2 Creating a dataset

This chapter covers

- Exploring R data structures
- Using data entry
- Importing data
- Annotating datasets

The first step in any data analysis is the creation of a dataset containing the information to be studied, in a format that meets your needs. In R, this task involves the following:

- Selecting a data structure to hold your data
- Entering or importing your data into the data structure

The first part of this chapter (sections 2.1–2.2) describes the wealth of structures that R can use for holding data. In particular, section 2.2 describes vectors, factors, matrices, data frames, and lists. Familiarizing yourself with these structures (and the notation used to access elements within them) will help you tremendously in understanding how R works. You might want to take your time working through this section.

The second part of this chapter (section 2.3) covers the many methods available for importing data into R. Data can be entered manually, or imported from an external source. These data sources can include text files, spreadsheets, statistical packages, and database management systems. For example, the data that I work with typically comes from SQL databases. On occasion, though, I receive data from legacy DOS systems, and from current SAS and SPSS databases. It's likely that you'll only have to use one or two of the methods described in this section, so feel free to choose those that fit your situation.

Once a dataset is created, you'll typically annotate it, adding descriptive labels for variables and variable codes. The third portion of this chapter (section 2.4) looks at annotating datasets and reviews some useful functions for working with datasets (section 2.5). Let's start with the basics.

2.1 Understanding datasets

A dataset is usually a rectangular array of data with rows representing observations and columns representing variables. Table 2.1 provides an example of a hypothetical patient dataset.

Table 2.1 A patient dataset

PatientID	AdmDate	Age	Diabetes	Status
1	10/15/2009	25	Type1	Poor
2	11/01/2009	34	Type2	Improved
3	10/21/2009	28	Type1	Excellent
4	10/28/2009	52	Type1	Poor

Different traditions have different names for the rows and columns of a dataset. Statisticians refer to them as observations and variables, database analysts call them records and fields, and those from the data mining/machine learning disciplines call them examples and attributes. We'll use the terms *observations* and *variables* throughout this book.

You can distinguish between the structure of the dataset (in this case a rectangular array) and the contents or data types included. In the dataset shown in table 2.1, `PatientID` is a row or case identifier, `AdmDate` is a date variable, `Age` is a continuous variable, `Diabetes` is a nominal variable, and `Status` is an ordinal variable.

R contains a wide variety of structures for holding data, including scalars, vectors, arrays, data frames, and lists. Table 2.1 corresponds to a data frame in R. This diversity of structures provides the R language with a great deal of flexibility in dealing with data.

The data types or modes that R can handle include numeric, character, logical (TRUE/FALSE), complex (imaginary numbers), and raw (bytes). In R, `PatientID`, `AdmDate`, and `Age` would be numeric variables, whereas `Diabetes` and `Status` would be character variables. Additionally, you'll need to tell R that `PatientID` is a case identifier, that `AdmDate` contains dates, and that `Diabetes` and `Status` are nominal and ordinal variables, respectively. R refers to case identifiers as `rownames` and categorical variables (nominal, ordinal) as `factors`. We'll cover each of these in the next section. You'll learn about dates in chapter 3.

2.2 Data structures

R has a wide variety of objects for holding data, including scalars, vectors, matrices, arrays, data frames, and lists. They differ in terms of the type of data they can hold, how they're created, their structural complexity, and the notation used to identify and access individual elements. Figure 2.1 shows a diagram of these data structures.

Let's look at each structure in turn, starting with vectors.

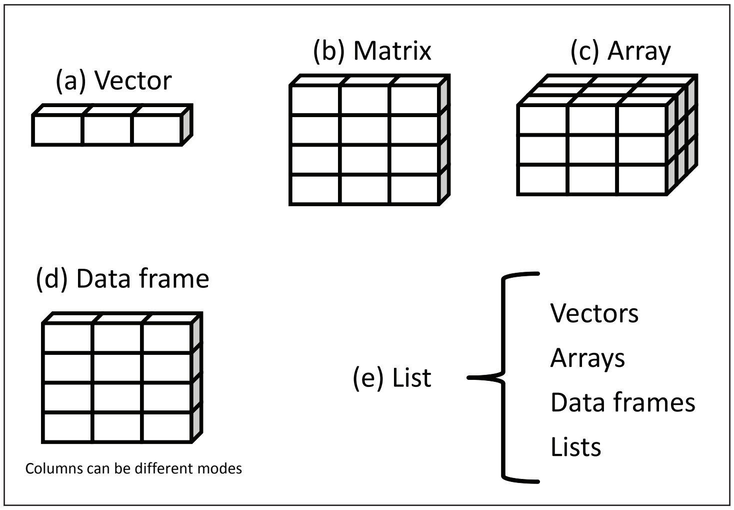


Figure 2.1 R data structures

Some definitions

There are several terms that are idiosyncratic to R, and thus confusing to new users.

In R, an *object* is anything that can be assigned to a variable. This includes constants, data structures, functions, and even graphs. Objects have a mode (which describes how the object is stored) and a class (which tells generic functions like `print` how to handle it).

A *data frame* is a structure in R that holds data and is similar to the datasets found in standard statistical packages (for example, SAS, SPSS, and Stata). The columns are variables and the rows are observations. You can have variables of different types (for example, numeric, character) in the same data frame. Data frames are the main structures you'll use to store datasets.

(continued)

Factors are nominal or ordinal variables. They're stored and treated specially in R. You'll learn about factors in section 2.2.5.

Most other terms should be familiar to you and follow the terminology used in statistics and computing in general.

2.2.1 Vectors

Vectors are one-dimensional arrays that can hold numeric data, character data, or logical data. The combine function `c()` is used to form the vector. Here are examples of each type of vector:

```
a <- c(1, 2, 5, 3, 6, -2, 4)
b <- c("one", "two", "three")
c <- c(TRUE, TRUE, TRUE, FALSE, TRUE, FALSE)
```

Here, `a` is numeric vector, `b` is a character vector, and `c` is a logical vector. Note that the data in a vector must only be one type or mode (numeric, character, or logical). You can't mix modes in the same vector.

NOTE Scalars are one-element vectors. Examples include `f <- 3`, `g <- "US"` and `h <- TRUE`. They're used to hold constants.

You can refer to elements of a vector using a numeric vector of positions within brackets. For example, `a[c(2, 4)]` refers to the 2nd and 4th element of vector a. Here are additional examples:

```
> a <- c(1, 2, 5, 3, 6, -2, 4)
> a[3]
[1] 5
> a[c(1, 3, 5)]
[1] 1 5 6
> a[2:6]
[1]  2  5  3  6 -2
```

The colon operator used in the last statement is used to generate a sequence of numbers. For example, a <- c(2:6) is equivalent to a <- c(2, 3, 4, 5, 6).

2.2.2 Matrices

A matrix is a two-dimensional array where each element has the same mode (numeric, character, or logical). Matrices are created with the `matrix` function. The general format is

```
myymatrix <- matrix(vector, nrow=number_of_rows, ncol=number_of_columns,
                    byrow=logical_value, dimnames=list(
                    char_vector_rownames, char_vector_colnames))
```

where *`vector`* contains the elements for the matrix, `nrow` and `ncol` specify the row and column dimensions, and `dimnames` contains optional row and column labels stored in character vectors. The option `byrow` indicates whether the matrix should be filled in by row (`byrow=TRUE`) or by column (`byrow=FALSE`). The default is by column. The following listing demonstrates the `matrix` function.

Listing 2.1 Creating matrices

```
  > y <- matrix(1:20, nrow=5, ncol=4)
> y
     [,1] [,2] [,3] [,4]
[1,]    1    6   11   16
[2,]    2    7   12   17
[3,]    3    8   13   18
[4,]    4    9   14   19
[5,]    5   10   15   20
> cells    <- c(1,26,24,68)
> rnames   <- c("R1", "R2")
> cnames   <- c("C1", "C2")
> mymatrix <- matrix(cells, nrow=2, ncol=2, byrow=TRUE,
                     dimnames=list(rnames, cnames))
> mymatrix
   C1 C2
R1  1 26
R2 24 68
> mymatrix <- matrix(cells, nrow=2, ncol=2, byrow=FALSE,
                     dimnames=list(rnames, cnames))
> mymatrix
  C1 C2
R1  1 24
R2 26 68
```

1 Create a 5x4 matrix

2 2x2 matrix filled by rows

3 2x2 matrix filled by columns

First, you create a 5x4 matrix 1. Then you create a 2x2 matrix with labels and fill the matrix by rows 2. Finally, you create a 2x2 matrix and fill the matrix by columns 3.

You can identify rows, columns, or elements of a matrix by using subscripts and brackets. `X`[*i*,] refers to the *i*th row of matrix `X`, `X`[,*j*] refers to *j*th column, and `X`[*i*, *j*] refers to the *ij*th element, respectively. The subscripts *i* and *j* can be numeric vectors in order to select multiple rows or columns, as shown in the following listing.

Listing 2.2 Using matrix subscripts

```
> x <- matrix(1:10, nrow=2)
> x
     [,1] [,2] [,3] [,4] [,5]
[1,]    1    3    5    7    9
[2,]    2    4    6    8   10
> x[2,]
  [1]  2  4  6  8 10
> x[,2]
[1] 3 4
> x[1,4]
[1] 7
> x[1, c(4,5)]
[1] 7 9
```

First a 2 x 5 matrix is created containing numbers 1 to 10. By default, the matrix is filled by column. Then the elements in the 2nd row are selected, followed by the elements in the 2nd column. Next, the element in the 1st row and 4th column is selected. Finally, the elements in the 1st row and the 4th and 5th columns are selected.

Matrices are two-dimensional and, like vectors, can contain only one data type. When there are more than two dimensions, you'll use arrays (section 2.2.3). When there are multiple modes of data, you'll use data frames (section 2.2.4).

2.2.3 Arrays

Arrays are similar to matrices but can have more than two dimensions. They're created with an array function of the following form:

```
myarray <- array(vector, dimensions, dimnames)
```

where *vector* contains the data for the array, *dimensions* is a numeric vector giving the maximal index for each dimension, and *dimnames* is an optional list of dimension labels. The following listing gives an example of creating a three-dimensional (2x3x4) array of numbers.

Listing 2.3 Creating an array

```
> dim1 <- c("A1", "A2")
> dim2 <- c("B1", "B2", "B3")
> dim3 <- c("C1", "C2", "C3", "C4")
> z <- array(1:24, c(2, 3, 4), dimnames=list(dim1, dim2, dim3))
> z
, , C1

   B1 B2 B3
A1  1  3  5
A2  2  4  6

, , C2

   B1 B2 B3
A1  7  9 11
A2  8 10 12

, , C3

   B1 B2 B3
A1 13 15 17
A2 14 16 18

, , C4

   B1 B2 B3
A1 19 21 23
A2 20 22 24
```

As you can see, arrays are a natural extension of matrices. They can be useful in programming new statistical methods. Like matrices, they must be a single mode.

Identifying elements follows what you've seen for matrices. In the previous example, the `z[1,2,3]` element is 15.

2.2.4 Data frames

A data frame is more general than a matrix in that different columns can contain different modes of data (numeric, character, etc.). It's similar to the datasets you'd typically see in SAS, SPSS, and Stata. Data frames are the most common data structure you'll deal with in R.

The patient dataset in table 2.1 consists of numeric and character data. Because there are multiple modes of data, you can't contain this data in a matrix. In this case, a data frame would be the structure of choice.

A data frame is created with the `data.frame()` function:

```
mydata <- data.frame(col1, col2, col3,…)
```

where *`col1, col2, col3,`* … are column vectors of any type (such as character, numeric, or logical). Names for each column can be provided with the `names` function. The following listing makes this clear.

Listing 2.4 Creating a data frame

```
> patientID <- c(1, 2, 3, 4)
> age <- c(25, 34, 28, 52)
> diabetes <- c("Type1", "Type2", "Type1", "Type1")
> status <- c("Poor", "Improved", "Excellent", "Poor")
> patientdata <- data.frame(patientID, age, diabetes, status)
> patientdata
  patientID age diabetes    status
1         1  25    Type1      Poor
2         2  34    Type2  Improved
3         3  28    Type1 Excellent
4         4  52    Type1      Poor
```

Each column must have only one mode, but you can put columns of different modes together to form the data frame. Because data frames are close to what analysts typically think of as datasets, we'll use the terms *columns* and *variables* interchangeably when discussing data frames.

There are several ways to identify the elements of a data frame. You can use the subscript notation you used before (for example, with matrices) or you can specify column names. Using the `patientdata` data frame created earlier, the following listing demonstrates these approaches.

Listing 2.5 Specifying elements of a data frame

```
> patientdata[1:2]
  patientID age
1         1  25
2         2  34
3         3  28
4         4  52
> patientdata[c("diabetes", "status")]
```

```
  diabetes    status
1    Type1      Poor
2    Type2  Improved
3    Type1 Excellent
4    Type1      Poor
> patientdata$age
[1] 25 34 28 52
```

1 **Indicates age variable in patient data frame**

The $ notation in the third example is new 1. It's used to indicate a particular variable from a given data frame. For example, if you want to cross tabulate diabetes type by status, you could use the following code:

```
> table(patientdata$diabetes, patientdata$status)

        Excellent Improved Poor
  Type1         1        0    2
  Type2         0        1    0
```

It can get tiresome typing `patientdata$` at the beginning of every variable name, so shortcuts are available. You can use either the `attach()` and `detach()` or `with()` functions to simplify your code.

ATTACH, DETACH, AND WITH

The `attach()` function adds the data frame to the R search path. When a variable name is encountered, data frames in the search path are checked in order to locate the variable. Using the `mtcars` data frame from chapter 1 as an example, you could use the following code to obtain summary statistics for automobile mileage (`mpg`), and plot this variable against engine displacement (`disp`), and weight (`wt`):

```
summary(mtcars$mpg)
plot(mtcars$mpg, mtcars$disp)
plot(mtcars$mpg, mtcars$wt)
```

This could also be written as

```
attach(mtcars)
  summary(mpg)
  plot(mpg, disp)
  plot(mpg, wt)
detach(mtcars)
```

The `detach()` function removes the data frame from the search path. Note that `detach()` does nothing to the data frame itself. The statement is optional but is good programming practice and should be included routinely. (I'll sometimes ignore this sage advice in later chapters in order to keep code fragments simple and short.)

The limitations with this approach are evident when more than one object can have the same name. Consider the following code:

```
> mpg <- c(25, 36, 47)
> attach(mtcars)

The following object(s) are masked _by_ '.GlobalEnv':    mpg
```

```
> plot(mpg, wt)
Error in xy.coords(x, y, xlabel, ylabel, log) :
  ‘x’ and ‘y’ lengths differ
> mpg
[1] 25 36 47
```

Here we already have an object named `mpg` in our environment when the `mtcars` data frame is attached. In such cases, the original object takes precedence, which isn't what you want. The `plot` statement fails because `mpg` has 3 elements and `disp` has 32 elements. The `attach()` and `detach()` functions are best used when you're analyzing a single data frame and you're unlikely to have multiple objects with the same name. In any case, be vigilant for warnings that say that objects are being masked.

An alternative approach is to use the `with()` function. You could write the previous example as

```
with(mtcars, {
  summary(mpg, disp, wt)
  plot(mpg, disp)
  plot(mpg, wt)
})
```

In this case, the statements within the `{}` brackets are evaluated with reference to the `mtcars` data frame. You don't have to worry about name conflicts here. If there's only one statement (for example, `summary(mpg)`), the `{}` brackets are optional.

The limitation of the `with()` function is that assignments will only exist within the function brackets. Consider the following:

```
> with(mtcars, {
   stats <- summary(mpg)
   stats
  })
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  10.40   15.43   19.20   20.09   22.80   33.90
> stats
Error: object ‘stats’ not found
```

If you need to create objects that will exist outside of the `with()` construct, use the special assignment operator <<- instead of the standard one (<-). It will save the object to the global environment outside of the `with()` call. This can be demonstrated with the following code:

```
> with(mtcars, {
   nokeepstats <- summary(mpg)
   keepstats <<- summary(mpg)
})
> nokeepstats
Error: object ‘nokeepstats’ not found
> keepstats
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    10.40   15.43   19.20   20.09   22.80   33.90
```

Most books on R recommend using `with()` over `attach()`. I think that ultimately the choice is a matter of preference and should be based on what you're trying to achieve and your understanding of the implications. We'll use both in this book.

CASE IDENTIFIERS

In the patient data example, `patientID` is used to identify individuals in the dataset. In R, case identifiers can be specified with a `rowname` option in the data frame function. For example, the statement

```
patientdata <- data.frame(patientID, age, diabetes, status,
   row.names=patientID)
```

specifies `patientID` as the variable to use in labeling cases on various printouts and graphs produced by R.

2.2.5 Factors

As you've seen, variables can be described as nominal, ordinal, or continuous. Nominal variables are categorical, without an implied order. `Diabetes` (`Type1, Type2`) is an example of a nominal variable. Even if `Type1` is coded as a 1 and `Type2` is coded as a 2 in the data, no order is implied. Ordinal variables imply order but not amount. `Status` (`poor, improved, excellent`) is a good example of an ordinal variable. You know that a patient with a poor status isn't doing as well as a patient with an improved status, but not by how much. Continuous variables can take on any value within some range, and both order and amount are implied. `Age` in years is a continuous variable and can take on values such as 14.5 or 22.8 and any value in between. You know that someone who is 15 is one year older than someone who is 14.

Categorical (nominal) and ordered categorical (ordinal) variables in R are called factors. Factors are crucial in R because they determine how data will be analyzed and presented visually. You'll see examples of this throughout the book.

The function `factor()` stores the categorical values as a vector of integers in the range [1... *k*] (where *k* is the number of unique values in the nominal variable), and an internal vector of character strings (the original values) mapped to these integers.

For example, assume that you have the vector

```
diabetes <- c("Type1", "Type2", "Type1", "Type1")
```

The statement `diabetes <- factor(diabetes)` stores this vector as (1, 2, 1, 1) and associates it with 1=Type1 and 2=Type2 internally (the assignment is alphabetical). Any analyses performed on the vector `diabetes` will treat the variable as nominal and select the statistical methods appropriate for this level of measurement.

For vectors representing ordinal variables, you add the parameter `ordered=TRUE` to the `factor()` function. Given the vector

```
status <- c("Poor", "Improved", "Excellent", "Poor")
```

the statement `status <- factor(status, ordered=TRUE)` will encode the vector as (3, 2, 1, 3) and associate these values internally as 1=Excellent, 2=Improved, and

3=Poor. Additionally, any analyses performed on this vector will treat the variable as ordinal and select the statistical methods appropriately.

By default, factor levels for character vectors are created in alphabetical order. This worked for the `status` factor, because the order "Excellent," "Improved," "Poor" made sense. There would have been a problem if "Poor" had been coded as "Ailing" instead, because the order would be "Ailing," "Excellent," "Improved." A similar problem exists if the desired order was "Poor," "Improved," "Excellent." For ordered factors, the alphabetical default is rarely sufficient.

You can override the default by specifying a `levels` option. For example,

```
status <- factor(status, order=TRUE,
                 levels=c("Poor", "Improved", "Excellent"))
```

would assign the levels as 1=Poor, 2=Improved, 3=Excellent. Be sure that the specified levels match your actual data values. Any data values not in the list will be set to missing.

The following listing demonstrates how specifying factors and ordered factors impact data analyses.

Listing 2.6 Using factors

```
> patientID <- c(1, 2, 3, 4)                          ◁── ❶ Enter data as vectors
> age <- c(25, 34, 28, 52)
> diabetes <- c("Type1", "Type2", "Type1", "Type1")
> status <- c("Poor", "Improved", "Excellent", "Poor")
> diabetes <- factor(diabetes)
> status <- factor(status, order=TRUE)
> patientdata <- data.frame(patientID, age, diabetes, status)
> str(patientdata)                                      ◁─┐ Display object
'data.frame':   4 obs. of  4 variables:                   ❷ structure
 $ patientID: num  1 2 3 4
 $ age      : num  25 34 28 52
 $ diabetes : Factor w/ 2 levels "Type1","Type2": 1 2 1 1
 $ status   : Ord.factor w/ 3 levels "Excellent"<"Improved"<..: 3 2 1 3
> summary(patientdata)                                   ◁─┐ Display object
   patientID          age          diabetes       status   ❸ summary
 Min.   :1.00   Min.   :25.00   Type1:3   Excellent:1
 1st Qu.:1.75   1st Qu.:27.25   Type2:1   Improved :1
 Median :2.50   Median :31.00             Poor     :2
 Mean   :2.50   Mean   :34.75
 3rd Qu.:3.25   3rd Qu.:38.50
 Max.   :4.00   Max.   :52.00
```

First, you enter the data as vectors ❶. Then you specify that `diabetes` is a factor and `status` is an ordered factor. Finally, you combine the data into a data frame. The function `str(`*`object`*`)` provides information on an object in R (the data frame in this case) ❷. It clearly shows that `diabetes` is a factor and `status` is an ordered factor, along with how it's coded internally. Note that the `summary()` function treats the variables differently ❸. It provides the minimum, maximum, mean, and quartiles for the continuous variable age, and frequency counts for the categorical variables `diabetes` and `status`.

2.2.6 Lists

Lists are the most complex of the R data types. Basically, a list is an ordered collection of objects (components). A list allows you to gather a variety of (possibly unrelated) objects under one name. For example, a list may contain a combination of vectors, matrices, data frames, and even other lists. You create a list using the `list()` function:

```
mylist <- list(object1, object2, …)
```

where the objects are any of the structures seen so far. Optionally, you can name the objects in a list:

```
mylist <- list(name1=object1, name2=object2, …)
```

The following listing shows an example.

Listing 2.7 Creating a list

```
> g <- "My First List"
> h <- c(25, 26, 18, 39)
> j <- matrix(1:10, nrow=5)
> k <- c("one", "two", "three")
> mylist <- list(title=g, ages=h, j, k)          <- Create list
> mylist                                         <- Print entire list
$title
[1] "My First List"

$ages
[1] 25 26 18 39

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

[[4]]
[1] "one"   "two"   "three"

> mylist[[2]]                               <- Print second
[1] 25 26 18 39                                component
> mylist[["ages"]]
[[1] 25 26 18 39
```

In this example, you create a list with four components: a string, a numeric vector, a matrix, and a character vector. You can combine any number of objects and save them as a list.

You can also specify elements of the list by indicating a component number or a name within double brackets. In this example, `mylist[[2]]` and `mylist[["ages"]]` both refer to the same four-element numeric vector. Lists are important R structures for two reasons. First, they allow you to organize and recall disparate information in a simple way. Second, the results of many R functions return lists. It's up to the analyst to pull out the components that are needed. You'll see numerous examples of functions that return lists in later chapters.

A note for programmers

Experienced programmers typically find several aspects of the R language unusual. Here are some features of the language you should be aware of:

- The period (.) has no special significance in object names. But the dollar sign ($) has a somewhat analogous meaning, identifying the parts of an object. For example, `A$x` refers to variable `x` in data frame A.
- R doesn't provide multiline or block comments. You must start each line of a multiline comment with `#`. For debugging purposes, you can also surround code that you want the interpreter to ignore with the statement `if(FALSE){…}`. Changing the `FALSE` to `TRUE` allows the code to be executed.
- Assigning a value to a nonexistent element of a vector, matrix, array, or list will expand that structure to accommodate the new value. For example, consider the following:

  ```
  > x <- c(8, 6, 4)
  > x[7] <- 10
  > x
  [1]  8  6  4 NA NA NA 10
  ```

  The vector `x` has expanded from three to seven elements through the assignment.
  `x <- x[1:3]` would shrink it back to three elements again.
- R doesn't have scalar values. Scalars are represented as one-element vectors.
- Indices in R start at 1, not at 0. In the vector earlier, `x[1]` is 8.
- Variables can't be declared. They come into existence on first assignment.

To learn more, see John Cook's excellent blog post, *R programming for those coming from other languages* (www.johndcook.com/R_language_for_programmers.html).

Programmers looking for stylistic guidance may also want to check out *Google's R Style Guide* (http://google-styleguide.googlecode.com/svn/trunk/google-r-style.html).

2.3 Data input

Now that you have data structures, you need to put some data in them! As a data analyst, you're typically faced with data that comes to you from a variety of sources and in a variety of formats. Your task is to import the data into your tools, analyze the data,

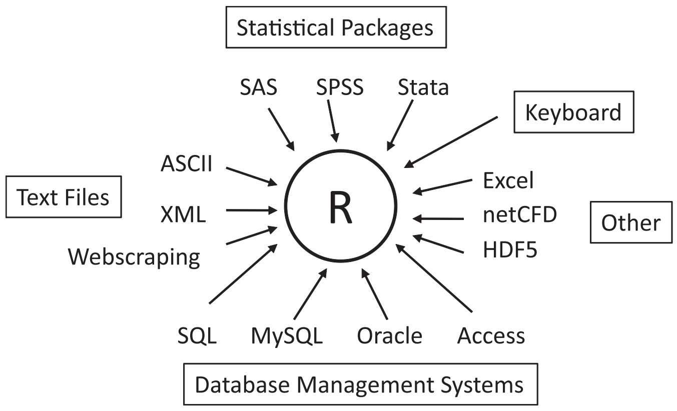


Figure 2.2 Sources of data that can be imported into R

and report on the results. R provides a wide range of tools for importing data. The definitive guide for importing data in R is the *R Data Import/Export* manual available at http://cran.r-project.org/doc/manuals/R-data.pdf.

As you can see in figure 2.2, R can import data from the keyboard, from flat files, from Microsoft Excel and Access, from popular statistical packages, from specialty formats, and from a variety of relational database management systems. Because you never know where your data will come from, we'll cover each of them here. You only need to read about the ones you're going to be using.

2.3.1 Entering data from the keyboard

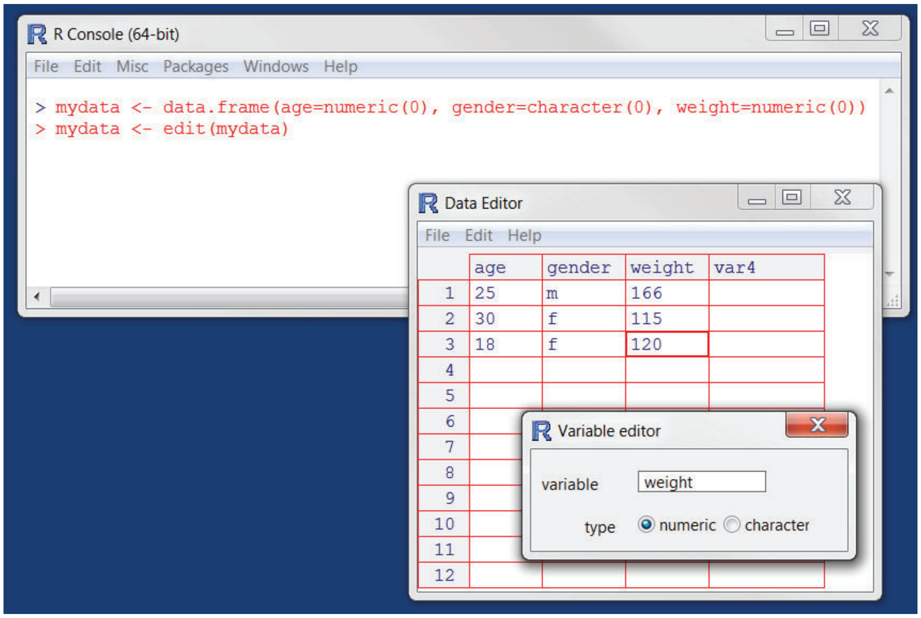
Perhaps the simplest method of data entry is from the keyboard. The `edit()` function in R will invoke a text editor that will allow you to enter your data manually. Here are the steps involved:

1. Create an empty data frame (or matrix) with the variable names and modes you want to have in the final dataset.
2. Invoke the text editor on this data object, enter your data, and save the results back to the data object.

In the following example, you'll create a data frame named `mydata` with three variables: `age` (numeric), `gender` (character), and `weight` (numeric). You'll then invoke the text editor, add your data, and save the results.

```
mydata <- data.frame(age=numeric(0),
  gender=character(0), weight=numeric(0))
mydata <- edit(mydata)
```

Assignments like `age=numeric(0)` create a variable of a specific mode, but without actual data. Note that the result of the editing is assigned back to the object itself. The `edit()` function operates on a copy of the object. If you don't assign it a destination, all of your edits will be lost!



```
> mydata <- data.frame(age=numeric(0), gender=character(0), weight=numeric(0))
> mydata <- edit(mydata)
```

	age	gender	weight	var4
1	25	m	166	
2	30	f	115	
3	18	f	120	

variable: weight
type: [✓ numeric] character

Figure 2.3 Entering data via the built-in editor on a Windows platform

The results of invoking the edit() function on a Windows platform can be seen in figure 2.3.

In this figure, I've taken the liberty of adding some data. If you click on a column title, the editor gives you the option of changing the variable name and type (numeric, character). You can add additional variables by clicking on the titles of unused columns. When the text editor is closed, the results are saved to the object assigned (`mydata` in this case). Invoking `mydata <- edit(mydata)` again allows you to edit the data you've entered and to add new data. A shortcut for `mydata <- edit(mydata)` is simply `fix(mydata)`.

This method of data entry works well for small datasets. For larger datasets, you'll probably want to use the methods we'll describe next: importing data from existing text files, Excel spreadsheets, statistical packages, or database management systems.

2.3.2 *Importing data from a delimited text file*

You can import data from delimited text files using `read.table()`, a function that reads a file in table format and saves it as a data frame. Here's the syntax:

```
mydataframe <- read.table(file, header=logical_value,
  sep="delimiter", row.names="name")
```

where *`file`* is a delimited ASCII file, header is a logical value indicating whether the first row contains variable names (`TRUE` or `FALSE`), `sep` specifies the delimiter separating data values, and row.names is an optional parameter specifying one or more variables to represent row identifiers.

For example, the statement

```
grades <- read.table("studentgrades.csv", header=TRUE, sep=",",
  row.names="STUDENTID")
```

reads a comma-delimited file named studentgrades.csv from the current working directory, gets the variable names from the first line of the file, specifies the variable STUDENTID as the row identifier, and saves the results as a data frame named grades.

Note that the sep parameter allows you to import files that use a symbol other than a comma to delimit the data values. You could read tab-delimited files with sep="\t". The default is sep="", which denotes one or more spaces, tabs, new lines, or carriage returns.

By default, character variables are converted to factors. This behavior may not always be desirable (for example, a variable containing respondents' comments). You can suppress this behavior in a number of ways. Including the option stringsAs Factors=FALSE will turn this behavior off for all character variables. Alternatively, you can use the colClasses option to specify a class (for example, logical, numeric, character, factor) for each column.

The read.table() function has many additional options for fine-tuning the data import. See help(read.table) for details.

NOTE Many of the examples in this chapter import data from files that exist on the user's computer. R provides several mechanisms for accessing data via connections as well. For example, the functions file(), gzfile(), bzfile(), xzfile(), unz(), and url() can be used in place of the filename. The file() function allows the user to access files, the clipboard, and C-level standard input. The gzfile(), bzfile(), xzfile(), and unz() functions let the user read compressed files. The url() function lets you access internet files through a complete URL that includes http://, ftp://, or file://. For HTTP and FTP, proxies can be specified. For convenience, complete URLs (surrounded by "" marks) can usually be used directly in place of filenames as well. See help(file) for details.

2.3.3 Importing data from Excel

The best way to read an Excel file is to export it to a comma-delimited file from within Excel and import it to R using the method described earlier. On Windows systems you can also use the RODBC package to access Excel files. The first row of the spreadsheet should contain variable/column names.

First, download and install the RODBC package.

```
install.packages("RODBC")
```

You can then use the following code to import the data:

```
library(RODBC)
channel <- odbcConnectExcel("myfile.xls")
mydataframe <- sqlFetch(channel, "mysheet")
odbcClose(channel)
```

Here, `myfile.xls` is an Excel file, `mysheet` is the name of the Excel worksheet to read from the workbook, `channel` is an `RODBC` connection object returned by `odbcConnectExcel()`, and `mydataframe` is the resulting data frame. `RODBC` can also be used to import data from Microsoft Access. See `help(RODBC)` for details.

Excel 2007 uses an XLSX file format, which is essentially a zipped set of XML files. The `xlsx` package can be used to access spreadsheets in this format. Be sure to download and install it before first use. The `read.xlsx()` function imports a worksheet from an XLSX file into a data frame. The simplest format is `read.xlsx`*`(file, n)`* where *`file`* is the path to an Excel 2007 workbook and *`n`* is the number of the worksheet to be imported. For example, on a Windows platform, the code

```
library(xlsx)
workbook <- "c:/myworkbook.xlsx"
mydataframe <- read.xlsx(workbook, 1)
```

imports the first worksheet from the workbook `myworkbook.xlsx` stored on the C: drive and saves it as the data frame `mydataframe`. The `xlsx` package can do more than import worksheets. It can create and manipulate Excel XLSX files as well. Programmers who need to develop an interface between R and Excel should check out this relatively new package.

2.3.4 Importing data from XML

Increasingly, data is provided in the form of files encoded in XML. R has several packages for handling XML files. For example, the `XML` package written by Duncan Temple Lang allows users to read, write, and manipulate XML files. Coverage of XML is beyond the scope of this text. Readers interested in the accessing XML documents from within R are referred to the excellent package documentation at www.omegahat.org/RSXML.

2.3.5 Webscraping

In *webscraping*, the user extracts information embedded in a web page available over the internet and saves it into R structures for further analysis. One way to accomplish this is to download the web page using the `readLines()` function and manipulate it with functions such as `grep()` and `gsub()`. For complex web pages, the `RCurl` and `XML` packages can be used to extract the information desired. For more information, including examples, see “Webscraping using readLines and RCurl,” available from the website *Programming with R* (www.programmingr.com).

2.3.6 *Importing data from SPSS*

SPSS datasets can be imported into R via the `read.spss()` function in the `foreign` package. Alternatively, you can use the `spss.get()` function in the `Hmisc` package. `spss.get()` is a wrapper function that automatically sets many parameters of `read.spss()` for you, making the transfer easier and more consistent with what data analysts expect as a result.

First, download and install the `Hmisc` package (the `foreign` package is already installed by default):

```
install.packages("Hmisc")
```

Then use the following code to import the data:

```
library(Hmisc)
mydataframe <- spss.get("mydata.sav", use.value.labels=TRUE)
```

In this code, `mydata.sav` is the SPSS data file to be imported, `use.value.labels=TRUE` tells the function to convert variables with value labels into R factors with those same levels, and `mydataframe` is the resulting R data frame.

2.3.7 *Importing data from SAS*

A number of functions in R are designed to import SAS datasets, including `read.ssd()` in the foreign package and `sas.get()` in the `Hmisc` package. Unfortunately, if you're using a recent version of SAS (SAS 9.1 or higher), you're likely to find that these functions don't work for you because R hasn't caught up with changes in SAS file structures. There are two solutions that I recommend.

You can save the SAS dataset as a comma-delimited text file from within SAS using `PROC EXPORT`, and read the resulting file into R using the method described in section 2.3.2. Here's an example:

```
SAS program:

proc export data=mydata
     outfile="mydata.csv"
     dbms=csv;
run;
```

```
R program:

mydata <- read.table("mydata.csv", header=TRUE, sep=",")
```

Alternatively, a commercial product called Stat Transfer (described in section 2.3.12) does an excellent job of saving SAS datasets (including any existing variable formats) as R data frames.

2.3.8 *Importing data from Stata*

Importing data from Stata to R is straightforward. The necessary code looks like this:

```
library(foreign)
mydataframe <- read.dta("mydata.dta")
```

Here, `mydata.dta` is the Stata dataset and `mydataframe` is the resulting R data frame.

2.3.9 Importing data from netCDF

Unidata's netCDF (network Common Data Form) open source software contains machine-independent data formats for the creation and distribution of array-oriented scientific data. netCDF is commonly used to store geophysical data. The `ncdf` and `ncdf4` packages provide high-level R interfaces to netCDF data files.

The `ncdf` package provides support for data files created with Unidata's netCDF library (version 3 or earlier) and is available for Windows, Mac OS X, and Linux platforms. The `ncdf4` package supports version 4 or earlier, but isn't yet available for Windows.

Consider this code:

```
library(ncdf)
nc <- nc_open("mynetCDFfile")
myarray <- get.var.ncdf(nc, myvar)
```

In this example, all the data from the variable `myvar`, contained in the netCDF file `mynetCDFfile`, is read and saved into an R array called `myarray`.

Note that both `ncdf` and `ncdf4` packages have received major recent upgrades and may operate differently than previous versions. Additionally, function names in the two packages differ. Read the online documentation for details.

2.3.10 Importing data from HDF5

HDF5 (Hierarchical Data Format) is a software technology suite for the management of extremely large and complex data collections. The `hdf5` package can be used to write R objects into a file in a form that can be read by software that understands the HDF5 format. These files can be read back into R at a later time. The package is experimental and assumes that the user has the HDF5 library (version 1.2 or higher) installed. At present, support for the HDF5 format in R is extremely limited.

2.3.11 Accessing database management systems (DBMSs)

R can interface with a wide variety of relational database management systems (DBMSs), including Microsoft SQL Server, Microsoft Access, MySQL, Oracle, PostgreSQL, DB2, Sybase, Teradata, and SQLite. Some packages provide access through native database drivers, whereas others offer access via ODBC or JDBC. Using R to access data stored in external DMBSs can be an efficient way to analyze large datasets (see appendix G), and leverages the power of both SQL and R.

THE ODBC INTERFACE

Perhaps the most popular method of accessing a DBMS in R is through the `RODBC` package, which allows R to connect to any DBMS that has an ODBC driver. This includes all of the DBMSs listed.

The first step is to install and configure the appropriate ODBC driver for your platform and database—they're not part of R. If the requisite drivers aren't already installed on your machine, an internet search should provide you with options.

Once the drivers are installed and configured for the database(s) of your choice, install the `RODBC` package. You can do so by using the `install.packages("RODBC")` command.

The primary functions included with the `RODBC` package are listed in table 2.2.

Table 2.2 `RODBC` functions

Function	Description
`odbcConnect(`*`dsn`*`,uid="",pwd="")`	Open a connection to an ODBC database
`sqlFetch(`*`channel`*`,`*`sqltable`*`)`	Read a table from an ODBC database into a data frame
`sqlQuery(`*`channel`*`,`*`query`*`)`	Submit a query to an ODBC database and return the results
`sqlSave(`*`channel`*`,`*`mydf`*`,tablename = `*`sqtable`*`,append=FALSE)`	Write or update `(append=TRUE)` a data frame to a table in the ODBC database
`sqlDrop(`*`channel`*`,`*`sqtable`*`)`	Remove a table from the ODBC database
`close(`*`channel`*`)`	Close the connection

The `RODBC` package allows two-way communication between R and an ODBC-connected SQL database. This means that you can not only read data from a connected database into R, but you can use R to alter the contents of the database itself. Assume that you want to import two tables (Crime and Punishment) from a DBMS into two R data frames called `crimedat` and `pundat`, respectively. You can accomplish this with code similar to the following:

```
library(RODBC)
myconn <-odbcConnect("mydsn", uid="Rob", pwd="aardvark")
crimedat <- sqlFetch(myconn, Crime)
pundat <- sqlQuery(myconn, "select * from Punishment")
close(myconn)
```

Here, you load the `RODBC` package and open a connection to the ODBC database through a registered data source name (`mydsn`) with a security UID (`rob`) and password (`aardvark`). The connection string is passed to `sqlFetch`, which copies the table Crime into the R data frame `crimedat`. You then run the SQL `select` statement against the table Punishment and save the results to the data frame `pundat`. Finally, you close the connection.

The `sqlQuery()` function is very powerful because any valid SQL statement can be inserted. This flexibility allows you to select specific variables, subset the data, create new variables, and recode and rename existing variables.

DBI-RELATED PACKAGES

The DBI package provides a general and consistent client-side interface to DBMS. Building on this framework, the RJDBC package provides access to DBMS via a JDBC driver. Be sure to install the necessary JDBC drivers for your platform and database. Other useful DBI-based packages include RMySQL, ROracle, RPostgreSQL, and RSQLite. These packages provide native database drivers for their respective databases but may not be available on all platforms. Check the documentation on CRAN (http://cran.r-project.org) for details.

2.3.12 Importing data via Stat/Transfer

Before we end our discussion of importing data, it's worth mentioning a commercial product that can make the task significantly easier. Stat/Transfer (www.stattransfer.com) is a stand-alone application that can transfer data between 34 data formats, including R (see figure 2.4).

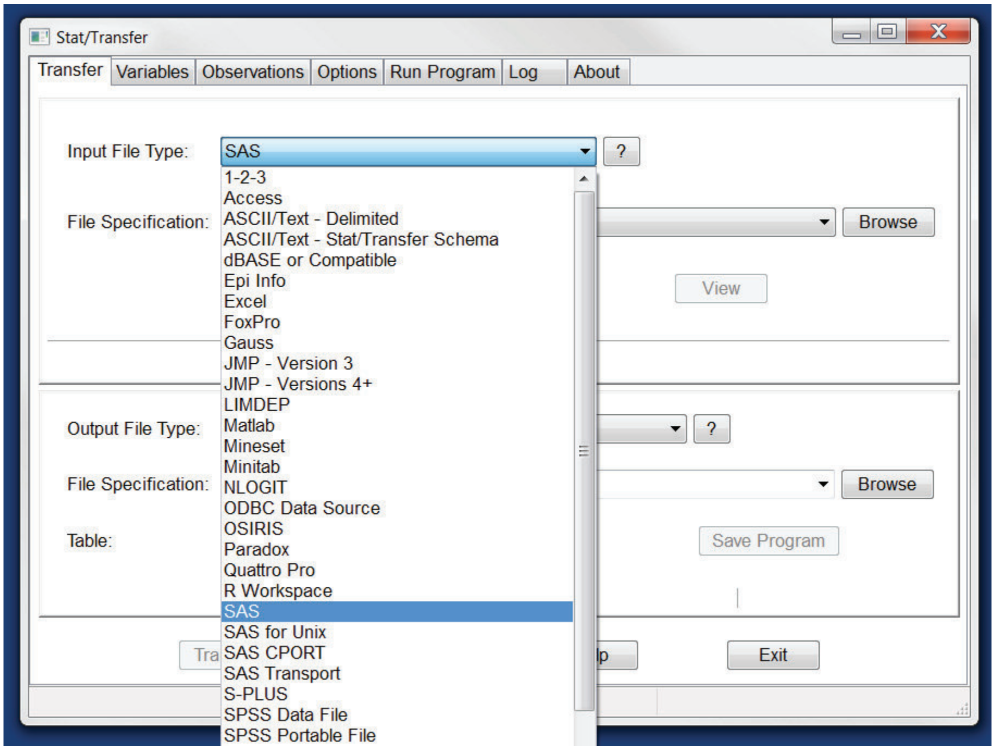


Figure 2.4 **Stat/Transfer's main dialog on Windows**

It's available for Windows, Mac, and Unix platforms and supports the latest versions of the statistical packages we've discussed so far, as well as ODBC-accessed DBMSs such as Oracle, Sybase, Informix, and DB/2.

2.4 Annotating datasets

Data analysts typically annotate datasets to make the results easier to interpret. Typically annotation includes adding descriptive labels to variable names and value labels to the codes used for categorical variables. For example, for the variable `age`, you might want to attach the more descriptive label "Age at hospitalization (in years)." For the variable gender coded 1 or 2, you might want to associate the labels "male" and "female."

2.4.1 Variable labels

Unfortunately, R's ability to handle variable labels is limited. One approach is to use the variable label as the variable's name and then refer to the variable by its position index. Consider our earlier example, where you have a data frame containing patient data. The second column, named `age`, contains the ages at which individuals were first hospitalized. The code

```
names(patientdata)[2] <- "Age at hospitalization (in years)"
```

renames `age` to `"Age at hospitalization (in years)"`. Clearly this new name is too long to type repeatedly. Instead, you can refer to this variable as `patientdata[2]` and the string `"Age at hospitalization (in years)"` will print wherever age would've originally. Obviously, this isn't an ideal approach, and you may be better off trying to come up with better names (for example, `admissionAge`).

2.4.2 Value labels

The `factor()` function can be used to create value labels for categorical variables. Continuing our example, say that you have a variable named `gender`, which is coded 1 for male and 2 for female. You could create value labels with the code

```
patientdata$gender <- factor(patientdata$gender,
                             levels = c(1,2),
                             labels = c("male", "female"))
```

Here `levels` indicate the actual values of the variable, and `labels` refer to a character vector containing the desired labels.

2.5 Useful functions for working with data objects

We'll end this chapter with a brief summary of useful functions for working with data objects (see table 2.3).

Table 2.3 Useful functions for working with data objects

Function	Purpose
`length(object)`	Number of elements/components.
`dim(object)`	Dimensions of an object.
`str(object)`	Structure of an object.
`class(object)`	Class or type of an object.
`mode(object)`	How an object is stored.
`names(object)`	Names of components in an object.
`c(object, object,...)`	Combines objects into a vector.
`cbind(object, object, ...)`	Combines objects as columns.
`rbind(object, object, ...)`	Combines objects as rows.
`object`	Prints the object.
`head(object)`	Lists the first part of the object.
`tail(object)`	Lists the last part of the object.
`ls()`	Lists current objects.
`rm(object, object, ...)`	Deletes one or more objects. The statement `rm(list = ls())` will remove most objects from the working environment.
`newobject <- edit(object)`	Edits object and saves as newobject.
`fix(object)`	Edits in place.

We've already discussed most of these functions. The functions `head()` and `tail()` are useful for quickly scanning large datasets. For example, `head(patientdata)` lists the first six rows of the data frame, whereas `tail(patientdata)` lists the last six. We'll cover functions such as `length()`, `cbind()`, and `rbind()` in the next chapter. They're gathered here as a reference.

2.6 Summary

One of the most challenging tasks in data analysis is data preparation. We've made a good start in this chapter by outlining the various structures that R provides for holding data and the many methods available for importing data from both keyboard and external sources. In particular, we'll use the definitions of a vector, matrix, data frame, and list again and again in later chapters. Your ability to specify elements of these structures via the bracket notation will be particularly important in selecting, subsetting, and transforming data.

As you've seen, R offers a wealth of functions for accessing external data. This includes data from flat files, web files, statistical packages, spreadsheets, and databases. Although the focus of this chapter has been on importing data into R, you can also export data from R into these external formats. Exporting data is covered in appendix C, and methods of working with large datasets (in the gigabyte to terabyte range) are covered in appendix G.

Once you get your datasets into R, it's likely that you'll have to manipulate them into a more conducive format (actually, I find guilt works well). In chapter 4, we'll explore ways of creating new variables, transforming and recoding existing variables, merging datasets, and selecting observations.

But before turning to data management tasks, let's spend some time with R graphics. Many readers have turned to R out of an interest in its graphing capabilities, and I don't want to make you wait any longer. In the next chapter, we'll jump directly into the creation of graphs. Our emphasis will be on general methods for managing and customizing graphs that can be applied throughout the remainder of this book.