	Status, where 0 = Censored, 1 = Censored due to liver treatment, and 2 = Death
`Drug`	Treatment, where 1 = D-penicillamine and 2 = Placebo
`Age`	Age in days
`Sex`	Gender, Male/Female
`Ascites`	Presence of ascites, No/Yes
`Bili`	Serum bilirubin in mg/dl
`Chol`	Serum cholesterol in mg/dl
`Album`	Albumin in gm/dl
`Stage`	Histological stage of disease

<u>MICROSOFT EXCEL FILES:</u> Your data file is often stored as a Microsoft Excel file, but unfortunately, R can not directly read such a file. R generally wants to read in a delimited text file. Luckily, it is very easy to use Microsoft Excel to export your data file in a tab-delimited or comma-delimited form. You can then use the `read.table()` function, which we'll discuss in detail, to read the exported data file into R. You can convert a file from Microsoft Excel to another file format by saving it with the Save As command from the File drop menu. Use the Save as type: drop box to choose the desired file format, such as tab-delimited text (.txt) or comma-delimited text (.csv). Remember, for most file formats, Excel converts only the active sheet. To convert the other sheets, switch to each sheet and save it separately.

SOME GOOD PROGRAMMING PRACTICES: Before you read in *any* data file:

1. Create a directory (folder) where you will keep all your data, code, and output related to a particular project. This can be thought of as your *'working directory'* whenever you use R for that particular project.

   → *Practice Exercise:* Create a folder on your desktop named `IntroToR` and save the `pbc.xls` Microsoft Excel file to this folder.

2. Start your R session from within your relevant working directory. It is quite common for objects that have the same name to be created during an analysis (e.g., `x`, `y`). Names like this are often meaningful in the context of a single analysis, but it can be quite hard to decode what they might be when several analyses have been conducted in the same directory. Starting your R session from within the relevant working directory will also allow you to easily reference the names of your data files without having to include long path names (i.e., `C:/MyDocuments/MyProjects/ProjectName/.../filename.txt`). Under R for Windows/Mac, use Change dir... from the File drop-menu to Browse for and select the relevant working directory after starting R. For the Linux/Unix versions of R, you can use the `cd` (i.e. change directory) command at the shell prompt to move to the relevant working directory *before* starting R, or you can use the `setwd()` function to specify the path (in quotes) to the desired working directory *after* starting R. Users of the Windows/Mac versions of R can also use the `setwd()` function.

   → *Practice Exercise:* Change your working directory to the `IntroToR` folder on your desktop. For example, we could specify `setwd("~/Desktop/IntroToR")` in the Linux/Unix version of R or `setwd("C:/windows/Desktop/IntroToR")` in the Windows/Mac versions of R.

3. Make sure each data file is '*clean*'.

   - All variable names are valid (i.e., contain no spaces or special characters).
   - Missing values are consistently represented (e.g., `NA` or a blank cell if originally a Microsoft Excel file).
   - All quotation marks are 'matched' (i.e., each opening quotation mark has a closing quotation mark).
     - *NOTE:* With R, non-numeric text data need not be quoted.
   - Microsoft Excel files are appropriately saved as either tab or comma delimited text files.
     - Make sure blank cells contain no spaces.
     - If saving as a tab delimited text file, make sure all character fields that contain spaces are wrapped with (single or double) quotation marks (e.g., `Disease free` to `"Disease free"`).
     - If saving as a comma delimited text file, make sure character fields that contain commas are wrapped with quotation marks and thousands separators are removed from all numeric fields (e.g., `1,250` to `1250`).

   → *Practice Exercise:* Using the File > `Save As` technique, convert `pbc.xls` to a comma-delimited file (i.e., `pbc.csv`) and save it to the same folder where `pbc.xls` is located.

It is also worthwhile to create and use an R *code file* to completely and cumulatively record your analysis, including the code to load any necessary packages and to read in your data set. This is easily done using a text editor such as WordPad (on a Windows machine) or xemacs (on a Linux/Unix machine) – simply type and/or copy and paste the desired code (and/or output) from the R command line subwindow to your code file, and vice versa. Doing so ensures reproducible results. It also allows you to 'cannibalize' your code for other projects.

→ *Practice Exercise:* Save the `Scott.IntroToR.I.R` file, which contains the extracted R code from this lecture, to the same folder where `pbc.xls` and `pbc.csv` are located and open it with an appropriate text editor.

THE* `read.table()` *FUNCTION: Whether or not your data set starts out as a Microsoft Excel file, most often, the data you want to read into R is a simple delimited text file with records corresponding to the rows and variables to the columns. For such files, the `read.table()` function is the most flexible function to use to read-in your data set. The columns of the text file can be separated by blanks, commas, or some other known separator. And the first line of the text file can also contain a *header* giving the names of the variables (i.e., columns) – a highly recommended practice. The `read.table()` function creates a data frame from the read in data set. The arguments of the `read.table()` function, and their default values (if any) are:

```
> args(read.table)

function (file, header = FALSE, sep = "", quote = "\"'", dec = ".",
    row.names, col.names, as.is = !stringsAsFactors, na.strings = "NA",
    colClasses = NA, nrows = -1, skip = 0, check.names = TRUE,
    fill = !blank.lines.skip, strip.white = FALSE, blank.lines.skip = TRUE,
    comment.char = "#", allowEscapes = FALSE, flush = FALSE,
    stringsAsFactors = default.stringsAsFactors(), encoding = "unknown")
NULL
```

The first argument is the `file=` argument. We will need to specify the name of the data file in quotes, including the file extension – and ***DON'T FORGET***, R is case sensitive. If the file is not in the current working directory, the file name must be specified along with its *path*. The syntax of the path varies depending on operating system, but *forward* slashes (/; not backslashes) should always be used in the path name (even in the Windows version of R). For example, in the Windows version of R, use something similar to `file = "C:/MyDocuments/MyProjects/ProjectName/filename.txt"`. And in the Unix/Linux version of R, use something similar to `file = "/home/username/MyDocuments/ProjectName/filename.txt"` (the tilde, ~, expansion can be used where supported). If the directory name and/or file name contains spaces, use a backslash *before* the space. For example,`file = "C:/My\ Documents/My\ Projects/Project\ Name/filename.txt"`. Lastly, the name of the file can also be specified as a complete URL, in which case the `read.table()` function reads the website as if it were a local file. For example, `file = "http://www.math.csi.cuny.edu/UsingR/Data/whale.txt"`. The `header=` argument is a logical value (`TRUE` or `FALSE`) specifying whether the file contains the names of the columns as its first line – specify `header = TRUE` if it does. Like with the `data.frame()` function, all invalid characters (e.g., spaces, dashes, or question marks) in the column names are converted to periods (`.`). The `sep=` argument allows you to specify the 'field separator character' – the character separating the columns on each line of the file. By default, `sep=` is defined to be any *whitespace* (i.e., `sep = ""`), which is defined as one or more spaces, tabs, or newlines. Use `sep = " "` for space delimited files; use `sep = ","` for comma-separated files (i.e., .csv files); and use `sep = "\t"` for tab-delimited files (i.e., .txt files). The `na.strings=` argument specifies what character strings are to be interpreted as `NA` (missing) values – by default, `na.strings = "NA"`. Blank fields can be specified as missing values using `na.strings = ""`. You can also specify multiple character strings by using the `c()` (concatenate) function – for instance, if `NA` and `N/A` should be considered missing values, then specify `na.strings = c("NA", "N/A")`. Lastly, specify `fill = TRUE` when the file's separator is some form of whitespace like spaces or tabs and some rows have trailing 'empty fields'. Doing so implicitly adds blank fields when the rows have unequal length. See the `Arguments` section of the `read.table()` function's help file for details regarding the other arguments – `help(read.table)`.

Note, if you incorrectly specify the values that should be considered missing values using the `na.strings=` argument, the character(s) representing missing values will be interpreted as an additional value. In turn, any numeric variables will be coerced to character fields.

→ *Practice Exercise:* We're now ready to import our PBC data file using the `read.table()` function. Recall, the name of our file is `pbc.csv`, the first row does contain column names, and the columns of the delimited file are separated by commas (i.e., a comma-delimited file). In addition, we need to be aware that missing values are represented by blank cells in `pbc.csv`. Putting this all together,

```
> pbc <- read.table("pbc.csv", header = TRUE, sep = ",", na.strings = "")
```

→ *Practice Exercise:* How would you change the previous code if our `pbc.xls` file had been saved as a tab delimited file with the first row containing column names and missing values represented by `NA`?

BE AWARE: The `read.table()` function can be an inefficient way to read in very large datasets. By default, the `read.table()` function needs to read in every column as character data, and then try to figure out which variables to convert to numeric or *factor*. For a large dataset, this takes considerable amounts of time and memory. The performance of the `read.table()` function can be improved by any of the following: (1) use the `colClasses=` argument to specify the classes as one of the atomic vector types (logical, integer, numeric, complex, character, or perhaps raw) for each column; (2) specify `comment.char = ""`; and/or (3) use the `nrows=` argument to give the number of rows to be read – a mild over-estimate is better than not specifying this at all. Another alternative is to use the `scan()` function instead of the `read.table()` function.

Irregardless of how you read your data file(s) into R, if no errors are given, it is always a good practice to check that your data was read in correctly. An easy way to do this is to view the *attributes* of your read in data set. ***REMEMBER:*** In R, your read in data set has the data structure of a *data frame*.

ATTRIBUTES OF A READ-IN DATA SET: Use the `dim()` function to check the dimensions (number of rows and number of columns, respectively) of your data frame. Use the `names()` function to check the variable names of your data frame. You can also use the `Hmisc` package's `contents()` function to display both of these attributes and more. Specifically, the `contents()` function displays the *meta-data* of your data frame, which includes the number of observations (rows) and columns, the variable names, the variable labels (if any), the variable units of measurement (if any), the number of levels for *factor* variables (if any), the storage mode of each variable, and the number of missing values (`NA`s) for each variable. The `contents()` function also displays the maximum number of `NA`s across all variables, and the level labels of each *factor* variable (if any). Lastly, use the `head()` function to print the first 6 (by default) rows of a data frame.

DON'T FORGET to install and/or load the `Hmisc` package if you haven't already done so.

→ *Practice Exercise:* Let's use the `dim()`, `names()`, `Hmisc` package's `contents()`, and `head()` functions to print the attributes of our `pbc` data frame

```
> dim(pbc)

[1] 100  11

> names(pbc)

 [1] "ID"      "FUDays"  "Status"  "Drug"    "Age"     "Sex"     "Ascites" "Bili"
 [9] "Chol"    "Album"   "Stage"

> library(Hmisc)
> contents(pbc)

Data frame:pbc        100 observations and 11 variables    Maximum # NAs:32


        Levels Storage NAs
ID             integer   0
```

```
FUDays          integer   0
Status          integer   0
Drug            integer  25
Age             integer   0
Sex           2 integer   0
Ascites       2 integer  25
Bili             double   0
Chol            integer  32
Album            double   0
Stage           integer   2

+--------+-----------+
|Variable|Levels     |
+--------+-----------+
| Sex    |Female,Male|
+--------+-----------+
| Ascites|No,Yes     |
+--------+-----------+
```

```
> head(pbc)
```

```
  ID FUDays Status Drug   Age    Sex Ascites Bili Chol Album Stage
1  6   2503      2    2 24201 Female      No  0.8  248  3.98     3
2  9   2400      2    1 15526 Female      No  3.2  562  3.08     2
3 20   1356      2    2 21898 Female      No  5.1  374  3.51     4
4 26   1444      2    2 19002 Female      No  5.2 1128  3.68     3
5 30    321      2    2 15116 Female      No  3.6  260  2.54     4
6 37    223      2    1 22546 Female     Yes  7.1  334  3.01     4
```

From the output of the `Hmisc` package's `contents()` function, we can see that the blank cells in the `Drug`, `Ascites`, `Chol`, and `Stage` columns were converted to missing values (`NA`).

FACTORS: It is common in statistical data to have *categorical variables*, indicating some subdivision of data, such as gender, race, disease diagnosis, or tumor stage. In R, categorical variables can be coded with character values, such as the `"No"` and `"Yes"` values of the `Ascites` variable in our `pbc` data frame, or numeric values, such as the `0`, `1`, and `2` values of the `Status` variable. In either case, the elements of the categorical variable may only take one of a finite set of values, such as `"male"` and `"female"` for a gender variable. In R, categorical variables should be defined as *factors*. This is a data structure that (among other things) makes it possible to assign meaningful names to the categories – for example, assign `"Black"` to `"B"` and `"White"` to `"W"` of a race variable or `"Censored"` to `0`, `"Censored due to liver treatment"` to `1`, and `"Death"` to `2` for the `Status` variable in our `pbc` data set. Factors are also essential for R to be able to distinguish between categorical variables and variables whose values have a direct numerical meaning – for example, in R, the raw `1`, `2`, and `3` values of `Status` would be interpreted as a continuous variable in a regression model, not a categorical one.

At first glance, factors appear to be similar to numeric or character vectors, but they are not. Specifically, factors are numeric or character vectors that have an associated set of *levels* – the finite set of values the categorical variable can take. As an example, let's use the `factor()` function to explicitly generate some factors and show this difference:

```
> 5:1
```

```
[1] 5 4 3 2 1
```

```
> factor(5:1)
```

```
[1] 5 4 3 2 1
Levels: 1 2 3 4 5

> c("cat", "horse", "dog", "cat", "dog", "dog")

[1] "cat"   "horse" "dog"   "cat"   "dog"   "dog"

> factor(c("cat", "horse", "dog", "cat", "dog", "dog"))

[1] cat   horse dog   cat   dog   dog
Levels: cat dog horse
```

Notice the additional `Levels:` attribute printed with the factors. As seen, by default, the *sorted unique* values of the vector are used to define the levels of the factor. The levels are sorted based on the type of the supplied vector (i.e., either alphabetical or numerical order). Also, by default, missing values (`NA`) are not defined as a level. For example,

```
> factor(c(TRUE, NA, FALSE, TRUE, FALSE, FALSE, NA))

[1] TRUE  <NA>  FALSE TRUE  FALSE FALSE <NA>
Levels: FALSE TRUE
```

NOTICE: R prints a missing value (`NA`) differently depending on whether it is an element of a factor vector or a vector that has not been defined as a factor. In the previous output, `NA` was printed as `<NA>` in the logical vector that was defined as a factor. On the other hand, `NA` is printed as merely `NA` when a plain numeric, logical, or character vector is printed – see the discussion of the `c()` (concatenate) function in the 'Vectors' section of the first chapter.

It is also important to know that the values of a numeric factor are not interpreted as numeric values. For example,

```
> mean(factor(1:5))

[1] NA

Warning message:
argument is not numeric or logical:  returning NA in:  mean.default(factor(1:5))
```

An important piece of information to know about factors is that non-logical (case sensitive `TRUE` and `FALSE`) character columns (whether or not enclosed in quotation marks) are automatically converted to factors when read-in with the `read.table()` and similar functions. This is apparent when we look at the output of the `Hmisc` package's `contents()` function of our `pbc` data frame – the `Sex` and `Ascites` variables were converted to factors. Specifically, an extra column labeled `Levels` is printed in the initial output and an additional table of `Variable` and `Levels` is also printed. Luckily, with the `read.table()` function, there are several arguments (`as.is=`, `colClasses=`, and `stringsAsFactors=`) that allow you to change this if needed – personally, I always set `stringsAsFactors = FALSE` in my `read.table()` invocation and then explicitly define each factor using the `factor()` function. In addition, irregardless of how a factor is originally specified (as numeric or character), the levels of a factor are internally stored as a vector of integers starting at 1. For example, in the output of `contents()` function of our `pbc` data frame, notice the value of the `Storage` column for the `Sex` and `Ascites` variables – `integer`.

Up to this point, the factors we have created have used the default process of defining the sorted unique values (excluding `NA`s) of the vector as the levels of the factor. However, the `factor()` function has some additional arguments that allow us to be even more explicit about how the levels are defined. Specifically,

```
> args(factor)
```

```
function (x = character(), levels = sort(unique.default(x), na.last = TRUE),
    labels = levels, exclude = NA, ordered = is.ordered(x))
NULL
```

The `levels=` argument can be used to explicitly define the levels of a factor. For example, we can construct a factor with an additional level that is not present in the data:

```
> factor(c(3, 3, 1, 2, 2), levels = 1:4)

[1] 3 3 1 2 2
Levels: 1 2 3 4
```

We can also use the `levels=` argument to change the default order of the levels. For example, we can change the default order of the levels of a race factor from `Black`, `Other`, `White` (i.e., alphabetical order) to `White`, `Black`, `Other`.

```
> factor(c("White", "Black", "Other", "White", "Other", "Black"))

[1] White Black Other White Other Black
Levels: Black Other White

> factor(c("White", "Black", "Other", "White", "Other", "Black"),
+     levels = c("White", "Black", "Other"))

[1] White Black Other White Other Black
Levels: White Black Other
```

The `labels=` argument can be used to define a more descriptive label for each level of a factor. For example, we can add character level labels to a factor that is originally coded with numeric levels.

```
> factor(c(1, 1, 2, NA, 1, 2), labels = c("Case", "Control"))

[1] Case    Case    Control <NA>    Case    Control
Levels: Case Control
```

IMPORTANT: The labels given in the `labels=` argument must be in the same *order* as the factor's levels. For example, suppose we want to add labels to a factor representing race with the levels (in order) of `W`, `B`, `O`, and `H`. Therefore, you would need to specify `labels = c("White", "Black", "Other", "Hispanic")` to properly match the order of the levels. If you had specified `labels = c("Black", "Hispanic", "Other", "White")` (alphabetical order), none of the level labels would match the corresponding levels. In addition, if modifying the order of the levels and defining more descriptive labels, we need to use both the `levels=` and `labels=` arguments.

→ *Practice Exercise:* Using the `factor()` function, convert the following character vector to a factor with the levels (in order) of 'Strongly disagree' (`SD`), 'Disagree' (`D`), 'Neutral' (`N`), 'Agree' (`A`), and 'Strongly agree' (`SA`). ***NOTE:*** The solution to this Practice Exercise, and others where the solution is not shown, can be found in the `Scott.IntroToR.I.R` code file.

```
> x <- c("A", "SA", "D", "D", "SA", "SA", "SA", "A", "N", "SD")
```

The `factor()` function also allows you to define a special kind of factor in which the levels are *ordered*, using its `ordered=` argument. Specifying `ordered = TRUE` allows you to distinguish nominal categorical variables from ordinal ones. For most purposes the only difference between ordered and unordered factors is that the former are printed showing the ordering of the levels. For example,

```
> x <- c("A", "SA", "D", "D", "SA", "SA", "SA", "A", "N", "SD")
> y <- factor(x, levels = c("SD", "D", "N", "A", "SA"), labels = c("Strongly disagree",
+     "Disagree", "Neutral", "Agree", "Strongly agree"), ordered = TRUE)
> y
```

```
 [1] Agree             Strongly agree    Disagree          Disagree
 [5] Strongly agree    Strongly agree    Strongly agree    Agree
 [9] Neutral           Strongly disagree
Levels: Strongly disagree < Disagree < Neutral < Agree < Strongly agree
```

As you can see, when printed, the levels of an ordered factor display the ordering relation (<) between the levels of the factor. This can also be useful when you wish to compare the levels of an ordered factor. For example,

```
> y < "Neutral"
```

```
 [1] FALSE FALSE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE  TRUE
```

We'll discuss *comparison operators*, like `<`, in the second document.

Once a factor has been created, the `levels()` function can be used to return, reorder, and/or redefine its levels (including assigning new level labels, defining new levels, and collapsing existing levels into new levels). To redefine the levels of a factor using the `levels()` function, we can specify a *named* list specifying how to redefine/reorder the levels (i.e., `list(NEWlevel = "OLDlevel")`). The list can also specify new levels. For example,

```
> test <- factor(c("positive", "negative", "negative"))
> levels(test)
```

```
[1] "negative" "positive"
```

```
> levels(test) <- list(positive = "positive", negative = "negative")
> levels(test)
```

```
[1] "positive" "negative"
```

```
> levels(test) <- list(Positive = "positive", Negative = "negative")
> test
```

```
[1] Positive Negative Negative
Levels: Positive Negative
```

```
> levels(test) <- list(Undetermined = "Undetermined", Positive = "Positive",
+     Negative = "Negative")
> test
```

```
[1] Positive Negative Negative
Levels: Undetermined Positive Negative
```

```
> levels(test) <- list(Combined = c("Undetermined", "Positive"), Negative = "Negative")
> test
```

```
[1] Combined Negative Negative
Levels: Combined Negative
```

As a side note, when manipulating factors, it is always a good idea to generate a frequency table of the factor both before and after you modify its levels and/or labels – see the `table()` function, which is explained in the 'Tables of categorical variables' section of the 'Descriptive Statistics' chapter.

→ *Practice Exercise:* Using the `levels()` function, collapse the five-level factor you created in the previous practice exercise to a three level factor with the levels of 'Disagree' (strongly disagree or disagree), 'Neutral', and 'Agree' (agree or strongly agree).

CUSTOMIZING DATA SETS AFTER INPUT: Now that we've read in our data file and have ensured it was read in correctly, we may want to make some modifications. There are many ways you can customize a data frame, including renaming variables, adding new variables, deleting variables, adding or changing the levels of a factor variable, adding or changing variable labels, and/or adding or changing the units of measurement of a variable. There are many functions that are useful in performing some of the modifications mentioned and we could make many of our desired modifications using individual function invocations, but there is an easier way using the `Hmisc` package's `upData()` function. The `Hmisc` package's `upData()` function provides a unified framework for updating a data frame. It accomplishes the following, listed in the order in which the changes are executed:

1. Optionally changes names of variables to lower case.
2. Renames variables.
3. Adds new variables.
4. Recomputes existing variables from the original variables and/or from other variables in the data frame.
5. Changes the storage mode of variables to the most efficient mode.
6. Drops (deletes) variables.
7. Adds, changes, and combines levels of factor variables.
8. Adds or changes variable labels.
9. Adds or changes variable units.

Making any of these changes upfront will allow you take full advantage of any of them during your analyses. For example, many functions will automatically print variable labels and units as part of their output, making interpretation of the results a lot easier. Using the `Hmisc` package's `upData()` function also allows you to define all of the modifications in one function invocation, making all of the modifications much easier to manage.

The arguments of the `Hmisc` package's `upData()` function are (remember, we've already loaded the `Hmisc` package)

```
> args(upData)

function (object, ..., rename = NULL, drop = NULL, labels = NULL,
    units = NULL, levels = NULL, force.single = TRUE, lowernames = FALSE,
    moveUnits = FALSE, charfactor = FALSE)
NULL
```

Specify the name of the data frame using the `object=` argument. Specify one or more expression of the form `VARname = `*`expression`* in the `...` argument position to derive new variables or modify old ones. Use the `rename=` argument to rename variables by specifying a *named* vector of old and new variable names using the `c()` (concatenate) function – e.g., `rename = c(oldVARname1 = "newVARname1", oldVARname2 = "newVARname2")`. Variables are renamed before any other operations are done, so variable names given inside the other `upData()` arguments need to use the new names. Use the `drop=` argument to specify a vector of variable names (using the `c()` function) to remove from the data frame. Use the `labels=` argument to add or modify existing variable labels by specifying a *named* vector, like the `rename=` argument. Use the `units=` argument to add or modify existing variable units by specifying a *named* vector, like the `rename=` and `labels=` argument. Use the `levels=` argument to add or modify the levels for factor variables by specifying a *named list* (not vector) using the `list()` and `c()` (concatenate) functions – e.g., `levels = list(VARname1 = c("`*`level1`*`", "`*`level2`*`", ...), VARname2 = ...)`. It was important to be aware of the `factor()` function's `levels=` and `labels=` arguments and the `levels()` function in order to understand the many things you can do with the `upData()` function's `levels=` argument. We will be demonstrating some of these when we 'update' our `pbc` data frame. Lastly, specifying `lowernames = TRUE` in an `upData()`

function invocation will coerce all the column names to lower-case.

When you invoke the `Hmisc` package's `upData()` function, you can either overwrite the original data frame by assigning the function invocation to original data frame (e.g., `pbc <- upData(pbc, ...)`), or you can assign the function invocation to a new data frame (e.g., `new.pbc <- upData(pbc, ...)`).

→ *Practice Exercise:* Let's make some changes to our `pbc` data using the `Hmisc` package's `upData()` function. Specifically, let's convert the variable names to lower case, and define some variable labels and units (where appropriate) using the `labels=` and `units=` arguments. In addition, let's convert the `Status` and `Drug` variables to factors and define character level labels for them using the `levels=` argument. We can also define the `Stage` variable as a *numeric* factor using the `factor()` function. Lastly, let's also define some new variables, `ageyrs` (age in years), `fuyrs` (follow-up in years), and `censored` (collapsed version of `status` – Censored/Censored due to liver treatment, Dead), and their corresponding value labels, units, and levels. Once we've made all of these changes, let's then view the implemented changes using the `Hmisc` package's `contents()` function.

```
> pbc <- upData(pbc, lowernames = TRUE, stage = factor(stage, levels = 1:4),
+     ageyrs = age/365.25, fuyrs = fudays/365.25, censored = factor(status),
+     labels = c(ageyrs = "Age", fuyrs = "Follow Up", censored = "Collapsed Survival Status",
+         fudays = "Follow Up", status = "Original Survival Status",
+         drug = "Treatment", sex = "Gender", age = "Age", ascites = "Presence of Ascites",
+         bili = "Serum Bilirubin", chol = "Serum Cholesterol", album = "Serum Albumin",
+         stage = "Histological stage of disease"), units = c(fudays = "days",
+         fuyrs = "years", age = "days", ageyrs = "years", bili = "mg/dL",
+         chol = "mg/dL", album = "mg/dL"), levels = list(status = c("Censored",
+         "Censored due to liver treatment", "Dead"), censored = list(Censored = c(0,
+         1), Dead = 2), drug = c("D-penicillamine", "Placebo")))

Input object size:         6776 bytes;         11 variables
Modified variable         stage
Added variable                 ageyrs
Added variable                 fuyrs
Added variable                 censored
New object size:         13928 bytes;         14 variables

> contents(pbc)

Data frame:pbc        100 observations and 14 variables    Maximum # NAs:32

                                Labels Units Levels Storage NAs
id                                                  integer   0
fudays                       Follow Up  days        integer   0
status        Original Survival Status            3 integer   0
drug                         Treatment            2 integer  25
age                                Age  days        integer   0
sex                             Gender            2 integer   0
ascites            Presence of Ascites            2 integer  25
bili                   Serum Bilirubin mg/dL         double   0
chol                 Serum Cholesterol mg/dL        integer  32
album                    Serum Albumin mg/dL         double   0
stage    Histological stage of disease            4 integer   2
ageyrs                             Age years         double   0
fuyrs                        Follow Up years         double   0
censored     Collapsed Survival Status            2 integer   0
```

```
+--------+-------------------------------------------+
|Variable|Levels                                     |
+--------+-------------------------------------------+
|status  |Censored,Censored due to liver treatment,Dead|
+--------+-------------------------------------------+
|drug    |D-penicillamine,Placebo                    |
+--------+-------------------------------------------+
|sex     |Female,Male                                |
+--------+-------------------------------------------+
|ascites |No,Yes                                     |
+--------+-------------------------------------------+
|stage   |1,2,3,4                                    |
+--------+-------------------------------------------+
|censored|Censored,Dead                              |
+--------+-------------------------------------------+
```

Note, I often do not use the `upData()` function's `levels=` argument as I have in this *Practice Exercise*. On the other hand, I first, as mentioned, specify `stringsAsFactors = FALSE` in my `read.table()` function invocation, causing all character columns in the read-in data file to remain as character columns (ie, they are not automatically converted to factors). I then explicitly convert each character column (and other columns if appropriate) to factors using the `factor()` function. This allows me to specify both the `levels=` and the `labels=` argument in each `factor()` function invocation, which in turn makes the pairing of each level with a corresponding label crystal clear. It also allows me to more easily define factors that have more levels defined than are present in the data. With all of this in mind, the following is alternative code for reading in our `pbc` data and defining all of the appropriate factors – the end result is the same. Notice, unlike previously, we must explicitly define the `Sex` and `Ascites` as factors.

```
> pbc <- read.table("pbc.csv", header = TRUE, sep = ",", na.strings = "",
+     stringsAsFactors = FALSE)
> contents(pbc)

Data frame:pbc        100 observations and 11 variables    Maximum # NAs:32

          Storage NAs
ID        integer   0
FUDays    integer   0
Status    integer   0
Drug      integer  25
Age       integer   0
Sex     character   0
Ascites character  25
Bili       double   0
Chol      integer  32
Album      double   0
Stage     integer   2

> pbc <- upData(pbc, lowernames = TRUE, status = factor(status, levels = 0:2,
+     labels = c("Censored", "Censored due to liver treatment", "Dead")),
+     censored = status, drug = factor(drug, levels = 1:2, labels = c("D-penicillamine",
+         "Placebo")), sex = factor(sex, levels = c("Female", "Male")),
+     ascites = factor(ascites, levels = c("No", "Yes")), stage = factor(stage,
+         levels = 1:4), ageyrs = age/365.25, fuyrs = fudays/365.25,
+     labels = c(ageyrs = "Age", fuyrs = "Follow Up", censored = "Collapsed Survival Status",
+         fudays = "Follow Up", status = "Original Survival Status",
+         drug = "Treatment", sex = "Gender", age = "Age", ascites = "Presence of Ascites",
+         bili = "Serum Bilirubin", chol = "Serum Cholesterol", album = "Serum Albumin",
+         stage = "Histological stage of disease"), units = c(fudays = "days",
+         fuyrs = "years", age = "days", ageyrs = "years", bili = "mg/dL",
+         chol = "mg/dL", album = "mg/dL"), levels = list(censored = list(Censored = c("Censored",
+         "Censored due to liver treatment"), Dead = "Dead")))

Input object size:         6360 bytes;         11 variables
Modified variable         status
Added variable                 censored
Modified variable         drug
Modified variable         sex
Modified variable         ascites
Modified variable         stage
Added variable                 ageyrs
Added variable                 fuyrs
New object size:         13928 bytes;         14 variables

> contents(pbc)

Data frame:pbc        100 observations and 14 variables    Maximum # NAs:32

                                Labels Units Levels Storage NAs
id                                                  integer   0
fudays                       Follow Up  days        integer   0
status        Original Survival Status           3 integer   0
drug                         Treatment           2 integer  25
age                                Age  days        integer   0
sex                             Gender           2 integer   0
ascites            Presence of Ascites           2 integer  25
bili                   Serum Bilirubin mg/dL         double   0
chol                 Serum Cholesterol mg/dL        integer  32
album                    Serum Albumin mg/dL         double   0
stage    Histological stage of disease           4 integer   2
censored     Collapsed Survival Status           2 integer   0
ageyrs                             Age years         double   0
fuyrs                        Follow Up years         double   0

+--------+---------------------------------------------+
|Variable|Levels                                       |
+--------+---------------------------------------------+
|status  |Censored,Censored due to liver treatment,Dead|
+--------+---------------------------------------------+
|drug    |D-penicillamine,Placebo                      |
+--------+---------------------------------------------+
|sex     |Female,Male                                  |
+--------+---------------------------------------------+
|ascites |No,Yes                                       |
+--------+---------------------------------------------+
|stage   |1,2,3,4                                      |
+--------+---------------------------------------------+
|censored|Censored,Dead                                |
+--------+---------------------------------------------+
```

A THOUGHT TO END WITH: Creating and using an R *code file* to completely and cumulatively record your analysis is invaluable. Luckily, it is very easy to type and/or copy and paste the desired code (and/or output) from the R command line subwindow to your code file, and vice versa. If you are on a Windows machine, I would recommend formatting your code and output using the Courier New (monospace) font, which is very similar to what is used in R.

Even though it is very easy create a code file, it is imperative that you try make your code files well readable and as much self-explaining as possible. This includes

- indenting and using spaces appropriately;
- explicitly specifying function arguments by their `ARGname` tag;
- wrapping long lines of code by explicitly breaking long expressions;
  - Explicitly break long expression by inserting a newline (i.e., a carriage return) after a *known separator* that is syntactically relevant. In particular, break a long expression after a comma separating the arguments of a function; after a *logical operator* (`&` = 'and' or `|` = 'or') within a logical statement; or after a plus sign (`+`) within a formula statement (e.g., `Y ~ X1 + X2`).
- and adding copious *comments* to your code.
  - Any text following a `#` on the command line, to the end of the line, is taken as a 'comment' and ignored by R. Comments can be put almost anywhere, except inside quoted strings, and within the argument list of a function definition. For example,

    ```
    > 175*(8/5) # convert 175 miles to kms
    [1] 280
    ```

See the `Scott.IntroToR.I.R` code file for an illustration of all of these tips. You'll notice that the `Scott.IntroToR.I.R` code file includes the R code to set the working directory (`setwd()`) and load any necessary packages (`library()`).

When all your R code is collected and recorded in a code file, the results can be reproduced at any time. In addition, if your R code is stored in an external file, say `Rcode.R` in the current working directory, all of the expressions can be executed at any time in an R session with the expression `source("Rcode.R")`. This is extremely useful if you have defined your own function (as we will discuss in more detail) in an external file and wish to source the function. The `source()` function also has a `verbose=` argument, which (when set to `TRUE`) will cause each expression and additional diagnostics to be printed during the parsing and evaluation of the input file.

Chapter 3

Generating Descriptive Statistics

Learning objective
To understand how to generate frequency tables of categorical data, simple univariate and group-wise summary statistics of continuous data, and descriptive tables that automatically summarize both continuous and categorical data.

After successfully reading in our data set and making the desired changes to it, we're now in the position to start exploring our data using various descriptive statistics. However, before we do this, we need to briefly discuss another fundamental of the R programming language.

ACCESSING VARIABLES IN YOUR DATA FRAME: The `$` *operator* is the main way a column of a data frame can be extracted – that is, you can access the values of a desired column using a `dfname$colname` construct, where `dfname` is the name of your data frame and `colname` is the name of the desired column. For example, we can return (print) the first 15 values of `ageyrs` using

```
> head(pbc$ageyrs, n = 15)

Age [years]
 [1] 66.25873 42.50787 59.95346 52.02464 41.38535 61.72758 33.63450 33.69473 49.13621
[10] 53.50856 32.61328 32.49281 46.51608 67.31006 55.83025
```

It is important to remember that in order to access the values of a desired column, we must also include the name of the data frame. Unlike some statistical software programs, in R, you can have many data frames assigned in memory, so you have to direct R to the data frame you wish to use. Unfortunately, having to type the name of the data frame each time we reference a variable can be cumbersome when multiple references are performed. And, as you can imagine, depending on the length of the name of both the data frame and column, the typed expression can be quite long and inconvenient. For example,

```
> pbc[pbc$ageyrs > 70 & !is.na(pbc$ageyrs) & pbc$drug == "D-penicillamine" &
+     !is.na(pbc$drug) & pbc$sex == "Female" & !is.na(pbc$sex), c("id",
+     "status")]
```

Luckily, there are a few alternative ways in R to access the variables of a data frame without involving the `dfname$colname` construct. The first alternative, the `attach()` function, is one that I have to mention because it is often used in various R documentation, but is the one alternative that I do not recommend.

As its name implies, the `attach()` function attaches R objects, assigned data frames or lists, to the *search path.* The search path is a group of 'databases' that R searches when evaluating a named object or function name. We can print (return) the search path using the `search()` function. Recall, we've encountered the `search()` function before in the 'Packages' section.

```
> search()

 [1] ".GlobalEnv"        "package:Hmisc"     "package:tools"     "package:stats"
 [5] "package:graphics"  "package:grDevices" "package:utils"     "package:datasets"
 [9] "package:methods"   "Autoloads"         "package:base"
```

The ‘databases’ are searched in the order they are printed. Therefore, the *global environment* database (`.GlobalEnv`), which is more often known as your *workspace*, is the first database searched. Your workspace contains all the objects you have assigned during an R session, which we will discuss in more detail in the ‘Object Management’ section of the second document. R then searches through the various loaded packages. The `Autoloads` entry is R’s way of automatically loading additional installed packages (such as `tools`) that are needed by specific functions.

When we attach an assigned data frame or list using the `attach()` function, it is placed at the number 2 position in the search path. For example,

```
> attach(pbc)
> search()

 [1] ".GlobalEnv"        "pbc"               "package:Hmisc"     "package:tools"
 [5] "package:stats"     "package:graphics"  "package:grDevices" "package:utils"
 [9] "package:datasets"  "package:methods"   "Autoloads"         "package:base"
```

Attaching a data frame or list allows us to access the columns of a data frame (or components of a list) by simply using their names; we no longer have to direct R through the data frame to find the column. For example,

```
> head(ageyrs, n = 15)

Age [years]
 [1] 66.25873 42.50787 59.95346 52.02464 41.38535 61.72758 33.63450 33.69473 49.13621
[10] 53.50856 32.61328 32.49281 46.51608 67.31006 55.83025
```

It is possible to attach more than one data frame (or list) – with the current release of R the search path can contain at most 20 items. New data frames (or lists) are inserted into position 2 by default, and everything except `.GlobalEnv` (i.e., the workspace) moves one step to the right.

Even though you will often see the `attach()` function used in many of the introductory R documentation, it can be very misleading if you are not careful with it’s use. Specifically, avoid attaching the same data frame more than once (e.g., subsets of the data frame) or multiple data frames with some names of variables in common. In actuality, there may be several objects of the same name in different parts of the search path. In that case, R chooses the first one (that is, it searches first in the `.GlobalEnv`, then in `pbc`, and so forth). For this reason you need to be a little careful with ‘loose’ objects that are defined in the workspace outside a data frame since they will be used before any vectors and factors of the same name in an attached data frame. For example, if you created an assigned object with the same name as one of the columns in your data frame. For the same reason, it is not a good idea to give a data frame the same name as one of the variables inside it.

Also, always *detach* the data frame (or list) from the search path as soon as you have finished using its columns (components). You can remove a data frame from the search path using the `detach()` function. For example

```
> detach("pbc")
> search()

 [1] ".GlobalEnv"        "package:Hmisc"     "package:tools"     "package:stats"
 [5] "package:graphics"  "package:grDevices" "package:utils"     "package:datasets"
 [9] "package:methods"   "Autoloads"         "package:base"
```

Note, the `.Globalenv` and `package:base` items of the search path can not be detached.

Another pitfall of the `attach()` function is it is not possible to directly assign into an attached list or data frame (thus, to some extent they are static). For example, suppose we attached a data frame `dframe` which contained variables `u`, `v` and `w`. At this point an assignment such as `u <- v+w` does not replace the component `u` of the data frame, but rather masks it with another variable `u` defined in your workspace at position 1 on the search path (i.e, the `.GlobalEnv`). To make a permanent change to the data frame itself, the simplest way is to resort once again to the `$` notation: `dframe$u <- v+w`. However, the new value of component `u` is not visible until the data frame is *detached* and attached again.

So, even though the `attach()` function appears very useful, I never use it because of the many pitfalls associated with it. Plus, I find it makes my code harder to read. More specifically, it is often difficult to determine what data frame (or list) the columns (components) you are specifying in your code are coming from, especially if you are performing the same tasks on several subsets of the same data frame or list. Instead, I use the `with()` function as an alternative.

Like the `attach()` function, the `with()` function saves us some typing by allowing us to not have to use the `dfname$colname` construct. However, the `with()` function essentially performs the `attach()` and `detach()` commands at once, which saves us many headaches. More specifically, the `with()` function evaluates an R expression in an environment constructed from some data, which is most often a data frame. The syntax of the `with()` function is

```
> args(with)

function (data, expr, ...)
NULL
```

where `data` is the data to use for constructing an environment, and `expr` is the expression to evaluate, which will reference various columns in the data frame. Because we have to specify the data frame as an argument, it is always apparent what data frame the columns are coming from.

By default, the `with()` function only accepts one expression. For example,

```
> with(pbc, head(ageyrs))

Age [years]
[1] 66.25873 42.50787 59.95346 52.02464 41.38535 61.72758
```

However, we can incorporate *braces* ({ and }) into the `with()` function, which will allow us to define a *block* of R code, which includes multiple expressions. This will be very useful when building plots and will be used often in the ‘R graphics’ chapter of this document.

Lastly, as an alternative to the `with()` function, many functions have a `data=` argument, which allows you to specify the data frame containing the variables being used in the function call. Some of these functions include most of the modeling functions and the `subset()` function. In practice, get into the habit of looking at the `Arguments` section of a function’s help file to determine if a `data=` argument is available.

Now let’s get back to generating various descriptive statistics of our data.

TABLES OF CATEGORICAL VARIABLES: Categorical data are usually described in the form of *frequency* tables. In R, frequency tables can be easily generated using the `table()` function, which uses one or more cross-classifying variables to build a contingency table of the counts at each combination of the ‘levels’ of the variables. To generate a *one*-way table, we simply specify one variable in the `table()` function. The `table()` function does not have a `data=` argument to specify the name of the corresponding data frame, so we’ll use the `with()` function instead. For example,

```
> with(pbc, table(sex))

sex
Female   Male
    86     14
```

The `table()` function can easily be extended to generate *two-*, *three-*, and *n*-way tables. In general, we merely need to specify one vector of values for each table margin that is desired. For example,

```
> with(pbc, table(sex, drug))

        drug
sex      D-penicillamine Placebo
  Female              34      30
  Male                 6       5

> with(pbc, table(sex, drug, censored))

, , censored = Censored

        drug
sex      D-penicillamine Placebo
  Female              21      19
  Male                 3       4

, , censored = Dead

        drug
sex      D-penicillamine Placebo
  Female              13      11
  Male                 3       1
```

As seen, the first argument in a `table()` function expression defines the rows of the table (though it is printed horizontally if there is just one column, as we saw above); the second argument defines the columns; and the table slices (rows by columns) that correspond to different values of the third argument appear in succession down the page. In other words, the `table()` function uses the first two arguments for the main (two-way) table and the remaining arguments to construct different tables for each combination of the arguments. In our three-way table example, a two-way table was generated for each level of `censored`. Any *three*-way or higher table can be formatted differently to save space using the `ftable()` ('flatten table') function in place of the `table()` function. For example,

```
> with(pbc, ftable(sex, drug, censored))

                       censored Censored Dead
sex    drug
Female D-penicillamine                21   13
       Placebo                        19   11
Male   D-penicillamine                 3    3
       Placebo                         4    1
```

The layout of a flat table (or any table) can be modified by shifting the order of the arguments. For example,

```
> with(pbc, ftable(sex, censored, drug))

                drug D-penicillamine Placebo
sex    censored
Female Censored                   21      19
       Dead                       13      11
Male   Censored                    3       4
       Dead                        3       1
```

IMPORTANT, you might not have realized, but *missing values* are automatically excluded from any frequency table and are not reported. For example, if we sum the frequencies in the `sex` by `drug` two-way table, we notice they only sum to N = 75 not 100 (the number of rows in our data frame) – remember, the `drug` variable in our `pbc` data set has N = 25 missing values. In R, the `table()` function coerces any of its arguments to a factor if not already defined as one before tabulating them. In turn, any missing values are dumped from being tabulated because of the default habits of the `factor()` function – recall, the `factor()` function automatically excludes missing values from the set of levels it defines.

`NA`s can be included in the tabulation in one of two ways. If the table is being generated from a non-factor object, specify `exclude = NULL` in your `table()`/`ftable()` function invocation. This will cause the `table()`/`ftable()` function to include an additional category in the table which counts the frequencies of `NA`s. For example, let's tabulate the frequency of `chol` values rounded to 1 significant digit. I chose to round the `chol` values using the `signif()` function because of the large number of unique values (N = 66 including `NA`).

```
> with(pbc, table(signif(chol, digits = 1), exclude = NULL))

 100  200  300  400  500  600  700  900 1000 <NA> 
   1   14   24   12    8    5    1    1    2   32 
```

If the table is being generated from an already defined factor object, for which `NA` is not a defined level, the `as.character()` function can be used in conjunction with `exclude = NULL` in your `table()`/`ftable()` function invocation. In general, the `as.character()` function is used to coerce the type of an object to character. In this case, coercing the factor variable to a character vector and specifying `exclude = NULL` causes the `table()`/`ftable()` function to reconstruct the factor with `NA` as a defined level. For example, we can use this construct to tabulate the `drug` variable of our `pbc` data frame and its missing values.

```
> with(pbc, table(as.character(drug), exclude = NULL))

D-penicillamine          Placebo             <NA> 
             40               35               25 
```

The `exclude=` argument can also be used to specify non-missing values to be excluded. For example,

```
> with(pbc, table(stage, exclude = 4))

stage
 1  2  3 
 6 24 39 

> with(pbc, table(as.character(stage), exclude = 4))

   1    2    3 <NA> 
   6   24   39    2 
```

→ *Practice Exercise:* Using the `table()` function, tabulate the number of subjects whose follow-up was greater than 5 years were censored due to liver treatment – use the comparison operator `>` to build a conditional expression that evaluates whether each value of `fuyrs` is greater than 5. Note, comparison *operators* in R are *vectorized*, meaning they operate on each element of a vector (i.e., *element-by-element*) and return a vector. We will discuss vectorization and comparison operators in more detail in the second document.

UNIVARIATE SUMMARY STATISTICS OF CONTINUOUS VARIABLES: There are several functions in R that easily calculate simple *univariate summary statistics* of a single continuous variable's central tendency, range, spread, and more. These include the `mean()`, `median()`, `min()` (minimum), `max()` (maximum), `range()`, `sd()` (standard deviation), and `quantile()` functions. Like the `table()` function, none of these functions have a `data=` argument to specify the name of the corresponding data frame. Instead, we'll use the `with()` function. All the mentioned functions take a numeric vector (i.e., numeric column of your data frame) as its first (main) argument. For example,

```
> with(pbc, mean(ageyrs))
```

```
[1] 49.92134
```

```
> with(pbc, median(ageyrs))
```

```
[1] 49.06776
```

```
> with(pbc, min(ageyrs))
```

```
[1] 30.57358
```

```
> with(pbc, max(ageyrs))
```

```
[1] 78.43943
```

```
> with(pbc, range(ageyrs))
```

```
[1] 30.57358 78.43943
```

```
> with(pbc, sd(ageyrs))
```

```
[1] 11.89152
```

```
> with(pbc, quantile(ageyrs))
```

```
Age [years]
      0%      25%      50%      75%     100%
30.57358 41.31896 49.06776 58.60370 78.43943
```

As you can see, the `range()` function returns a two element vector containing the minimum and maximum of the supplied numeric vector argument. By default, the `quantile()` function returns the minimum, the maximum, and the three *quartiles* in between, which represent the 0.25, 0.50 (ie, median), and 0.75 quantiles. These default probabilities are defined using the `quantile()` function's `probs=` argument – `probs = seq(0, 1, by = 0.25)`. This `probs=` argument can be modified to specify any numeric vector of the desired probabilities with values in [0, 1]. For example,

```
> with(pbc, quantile(ageyrs, probs = seq(0, 1, by = 0.1)))
```

```
Age [years]
      0%      10%      20%      30%      40%      50%      60%      70%      80%
30.57358 34.00520 39.80014 42.59986 44.98234 49.06776 52.00986 56.50568 61.11540
     90%     100%
67.03162 78.43943
```

IMPORTANT: All of these functions have a `na.rm=` argument, which is a logical value (`TRUE` or `FALSE`) indicating whether `NA`s (missing values) should be stripped from the numeric vector data argument before the computation proceeds. By default, `na.rm = FALSE`, which causes all of these functions to return `NA` if the supplied numeric vector contains missing values – in R, any operation involving `NA`s returns an `NA`. For example, let's try to calculate the mean serum cholesterol (`chol`) value in our `pbc` data frame – recall, `chol` has N = 32 missing values.

```
> with(pbc, mean(chol))
```

```
[1] NA
```

As mentioned, specifying `na.rm = TRUE` will explicitly remove any missing values before the computation is evaluated.

```
> with(pbc, mean(chol, na.rm = TRUE))

[1] 381.6176
```

There are many other basic statistics functions in R that have a similar `na.rm=` argument, but only some have a default value of `TRUE`. In addition, many functions have other `na.X=` arguments that dictate how missing values should be treated. For example, the `lm()` (linear model) function has a `na.action=` argument that is specified as `"na.fail"`, `"na.omit"`, or `"na.exclude"`. Make sure you look in the function's help file to ensure any missing values are handled correctly.

→ *Practice Exercise:* Use the `mean()`, and `sd()` functions to calculate the lower- and upper-limits of a 95% confidence interval around the mean of age (in years).

MORE ON MISSING VALUES: The following results may seem surprising. Note, arithmetic, comparison, and logic operators in R, which we will discuss in more detail in the second document, are *vectorized*, meaning they operate on each element of a vector (i.e., *element-by-element*).

```
> x <- c(9, 5, 12, NA, 2, NA, NA, 1)
> x + 5

[1] 14 10 17 NA  7 NA NA  6

> x > 2

[1]  TRUE  TRUE  TRUE    NA FALSE    NA    NA FALSE

> x == NA

[1] NA NA NA NA NA NA NA NA
```

In general, any *operator* (arithmetic, comparison, or logical) performed on an `NA` returns an `NA`. Therefore, using `x == NA` to test whether an element is equal to `NA` does not work. Instead, you must use the `is.na()` function, which returns a logical vector that indicates if each element is missing (`NA`). For example (the `!` = 'not'),

```
> is.na(x)

[1] FALSE FALSE FALSE  TRUE FALSE  TRUE  TRUE FALSE

> x > 2 & !is.na(x)

[1]  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE
```

Missing values (`NA`s) can cause problems in a number of functions. It is always a good idea to look at an individual function's help file to determine how it will handle `NA`s.

→ *Practice Exercise:* Use the `is.na()` and `table()` functions to tabulate the number of missing `ascites` values.

GROUP-WISE SUMMARY STATISTICS OF CONTINUOUS VARIABLES: Up to this point we have generated univariate summary statistics of single continuous variables ignoring any other possible classifying categorical variables. However, you will often want to generate summary statistics of continuous variables at each level of various categorical ones, or at each combination of several categorical variables. Such summaries are often referred to as *group-wise summary statistics*. Like univariate summary statistics, there are many functions in R that can be used to generate group-wise summary statistics. However, we will only cover the `Hmisc` package's `summary.formula()` function in this document. The `Hmisc` package's `summary.formula()` function works from three main arguments: the `formula=`, `method=`, and `data=` arguments. In general, the `formula=` argument specifies the continuous variable you would like to summarize and the categorical variable(s) that specify the groups using a *formula interface* of `LHS ~ RHS`. The `method=` argument specifies whether the continuous variable should be summarized *separately* for each categorical variable specified (`method = "response"`) or *jointly* for the cross-classification of the specified categorical variables (`method = "cross"`). And the `data=` argument specifies the data frame from which the continuous and categorical variables should come. Therefore, unlike with the `table()` and univariate summary statistics functions mentioned, we will not need to use the `dfname$colname` construct or the `with()` function. With these three main arguments in mind, let's discuss the `method = "response"` and `method = "cross"` forms of the `Hmisc` package's `summary.formula()` function in more detail.

REMEMBER, when using the `summary.formula()` function, ***DON'T FORGET*** to load the `Hmisc` package with the `library()` function (i.e., `library(Hmisc)`) if you haven't already done so. If you haven't previously installed the package, you must do this first.

In the `method = "response"` form, which is actually the default method of the `Hmisc` package's `summary.formula()` function, a numeric 'response' variable is specified on the `LHS` of the formula and one or more 'independent' variables are specified on the `RHS` of the formula separated by `+` signs. In turn, as mentioned, the response variable is summarized *separately* for each independent variable. By default, the *mean* of the response variable is the summary statistic calculated for each 'level' of each independent variable. For example,

```
> summary.formula(bili ~ censored + sex, data = pbc, method = "response")

Serum Bilirubin    N=100

+--------------------------+--------+---+--------+
|                          |        |N  |bili    |
+--------------------------+--------+---+--------+
|Collapsed Survival Status|Censored| 68|1.967647|
|                          |Dead    | 32|5.534375|
+--------------------------+--------+---+--------+
|Gender                    |Female  | 86|2.998837|
|                          |Male    | 14|3.785714|
+--------------------------+--------+---+--------+
|Overall                   |        |100|3.109000|
+--------------------------+--------+---+--------+
```

Notice, the defined variable labels and level labels were automatically shown in the resulting table (a benefit of using the `Hmisc` package's `updata()` function discussed in the second chapter of this document).

You can change the function used to summarize the data in each cell by incorporating the `fun=` argument. For example, we can easily calculate the range instead of the mean.

```
> summary.formula(bili ~ censored + sex, data = pbc, method = "response",
+     fun = range)

Serum Bilirubin    N=100

+--------------------------+--------+---+-----+-----+
|                          |        |N  |bili1|bili2|
+--------------------------+--------+---+-----+-----+
|Collapsed Survival Status|Censored| 68|0.4  | 8.6 |
|                          |Dead    | 32|0.6  |25.5 |
+--------------------------+--------+---+-----+-----+
|Gender                    |Female  | 86|0.4  |25.5 |
|                          |Male    | 14|0.9  | 9.5 |
+--------------------------+--------+---+-----+-----+
|Overall                   |        |100|0.4  |25.5 |
+--------------------------+--------+---+-----+-----+
```

The function you specify with the `fun=` argument can even be *self-defined*. For example,

```
> summary.formula(bili ~ censored + sex, data = pbc, method = "response",
+     fun = function(x) {
+         c(Median = median(x), Min = min(x), Max = max(x))
+     })

Serum Bilirubin    N=100

+-------------------------+--------+---+------+---+----+
|                         |        |N  |Median|Min|Max |
+-------------------------+--------+---+------+---+----+
|Collapsed Survival Status|Censored| 68|1.05  |0.4| 8.6|
|                         |Dead    | 32|3.55  |0.6|25.5|
+-------------------------+--------+---+------+---+----+
|Gender                   |Female  | 86|1.35  |0.4|25.5|
|                         |Male    | 14|2.70  |0.9| 9.5|
+-------------------------+--------+---+------+---+----+
|Overall                  |        |100|1.60  |0.4|25.5|
+-------------------------+--------+---+------+---+----+
```

You'll notice that a final row labeled `Overall` is automatically (by default) calculated and printed, which specifies the global summary of the response variable. You can suppress this calculation and printing by specifying `overall = FALSE` in your `summary.formula()` function invocation. In addition, unlike the univariate summary statistics functions mentioned, the `Hmisc` package's `summary.formula()` function by default also removes any missing values from the response variable before calculating any summary statistics – `na.rm = TRUE`. For example,

```
> summary.formula(chol ~ drug + ascites, data = pbc, method = "response",
+     fun = median)

Serum Cholesterol    N=68, 32 Missing

+--------------------+---------------+--+-----+
|                    |               |N |chol |
+--------------------+---------------+--+-----+
|Treatment           |D-penicillamine|36|335.0|
|                    |Placebo        |32|324.5|
+--------------------+---------------+--+-----+
|Presence of Ascites|No             |64|329.5|
|                    |Yes            | 4|288.5|
+--------------------+---------------+--+-----+
|Overall             |               |68|329.5|
+--------------------+---------------+--+-----+
```

If an independent variable(s) specified on the `RHS` of the formula contain(s) more missing values than the response variable then missing values are counted as their own category when subsetting the response variable by the 'levels' of each categorical variable – `na.include = TRUE`. For example,

```
> summary.formula(fuyrs ~ drug + ascites, data = pbc, method = "response",
+     fun = median)

Follow Up    N=100

+-------------------+---------------+---+--------+
|                   |               |N  |fuyrs   |
+------------------+--------------+---+--------+
|Treatment         |D-penicillamine| 40|4.746064|
|                  |Placebo       | 35|3.953457|
|                  |Missing       | 25|3.885010|
+------------------+--------------+---+--------+
|Presence of Ascites|No           | 70|4.580424|
|                  |Yes           |  5|1.062286|
|                  |Missing       | 25|3.885010|
+------------------+--------------+---+--------+
|Overall           |              |100|4.343600|
+------------------+--------------+---+--------+
```

You can suppress the inclusion of the missing categories by specifying `na.include = FALSE` in your `summary.formula()` function invocation. Lastly, there are two additional modifications of the `method = "response"` form of the `Hmisc` package's `summary.formula()` function worth mentioning, but are outside the scope of this introductory document and so will not be covered in detail. Specifically, (1) more than one continuous response variable can be specified on the `LHS` of the formula and (2) one or more continuous independent variables can be specified on the `RHS` of the formula. In case (1), each response variable is summarized separately for each independent variable. In case (2), any continuous independent variable (of at least 10 unique values) is, by default, stratified into groups based on its quartiles. The response variable(s) is/are then summarized based on each quartile.

→ *Practice Exercise:* Use the `Hmisc` package's `summary.formula()` function with `method = "response"` and the `quantile()` function to calculate the minimum, 0.25 quantile, median, 0.75 quantile, and maximum value of `ageyrs` for each level of `sex`, `censored`, and `stage`. In addition, incorporate the `round()` function by modifying the `fun=` argument to be a self-defined function such that the calculated quantiles are rounded to 2 decimal places.

The `method = "cross"` form of the `Hmisc` package's `summary.formula()` function is very similar to the `method = "response"` form. Like the `method = "response"` form, the `method = "cross"` form calculates the mean of the response variable by default and the summary function used can be modified using the `fun=` argument. It returns (prints) an `N` column and, by default, a 'combined' row labeled `ALL`. Also by default, it removes any missing values from the response variable before calculating any summary statistics and returns (prints) missing categories (labeled `NA` or `Missing`) if applicable. However, there are some differences between the `method = "response"` and `method = "cross"` forms regarding the specification of the formula, how the response variable is summarized, and the form of the output. Like the `method = "response"` formula, a numeric response variable is specified on the `LHS` of the `method = "cross"` formula, but the `RHS` of the `method = "cross"` formula can only specify *up to three* independent variables on the `RHS` of the formula. Also, recall, when `method = "cross"`, the response variable is *jointly* summarized for the cross-classification of the categorical independent variable(s). In addition, the form of the output of the `method = "cross"` form is a *data frame*, but it may not look like one depending on how the formula is specified. Specifically, the output really only looks like a data frame if the `RHS` of the formula specifies one or three independent variables. For example,

```
> summary.formula(bili ~ ascites, data = pbc, method = "cross", fun = median)

 UseMethod by ascites

  ascites   N bili
1      No  70  1.6
2     Yes   5  7.1
3      NA  25  1.5
4     ALL 100  1.6

> summary.formula(bili ~ drug + censored + sex, data = pbc, method = "cross",
+     fun = function(x) {
```

```
+         c(Mean = mean(x), SD = sd(x), Median = median(x), Min = min(x),
+             Max = max(x))
+     })

 function by drug, censored, sex list(x = ) by drug, censored, sex { by drug, censored, sex NULL by drug

               drug censored    sex   N     Mean  SD.bili Median Min  Max
1  D-penicillamine Censored Female  21 1.304762 1.173233   0.90 0.4  5.5
2          Placebo Censored Female  19 1.784211 1.682677   1.00 0.4  6.4
3               NA Censored Female  19 2.021053 2.278542   1.00 0.6  8.1
4              ALL Censored Female  59 1.689831 1.748467   1.00 0.4  8.1
5  D-penicillamine     Dead Female  13 3.238462 2.087478   3.20 0.6  7.1
6          Placebo     Dead Female  11 8.254545 8.798791   5.10 0.8 25.5
7               NA     Dead Female   3 8.433333 6.995951   7.10 2.2 16.0
8              ALL     Dead Female  27 5.859259 6.494510   3.60 0.6 25.5
9  D-penicillamine      ALL Female  34 2.044118 1.824445   1.15 0.4  7.1
10         Placebo      ALL Female  30 4.156667 6.205708   2.10 0.4 25.5
11              NA      ALL Female  22 2.895455 3.766200   1.35 0.6 16.0
12             ALL      ALL Female  86 2.998837 4.333142   1.35 0.4 25.5
13 D-penicillamine Censored   Male   3 4.333333 2.458319   3.50 2.4  7.1
14         Placebo Censored   Male   4 4.250000 3.535062   3.75 0.9  8.6
15              NA Censored   Male   2 2.050000 1.343503   2.05 1.1  3.0
16             ALL Censored   Male   9 3.788889 2.719579   3.00 0.9  8.6
17 D-penicillamine     Dead   Male   3 2.633333 1.234234   2.30 1.6  4.0
18         Placebo     Dead   Male   1 1.500000       NA   1.50 1.5  1.5
19              NA     Dead   Male   1 9.500000       NA   9.50 9.5  9.5
20             ALL     Dead   Male   5 3.780000 3.350672   2.30 1.5  9.5
21 D-penicillamine      ALL   Male   6 3.483333 1.973238   2.95 1.6  7.1
22         Placebo      ALL   Male   5 3.700000 3.299242   1.90 0.9  8.6
23              NA      ALL   Male   3 4.533333 4.404921   3.00 1.1  9.5
24             ALL      ALL   Male  14 3.785714 2.829476   2.70 0.9  9.5
25 D-penicillamine Censored    ALL  24 1.683333 1.664114   1.05 0.4  7.1
26         Placebo Censored    ALL  23 2.213043 2.221241   1.00 0.4  8.6
27              NA Censored    ALL  21 2.023810 2.182408   1.10 0.6  8.1
28             ALL Censored    ALL  68 1.967647 2.010750   1.05 0.4  8.6
29 D-penicillamine     Dead    ALL  16 3.125000 1.936147   3.20 0.6  7.1
30         Placebo     Dead    ALL  12 7.691667 8.612935   4.35 0.8 25.5
31              NA     Dead    ALL   4 8.700000 5.737014   8.30 2.2 16.0
32             ALL     Dead    ALL  32 5.534375 6.116588   3.55 0.6 25.5
33 D-penicillamine      ALL    ALL  40 2.260000 1.893823   1.60 0.4  7.1
34         Placebo      ALL    ALL  35 4.091429 5.844171   2.10 0.4 25.5
35              NA      ALL    ALL  25 3.092000 3.784609   1.50 0.6 16.0
36             ALL      ALL    ALL 100 3.109000 4.153010   1.60 0.4 25.5
```

However, if the RHS of the formula specifies two independent variables then the output is printed in a table format, where the levels of the first independent variable denote the rows, the levels of the second independent variable denote the columns, and the values in each cell represent the summary of the response variable. For example,

```
> summary.formula(bili ~ censored + sex, data = pbc, method = "cross",
+     fun = function(x) {
+         c(Mean = mean(x), SD = sd(x), Median = median(x), Min = min(x),
+             Max = max(x))
+     })
```

```
 function by censored, sex list(x = ) by censored, sex { by censored, sex NULL by censored, sex

+-------+
|N      |
|Mean   |
|SD.bili|
|Median |
|Min    |
|Max    |
+-------+
+--------+--------+--------+--------+
|censored| Female |  Male  |   ALL  |
+--------+--------+--------+--------+
|Censored| 59     |  9     | 68     |
|        |1.689831|3.788889|1.967647|
|        |1.748467|2.719579|2.010750|
|        |1.00    |3.00    |1.05    |
|        |0.4     |0.9     |0.4     |
|        | 8.1    | 8.6    | 8.6    |
+--------+--------+--------+--------+
|Dead    | 27     |  5     | 32     |
|        |5.859259|3.780000|5.534375|
|        |6.494510|3.350672|6.116588|
|        |3.60    |2.30    |3.55    |
|        |0.6     |1.5     |0.6     |
|        |25.5    | 9.5    |25.5    |
+--------+--------+--------+--------+
|ALL     | 86     | 14     |100     |
|        |2.998837|3.785714|3.109000|
|        |4.333142|2.829476|4.153010|
|        |1.35    |2.70    |1.60    |
|        |0.4     |0.9     |0.4     |
|        |25.5    | 9.5    |25.5    |
+--------+--------+--------+--------+
```

AUTOMATIC SUMMARIES OF BOTH CATEGORICAL AND CONTINUOUS DATA: So far we have had to summarize each categorical and continuous 'response' variable using various functions and a *separate* function invocation for each 'response' and desired summary. In turn, we've been generating a lot of bits and pieces of output. It would be a lot more efficient if we could use *one* function to generate *one* table that appropriately summarized each of several categorical and/or continuous 'response' variables both 'overall' and for each 'level' of a possible grouping categorical variable. Such a thing is possible with a third method of the `Hmisc` package's `summary.formula()` function – `method = "reverse"`. With `method = "reverse"`, the variable specified on `LHS` of the formula is actually the variable that is used to stratify all the variables specified on the `RHS` of the formula – the *reverse* of normal formula specification. Furthermore, the *single* variable specified on the `LHS` must be a categorical variable (either a factor, character, or discrete numeric). For example, if we wanted to summarize `fuyrs` and `chol` across the levels of `sex`, we would use the formula `sex ~ fuyrs + chol`. With this type of specification, the one or more variables specified on the `RHS` of the formula are broken down one at a time by the 'dependent' variable specified on the `LHS` of the formula. That is, the one or more variables specified on the `RHS` of the formula are appropriately summarized at each 'level' (i.e., unique value) of the variable specified on the `LHS` of the formula.

With `method = "reverse"`, continuous variables are, by default, summarized by the 25th, 50th (i.e., median), and 75th quantiles, and categorical variables are described by frequencies and (column) percentages. Unfortunately, there is not a `fun=` argument that allows you to modify the summary statistics used. However, the mean and standard deviation can be printed in addition to these three quantiles, which we will demonstrate momentarily. By default, any numeric variable that has at least 10 unique values is deemed 'continuous' (`continuous = 10`). Therefore, by default, any numeric variable that has less than 10 unique values (i.e., a discrete numeric variable) is summarized as a categorical variable. If you wish to summarize a discrete numeric variable as a continuous one, use the `continuous=` argument to modify the number of unique levels needed to be interpreted as 'continuous.' By default, any character, factor, or discrete numeric variables are deemed categorical. This includes logical vectors, which are coerced to a discrete numeric vector of `0`s and `1`s.

Here's an example:

```
> summary.formula(sex ~ ageyrs + chol + drug + stage, data = pbc,
+     method = "reverse")
```

```
Descriptive Statistics by Gender

+----------------------------------+---+--------------------------+--------------------------+
|                                  |N  |Female                    |Male                      |
|                                  |   |(N=86)                    |(N=14)                    |
+----------------------------------+---+--------------------------+--------------------------+
|Age [years]                       |100|41.20808/47.10883/57.75086|45.28405/52.12320/67.89322|
+----------------------------------+---+--------------------------+--------------------------+
|Serum Cholesterol [mg/dL]         | 68|       257/321/442        |       292/346/566        |
+----------------------------------+---+--------------------------+--------------------------+
|Treatment : Placebo               | 75|        47% (30)          |        45% ( 5)          |
+----------------------------------+---+--------------------------+--------------------------+
|Histological stage of disease : 1| 98|         7% ( 6)          |         0% ( 0)          |
+----------------------------------+---+--------------------------+--------------------------+
|    2                             |   |        25% (21)          |        21% ( 3)          |
+----------------------------------+---+--------------------------+--------------------------+
|    3                             |   |        37% (31)          |        57% ( 8)          |
+----------------------------------+---+--------------------------+--------------------------+
|    4                             |   |        31% (26)          |        21% ( 3)          |
+----------------------------------+---+--------------------------+--------------------------+
```

The `N` column reports the number of non-missing values for each variable. You'll also notice that in addition to any defined variable labels and level labels, defined units of a continuous variable are also automatically shown in the resulting table.

As you noticed in the previous example, by default, with `method = "reverse"`, no 'overall' summary statistics are calculated for each variable (`overall = FALSE`). Use `overall = TRUE` to add an additional column, titled as `Combined`, which reports these 'overall' summary statistics. For example,

```
> summary.formula(sex ~ ageyrs + chol + drug + stage, data = pbc,
+     method = "reverse", overall = TRUE)

Descriptive Statistics by Gender

+----------------------------------+---+-------------------------+-------------------------+-------------------------+
|                                  |N  |Female                   |Male                     |Combined                 |
|                                  |   |(N=86)                   |(N=14)                   |(N=100)                  |
+----------------------------------+---+-------------------------+-------------------------+-------------------------+
|Age [years]                       |100|41.20808/47.10883/57.75086|45.28405/52.12320/67.89322|41.31896/49.06776/58.60370|
+----------------------------------+---+-------------------------+-------------------------+-------------------------+
|Serum Cholesterol [mg/dL]         | 68|     257.0/321.0/442.0   |     292.0/346.0/566.0   |     258.5/329.5/450.5   |
+----------------------------------+---+-------------------------+-------------------------+-------------------------+
|Treatment : Placebo               | 75|         47% (30)        |         45% ( 5)        |         47% (35)        |
+----------------------------------+---+-------------------------+-------------------------+-------------------------+
|Histological stage of disease : 1| 98|          7% ( 6)        |          0% ( 0)        |          6% ( 6)        |
+----------------------------------+---+-------------------------+-------------------------+-------------------------+
|    2                             |   |         25% (21)        |         21% ( 3)        |         24% (24)        |
+----------------------------------+---+-------------------------+-------------------------+-------------------------+
|    3                             |   |         37% (31)        |         57% ( 8)        |         40% (39)        |
+----------------------------------+---+-------------------------+-------------------------+-------------------------+
|    4                             |   |         31% (26)        |         21% ( 3)        |         30% (29)        |
+----------------------------------+---+-------------------------+-------------------------+-------------------------+
```

We can also generate *only* the 'overall' summary statistics of each variable by not specifying a variable on the LHS of the formula (e.g., ~ ageyrs + chol). If there is no LHS variable specified, the summary.formula() function assumes that there is only one group in the data and only one column of summaries will appear. Also, if there is no LHS variable specified in the formula, the method= argument defaults to "reverse" automatically. Here's an example,

```
> summary.formula(~ageyrs + chol + drug + stage + sex, data = pbc,
+     method = "reverse")

Descriptive Statistics  (N=100)

+---------------------------------+---+--------------------------+
|                                 |N  |                          |
+---------------------------------+---+--------------------------+
|Age [years]                      |100|41.31896/49.06776/58.60370|
+---------------------------------+---+--------------------------+
|Serum Cholesterol [mg/dL]        | 68|     258.5/329.5/450.5    |
+---------------------------------+---+--------------------------+
|Treatment : Placebo              | 75|         47% (35)         |
+---------------------------------+---+--------------------------+
|Histological stage of disease : 1| 98|          6% ( 6)         |
+---------------------------------+---+--------------------------+
|    2                            |   |         24% (24)         |
+---------------------------------+---+--------------------------+
|    3                            |   |         40% (39)         |
+---------------------------------+---+--------------------------+
|    4                            |   |         30% (29)         |
+---------------------------------+---+--------------------------+
|Gender : Male                    |100|         14% (14)         |
+---------------------------------+---+--------------------------+
```

So far, all of the examples we have shown have explicitly specified all of the variables on the RHS of the formula. With method = "reverse", you may wish to summarize every variable in your data frame, or in a subset of your data frame – which can be a lot of typing depending on how many variables there are. Luckily, there is a shortcut that can be used to specify all of the variables in the data frame that is specified as the data= argument. Specifically, use a '.' (period) on the RHS of your formula. For example, if we wanted to summarize all of the variables in our pbc data frame, we would use the formula ~ ., with an optional variable specified on the LHS of the formula. We can also use the subset() function and its select= argument (and/or its subset= argument) to specify a subset of the desired data frame as the data= argument.

With method = "reverse" and a variable specified on the LHS of the formula, we can also specify test = TRUE to perform association tests between the variable on the LHS and each variable on the RHS of the formula. The tests used are specified in the conTest= and catTest= arguments. By default, the continuous and categorical tests of association used are the Wilcoxon rank-sum or Kruskal-Wallis test using the F distribution (i.e., the Hmisc package's spearman2() function), and the Pearson chi-square test, without the continuity correction (i.e., the chisq.test() function with correct = FALSE), respectively. For example,

```
> summary.formula(sex ~ ageyrs + chol + drug + stage, test = TRUE,
+     data = pbc, method = "reverse")

Descriptive Statistics by Gender

+----------------------------------+---+-----------------------------+-----------------------------+-------------------------------+
|                                  |N  |Female                       |Male                         |  Test                         |
|                                  |   |(N=86)                       |(N=14)                       |Statistic                      |
+----------------------------------+---+-----------------------------+-----------------------------+-------------------------------+
|Age [years]                       |100|  41.20808/47.10883/57.75086|  45.28405/52.12320/67.89322|   F=2.37 d.f.=1,98 P=0.127    |
+----------------------------------+---+-----------------------------+-----------------------------+-------------------------------+
|Serum Cholesterol [mg/dL]         | 68|         257/321/442         |         292/346/566         |   F=1.23 d.f.=1,66 P=0.271    |
+----------------------------------+---+-----------------------------+-----------------------------+-------------------------------+
|Treatment : Placebo               | 75|          47% (30)           |          45% ( 5)           | Chi-square=0.01 d.f.=1 P=0.93|
+----------------------------------+---+-----------------------------+-----------------------------+-------------------------------+
|Histological stage of disease : 1| 98|           7% ( 6)           |           0% ( 0)           |Chi-square=2.67 d.f.=3 P=0.446|
+----------------------------------+---+-----------------------------+-----------------------------+-------------------------------+
|    2                             |   |          25% (21)           |          21% ( 3)           |                               |
+----------------------------------+---+-----------------------------+-----------------------------+-------------------------------+
|    3                             |   |          37% (31)           |          57% ( 8)           |                               |
+----------------------------------+---+-----------------------------+-----------------------------+-------------------------------+
|    4                             |   |          31% (26)           |          21% ( 3)           |                               |
+----------------------------------+---+-----------------------------+-----------------------------+-------------------------------+
```

You can also optionally specify `overall = TRUE` with `test = TRUE`. In this case, the tests are correctly performed (i.e., they ignore the values in the `Combined` column).

As you probably noticed, the way the output of the `Hmisc` package's `summary.formula()` function with `method = "reverse"` is printed by default is not that desirable. For instance, there are varying numbers of decimal places and not all levels of all categorical variables are shown. Luckily there is a print method that corresponds to the `summary.formula()` function with `method = "reverse"` output – `print.summary.formula.reverse()`. We can specify our `method = "reverse"` form of our `summary.formula()` function invocation as the data argument to a `print.summary.formula.reverse()` method invocation and use the `print.summary.formula.reverse()` arguments to print the output as desired.

Specifically, use the `digits=` argument to specify the number of significant digits to print. By default, the current value of the digits system option (i.e., `options("digits")`) is used, which is 7.

By default, the number of non-missing observations for each `RHS` variable (i.e., the `N` column) is printed only if any of the counts of non-missing values of the `RHS` variables differs from the total number of non-missing values of the `LHS` variable. Specify `prn = TRUE` to always print the number of non-missing observations for each `RHS` variable.

You can modify the way the frequencies and column percentages for categorical variables are printed using the `npct=` and `pctdig=` arguments. In general, the `npct=` argument specifies which counts are to be printed to the right of percentages. By default, only the numerator of the percentage is printed (`npct = "numerator"`). Use `npct = "both"` to print both numerator and denominator, which is very useful when your data (both the `LHS` and `RHS` variables) contain missing values. You can also specify `npct = "denominator"` or `npct = "none"`. The `pctdig=` argument specifies the number of digits to the right of the decimal place for printing percentages. By default, `pctdig = 0`, so percents will be rounded to the nearest percent.

By default, for `method="reverse"`, `summary.formula()` function objects will be printed by removing 'redundant' entries from percentage tables for binary categorical variables – `exclude1 = TRUE`. This means that only one of the two levels for any binary categorical variable will be printed. For example, only the `Placebo` level of `drug` was summarized in our printed output. The idea is that, for a binary categorical variable, if you know the frequency of one level and the denominator then you can easily calculate the frequency of the other level. To override this, use `exclude1 = FALSE`.

Going one step further, you probably noticed that the summary of the first level of any categorical variable (binary or more levels) was printed on the same line as the variable label – `long = FALSE`. To print the result for the first level on a new line, use `long = TRUE`.

When you use `test = TRUE`, you can optionally specify the `pdig=`, `eps=`, and `prtest=` arguments to control the number of digits to the right of the decimal place for printing *p*-values, the *p*-value 'cutoff', and the test statistic components that are printed, respectively. By default, `pdig = 3`, `eps = 0.001`, which mean any *p*-values less than 0.001 will be printed as `< 0.001`, and `prtest = c("P", "stat", "df", "name")`, which means the name of the test statistic (`F` or `Chi-square`), the value of the test statistic, the degree(s) of freedom, and the p-value are all printed. An alternative is to use `prtest = "P"`, which prints only the p-values.

Lastly, specify `prmsd = TRUE` to print the mean and standard deviation of a continuous variable in addition to the three quantiles. Keep in mind though, that this will make the individual columns even wider.

As an example, let's incorporate some of these printing arguments,

```
> print(summary.formula(sex ~ ageyrs + chol + drug + stage, overall = TRUE,
+     method = "reverse", data = pbc), digits = 3, npct = "both",
+     pctdig = 2, exclude1 = FALSE, long = TRUE)
```

```
Descriptive Statistics by Gender

+------------------------------+---+--------------+--------------+--------------+
|                              |N  |Female        |Male          |Combined      |
|                              |   |(N=86)        |(N=14)        |(N=100)       |
+------------------------------+---+--------------+--------------+--------------+
|Age [years]                   |100|41.2/47.1/57.8|45.3/52.1/67.9|41.3/49.1/58.6|
+------------------------------+---+--------------+--------------+--------------+
|Serum Cholesterol [mg/dL]     | 68| 257/321/442  | 292/346/566  | 258/330/450  |
+------------------------------+---+--------------+--------------+--------------+
|Treatment                     | 75|              |              |              |
+------------------------------+---+--------------+--------------+--------------+
|    D-penicillamine           |   | 53.1% 34/64  | 54.5%  6/11  | 53.3% 40/75  |
+------------------------------+---+--------------+--------------+--------------+
|    Placebo                   |   | 46.9% 30/64  | 45.5%  5/11  | 46.7% 35/75  |
+------------------------------+---+--------------+--------------+--------------+
|Histological stage of disease| 98|              |              |              |
+------------------------------+---+--------------+--------------+--------------+
|    1                         |   |  7.14%  6/84 |  0.00%  0/14 |  6.12%  6/98 |
+------------------------------+---+--------------+--------------+--------------+
|    2                         |   | 25.00% 21/84 | 21.43%  3/14 | 24.49% 24/98 |
+------------------------------+---+--------------+--------------+--------------+
|    3                         |   | 36.90% 31/84 | 57.14%  8/14 | 39.80% 39/98 |
+------------------------------+---+--------------+--------------+--------------+
|    4                         |   | 30.95% 26/84 | 21.43%  3/14 | 29.59% 29/98 |
+------------------------------+---+--------------+--------------+--------------+
```

DIVERTING SCREEN OUTPUT TO A FILE: As you can imagine, with all of the printing arguments we just discussed, we might have some problems printing a wide table to the screen – as seen when we specified `test = TRUE` and `overall = TRUE`. That's why I suggest using the `sink()` function, which diverts R output to a file, to write the `summary.formula()` with `method = "reverse"` output to a file instead of the screen. In turn, you can print the paper in a *landscape* format instead of a portrait one. Doing so will increase your chances of having the wide table print nicely. To start the diversion of the output, the `sink()` function is invoked with the `file=` argument specifying the name of the file to write to (possibly including the path – if no path is specified, the file is created in the current working directory). In turn, a file connection with that named file is established for the duration of the diversion. Once the connection is established, you then evaluate any desired expressions at the command line prompt. Any results that are normally returned (printed) to the screen are written to the named file. Once you have evaluated all desired expressions, the diversion of the output is ended by invoking `sink()` (no formal arguments specified; actually invoking `sink(file = NULL)`). For example,

```
> sink("output.txt")
> print(summary.formula(drug ~ ageyrs + censored,
+    data = pbc, method = "reverse", overall = TRUE, test = TRUE),
+    digits = 3, exclude1 = FALSE, long = TRUE)
> sink()
```

You can write more output to the same file by specifying `append = TRUE` in your subsequent `sink()` function invocations. Otherwise, any previous output is overwritten if 'sinked' to the same file.

In general, you can use the `sink()` function to divert any screen output to a file. In turn, it is very helpful to take advantage of the many `print()` functions. Doing so will allow you to customize how the object is printed to the screen, and therefore diverted to the file – as we demonstrated with the print of the `summary.formula()` function output. As we will see in the next section, there are print functions for hundreds of different types of objects. Other helpful functions to use in conjunction with the `sink()` function are the `cat()` and `paste()` functions, which we discuss in the 'Data Export' section of the second document.

The major draw back to the `sink()` function is that it doesn't write the invoked function expressions to the specified file. Therefore the file contains only evaluated results, not the function expressions used to generate those results. If you are interested in capturing this information too, I would recommend copying desired output that has been returned (printed) to the screen and pasting it into your code file below the function expression that generated it. In turn, you can use the `#` symbol to *comment* out the copied output.

In the Windows version of R you also have two options under the `File` drop-menu: (1) Print...; or (2) Save to file.... These two options will print or save, respectively, the whole command line subwindow including all submitted function expressions and all returned output and warning/error messages.

Lastly, another option for generating reproducible research with R and LaTeX is `Sweave` – see the 'Sweave, part I: Mixing R and LATEX' article by Friedrich Leisch in the December 2002 issue of the *R News* newsletter, and `http://www.ci.tuwien.ac.at/~leisch/Sweave/` for more information. Feel free to also check-out my 'Reproducible Research with R, LaTeX, and Sweave' lecture on my website.

→ *Practice Exercise:* Let's summarize `ageyrs`, `sex`, `bili`, `chol`, `album`, `ascites`, `drug`, `censored`, and `fuyrs` across the levels of `stage`. Let's generate an 'overall' summary for each variable and test for any associations between `stage` and any of the 'response' variables. Let's direct the output to a file named `"output.txt"` and modify the printed output to include the mean and standard deviation of all continuous variables, to 'round' to three significant digits, to show both the numerator and denominator of the frequencies, to print the percentages to two decimal places, to show both levels of all binary categorical variables, to print the first level of all categorical variable on a new line, and to print only the p-values (rounded to 4 decimal places) as the test output. Let's then open the `output.txt` file with an appropriate text editor and see the result – you might have to turn off any word-wrapping to see the output nicely.

A THOUGHT TO END WITH: The action of many functions in R depend on the kind of object given as the main argument. More specifically, these functions act with respect to the *class* (i.e., the definition) of the object specified as its main argument. These functions are called *generic*. In turn, for any generic function, there can be a number of different *class specific methods* where each method is a different function that corresponds to the action to be taken for a particular class of objects. For example, the `summary()` function is generic and generates a different summary for a vector, a data frame, or a formula:

```
> summary(pbc$ageyrs)

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  30.57   41.32   49.07   49.92   58.60   78.44

> summary(pbc)

       id            fudays                                     status
 Min.   :  6.0   Min.   : 216   Censored                           :62
 1st Qu.:118.8   1st Qu.:1150   Censored due to liver treatment: 6
 Median :238.0   Median :1586   Dead                               :32
 Mean   :223.2   Mean   :1870
 3rd Qu.:313.2   3rd Qu.:2546
 Max.   :417.0   Max.   :4453

              drug          age             sex       ascites        bili
 D-penicillamine:40   Min.   :11167   Female:86   No  :70   Min.   : 0.400
 Placebo        :35   1st Qu.:15092   Male  :14   Yes : 5   1st Qu.: 0.800
 NA's           :25   Median :17922               NA's:25   Median : 1.600
                      Mean   :18234                         Mean   : 3.109
                      3rd Qu.:21405                         3rd Qu.: 3.600
                      Max.   :28650                      Max.   :25.500

      chol           album        stage       censored      ageyrs     
 Min.   : 120.0   Min.   :1.960   1   : 6   Censored:68   Min.   :30.57  
 1st Qu.: 258.5   1st Qu.:3.260   2   :24   Dead    :32   1st Qu.:41.32  
 Median : 329.5   Median :3.530   3   :39                 Median :49.07  
 Mean   : 381.6   Mean   :3.518   4   :29                 Mean   :49.92  
 3rd Qu.: 450.5   3rd Qu.:3.775   NA's: 2                 3rd Qu.:58.60  
 Max.   :1128.0   Max.   :4.240                           Max.   :78.44  
 NA's   :  32.0                                                          
     fuyrs        
 Min.   : 0.5914  
 1st Qu.: 3.1478  
 Median : 4.3436  
 Mean   : 5.1208  
 3rd Qu.: 6.9692  
 Max.   :12.1916  
```

```
> summary(ageyrs ~ drug, data = pbc)
```

```
Age    N=100

+---------+---------------+---+--------+
|         |               |N  |ageyrs  |
+---------+---------------+---+--------+
|Treatment|D-penicillamine| 40|50.90849|
|         |Placebo        | 35|47.76525|
|         |Missing        | 25|51.36044|
+---------+---------------+---+--------+
|Overall  |               |100|49.92134|
+---------+---------------+---+--------+
```

When a generic function is called, R uses a process called *method dispatch* to determine which class specific method to use. Specifically, the class of the object specified as the main argument is first determined, which is a character vector of at least one element returned by the `class()` function. For example,

```
> class(pbc)

[1] "data.frame"

> class(pbc$ageyrs)

[1] "labelled"

> class(ageyrs ~ drug)

[1] "formula"
```

Each element of the class of the object is then compared to each method of the generic function, which is returned by the `methods()` function, until one matches a method. For example,

```
> methods(summary)

 [1] summary.agnes*         summary.aov            summary.aovlist       
 [4] summary.areg.boot      summary.clara*         summary.connection    
 [7] summary.data.frame     summary.Date           summary.default       
[10] summary.diana*         summary.dissimilarity* summary.ecdf*         
```

```
[13] summary.factor         summary.fanny*         summary.find.matches
[16] summary.formula        summary.glm            summary.impute
[19] summary.infl           summary.ldBands        summary.lm
[22] summary.loess*         summary.manova         summary.matrix
[25] summary.mChoice        summary.mlm            summary.mona*
[28] summary.nls*           summary.packageStatus* summary.pam*
[31] summary.POSIXct        summary.POSIXlt        summary.ppr*
[34] summary.prcomp*        summary.princomp*      summary.shingle*
[37] summary.silhouette*    summary.stepfun        summary.stl*
[40] summary.table          summary.transcan       summary.trellis*
[43] summary.tukeysmooth*

   Non-visible functions are asterisked
```

Note, the message `no methods are found` is returned if a function is not generic,(e.g., `methods(paste)`). In general, the name of a class specific method of a generic function is the name of the generic function followed by a period followed by the name of the class. So, in the case where we specified `ageyrs ~ drug` as the main argument of the `summary()` function, the class of the object was determined to be `"formula"` and the class specific `summary.formula()` function was chosen. When we specified `pbc` as the main argument, which has a class of `"data.frame"`, the class specific `summary.data.frame()` function was chosen.

If no element of the class matches a method or an object has no class, then the *default method* is used. For example, when we specified `pbc$ageyrs` as the first argument of the generic `summary()` function, which has a class of `"labelled"`, the default `summary.default()` function was chosen.

This method dispatch procedure is apparent when you look at the body of a generic function, like the `print()` function. Specifically, you will see the `UseMethod()` function.

```
> print

function (x, ...)
UseMethod("print")
<environment: namespace:base>
```

The `UseMethod()` function notes the class of the object, and then calls the relevant method for that class of object.

These concepts of *class* and *methods* are central to *object-oriented programming*. Object-orientation simplifies the programming of a language, like R, by accommodating the fact that you will have conceptually similar methods for different types of data, even though the implementations will have to be different. For example, it generally makes sense to summarize many kinds of data objects, but the way they are summarized will depend on what the data object is. With object-orientation, if you want to summarize an object, you don't need to find out what type of object it is, then try to remember the proper function to use on that type of object, and then do it. You merely use the generic `summary()` function and the right thing happens. In other words, the end result for the user is fewer function names to remember.

As an example, we have been using the `Hmisc` package's `summary.formula()` function for the majority of this chapter. Surprisingly, we could have evaluated all of the `summary.formula()` expressions in this chapter using the *generic* `summary()` function from the `base` package – as seen above. In the same sense, we mentioned the `Hmisc` package's `print.summary.formula.reverse()` function, but actually used the generic `print()` function instead. This is possible because R is an object-oriented programming language. In addition to the `summary()` and `print()` functions, the `plot()` function is one of many other generic functions.

Understanding the concept of object-oriented programming and method dispatch is indispensable when you need to consult a function's help file. For instance, if you weren't aware that the `plot()` function is a generic function, you would quickly become frustrated trying to use the plot help file (i.e., `help(plot)`) to determine which arguments you can specify when plotting various objects. As we can see, the plot function's arguments are not very specific:

```
> args(plot)

function (x, y, ...)
NULL
```

However, if you determined the class of the object you were trying to plot using the `class()` function and determined its corresponding class specific method using the `methods()` function, then you could consult the class specific method's help file. As an example, suppose I was trying to plot an object of class `stepfun`, an object generated by the step function `stepfun()`, then I would consult the class specific `plot.stepfun()` function's help file, and become aware of the following arguments:

```
> args(plot.stepfun)

function (x, xval, xlim, ylim = range(c(y, Fn.kn)), xlab = "x",
    ylab = "f(x)", main = NULL, add = FALSE, verticals = TRUE,
    do.points = TRUE, pch = par("pch"), col.points = par("col"),
    cex.points = par("cex"), col.hor = par("col"), col.vert = par("col"),
    lty = par("lty"), lwd = par("lwd"), ...)
NULL
```

Even looking at the help file of a function's default method (e.g., `plot.default()`) is more helpful than looking at the help file of the generic function:

```
> args(plot.default)

function (x, y = NULL, type = "p", xlim = NULL, ylim = NULL,
    log = "", main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
    ann = par("ann"), axes = TRUE, frame.plot = axes, panel.first = NULL,
    panel.last = NULL, asp = NA, ...)
NULL
```

Understanding the concept of object-oriented programming and method dispatch is also indispensable when you wish to look at the body of a function to truly understand what it is doing. As we have shown before, typing the name of a function *without parentheses* at the command line and pressing return will return (print) the body of the function. Unfortunately, 'non-visible' functions (as shown with an asterisk in the output of a `methods()` function expression) don't follow this common rule. Instead, use the `getAnywhere()` and `argsAnywhere()` functions to return (print) the body and arguments of a 'non-visible' function. For example, `getAnywhere(summary.ecdf)`.

Chapter 4

R Graphics

Learning objective
To understand how to incorporate high-level and low-level plotting functions and graphical parameters to generate a customized graph.

TRADITIONAL GRAPHICS: R provides the usual range of standard statistical plots, including scatterplots, boxplots, histograms, barplots, and basic 3D plots. Figure 4.1 on page 51 shows some examples from Paul Murrell's *R Graphics* book (Chapman & Hall/CRC, 2006). In R, these basic plots can be produced by a single function call, but plots can also be considered merely as starting points for producing more complex images. For example, in the first four cases in Figure 4.1 on page 51, the basic plot type has been augmented by adding additional labels, lines, and axes. This ability to add several graphical elements together to create the final result is a fundamental feature of R graphics. And, as demonstrated in the last case in Figure 4.1 on page 51, this ability also allows you to create a new plot 'from scratch' when no existing plot provides a sensible starting point for creating the final plot that you desire.

TRELLIS GRAPHICS: In addition to these *traditional* statistical plots, R also provides an implementation of *trellis* plots via the `lattice` package. Trellis plots embody a number of design principles proposed by Bill Cleveland in his *The Elements of Graphing Data* and *Visualizing Data* books that are 'aimed at ensuring accurate and faithful communication of information via statistical plots.' These principles are evident in a number of new plot types and in the default choice of colors, symbol shapes, and line styles provided by trellis plots. Furthermore, trellis plots provide a feature known as 'multi-panel conditioning,' which creates multiple plots by splitting the data being plotted according to the levels of other variables. Figure 4.2 on page 52 shows an example of a multi-panel trellis plot. The data are yields of several different varieties of barley at six sites, over two years. The plot consists of six 'panels,' one for each site. Each panel consists of a dotplot showing yield for each site with different symbols used to distinguish different years, and a 'strip' showing the name of the site.

In this document and the second document, we will only cover the traditional graphics system, which mainly consists of functions in the `graphics` and `grDevices` packages. If you are interested in learning more about trellis plots and the `lattice` package, I would highly recommend the book *R Graphics* by Paul Murrell (Chapman & Hall/CRC, 2006). We will also discuss some of the functions in the `Hmisc` package, as we have done in previous section. Unlike the `Hmisc` package, the `graphics` package is automatically installed with R and is loaded in every R session. ***REMEMBER***, when using the functions in the `Hmisc` package, ***DON'T FORGET*** to load the `Hmisc` package with the`library()` function (i.e., `library(Hmisc)`) if you haven't already done so. If you haven't previously installed the package, you must do this first.

BUILDING PLOTS IN LAYERS: Traditional R graphics follow a 'painters model,' which means that graphical output occurs in steps, with later output (possibly) obscuring any previous output that it overlaps. More specifically, in R, a traditional graphics plot is created by first calling a *high-level* plotting function

Figure 4.1: Examples of *traditional* graphics plots produced using R.

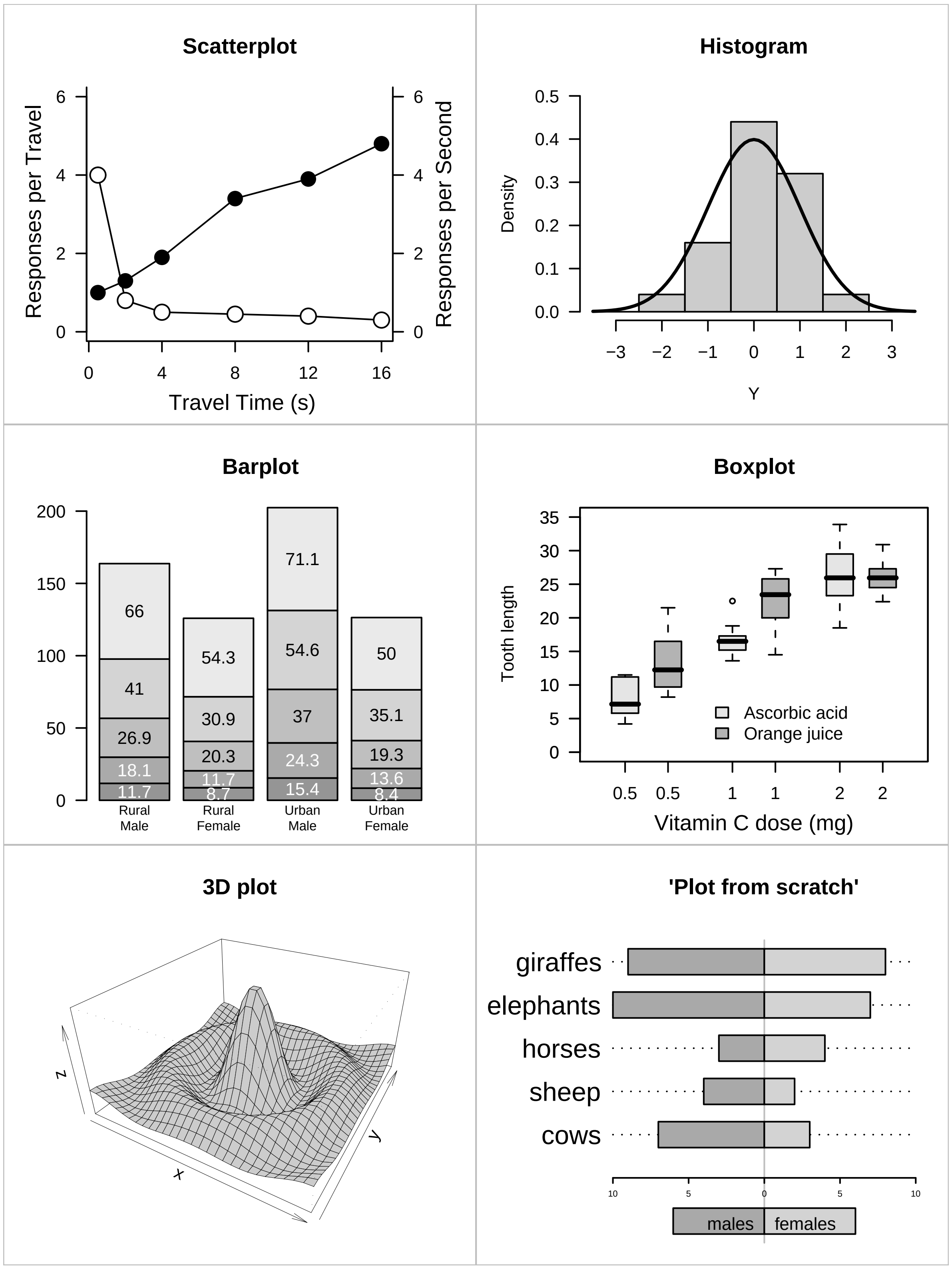
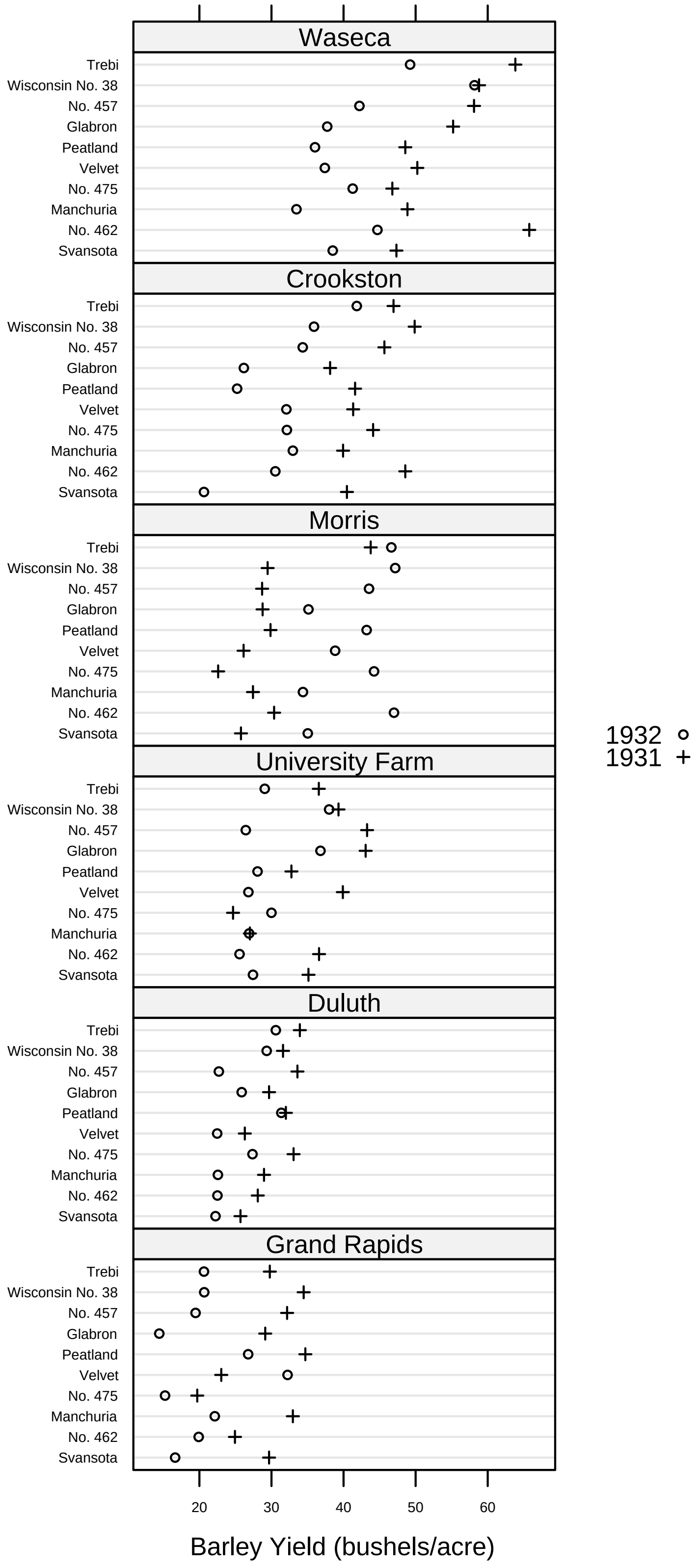


Figure 4.2: An example *trellis* plot produced using R.



that creates a 'complete' plot. This means that with high-level plotting functions, axes, labels and titles are automatically generated, where appropriate, and unless you request otherwise. In addition, high-level plotting functions always start a new plot, erasing the current plot if necessary. Examples of high-level plotting functions are the (generic) `plot()`, `hist()` (histogram), and `boxplot()` functions. Sometimes, though, the high-level plotting function doesn't produce exactly the kind of plot you desire. In this case, *low-level* plotting functions can be used to add more output (such as points, lines or text) to the current plot. Examples of low-level plotting functions are the `points()`, `legend()`, and `mtext()` (margin text) functions. In actuality, some high-level plotting functions can also be forced to act like low-level ones. With all of this in mind, it is helpful to think of building your graph in *layers* until the desired final product is created. The 'Plot from scratch' in Figure 4.1 is a good example of building a plot in layers – first the dotted and gray reference lines were added to the defined plotting grid; then the x-axis was added, then the rectangles, and then the text. Because of this 'painters model', the only way to 'edit' graphical output is to modify and rerun the R code, or to produce output in a format that can be edited using third-party software. So, ***BE PATIENT***. Creating the 'final' version of your graph takes a lot of trial-and-error.

ARGUMENTS OF PLOTTING FUNCTIONS: As we have seen with other non-plotting functions, all high- and low-level plotting functions have formal arguments that are specific to a particular function. For example, the `boxplot()` function has `width=` and `boxwex=` arguments (among others) for controlling the width of the boxes in the plot, and the `barplot()` function has a `horiz=` argument for controlling whether bars are drawn horizontally rather than vertically. In turn, various aspects of the graphical output can be modified or completely replaced. However, you are not limited to arguments that are specific to a single high- or low-level plotting function.

For high-level plotting functions, in addition to function-specific arguments, there are several arguments that are 'standard' in the sense that many high-level plotting functions will accept them. Specifically, most high-level plotting functions will accept graphical parameter arguments that control such things as the appearance of axes and labels, and the range of the axes scales. It is usually possible to modify the default range of the axes scales on a plot by specifying the `xlim=` and/or `ylim=` arguments in the high-level function invocation, which are each specified as two element vectors containing the minimum and maximum values (e.g., `xlim = c(0, 50)`). There is also a set of arguments for modifying the default labels (if any) on a plot: `main=` for a title, `sub=` for a sub-title, `xlab=` for an x-axis label, and `ylab=` for a y-axis label. Each of these arguments is specified as a character string. The title specified with the `main=` argument (if any) is placed at the top of the plot in a large font, and the sub-title specified with the `sub=` argument is placed just below the x-axis in a smaller font. Some high-level plotting functions have an `axes=` argument (by default `TRUE`), which allows you to suppress the drawing of the axes and therefore produce customized axes instead. Lastly, some high-level plotting function have an `add=` argument (by default `FALSE`), which, if set to `TRUE`, forces the function to act as a low-level plotting, superimposing the high-level plot onto the current plot.

Lastly, most high- *and* low-level plotting functions will also appropriately accept graphical parameter arguments that control such things as data symbols, axes, color, line type and width, and text font, justification, magnification, and rotation. In many cases though, these arguments are not given as explicitly named arguments to the high- or low-level function, but are accepted instead via a `...` argument. These unspecified graphical parameter arguments are a subset of the formal arguments of the `par()` function.

THE `par()` ***FUNCTION:*** The `par()` function is the main function used to access and modify numerous graphical parameters. These parameters describe and control things such as the general appearance of graphical output (the colors and line types that are used to draw lines, the fonts that are used to draw text, etc.), but also describe and control such things as the size and placement of the plot regions and coordinate systems. Invoking the `par()` function with no specified arguments will result in a complete listing of the graphical parameters you may set and their current values. Specific graphical parameters can be queried by supplying specific parameter names as arguments to the `par()` function. For example, the following code queries the current values of the `col=` (color) and `lty=` (line type) parameters.

```
> par(c("col", "lty"))
```

```
$col
[1] "black"

$lty
[1] "solid"
```

And specific parameters can be modified by specifying a value via an argument with the appropriate parameter name. For example, `par(col = "red", lty = "dashed")` sets new values for the `col=` and `lty=` arguments.

As mentioned, a specific subset of the `par()` function's arguments can be set not only via the `par()` function, but can also be used as arguments to other high- and low-level plotting functions, where appropriate. These arguments include:

Group	Argument	Description
Points	`pch=`	data symbol type ('point character')
	`type=`	type of plot (points, lines, both)
Lines	`lty=`	line type (solid, dashed)
	`lwd=`	line width
Text	`adj=`	justification of text
	`cex=`	size of text (magnification multiplier)
	`font=`	font face (bold, italic) for text
	`las=`	rotation of text in margins
Color	`col=`	color of lines and data symbols

On the other hand, some graphics settings can be set *only* via the `par()` function, which include:

Group	Argument	Description
Plotting regions & Margins	`mar=`	size of figure margins (lines of text)
	`oma=`	size of outer margins (lines of text)
Multiple plots	`mfrow=`	number of figures on a page
Overlaying output	`new=`	has a new plot been started?

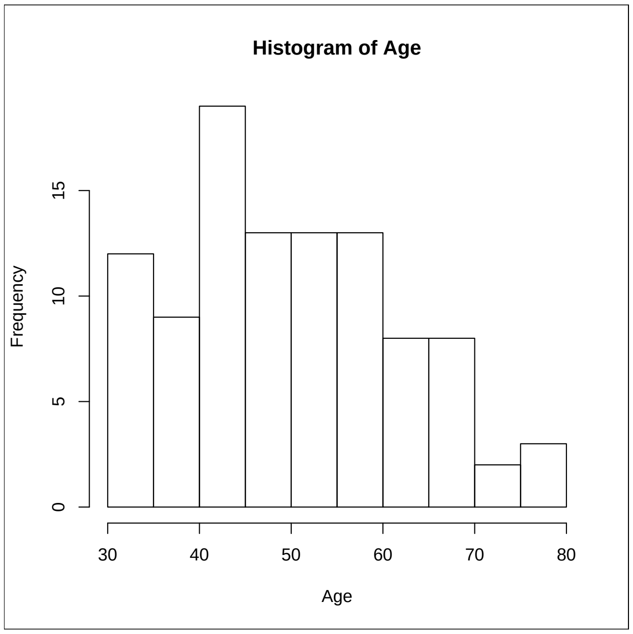
See the `par()` function's help file and the second document for a complete list and detailed description of the available arguments. We will be using many of these arguments soon.

TEMPORARY/PERSISTENT ALTERATIONS OF GRAPHICAL PARAMETERS: Modifying traditional graphical parameters via the `par()` function has a *persistent effect*. That is, parameters specified in this way hold until a different parameter is specified via another `par()` function invocation. In other words, when a graphical parameter is modified using the `par()` function, all future invocations of high- and low-level plotting functions will be appropriately affected by that new parameter, as if you set a 'default' value for that parameter. This 'default' parameter will be used by all subsequent plotting functions unless an alternative is given. In contrast, graphical parameters may also be *temporarily* modified by specifying a new value in the invocation of a high- or low-level plotting function such as the `plot()` function. The following code demonstrates this idea. First, the line type is permanently set as dashed using the `par()` function. Therefore, in the subsequent line plot (`plot(y, type = "l")`), the line will be dashed. However, in the next plot, a temporary line type parameter of `lty = "solid"` is specified, which causes the line in this plot to be solid. Lastly, when the third plot is drawn, the permanent line type parameter of `lty = "dashed"` comes back into effect and thus the line is again dashed.

```
> y <- rnorm(20)
> par(lty = "dashed")
> plot(y, type = "l") # line is dashed
> plot(y, type = "l", lty = "solid") # line is solid
> plot(y, type = "l") # line is dashed
```

HISTOGRAMS, STRIPCHARTS, and BOXPLOTS: Very often, a histogram or boxplot is used to graphically display the distribution of a continuous variable, which can be generated using the `hist()` and `boxplot()` functions, respectively. By default, the `hist()` function generates a histogram of the given data values (a numeric vector; often a numeric column from a data frame) based on equally-spaced breaks. The height of each rectangle is proportional to the number of data values falling within the bordering breaks. By default, the y-axis is labeled `Frequency`, the x-axis is labeled with the variable name, and a main title is generated – `Histogram of ....` We can use the `ylab=`, `xlab=`, and `main=` arguments, respectively, to modify any of these defaults.

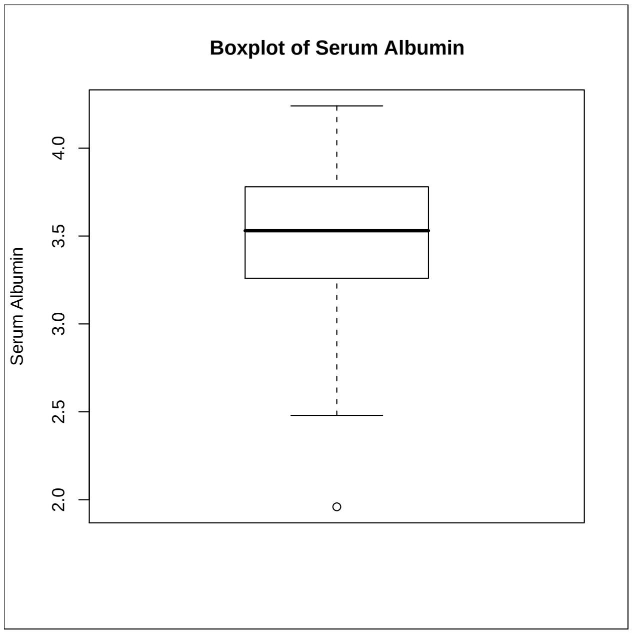
```
> with(pbc, hist(ageyrs, xlab = label(ageyrs), main = paste("Histogram of",
+     label(ageyrs))))
```



You'll notice that most plotting functions, like the `hist()` function, do not have a `data=` argument, so we will be using the `with()` function as needed. Also, the `Hmisc` package's `label()` function not only allows us to define a variable's label, but it also allows us to return (print) a variable's label – in this case, a variable label for `ageyrs` was defined in our `upData()` function invocation. Like the `with()` function, the `label()` function saves us some typing, but the label for a variable has to be already defined to take advantage of the `label()` function. We also used the `paste()` function to easily generate a main title. In general, the `paste()` function concatenates character strings.

As an alternative to the histogram, the `boxplot()` function graphically displays the *five-number* summary of a continuous variable, which contains the minimum, the *lower hinge*, the median, the *upper hinge*, and the maximum – see the `fivenum()` function help file for more information (`help(fivenum)`). The hinges essentially give the same information as the quartiles. Like the `hist()` function, the main data argument of the `boxplot()` function is a numeric vector (often a numeric column from a data frame). In addition, by default, the y-axis is not labeled, and a main title is not given. If desired, these can be specified using the `ylab=`, and `main=` arguments, respectively.

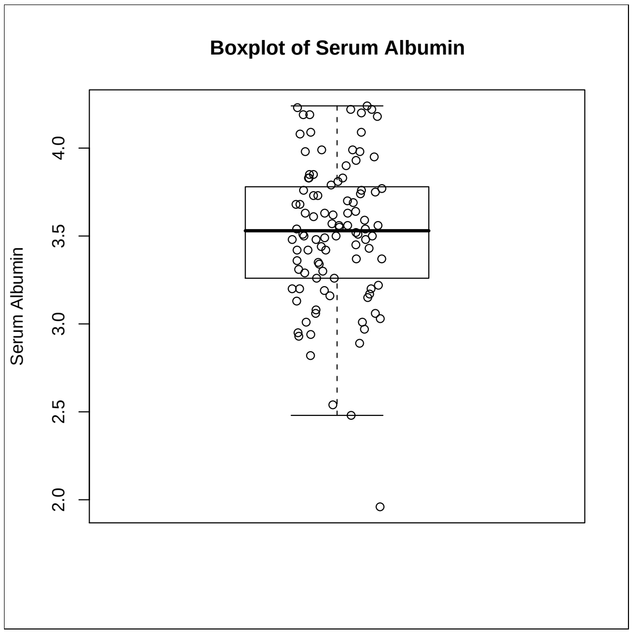
```
> with(pbc, boxplot(album, ylab = label(album), main = paste("Boxplot of",
+     label(album))))
```



In all boxplots, the two most outer lines show the largest/smallest observations that fall within a distance of 1.5 times the box size from the nearest hinge. If any observation falls farther away, the additional points are considered ‘extreme’ values (outliers) and are shown as open circles.

It is often useful to take the boxplot one step further by also showing where the raw data points fall along the y-axis. The `stripchart()` function produces a one dimensional scatter plot (i.e., dot plot) of the given data. By default, the stripchart is horizontal (`vertical = FALSE`) and coincident points are *overplotted* (`method = "overplot"`). We will specify `vertical = TRUE` and `method = "jitter"` to generate a vertical stripchart where a small amount of noise (in the x-direction) is added to each data point so coincident points are easily distinguished. In order to superimpose the stripchart on top of the boxplot, we will specify `add = TRUE`, causing the *high-level* `stripchart()` plotting function (by default, `add = FALSE`) to act like a *low-level* plotting function. We will also specify `outline = FALSE` in the `boxplot()` function invocation to suppress the plotting of the outlier. We are doing this because the outlier will also be plotted by the `stripchart()` function invocation.

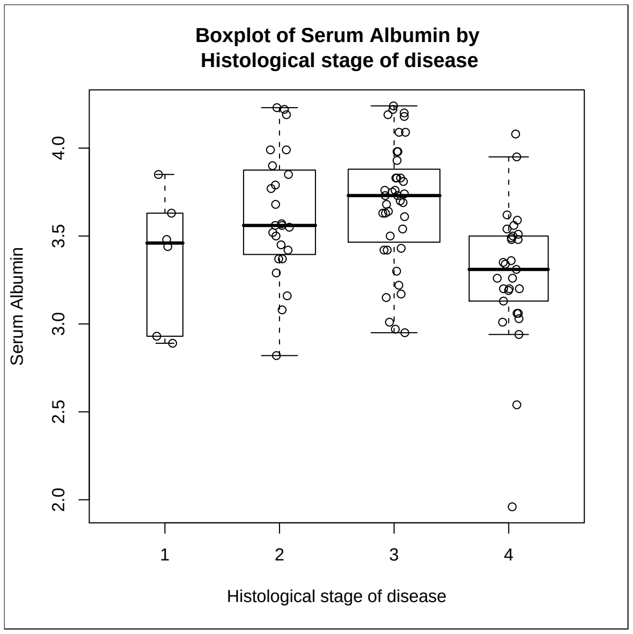
```
> with(pbc, {
+     boxplot(album, outline = FALSE, ylab = label(album), main = paste("Boxplot of",
+         label(album)))
+     stripchart(album, vertical = TRUE, method = "jitter", pch = 1,
+         add = TRUE)
+ })
```



We also specified `pch = 1` (open circle) in the `stripchart()` function invocation to modify the point character. The `Hmisc` package's `show.pch()` function (invoked without specifying any arguments) can be used to display the definition of the available `pch=` parameters. Alternatively, we could have changed to color of the points instead of the point character using the `col=` argument (e.g., `col = "gray"`). You'll also notice the incorporation of *braces* (`{` and `}`) into the `with()` function. Recall, by default, the `with()` function only accepts one expression. Using the braces allow us to define a *block* of R code, which includes multiple expressions.

The `boxplot()` function can also generate *side-by-side* boxplots illustrating the distribution of a continuous variable at each level of a categorical grouping variable. To do so, we can use the `boxplot()` function's *formula interface* to specify the data argument – `y ~ grp`, where `y` is a numeric vector of data values to be split into groups according to the grouping variable `grp`. `y` and `grp` (usually a factor) are most often columns in a data frame. The `stripchart()` function can also be specified using a similar formula interface. In addition, when generating a side-by-side boxplot, specify `varwidth = TRUE` in your `boxplot()` function invocation to draw the boxes with widths proportional to the square-root of the number of observations in each group.

```
> with(pbc, {
+     boxplot(album ~ stage, outline = FALSE, varwidth = TRUE, xlab = label(stage),
+         ylab = label(album), main = paste("Boxplot of", label(album),
+             "by\n", label(stage)))
+     stripchart(album ~ stage, method = "jitter", pch = 1, vertical = TRUE,
+         add = TRUE)
+ })
```

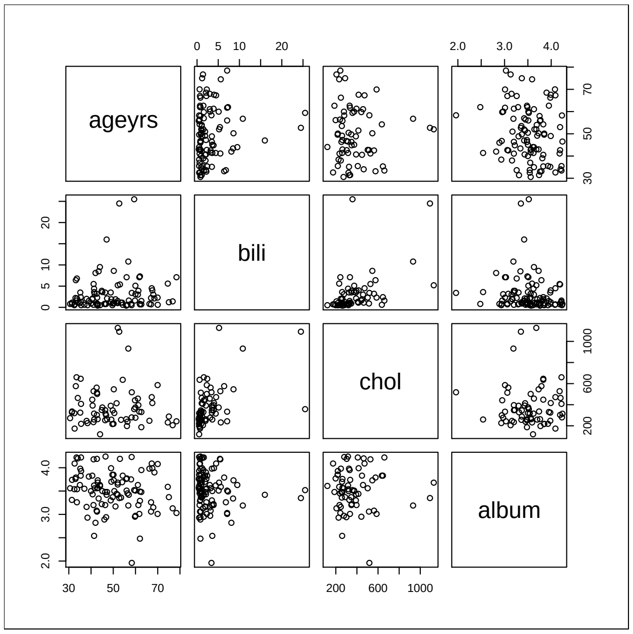


We specified the `\n` in the `main=` argument to break the title over two lines (i.e., insert a new line). As an alternative, we could have specified the `cex.main=` argument (as a value <1) in the `plot()` function to shrink the size of the main title.

→ *Practice Exercise:* Let's generate (1) a histogram of `bili`, (2) a single boxplot overlaid with a stripchart of `bili`, and (3) side-by-side boxplots of `bili` across the levels of `drug` overlaid with a corresponding stripchart. Your plots should include a main title, x- and y-labels, and should remove repeated plotting of any outliers.

SCATTERPLOTS, BARPLOTS, and DOTPLOTS: Graphical exploratory data analysis often includes generating scatter plots between all pertinent continuous variables (ie, between all pairwise combinations). In our `pbc` data frame, we have 4 continuous variables we might be interested in plotting – `ageyrs`, `bili`, `chol`, and `album`. We could generate all 10 possible pairwise scatterplots between these 4 continuous variables as *individual* graphs, but who has time for that? Instead, we can generate a *matrix of scatterplots* using the `pairs()` function. The primary argument of the `pairs()` function is a data frame with numeric columns – logical and factor columns are converted to numeric ones. The ijth scatterplot of the matrix of scatterplots contains the ith column of the data frame plotted against the jth. For example,

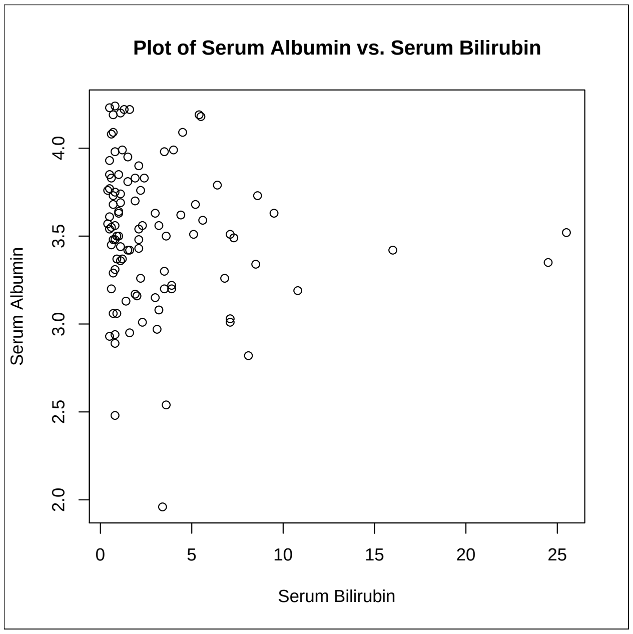
```
> pairs(subset(pbc, select = c(ageyrs, bili, chol, album)))
```



We used the `subset()` function to select only those variables we were interested in plotting (`select=`).

Now let's look at the relationship between `bili` and `album` a bit more closely. The default method of the generic `plot()` function generates a simple x-y scatterplot. With the `plot()` function, the x and y coordinates of the points to be plotted can be specified in one of two ways: (1) `plot(x, y)`; or (2) `plot(y ~ x)` (i.e., using a formula interface).

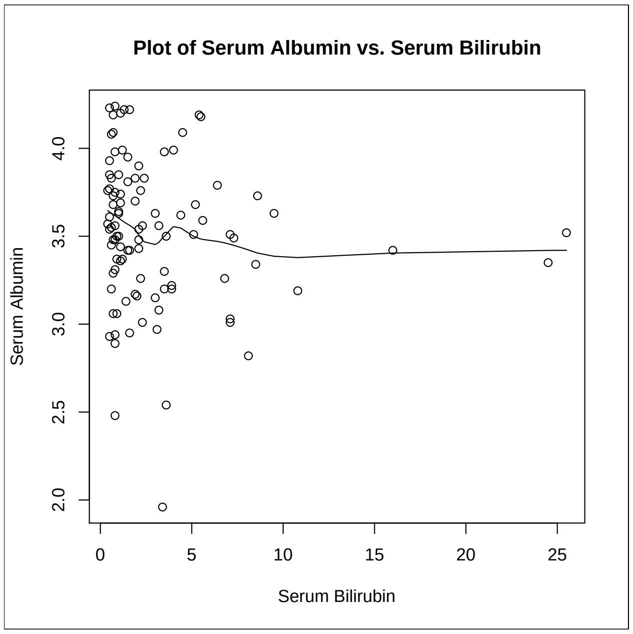
```
> with(pbc, plot(album ~ bili, xlab = label(bili), ylab = label(album),
+     main = paste("Plot of", label(album), "vs.", label(bili))))
```



Notice that `pch = 1` (open circle) is the default value of the `pch=` argument in the `plot()` function.

We can add more information to the simple x-y scatterplot by incorporating the `Hmisc` package's `plsmo()` (plot smoother) function. The `plsmo()` function generates a (non-parametric) plot smoothed estimate (line) of x vs. y. Because the `plsmo()` function is a *high-level* plotting function, we will need to specify `add = TRUE` to add the curve to the x-y scatterplot, as we did with the `stripchart()` function.

```
> with(pbc, {
+     plot(album ~ bili, xlab = label(bili), ylab = label(album),
+         main = paste("Plot of", label(album), "vs.", label(bili)))
+     plsmo(x = bili, y = album, add = TRUE)
+ })
```



Let's now switch to graphically displaying some categorical variables. A barplot or dotplot is often used to graphically display a categorical variable, which can be generated using the `barplot()` and `dotchart()` functions, respectively. Barplots and dotplots are often generated from count data (i.e., a frequency table). As we have seen, the easiest way to calculate this count data from a raw categorical variable is to use the `table()` function, which returns raw frequencies. For example,

```
> with(pbc, table(censored))

censored
Censored     Dead
      68       32
```

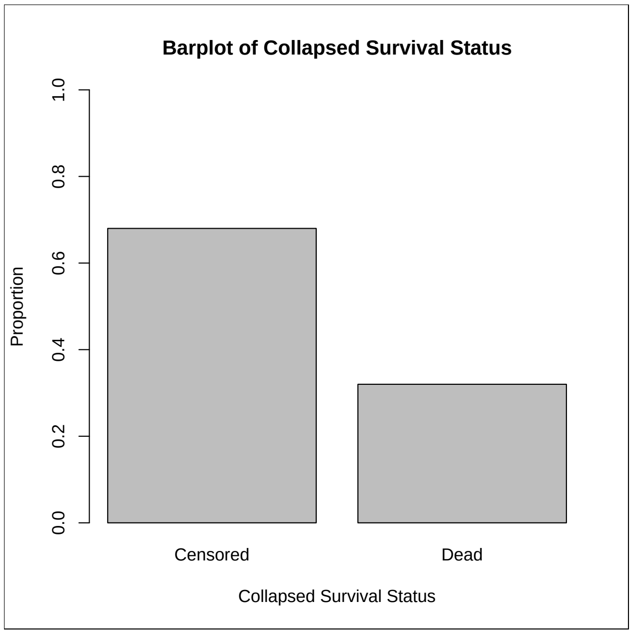
If proportions are desired, the `prop.table()` function can be used to express the table entries as relative frequencies.

```
> with(pbc, prop.table(table(censored)))

censored
Censored     Dead
    0.68     0.32
```

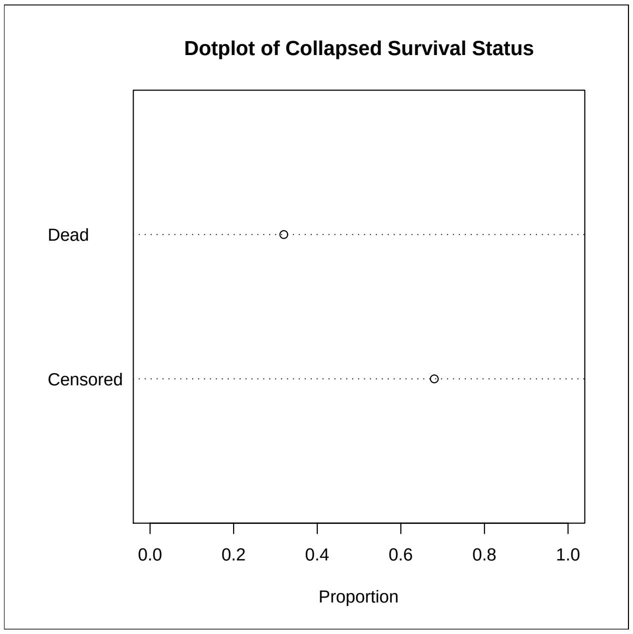
With this in mind, let's generate a barplot of `censored` based on proportions. By default, the `barplot()` function will label the bars appropriately if based on either a factor variable or a character variable. However, the `names.arg=` argument can be used to explicitly label the bars.

```
> with(pbc, barplot(prop.table(table(censored)), ylim = c(0, 1), xlab = label(censored),
+     ylab = "Proportion", main = paste("Barplot of", label(censored))))
```



We can generate a dotplot in a similar fashion. While the `barplot()` function displays bars aligned with the y-axis, the `dotchart()` function displays dots aligned with the x-axis. Because of this, `xlim=` is specified in the `dotchart()` function invocation instead of `ylim=`.

```
> with(pbc, dotchart(prop.table(table(censored)), lcolor = "black",
+     xlim = c(0, 1), xlab = "Proportion", main = paste("Dotplot of",
+         label(censored))))
```



By default, the horizontal dotted grid lines are plotted in gray (`lcolor = "gray"`), but because most copy machines don't copy gray well, I specified that they should be plotted in black – `lcolor = "black"`.

We can also easily extend both a barplot and a dotplot to graphically display the cross-tabulation of two categorical variables. To do this, we merely add a second variable to the `table()` function invocation. We can also specify the `margin=` argument of the `prop.table()` function in order to calculate the *row* (`margin`

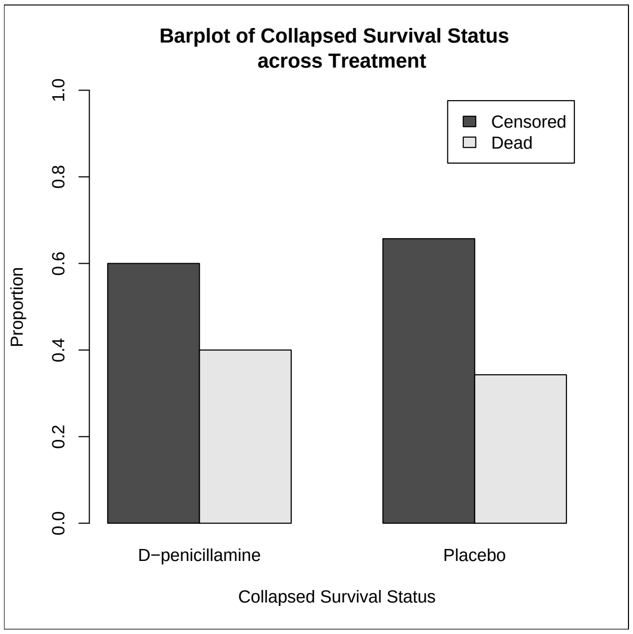
`= 1`) or *column* (`margin = 2`) proportions. For our example, we are interested in *column* proportions – we want to graphically depict the proportion of Censored/Dead within each treatment group.

```
> with(pbc, prop.table(table(censored, drug), margin = 2))
```

```
          drug
censored   D-penicillamine   Placebo
  Censored       0.6000000 0.6571429
  Dead           0.4000000 0.3428571
```

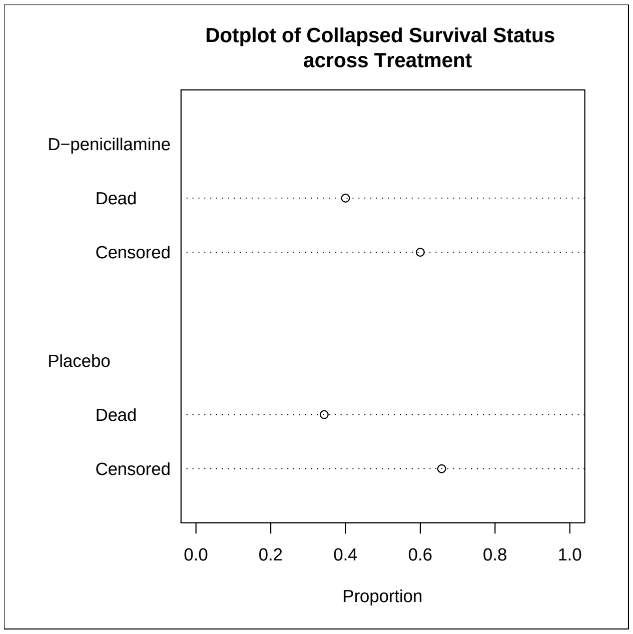
We also use the `barplot()` function's `legend.text=` argument to add a legend that denotes which bar represents the Censored and Dead groups of subjects.

```
> with(pbc, barplot(prop.table(table(censored, drug), margin = 2),
+     beside = TRUE, legend.text = levels(censored), ylim = c(0, 1),
+     xlab = label(censored), ylab = "Proportion", main = paste("Barplot of",
+         label(censored), "\n across", label(drug))))
```



Now let's graphically display the cross-tabulation of the two categorical variables using a dotplot:

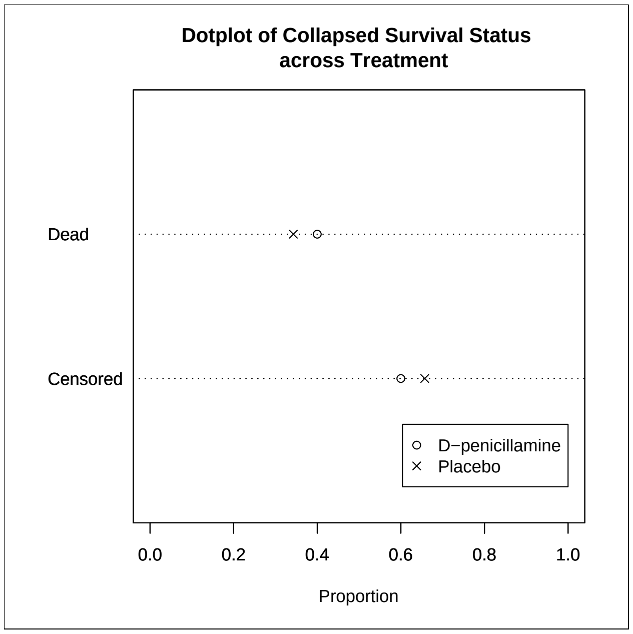
```
> with(pbc, dotchart(prop.table(table(censored, drug), margin = 2),
+     lcolor = "black", xlim = c(0, 1), xlab = "Proportion", main = paste("Dotplot of",
+         label(censored), "\n across", label(drug))))
```



As before, I specified `lcolor = "black"` instead of the default `lcolor = "gray"` for copying reasons.

As an alternative to the previous dotplot that displays the proportions of `censored`, and `dead` subjects in each `drug` group as two separates groups of lines, let's work through how to display the corresponding subject proportions from the two groups on the same line using two different point characters. To do this, we subset the `prop.table()` function output using single square bracket operators, `[ ]` – specifically, we desire the proportion of Dead and Censored (ie, the row proportions) in (1) the D-penicillamine column and (2) the Placebo column. We will learn more about subsetting output in the second document. Unlike in the previous examples where we used `add = TRUE`, we will use the `par()` function's `new=` argument to superimpose the second dotplot onto the first because the `dotchart()` function does not accept an `add=` argument. Lastly, we will use the `legend()` function to add a legend to the plot to denote the point characters of each group.

```
> with(pbc, dotchart(prop.table(table(censored, drug), margin = 2)[,
+     "D-penicillamine"], lcolor = "black", xlim = c(0, 1), xlab = "Proportion",
+     main = paste("Dotplot of", label(censored), "\n across", label(drug))))
> par(new = TRUE)
> with(pbc, dotchart(prop.table(table(censored, drug), margin = 2)[,
+     "Placebo"], lcolor = "black", xlim = c(0, 1), pch = 4))
> legend(x = 1, y = 0.25, xjust = 1, yjust = 0, legend = levels(pbc$drug),
+     pch = c(1, 4))
```

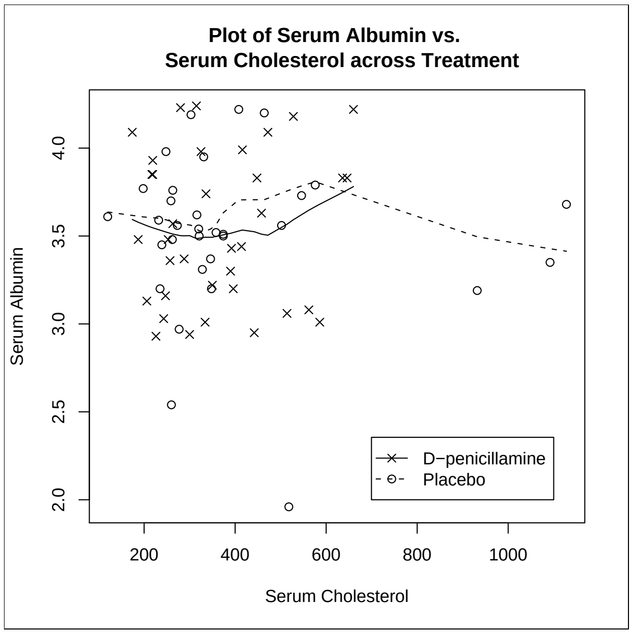


When you invoke the `par()` function, it is always a good idea to invoke it once again after you have generated your graph to reset any modified arguments to their default values.

```
> par(new = FALSE)
```

Lastly, let's discuss two ways you can graphically display the relationship between two continuous variables and a categorical one. The first suggested way uses different point characters and line types to distinguish the continuous data values in each level of the categorical variable. We first use the `plot()` function to set up the x- and y-axes, but we don't plot any points (`type = "n"` – i.e., 'null'). We then use the `points()` function to add points to the blank plot. Specifically, we add the points for each level of the categorical variable by using the `subset()` function to appropriately subset the rows of our `pbc` data frame. The groups of points are distinguished by point character (`pch=`) and line type (`lty=`). We add the plot smoothed line of x vs. y using the `plsmo()` function, by specifying the `group=` argument to generate a separate smoothed line for each level of the categorical variable. And lastly, we use the `legend()` function to add a legend to the plot to denote the point characters and line types.

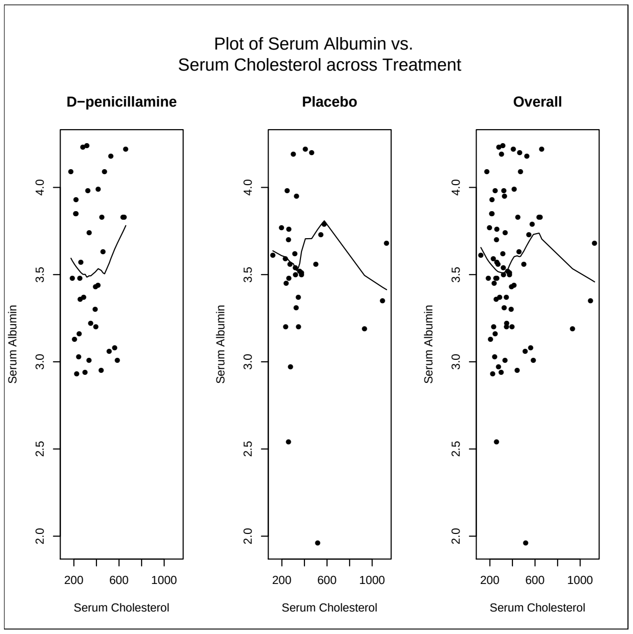
```
> with(pbc, plot(album ~ chol, type = "n", xlab = label(chol), ylab = label(album),
+     main = paste("Plot of", label(album), "vs. \n", label(chol),
+         "across", label(drug))))
> with(subset(pbc, drug == "D-penicillamine"), points(album ~ chol,
+     pch = 4))
> with(subset(pbc, drug == "Placebo"), points(album ~ chol))
> with(pbc, {
+     plsmo(chol, album, group = drug, add = TRUE, lty = c(1, 2))
+     legend(x = 1100, y = 2, xjust = 1, yjust = 0, legend = levels(drug),
+         lty = c(1, 2), pch = c(4, 1))
+ })
```



The second suggested way to graphically display the relationship between two continuous variables and a categorical one involves generating multiple side-by-side scatterplots – a scatterplot for each level of the categorical variable and one that does not distinguish the categorical variable (i.e., an 'overall' plot). To generate multiple plots (i.e., figures) on the same page, we use the `par()` function to specify the number of figures to place on one page using the `mfrow=` argument – `mfrow = c(nr, nc)`, where `nr` is the number of rows and `nc` is the number of columns. By default, `mfrow = c(1, 1)` – there is one figure per page. When changed from default, the number of figures on one page will be `nr*nc`. The figures will be drawn by rows – that is, across the columns (from left to right) in each subsequent row.

For our `pbc` data frame, we will want to generate three figures on one page – one for `"D-penicillamine"`, one for `"Placebo"`, and one 'overall' plot that does not distinguish `drug`. So, we will specify `par(mfrow = c(1, 3))` – one row and three columns. We then generate three separate figures using the `subset()`, `plot()` and `plsmo()` functions. We'll ensure that the limits of the x- and y-axes in each plot are consistent using the `xlim=` and `ylim=` arguments – setting them equal to the '*overall*' ranges of `chol` and `album`. To add a title across all three plots, we use the `par()` function's `oma=` argument to specify the desired size of the outer margins (specified in order: bottom, left, top, right). We then use the `mtext()` (margin text) function to add the desired title to the top (`side = 3`) outer (`outer = TRUE`) margin.

```
> xrange <- with(pbc, range(chol, na.rm = TRUE))
> yrange <- with(pbc, range(album, na.rm = TRUE))
> par(mfrow = c(1, 3), oma = c(0, 0, 5, 0))
> with(subset(pbc, drug == "D-penicillamine"), {
+     plot(album ~ chol, pch = 16, xlim = xrange, ylim = yrange, xlab = label(chol),
+         ylab = label(album), main = levels(drug)[1])
+     plsmo(chol, album, add = TRUE)
+ })
> with(subset(pbc, drug == "Placebo"), {
+     plot(album ~ chol, pch = 16, xlim = xrange, ylim = yrange, xlab = label(chol),
+         ylab = label(album), main = levels(drug)[2])
+     plsmo(chol, album, add = TRUE)
+ })
> with(pbc, {
+     plot(album ~ chol, pch = 16, xlim = xrange, ylim = yrange, xlab = label(chol),
+         ylab = label(album), main = "Overall")
+     plsmo(chol, album, add = TRUE)
+     mtext(text = paste("Plot of", label(album), "vs. \n", label(chol),
+         "across", label(drug)), side = 3, outer = TRUE)
+ })
```



Notice, we used the `range()` function to calculate and return the minimum and maximum values need for the `xlim=` and `ylim=` arguments – this is useful in case our data changes. The `[ ]` (square brackets) that we used in the `levels(drugs)` expressions to specify the `main=` argument are the operators used to subset vectors. We'll discuss this more in the next document. Also, in the past, when there was only one plot per page, we saw that a high-level plotting function starts a new plot on a new page. In this case, when there are multiple plots on a page, a high-level plotting function starts the next plot on the same page. A new page is started only when the number of plots per page is exceeded.

As we did previously, let's reset the modified `par()` functions arguments to their default values.

```
> par(mfrow = c(1, 1), oma = c(0, 0, 0, 0))
```

→ *Practice Exercise:* Let's generate: (1) A dotplot of the `ascites` genotypes across the `sex` genotypes, where the corresponding proportions are shown on the same line with different point characters (with a legend); and (2) a replicate plot of `album` versus `chol` across `drug` using the three separate graphs (one for each level of `drug` and one 'overall'). However, this time for (2), in the first two graphs, display all data points as a background layer of gray filled circles.

GRAPHICAL OUTPUT: As you have seen, when using R interactively, the main persistent record of graphical output is a window on your screen, which is also known as a GUI ('graphical user interface') screen *device*. When R is installed, an appropriate screen format is selected as the default GUI screen device and this default device is opened automatically the first time that any graphical output occurs. For example, on the various Unix systems, the default GUI screen device is an X11 window. These GUI screen devices are opened by internally calling the `x11()`, `windows()`, and `quartz()` functions in the Linux/Unix, Windows, and Mac versions of R, respectively. By default, the size of an X11 graphics window and a Windows graphics window are 7 inches by 7 inches. A Mac graphics window is, by default, 5 inches by 5 inches. The three mentioned functions all have `height=` and `width=` with arguments that can be used to open new GUI screen devices of the desired size.

In the Windows version of R, right-clicking on the graphics window offers you three options for outputting any desired graph from R: (1) Copy your graph as either a metafile or a bitmap; (2) Save your graph as either a metafile or postscript; and/or (3) Print your graph. For the Copy and Save options, it is very easy to then Paste or Insert, respectively, your graph into a Microsoft Word and/or Powerpoint document.

In any version of R, it is also possible to produce a *file* that contains your plot. Similar to the GUI screen devices, the graphical output can be directed to a particular *file device*, which dictates the output format that will be produced. And like the GUI screen devices, the file devices are controlled by specific functions, including the `pdf()` function that produces an Adobe PDF file. Like the GUI screen device functions, these file device functions allow you to specify things such as the name of the file and the size of the plot. Unlike sending graphical output to a window on your screen, directing graphical output to a file takes a few more steps. A file device must be created or 'opened to writing' in order to receive graphical output by invoking the desired file device function with at least the desired file name specified. Once you have opened the file to writing, you then execute all of your desired graphical function invocations. In turn, the specific file device that you opened converts the graphical function invocations from R (e.g., 'draw a line') into commands that the particular device can understand and your graphical output is generated. When you have finished writing the desired graphical output to a file, you then close the file to writing (and therefore close the file device) by invoking the `dev.off()` ('device off') function. For example, let's write a simple scatterplot to a PDF file named `myplot.pdf`:

```
> pdf("myplot.pdf", height = 8.5, width = 11)
> with(pbc, plot(ageyrs ~ chol,
+   main = "Age (years) vs. Serum Chol",
+   xlab = label(chol), ylab = label(ageyrs)))
> dev.off()
```

In the previous code, we also specified that the plot should be in a landscape orientation (i.e., height < width), with a height of 8.5" and a width of 11.0".

A THOUGHT TO END WITH: Keep in mind that there are always multiple ways of performing the same task in R. And remember to read, read, read – read the documentation, including help files and their examples; read others' code; and read the body of defined functions. Also, feel free to check out the website for the weekly 'R Clinic' that I run at Vanderbilt University – `http://biostat.mc.vanderbilt.edu/RClinic`. It contains the 'solutions' to problems that various 'R Clinic' attendees have posed.