Study Material. Do not distribute.

You can remove multiple elements this way, too:

```
> years[c("Carter","Clinton")] <- NULL  # Remove two elements
> years
$Kennedy
[1] 1960
```

5.11 Flatten a List into a Vector

Problem

You want to flatten all the elements of a list into a vector.

Solution

Use the unlist function.

Discussion

There are many contexts that require a vector. Basic statistical functions work on vectors but not on lists, for example. If **iq.scores** is a list of numbers, then we cannot directly compute their mean:

```
> mean(iq.scores)
[1] NA
Warning message:
In mean.default(iq.scores) :
    argument is not numeric or logical: returning NA
```

Instead, we must flatten the list into a vector using unlist and then compute the mean of the result:

```
> mean(unlist(iq.scores))
[1] 106.4452
```

Here is another example. We can cat scalars and vectors, but we cannot cat a list:

```
> cat(iq.scores, "\n")
Error in cat(list(...), file, sep, fill, labels, append) :
    argument 1 (type 'list') cannot be handled by 'cat'
```

One solution is to flatten the list into a vector before printing:

```
> cat("IQ Scores:", unlist(iq.scores), "\n")
IQ Scores: 89.73383 116.5565 113.0454
```

See Also

Conversions such as this are discussed more fully in Recipe 5.33.

5.12 Removing NULL Elements from a List

Problem

Your list contains NULL values. You want to remove them.

Solution

Suppose lst is a list some of whose elements are NULL. This expression will remove the NULL elements:

```
> lst[sapply(lst, is.null)] <- NULL</pre>
```

Discussion

Finding and removing NULL elements from a list is surprisingly tricky. I wrote the following expression after trying several other ways, including the obvious ones, and failing. Here's how it works:

- 1. R calls sapply to apply the is.null function to every element of the list.
- 2. **sapply** returns a vector of logical values that are **TRUE** wherever the corresponding list element is **NULL**.
- 3. R selects values from the list according to that vector.
- 4. R assigns NULL to the selected items, removing them from the list.

The curious reader may be wondering how a list can contain NULL elements, given that we remove elements by setting them to NULL (Recipe 5.10). The answer is that we can create a list containing NULL elements:

```
> lst <- list("Moe", NULL, "Curly")</pre>
                                                # Create list with NULL element
> 1st
[[1]]
[1] "Moe"
[[2]]
NULL
[[3]]
[1] "Curly"
> lst[sapply(lst, is.null)] <- NULL</pre>
                                                # Remove NULL element from list
> 1st
[[1]]
[1] "Moe"
[[2]]
[1] "Curly"
```

See Also

See Recipe 5.10 for how to remove list elements.

5.13 Removing List Elements Using a Condition

Problem

You want to remove elements from a list according to a conditional test, such as removing elements that are negative or smaller than some threshold.

Solution

Build a logical vector based on the condition. Use the vector to select list elements and then assign NULL to those elements. This assignment, for example, removes all negative value from 1st:

```
> lst[lst < 0] <- NULL
```

Discussion

This recipe is based on two useful features of R. First, a list can be indexed by a logical vector. Wherever the vector element is TRUE, the corresponding list element is selected. Second, you can remove a list element by assigning NULL to it.

Suppose we want to remove elements from lst whose value is zero. We construct a logical vector which identifies the unwanted values (lst == 0). Then we select those elements from the list and assign NULL to them:

> lst[lst == 0] <- NULL

This expression will remove NA values from the list:

```
> lst[is.na(lst)] <- NULL</pre>
```

So far, so good. The problems arise when you cannot easily build the logical vector. That often happens when you want to use a function that cannot handle a list. Suppose you want to remove list elements whose absolute value is less than 1. The **abs** function will not handle a list, unfortunately:

> lst[abs(lst) < 1] <- NULL Error in abs(lst) : non-numeric argument to function

The simplest solution is flattening the list into a vector by calling unlist and then testing the vector:

```
> lst[abs(unlist(lst)) < 1] <- NULL</pre>
```

A more elegant solution uses lapply to apply the function to every element of the list:

```
> lst[lapply(lst,abs) < 1] <- NULL</pre>
```

Lists can hold complex objects, too, not just atomic values. Suppose that **mods** is a list of linear models created by the lm function. This expression will remove any model whose R^2 value is less than 0.30:

```
> mods[sapply(mods, function(m) summary(m)$r.squared < 0.3)] <- NULL</pre>
```

See Also

See Recipes 5.7, 5.10, 5.11, 6.2, and 11.1.

5.14 Initializing a Matrix

Problem

You want to create a matrix and initialize it from given values.

Solution

Capture the data in a vector or list, and then use the matrix function to shape the data into a matrix. This example shapes a vector into a 2 × 3 matrix (i.e., two rows and three columns):

```
> matrix(vec, 2, 3)
```

Discussion

Suppose we want to create and initialize a 2×3 matrix. We can capture the initial data inside a vector and then shape it using the matrix function:

```
> theData <- c(1.1, 1.2, 2.1, 2.2, 3.1, 3.2)
> mat <- matrix(theData, 2, 3)
> mat
      [,1] [,2] [,3]
[1,] 1.1 2.1 3.1
[2,] 1.2 2.2 3.2
```

The first argument of matrix is the data, the second argument is the number of rows, and the third argument is the number of columns. Observe that the matrix was filled column by column, not row by row.

It's common to initialize an entire matrix to one value such as zero or NA. If the first argument of matrix is a single value, then R will apply the Recycling Rule and automatically replicate the value to fill the entire matrix:

```
> matrix(0, 2, 3)  # Create an all-zeros matrix
   [,1] [,2] [,3]
[1,] 0 0 0
[2,] 0 0 0
> matrix(NA, 2, 3)  # Create a matrix populated with NA
   [,1] [,2] [,3]
```

[1,] NA NA NA [2,] NA NA NA

You can create a matrix with a one-liner, of course, but it becomes difficult to read:

```
> mat <- matrix(c(1.1, 1.2, 1.3, 2.1, 2.2, 2.3), 2, 3)</pre>
```

A common idiom in R is typing the data itself in a rectangular shape that reveals the matrix structure:

```
> theData <- c(1.1, 1.2, 1.3,
+ 2.1, 2.2, 2.3)
> mat <- matrix(theData, 2, 3, byrow=TRUE)</pre>
```

Setting **byrow=TRUE** tells **matrix** that the data is row-by-row and not column-by-column (which is the default). In condensed form, that becomes:

> mat <- matrix(c(1.1, 1.2, 1.3, + 2.1, 2.2, 2.3), + 2, 3, byrow=TRUE)

Expressed this way, the reader quickly sees the two rows and three columns of data.

There is a quick-and-dirty way to turn a vector into a matrix: just assign dimensions to the vector. This was discussed in the "Introduction". The following example creates a vanilla vector and then shapes it into a 2×3 matrix:

```
> v <- c(1.1, 1.2, 1.3, 2.1, 2.2, 2.3)
> dim(v) <- c(2,3)
> v
      [,1] [,2] [,3]
[1,] 1.1 1.3 2.2
[2,] 1.2 2.1 2.3
```

Personally, I find this more opaque than using matrix, especially since there is no byrow option here.

See Also

See Recipe 5.3.

5.15 Performing Matrix Operations

Problem

You want to perform matrix operations such as transpose, matrix inversion, matrix multiplication, or constructing an identity matrix.

Solution

t(A)

```
Matrix transposition of A
```

```
solve(A)
    Matrix inverse of A
A %*% B
    Matrix multiplication of A and B
diag(n)
    An n-by-n diagonal (identity) matrix
```

Recall that A*B is element-wise multiplication whereas A %*% B is matrix multiplication.

All these functions return a matrix. Their arguments can be either matrices or data frames. If they are data frames then R will first convert them to matrices (although this is useful only if the data frame contains exclusively numeric values).

5.16 Giving Descriptive Names to the Rows and Columns of a Matrix

Problem

You want to assign descriptive names to the rows or columns of a matrix.

Solution

Every matrix has a **rownames** attribute and a **colnames** attribute. Assign a vector of character strings to the appropriate attribute:

```
> rownames(mat) <- c("rowname1", "rowname2", ..., "rownamem")
> colnames(mat) <- c("colname1", "colname2", ..., "colnamen")</pre>
```

Discussion

R lets you assign names to the rows and columns of a matrix, which is useful for printing the matrix. R will display the names if they are defined, enhancing the readability of your output. Consider this matrix of correlations between the prices of IBM, Microsoft, and Google stock:

```
> print(tech.corr)
      [,1] [,2] [,3]
[1,] 1.000 0.556 0.390
[2,] 0.556 1.000 0.444
[3,] 0.390 0.444 1.000
```

In this form, the matrix output's interpretation is not self-evident. Yet if we define names for the rows and columns, then R will annotate the matrix output with the names:

Now the reader knows at a glance which rows and columns apply to which stocks.

Another advantage of naming rows and columns is that you can refer to matrix elements by those names:

```
> tech.corr["IBM","GOOG"]  # What is the correlation between IBM and GOOG?
[1] 0.39
```

5.17 Selecting One Row or Column from a Matrix

Problem

You want to select a single row or a single column from a matrix.

Solution

The solution depends on what you want. If you want the result to be a simple vector, just use normal indexing:

> vec <- mat[1,] # First row > vec <- mat[,3] # Third column</pre>

If you want the result to be a one-row matrix or a one-column matrix, then include the drop=FALSE argument:

<pre>> row <- mat[1,,drop=FALSE]</pre>	# First row in a one-row matrix
<pre>> col <- mat[,3,drop=FALSE]</pre>	<pre># Third column in a one-column matrix</pre>

Discussion

Normally, when you select one row or column from a matrix, R strips off the dimensions. The result is a dimensionless vector:

```
> mat[1,]
[1] 1 4 7 10
> mat[,3]
[1] 7 8 9
```

When you include the **drop=FALSE** argument, however, R retains the dimensions. In that case, selecting a row returns a row vector (a $1 \times n$ matrix):

```
> mat[1,,drop=FALSE]
    [,1] [,2] [,3] [,4]
[1,] 1 4 7 10
```

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Likewise, selecting a column with **drop=FALSE** returns a column vector (an *n* × 1 matrix):

```
> mat[,3,drop=FALSE]
    [,1]
[1,] 7
[2,] 8
[3,] 9
```

5.18 Initializing a Data Frame from Column Data

Problem

Your data is organized by columns, and you want to assemble it into a data frame.

Solution

If your data is captured in several vectors and/or factors, use the data.frame function to assemble them into a data frame:

```
> dfrm <- data.frame(v1, v2, v3, f1, f2)</pre>
```

If your data is captured in a *list* that contains vectors and/or factors, use instead as.data.frame:

```
> dfrm <- as.data.frame(list.of.vectors)</pre>
```

Discussion

A data frame is a collection of columns, each of which corresponds to an observed variable (in the statistical sense, not the programming sense). If your data is already organized into columns, then it's easy to build a data frame.

The data.frame function can construct a data frame from vectors, where each vector is one observed variable. Suppose you have two numeric predictor variables, one categorical predictor variable, and one response variable. The data.frame function can create a data frame from your vectors:

```
> dfrm <- data.frame(pred1, pred2, pred3, resp)</pre>
> dfrm
       pred1
                  pred2 pred3
                                  resp
                           AM 12.57715
1 -2.7528917 -1.40784130
2 -0.3626909 0.31286963
                           AM 21.02418
3 -1.0416039 -0.69685664
                         PM 18.94694
4 1.2666820 -1.27511434 PM 18.98153
5 0.7806372 -0.27292745
                         AM 19.59455
6 -1.0832624 0.73383339
                         AM 20.71605
7 -2.0883305 0.96816822
                           PM 22.70062
8 -0.7063653 -0.84476203
                           PM 18.40691
                         PM 21.00930
9 -0.8394022 0.31530793
10 -0.4966884 -0.08030948
                         AM 19.31253
```

Notice that data.frame takes the column names from your program variables. You can override that default by supplying explicit column names:

Alternatively, your data may be organized into vectors but those vectors are held in a list, not individual program variables, like this:

```
> lst <- list(p1=pred1, p2=pred2, p3=pred3, r=resp)</pre>
```

No problem. Use the **as.data.frame** function to create a data frame from the list of vectors:

5.19 Initializing a Data Frame from Row Data

Problem

Your data is organized by rows, and you want to assemble it into a data frame.

Solution

Store each row in a one-row data frame. Store the one-row data frames in a list. Use **rbind** and **do.call** to bind the rows into one, large data frame:

> dfrm <- do.call(rbind, obs)</pre>

Here, **obs** is a list of one-row data frames.

Discussion

Data often arrives as a collection of observations. Each *observation* is a record or tuple that contains several values, one for each observed variable. The lines of a flat file are usually like that: each line is one record, each record contains several columns, and each column is a different variable (see Recipe 4.12). Such data is organized by

observation, not by *variable*. In other words, you are given rows one at a time rather than columns one at a time.

Each such row might be stored in several ways. One obvious way is as a vector. If you have purely numerical data, use a vector.

However, many datasets are a mixture of numeric, character, and categorical data, in which case a vector won't work. I recommend storing each such heterogeneous row in a one-row data frame. (You could store each row in a list, but this recipe gets a little more complicated.)

For concreteness, let's assume that you have ten rows with four variables per observation: pred1, pred2, pred2, and resp. Each row is stored in a one-row data frame, so you have ten such data frames. Those data frames are stored in a list called obs. The first element of obs might look like this:

```
> obs[[1]]
    pred1 pred2 pred3 resp
1 -1.197 0.36 AM 18.701
```

This recipe works also if your observations are stored in vectors rather than one-row data frames.

We need to bind together those rows into a data frame. That's what the **rbind** function does. It binds its arguments in such a way that each argument becomes one row in the result. If we **rbind** the first two observations, for example, we get a two-row data frame:

```
> rbind(obs[[1]], obs[[2]])
    pred1 pred2 pred3 resp
1 -1.197 0.36 AM 18.701
2 -0.952 1.23 PM 25.709
```

We want to bind together every observation, not just the first two, so we tap into the vector processing of R. The do.call function will expand obs into one, long argument list and call rbind with that long argument list:

```
    > do.call(rbind,obs)
    pred1 pred2 pred3 resp
    -1.197 0.360 AM 18.701
    -0.952 1.230 PM 25.709
    0.279 0.423 PM 21.572
    -1.445 -1.846 AM 14.392
    0.822 -0.246 AM 19.841
    1.247 1.254 PM 25.637
    -0.394 1.563 AM 24.585
    -1.248 -1.264 PM 16.770
    0.652 -2.344 PM 14.915
    10 -1.171 -0.776 PM 17.948
```

The result is a data frame built from our rows of data.

Sometimes, for reasons beyond your control, the rows of your data are stored in lists rather than one-row data frames. You may be dealing with rows returned by a database package, for example. In that case, **obs** will be a list of lists, not a list of data frames.

We first transform the rows into data frames using the Map function and then apply this recipe:

```
> dfrm <- do.call(rbind,Map(as.data.frame,obs))</pre>
```

See Also

See Recipe 5.18 if your data is organized by columns, not rows; see Recipe 12.18 to learn more about do.call.

5.20 Appending Rows to a Data Frame

Problem

You want to append one or more new rows to a data frame.

Solution

Create a second, temporary data frame containing the new rows. Then use the **rbind** function to append the temporary data frame to the original data frame.

Discussion

Suppose we want to append a new row to our data frame of Chicago-area cities. First, we create a one-row data frame with the new data:

```
> newRow <- data.frame(city="West Dundee", county="Kane", state="IL", pop=5428)</pre>
```

Next, we use the **rbind** function to append that one-row data frame to our existing data frame:

```
> suburbs <- rbind(suburbs, newRow)</pre>
```

> suburbs

-	JUDUIDJ			
	city	county	state	рор
1	Chicago	Cook	IL	2853114
2	Kenosha	Kenosha	WI	90352
3	Aurora	Kane	IL	171782
4	Elgin	Kane	IL	94487
5	Gary	Lake(IN)	IN	102746
6	Joliet	Kendall	IL	106221
7	Naperville	DuPage	IL	147779
8	Arlington Heights	Cook	IL	76031
9	Bolingbrook	Will	IL	70834
10	Cicero	Cook	IL	72616
11	Evanston	Cook	IL	74239
12	Hammond	Lake(IN)	IN	83048
13	Palatine	Cook	IL	67232
14	Schaumburg	Cook	IL	75386
15	Skokie	Cook	IL	63348
16	Waukegan	Lake(IL)	IL	91452
17	West Dundee	Kane	IL	5428

The **rbind** function tells R that we are appending a new row to **suburbs**, not a new column. It may be obvious to you that **newRow** is a row and not a column, but it is not obvious to R. (Use the **cbind** function to append a column.)

One word of caution. The new row must use the same column names as the data frame. Otherwise, **rbind** will fail.

We can combine these two steps into one, of course:

```
> suburbs <- rbind(suburbs,
+ data.frame(city="West Dundee", county="Kane", state="IL", pop=5428))
```

We can even extend this technique to multiple new rows because **rbind** allows multiple arguments:

```
> suburbs <- rbind(suburbs,
+ data.frame(city='
+ data.frame(city='
```



Do not use this recipe to append many rows to a large data frame. That would force R to reallocate a large data structure repeatedly, which is a very slow process. Build your data frame using more efficient means, such as those in Recipes 5.19 or 5.21.

5.21 Preallocating a Data Frame

Problem

You are building a data frame, row by row. You want to preallocate the space instead of appending rows incrementally.

Solution

Create a data frame from generic vectors and factors using the functions numeric(n), character(n), and factor(n):

```
> dfrm <- data.frame(colname1=numeric(n), colname2=character(n), ... etc. ... )</pre>
```

Here, n is the number of rows needed for the data frame.

Discussion

Theoretically, you can build a data frame by appending new rows, one by one. That's OK for small data frames, but building a large data frame in that way can be tortuous. The memory manager in R works poorly when one new row is repeatedly appended to a large data structure. Hence your R code will run very slowly.

One solution is to preallocate the data frame—assuming you know the required number of rows. By preallocating the data frame once and for all, you sidestep problems with the memory manager.

Suppose you want to create a data frame with 1,000,000 rows and three columns: two numeric and one character. Use the numeric and character functions to preallocate the columns; then join them together using data.frame:

```
> N <- 1000000
> dfrm <- data.frame(dosage=numeric(N), lab=character(N), response=numeric(N))</pre>
```

Now you have a data frame with the correct dimensions, $1,000,000 \times 3$, waiting to receive its contents.

Data frames can contain factors, but preallocating a factor is a little trickier. You can't simply call factor(n). You need to specify the factor's levels because you are creating it. Continuing our example, suppose you want the lab column to be a factor, not a character string, and that the possible levels are NJ, IL, and CA. Include the levels in the column specification, like this:

5.22 Selecting Data Frame Columns by Position

Problem

You want to select columns from a data frame according to their position.

Solution

To select a single column, use this list operator:

dfrm[[n]]

Returns *one column*—specifically, the *n*th column of dfrm.

To select one or more columns and package them in a data frame, use the following sublist expressions:

dfrm[*n*]

Returns a *data frame* consisting solely of the *n*th column of dfrm.

```
dfrm[c(n_1, n_2, ..., n_k)]
```

Returns a *data frame* built from the columns in positions $n_1, n_2, ..., n_k$ of dfrm.

You can use matrix-style subscripting to select one or more columns:

dfrm[, n]

Returns the nth column (assuming that n contains exactly one value).

```
dfrm[, c(n_1, n_2, ..., n_k)]
```

Returns a *data frame* built from the columns in positions $n_1, n_2, ..., n_k$.

Note that the matrix-style subscripting can return two different data types (either column or data frame) depending upon whether you select one column or multiple columns.

Discussion

There are a bewildering number of ways to select columns from a data frame. The choices can be confusing until you understand the logic behind the alternatives. As you read this explanation, notice how a slight change in syntax—a comma here, a double-bracket there—changes the meaning of the expression.

Let's play with the population data for the 16 largest cities in the Chicago metropolitan area:

> :	suburbs			
	city	county	state	рор
1	Chicago	Cook	IL	2853114
2	Kenosha	Kenosha	WI	90352
3	Aurora	Kane	IL	171782
4	Elgin	Kane	IL	94487
5	Gary	Lake(IN)	IN	102746
6	Joliet	Kendall	IL	106221
7	Naperville	DuPage	IL	147779
8	Arlington Heights	Cook	IL	76031
9	Bolingbrook	Will	IL	70834
10	Cicero	Cook	IL	72616
11	Evanston	Cook	IL	74239
12	Hammond	Lake(IN)	IN	83048
13	Palatine	Cook	IL	67232
14	Schaumburg	Cook	IL	75386
15	Skokie	Cook	IL	63348
16	Waukegan	Lake(IL)	IL	91452

Use simple list notation to select exactly one column, such as the first column:

<pre>> suburbs[[1]]</pre>			
<pre>[1] "Chicago"</pre>	"Kenosha"	"Aurora"	"Elgin"
[5] "Gary"	"Joliet"	"Naperville"	"Arlington Heights"
[9] "Bolingbrook"	"Cicero"	"Evanston"	"Hammond"
[13] "Palatine"	"Schaumburg"	"Skokie"	"Waukegan"

The first column of suburbs is a vector, so that's what suburbs[[1]] returns: a vector. If the first column were a factor, we'd get a factor.

The result differs when you use the single-bracket notation, as in suburbs[1] or suburbs[c(1,3)]. You still get the requested columns, but R wraps them in a data frame. This example returns the first column wrapped in a data frame:

> suburbs[1]

	city
1	Chicago
2	Kenosha
3	Aurora
4	Elgin

5	Gary
6	Joliet
7	Naperville
8	Arlington Heights
9	Bolingbrook
10	Cicero
11	Evanston
12	Hammond
13	Palatine
14	Schaumburg
15	Skokie
16	Waukegan

The next example returns the first and third columns wrapped in a data frame:

```
> suburbs[c(1,3)]
```

	city	рор
1	Chicago	2853114
2	Kenosha	90352
3	Aurora	171782
4	Elgin	94487
5	Gary	102746
6	Joliet	106221
7	Naperville	147779
8	Arlington Heights	76031
9	Bolingbrook	70834
10	Cicero	72616
11	Evanston	74239
12	Hammond	83048
13	Palatine	67232
14	Schaumburg	75386
15	Skokie	63348
16	Waukegan	91452

A major source of confusion is that suburbs[[1]] and suburbs[1] look similar but produce very different results:

```
suburbs[[1]]
```

This returns one column.

```
suburbs[1]
```

This returns a data frame, and the data frame contains exactly one column. This is a special case of $dfrm[c(n_1, n_2, \ldots, n_k)]$. We don't need the $c(\ldots)$ construct because there is only one n.

The point here is that "one column" is different from "a data frame that contains one column." The first expression returns a column, so it's a vector or a factor. The second expression returns a data frame, which is different.

R lets you use matrix notation to select columns, as shown in the Solution. But an odd quirk can bite you: you might get a column or you might get a data frame, depending upon many subscripts you use. In the simple case of one index you get a column, like this:

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> suburbs[,1]								
<pre>[1] "Chicago"</pre>	"Kenosha"	"Aurora"	"Elgin"					
[5] "Gary"	"Joliet"	"Naperville"	"Arlington Heights"					
<pre>[9] "Bolingbrook"</pre>	"Cicero"	"Evanston"	"Hammond"					
[13] "Palatine"	"Schaumburg"	"Skokie"	"Waukegan"					

But using the same matrix-style syntax with multiple indexes returns a data frame:

> :	suburbs[,c(1,4)]	
	city	рор
1	Chicago	2853114
2	Kenosha	90352
3	Aurora	171782
4	Elgin	94487
5	Gary	102746
6	Joliet	106221
7	Naperville	147779
8	Arlington Heights	76031
9	Bolingbrook	70834
10	Cicero	72616
11	Evanston	74239
12	Hammond	83048
13	Palatine	67232
14	Schaumburg	75386
15	Skokie	63348
16	Waukegan	91452

This creates a problem. Suppose you see this expression in some old R script:

dfrm[,vec]

Quick, does that return a column or a data frame? Well, it depends. If **vec** contains one value then you get a column; otherwise, you get a data frame. You cannot tell from the syntax alone.

To avoid this problem, you can include drop=FALSE in the subscripts; this forces R to return a data frame:

dfrm[,vec,drop=FALSE]

Now there is no ambiguity about the returned data structure. It's a data frame.

When all is said and done, using matrix notation to select columns from data frames is not the best procedure. I recommend that you instead use the list operators described previously. They just seem clearer.

See Also

See Recipe 5.17 for more about using drop=FALSE.

5.23 Selecting Data Frame Columns by Name

Problem

You want to select columns from a data frame according to their name.

Solution

To select a single column, use one of these list expressions:

```
dfrm[["name"]]
```

Returns one column, the column called name.

dfrm\$*name*

Same as previous, just different syntax.

To select one or more columns and package them in a data frame, use these list expressions:

```
dfrm["name"]
```

Selects one column and packages it inside a data frame object.

```
dfrm[c("name1", "name2", ..., "namek")]
```

Selects several columns and packages them in a data frame.

You can use matrix-style subscripting to select one or more columns:

dfrm[, "name"]
 Returns the named column.

```
dfrm[, c("name_1", "name_2", ..., "name_k")]
Selects several columns and packages in a data frame.
```

Once again, the matrix-style subscripting can return two different data types (column or data frame) depending upon whether you select one column or multiple columns.

Discussion

All columns in a data frame must have names. If you know the name, it's usually more convenient and readable to select by name, not by position.

The solutions just described are similar to those for Recipe 5.22, where we selected columns by position. The only difference is that here we use column names instead of column numbers. All the observations made in Recipe 5.22 apply here:

- dfrm[["name"]] returns one column, not a data frame.
- dfrm[c("name₁", "name₂", ..., "name_k")] returns a data frame, not a column.
- dfrm["name"] is a special case of the previous expression and so returns a data frame, not a column.

• The matrix-style subscripting can return either a column or a data frame, so be careful how many names you supply. See Recipe 5.22 for a discussion of this "gotcha" and using drop=FALSE.

There is one new addition:

dfrm\$name

This is identical in effect to dfrm[["name"]], but it's easier to type and to read.

See Also

See Recipe 5.22 to understand these ways to select columns.

5.24 Selecting Rows and Columns More Easily

Problem

You want an easier way to select rows and columns from a data frame or matrix.

Solution

Use the **subset** function. The **select** argument is a column name, or a vector of column names, to be selected:

```
> subset(dfrm, select=colname)
```

```
> subset(dfrm, select=c(colname1, ..., colnameN))
```

Note that you do *not* quote the column names.

The **subset** argument is a logical expression that selects rows. Inside the expression, you can refer to the column names as part of the logical expression. In this example, **response** is a column in the data frame, and we are selecting rows with a positive **response**:

```
> subset(dfrm, subset=(response > 0))
```

subset is most useful when you combine the select and subset arguments:

```
> subset(dfrm, select=c(predictor,response), subset=(response > 0))
```

Discussion

Indexing is the "official" way to select rows and columns from a data frame, as described in Recipes 5.22 and 5.23. However, indexing is cumbersome when the index expressions become complicated.

The **subset** function provides a more convenient and readable way to select rows and columns. It's beauty is that you can refer to the columns of the data frame right inside the expressions for selecting columns and rows.

Here are some examples using the Cars93 dataset in the MASS package. Recall that the dataset includes columns for Manufacturer, Model, MPG.city, MPG.highway, Min.Price, and Max.Price:

Select the model name for cars that can exceed 30 miles per gallon (MPG) in the city

Select the model name and price range for four-cylinder cars made in the United States

```
> subset(Cars93, select=c(Model,Min.Price,Max.Price),
        subset=(Cylinders == 4 & Origin == "USA"))
+
          Model Min.Price Max.Price
6
        Centurv
                     14.2
                               17.3
       Cavalier
                     8.5
                               18.3
12
13
        Corsica
                     11.4
                               11.4
. (etc.)
```

Select the manufacturer's name and the model name for all cars whose highway MPG value is above the median

```
> subset(Cars93, select=c(Manufacturer,Model),
+ subset=c(MPG.highway > median(MPG.highway)))
Manufacturer Model
1 Acura Integra
5 BMW 535i
6 Buick Century
.
. (etc.)
```

The **subset** function is actually more powerful than this recipe implies. It can select from lists and vectors, too. See the help page for details.

5.25 Changing the Names of Data Frame Columns

Problem

You converted a matrix or list into a data frame. R gave names to the columns, but the names are at best uninformative and at worst bizarre.

Solution

Data frames have a **colnames** attribute that is a vector of column names. You can update individual names or the entire vector:

> colnames(dfrm) <- newnames # newnames is a vector of character strings</pre>

Discussion

The columns of data frames must have names. If you convert a vanilla matrix into a data frame, R will synthesize names that are reasonable but boring—for example, V1, V2, V3, and so forth:

```
> mat
        [,1] [,2] [,3]
[1,] -0.818 -0.667 -0.494
[2,] -0.819 -0.946 -0.205
[3,] 0.385 1.531 -0.611
[4,] -2.155 -0.535 -0.316
> as.data.frame(mat)
        V1 V2 V3
1 -0.818 -0.667 -0.494
2 -0.819 -0.946 -0.205
3 0.385 1.531 -0.611
4 -2.155 -0.535 -0.316
```

If the matrix had column names defined, R would have used those names instead of synthesizing new ones.

However, converting a list into a data frame produces some strange synthetic names:

```
> 1st
[[1]]
[1] -0.284 -1.114 -1.097 -0.873
[[2]]
[1] -1.673 0.929 0.306 0.778
[[3]]
[1] 0.323 0.368 0.067 -0.080
> as.data.frame(lst)
  c..0.284...1.114...1.097...0.873. c..1.673..0.929..0.306..0.778.
1
                             -0.284
                                                             -1.673
2
                             -1.114
                                                             0.929
                                                              0.306
3
                             -1.097
4
                             -0.873
                                                              0.778
 c.0.323..0.368..0.067...0.08.
                          0.323
1
2
                          0.368
                          0.067
3
4
                         -0.080
```

Again, if the list elements had names then R would have used them.

Fortunately, you can overwrite the synthetic names with names of your own by setting the **colnames** attribute:

```
> dfrm <- as.data.frame(lst)
> colnames(dfrm) <- c("before","treatment","after")
> dfrm
    before treatment after
1 -0.284 -1.673 0.323
2 -1.114 0.929 0.368
3 -1.097 0.306 0.067
4 -0.873 0.778 -0.080
```

See Also

See Recipe 5.33.

5.26 Editing a Data Frame

Problem

Data in a data frame are incorrect or missing. You want a convenient way to edit the data frame contents.

Solution

R includes a data editor that displays your data frame in a spreadsheet-like window. Invoke the editor using the edit function:

```
> temp <- edit(dfrm)
> dfrm <- temp  # Overwrite only if you're happy with the changes!</pre>
```

Make your changes and then close the editor window. The edit function will return the updated data, which here are assigned to temp. If you are happy with the changes, overwrite your data frame with the results.

If you are feeling brave, the fix function invokes the editor and overwrites your variable with the result. There is no "undo", however:

> fix(dfrm)

Discussion

Figure 5-1 is a screenshot of the data editor on Windows during the editing of data from Recipe 5.22.

As of this writing, the editor is quite primitive. It does not include the common features of a modern editor—not even an "undo" command, for instance. I cannot recommend the data editor for regular use, but it's OK for emergency touch-ups.

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is a collabore	7	Naperville	DuPage	IL	147779			
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citation()' on	9	Bolingbrook	Will	IL	70834			
ype 'demo()' fo	10	Cicero	Cook	IL	72616			
help.start()':	11	Evanston	Cook	IL	74239			
'ype 'q()' to q	12	Hammond	Lake(IN)	IN	83048			
Previously save	13	Palatine	Cook	IL	67232			
Freviously save	14	Schaumburg	Cook	IL	75386			
edit(suburbs)	15	Skokie	Cook	IL	63348			
	16	Waukegan	Lake(IL)	WI	91452			
	17							
	18							
	19							

Figure 5-1. Editing a data frame

Since there is no undo, take note of the solution that assigns the edited result to a temporary, intermediate variable. If you mess up your data, you can just delete the temporary variable without affecting the original data.

See Also

Several of the add-on GUI frontends provide data editors that are better than the native editor.

5.27 Removing NAs from a Data Frame

Problem

Your data frame contains NA values, which is creating problems for you.

Solution

Use na.omit to remove rows that contain any NA values.

```
> clean <- na.omit(dfrm)</pre>
```

I frequently stumble upon situations where just a few NA values in my data frame cause everything to fall apart. One solution is simply to remove all rows that contain NAs. That's what na.omit does.

Here we can see cumsum fail because the input contains NA values:

```
> dfrm
          х
                      y
1 -0.9714511 -0.4578746
2
         NA 3.1663282
3 0.3367627
                     NΔ
4 1.7520504 0.7406335
5 0.4918786 1.4543427
> cumsum(dfrm)
          х
                     ۷
1 -0.971451 -0.4578746
2
        NA 2.7084536
3
        NA
                    NA
4
         NA
                    NA
5
         NA
                    NA
```

If we remove the NA values, cumsum can complete its summations:

This recipe works for vectors and matrices, too, but not for lists.

Will You Still Have Enough Data?

The obvious danger here is that simply dropping observations from your data could render the results computationally or statistically meaningless. Make sure that omitting data makes sense in your context. Remember that na.omit will remove entire rows, not just the NA values, which could eliminate a lot of useful information.

5.28 Excluding Columns by Name

Problem

You want to exclude a column from a data frame using its name.

Solution

Use the subset function with a negated argument for the select parameter:

We can exclude a column by position (e.g., dfrm[-1]), but how do we exclude a column by name? The subset function can exclude columns from a data frame. The select parameter is a normally a list of columns to include, but prefixing a minus sign (-) to the name causes the column to be excluded instead.

I often encounter this problem when calculating the correlation matrix of a data frame and I want to exclude nondata columns such as labels:

This correlation matrix includes the meaningless "correlation" between patient ID and other variables, which is annoying. We can exclude the patient ID column to clean up the output:

We can exclude multiple columns by giving a vector of negated names:

See Also

See Recipe 5.24 for more about the subset function.

5.29 Combining Two Data Frames

Problem

You want to combine the contents of two data frames into one data frame.

Solution

To combine the columns of two data frames side by side, use cbind:

```
> all.cols <- cbind(dfrm1,dfrm2)</pre>
```

To "stack" the rows of two data frames, use rbind:

```
> all.rows <- rbind(dfrm1,dfrm2)</pre>
```

You can combine data frames in one of two ways: either by putting the columns side by side to create a wider data frame; or by "stacking" the rows to create a taller data frame. The **cbind** function will combine data frames side by side, as shown here when combining **stooges** and **birth**:

```
> stooges
  name n.marry n.child
1 Moe
            1
                   2
2 Larry
            1
                   2
3 Curly
            4
                   2
> birth
 birth.year birth.place
1
       1887 Bensonhurst
       1902 Philadelphia
2
3
       1903
               Brooklyn
> cbind(stooges,birth)
  name n.marry n.child birth.year birth.place
1 Moe 1 2
                           1887 Bensonhurst
                   2
                           1902 Philadelphia
2 Larry
            1
3 Curly
            4
                   2
                           1903
                                   Brooklyn
```

You would normally combine columns with the same height (number of rows). Technically speaking, however, **cbind** does not require matching heights. If one data frame is short, it will invoke the Recycling Rule to extend the short columns as necessary (Recipe 5.3), which may or may not be what you want.

The **rbind** function will "stack" the rows of two data frames, as shown here when combining **stooges** and **guys**:

```
> stooges
  name n.marry n.child
1 Moe
                     2
             1
2 Larry
             1
                     2
3 Curly
             4
                     2
> guys
  name n.marry n.child
1 Tom
                     2
             4
2 Dick
             1
                     4
3 Harry
             1
                     1
> rbind(stooges,guys)
  name n.marry n.child
1
  Moe
           1
                     2
2 Larry
             1
                     2
3 Curly
             4
                     2
                     2
4 Tom
             4
5 Dick
             1
                     4
6 Harry
             1
                     1
```

The **rbind** function requires that the data frames have the same width: same number of columns and same column names. The columns need not be in the same *order*, however; **rbind** will sort that out.

Finally, this recipe is slightly more general than the title implies. First, you can combine more than two data frames because both **rbind** and **cbind** accept multiple arguments. Second, you can apply this recipe to other data types because **rbind** and **cbind** work also with vectors, lists, and matrices.

See Also

The merge function can combine data frames that are otherwise incompatible owing to missing or different columns. The reshape2 and plyr packages, available on CRAN, include some powerful functions for slicing, dicing, and recombining data frames.

5.30 Merging Data Frames by Common Column

Problem

You have two data frames that share a common column. You want to merge their rows into one data frame by matching on the common column.

Solution

Use the **merge** function to join the data frames into one new data frame based on the common column:

> m <- merge(*df*1, *df*2, by="*name*")

Here *name* is the name of the column that is common to data frames *df1* and *df2*.

Discussion

Suppose you have two data frames, **born** and **died**, that each contain a column called **name**:

```
> born
  name year.born
                   place.born
           1887 Bensonhurst
1 Moe
            1902 Philadelphia
2 Larry
                     Brooklyn
3 Curly
            1903
                       Moscow
4 Harry
            1964
> died
  name year.died
1 Curly
            1952
2 Moe
            1975
3 Larry
            1975
```

We can merge them into one data frame by using name to combine matched rows:

```
> merge(born, died, by="name")
name year.born place.born year.died
1 Curly 1903 Brooklyn 1952
2 Larry 1902 Philadelphia 1975
3 Moe 1887 Bensonhurst 1975
```

Notice that **merge** does not require the rows to be sorted or even to occur in the same order. It found the matching rows for Curly even though they occur in different positions. It also discards rows that appear in only one data frame or the other.

In SQL terms, the **merge** function essentially performs a join operation on the two data frames. It has many options for controlling that join operation, all of which are described on the help page for **merge**.

See Also

See Recipe 5.29 for other ways to combine data frames.

5.31 Accessing Data Frame Contents More Easily

Problem

Your data is stored in a data frame. You are getting tired of repeatedly typing the data frame name and want to access the columns more easily.

Solution

For quick, one-off expressions, use the with function to expose the column names:

> with(dataframe, expr)

Inside *expr*, you can refer to the columns of *dataframe* by their names—as if they were simple variables.

For repetitive access, use the **attach** function to insert the data frame into your search list. You can then refer to the data frame columns by name without mentioning the data frame:

> attach(dataframe)

Use the detach function to remove the data frame from your search list.

Discussion

A data frame is a great way to store your data, but accessing individual columns can become tedious. For a data frame called **suburbs** that contains a column called **pop**, here is the naïve way to calculate the *z*-scores of **pop**:

```
> z <- (suburbs$pop - mean(suburbs$pop)) / sd(suburbs$pop)</pre>
```

Call me a whiner, but all that typing gets tedious. The with function lets you expose the columns of a data frame as distinct variables. It takes two arguments, a data frame and an expression to be evaluated. Inside the expression, you can refer to the data frame columns by their names:

> z <- with(suburbs, (pop - mean(pop)) / sd(pop))</pre>

That is useful for one-liners. If you will be working repeatedly with columns in your data frame, attach the data frame to your search list and the columns will become available as variables:

```
> attach(suburbs)
```

After the attach, the second item in the search list is the suburbs data frame:

```
> search()
[1] ".GlobalEnv" "suburbs" "package:stats"
[4] "package:graphics" "package:grDevices" "package:utils"
[7] "package:datasets" "package:methods" "Autoloads"
[10] "package:base"
```

Now we can refer to the columns of the data frame as if they were variables:

```
> z <- (pop - mean(pop)) / sd(pop)</pre>
```

When you are done, use a **detach** (with no arguments) to remove the second location in the search list:

<pre>> detach()</pre>		
<pre>> search()</pre>		
<pre>[1] ".GlobalEnv"</pre>	"package:stats"	"package:graphics"
<pre>[4] "package:grDevices"</pre>	"package:utils"	"package:datasets"
<pre>[7] "package:methods"</pre>	"Autoloads"	"package:base"

Observe that suburbs is no longer in the search list.

Attaching a data frame has a big quirk: R attaches a *temporary copy* of the data frame, which means that changes to the original data frame are hidden. In this session fragment, notice how changing the data frame does not change our view of the attached data:

```
> attach(suburbs)
> pop
[1] 2853114
             90352 171782
                           94487 102746 106221 147779
                                                        76031
                                                                70834
[10] 72616 74239 83048 67232 75386 63348
                                                91452
> suburbs$pop <- 0
                       # Overwrite data frame contents
                         # Hey! It seems nothing changed
> pop
[1] 2853114 90352 171782 94487 102746 106221 147779
                                                                70834
                                                        76031
[10] 72616 74239 83048 67232
                                 75386 63348
                                                91452
                         # Contents of data frame did indeed change
> suburbs$pop
[1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
```

Another source of confusion is that assigning values to the exposed names does not work as you might expect. In the following fragment, you might think we are scaling **pop** by 1,000 but we are actually creating a new local variable:

```
> attach(suburbs)
> pop
[1] 2853114
             90352 171782
                            94487 102746 106221 147779
                                                          76031
                                                                  70834
             74239 83048 67232 75386 63348
[10] 72616
                                                 91452
                       # Achtung! This is creating a local variable called "pop"
> pop <- pop / 1000
                          # We can see the new variable in our workspace
> ls()
            "suburbs"
[1] "pop"
```

> subi	urbs\$pop	<pre># Original data is unchanged</pre>							
[1] 2	2853114	90352	171782	94487	102746	106221	147779	76031	70834
[10]	72616	74239	83048	67232	75386	63348	91452		

5.32 Converting One Atomic Value into Another

Problem

You have a data value which has an atomic data type: character, complex, double, integer, or logical. You want to convert this value into one of the other atomic data types.

Solution

For each atomic data type, there is a function for converting values to that type. The conversion functions for atomic types include:

- as.character(x)
- as.complex(x)
- as.numeric(x) or as.double(x)
- as.integer(x)
- as.logical(x)

Discussion

Converting one atomic type into another is usually pretty simple. If the conversion works, you get what you would expect. If it does not work, you get NA:

```
> as.numeric(" 3.14 ")
[1] 3.14
> as.integer(3.14)
[1] 3
> as.numeric("foo")
[1] NA
Warning message:
NAs introduced by coercion
> as.character(101)
[1] "101"
```

If you have a vector of atomic types, these functions apply themselves to every value. So the preceding examples of converting scalars generalize easily to converting entire vectors:

```
> as.numeric(c("1","2.718","7.389","20.086"))
[1] 1.000 2.718 7.389 20.086
> as.numeric(c("1","2.718","7.389","20.086", "etc."))
[1] 1.000 2.718 7.389 20.086 NA
Warning message:
NAs introduced by coercion
```

```
> as.character(101:105)
[1] "101" "102" "103" "104" "105"
```

When converting logical values into numeric values, R converts FALSE to $\mathbf{0}$ and TRUE to $\mathbf{1}:$

```
> as.numeric(FALSE)
[1] 0
> as.numeric(TRUE)
[1] 1
```

This behavior is useful when you are counting occurrences of TRUE in vectors of logical values. If **logvec** is a vector of logical values, then **sum(logvec)** does an implicit conversion from logical to integer and returns the number of TRUEs.

5.33 Converting One Structured Data Type into Another

Problem

You want to convert a variable from one structured data type to another—for example, converting a vector into a list or a matrix into a data frame.

Solution

These functions convert their argument into the corresponding structured data type:

- as.data.frame(x)
- as.list(x)
- as.matrix(x)
- as.vector(x)

Some of these conversions may surprise you, however. I suggest you review Table 5-1.

Discussion

Converting between structured data types can be tricky. Some conversions behave as you'd expect. If you convert a matrix into a data frame, for instance, the rows and columns of the matrix become the rows and columns of the data frame. No sweat.

Conversion	How	Notes
Vector→List	as.list(vec)	Don't use list(vec); that creates a 1-element list whose only element is a copy of vec.
Vector→Matrix	To create a 1-column matrix: cbind(vec) or as.matrix(vec) To create a 1-row matrix: rbind(vec)	See Recipe 5.14.

Table 5-1. Data conversions

Study Material. Do not distribute.

How	Notes
To create an <i>n</i> × <i>m</i> matrix: matrix(vec,n,m)	
To create a 1-column data frame: as.data.frame(vec)	
To create a 1-row data frame: as.data.frame(rbind(vec))	
unlist(lst)	Use unlist rather than as.vector; see Note 1 and Recipe 5.11.
To create a 1-column matrix: as.matrix(lst)	
To create a 1-row matrix: as.matrix(rbind(lst))	
To create an <i>n</i> × <i>m</i> matrix: matrix(lst,n,m)	
If the list elements are columns of data: as.data.frame(lst)	
If the list elements are rows of data: Recipe 5.19	
as.vector(mat)	Returns all matrix elements in a vector.
as.list(mat)	Returns all matrix elements in a list.
as.data.frame(mat)	
To convert a 1-row data frame: dfrm[1,]	See Note 2.
To convert a 1-column data frame: dfrm[,1] or dfrm[[1]]	
as.list(dfrm)	See Note 3.
as.matrix(dfrm)	See Note 4.
	To create an <i>n</i> × <i>m</i> matrix: matrix(vec,n,m) To create a 1-column data frame: as.data.frame(vec) To create a 1-row data frame: as.data.frame(rbind(vec)) unlist(lst) To create a 1-column matrix: as.matrix(lst) To create a 1-row matrix: as.matrix(rbind(lst)) To create a 1-row matrix: matrix(lst,n,m) If the list elements are columns of data: as.data.frame(lst) If the list elements are rows of data: Recipe 5.19 as.vector(mat) as.list(mat) To convert a 1-row data frame: dfrm[1,] To convert a 1-column data frame: dfrm[1,] or dfrm[[1]] as.list(dfrm)

In other cases, the results might surprise you. Table 5-1 summarizes some noteworthy examples. The following Notes are cited in that table:

- 1. When you convert a list into a vector, the conversion works cleanly if your list contains atomic values that are all of the same mode. Things become complicated if either (a) your list contains mixed modes (e.g., numeric and character), in which case everything is converted to characters; or (b) your list contains other structured data types, such as sublists or data frames—in which case very odd things happen, so don't do that.
- 2. Converting a data frame into a vector makes sense only if the data frame contains one row or one column. To extract all its elements into one, long vector, use as.vector(as.matrix(dfrm)). But even that makes sense only if the data frame is all-numeric or all-character; if not, everything is first converted to character strings.
- 3. Converting a data frame into a list may seem odd in that a data frame is already a list (i.e., a list of columns). Using as.list essentially removes the class (data.frame) and thereby exposes the underlying list. That is useful when you want R to treat your data structure as a list—say, for printing.

4. Be careful when converting a data frame into a matrix. If the data frame contains only numeric values then you get a numeric matrix. If it contains only character values, you get a character matrix. But if the data frame is a mix of numbers, characters, and/or factors, then all values are first converted to characters. The result is a matrix of character strings.

Problems with matrices

The matrix conversions detailed here assume that your matrix is homogeneous: all elements have the same mode (e.g, all numeric or all character). A matrix can to be heterogeneous, too, when the matrix is built from a list. If so, conversions become messy. For example, when you convert a mixed-mode matrix to a data frame, the data frame's columns are actually lists (to accommodate the mixed data).

See Also

See Recipe 5.32 for converting atomic data types; see the "Introduction" to this chapter for remarks on problematic conversions.