Chapter 4
Simple Functions

In previous chapters, we demonstrated how to enter data; read data from a spreadsheet, ascii file, or a database; and extract subsets of data. In this chapter, we discuss applying some simple functions to the data, such as the mean or the mean of a single data subset. These are functions that may be useful; however, they are not the tools that will convince you to become an R user. Use them when it is convenient. Upon first reading of the book, you may skip this chapter.

4.1 The `tapply` Function

R provides functions for calculating the mean, length, standard deviation, minimum, maximum, variance, and any other function of a single variable, multiple variables, or on subsets of observations. For illustration, we use a vegetation dataset. Sikkink et al. (2007) analysed grassland data from a monitoring program conducted in two temperate communities, Yellowstone National Park and the National Bison Range, USA. The aim of the study was to determine whether the biodiversity of these bunchgrass communities changed over time, and, if so, whether the changes in biodiversity related to particular environmental factors. For our purposes we use only the Yellowstone National Park data. To quantify biodiversity, the researchers calculated species richness, defined as the number of *different* species per site. The study identified about 90 species. The data were measured in 8 transects, with each transect being assessed at intervals of 4–10 years, for a total of 58 observations.

The following code can be used to import the data and gain basic information on the variables.

```
> setwd("C:/RBook/")
> Veg <- read.table(file="Vegetation2.txt",
                     header= TRUE)
> names(Veg)
```

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```
 [1] "TransectName" "Samples"      "Transect"
 [4] "Time"         "R"            "ROCK"
 [7] "LITTER"       "ML"           "BARESOIL"
[10] "FallPrec"     "SprPrec"      "SumPrec"
[13] "WinPrec"      "FallTmax"     "SprTmax"
[16] "SumTmax"      "WinTmax"      "FallTmin"
[19] "SprTmin"      "SumTmin"      "WinTmin"
[22] "PCTSAND"      "PCTSILT"      "PCTOrgC"
```

```
> str(Veg)
```

```
'data.frame':   58 obs. of 24 variables:
 $ TransectName: Factor w/ 58 levels ...
 $ Samples     : int 1 2 3 4 5 6 7 8 9 10 ...
 $ Transect    : int 1 1 1 1 1 1 1 2 2 2 ...
 $ Time        : int 1958 1962 1967 1974 1981 1994...
 $ R           : int 8 6 8 8 10 7 6 5 8 6 ...
 $ ROCK        : num 27 26 30 18 23 26 39 25 24 21 ...
 $ LITTER      : num 30 20 24 35 22 26 19 26 24 16 ...
                <Cut to reduce space>
```

The data are stored in the ascii file "Vegetation2.txt." Once the `read.table` function has been executed, we need to ensure that richness is indeed a numerical vector or integer. If, for some reason, R imports richness as a factor (e.g., because there is an alphanumerical in the column, or there are problems with the decimal separator), functions such as `mean`, `sd`, and the like will give an error message[1].

4.1.1 Calculating the Mean Per Transect

One of the first things we would like to know is whether the mean richness per transect differs. The code below calculates the mean richness, as well as mean richness for each transect (see Chapter 3 for selecting subsets of data):

```
> m <- mean(Veg$R)
> m1<- mean(Veg$R[Veg$Transect == 1])
> m2<- mean(Veg$R[Veg$Transect == 2])
> m3<- mean(Veg$R[Veg$Transect == 3])
```

[1] If you import data that are decimal comma separated with the default settings (i.e., with decimal point separation) or vice versa, R will see all variables as factors, and the `str` command will tell you so. Hence, to check that data were imported correctly, we recommend always using the `str` command on the imported data frame immediately after importing the data.

```
> m4<- mean(Veg$R[Veg$Transect == 4])
> m5<- mean(Veg$R[Veg$Transect == 5])
> m6<- mean(Veg$R[Veg$Transect == 6])
> m7<- mean(Veg$R[Veg$Transect == 7])
> m8<- mean(Veg$R[Veg$Transect == 8])
> c(m, m1, m2, m3, m4, m5, m6, m7, m8)

[1]  9.965517  7.571429  6.142857 10.375000 9.250000
[6] 12.375000 11.500000 10.500000 11.833333
```

The variable `m` contains the mean richness of all 8 transects, and `m1` through `m8` show the mean richness values per transect. Note that the `mean` command is applied to `Veg $R`, which is a vector of data. It is not a matrix; hence there is no need for a comma between the square brackets.

4.1.2 Calculating the Mean Per Transect More Efficiently

It is cumbersome to type eight commands to calculate the mean value per transect. The R function `tapply` performs the same operation as the code above (for `m1` through `m8`), but with a single line of code:

```
> tapply(Veg$R, Veg$Transect, mean)
        1         2         3        4         5
 7.571429  6.142857 10.375000 9.250000 12.375000
        6         7         8
11.500000 10.500000 11.833333
```

You can also run this code as

```
> tapply(X = Veg$R, INDEX = Veg$Transect, FUN = mean)
```

The `tapply` function splits the data of the first variable (`R`), based on the levels of the second variable (`Transect`). To each subgroup of data, it applies a function, in this case the mean, but we can also use the standard deviation (function `sd`), variance (function `var`), length (function `length`), and so on. The following lines of code calculate some of these functions for the vegetation data.

```
> Me <- tapply(Veg$R, Veg$Transect, mean)
> Sd <- tapply(Veg$R, Veg$Transect, sd)
> Le <- tapply(Veg$R, Veg$Transect, length)
> cbind(Me, Sd, Le)
         Me        Sd Le
1  7.571429 1.3972763  7
2  6.142857 0.8997354  7
3 10.375000 3.5831949  8
```

```
4  9.250000 2.3145502  8
5 12.375000 2.1339099  8
6 11.500000 2.2677868  8
7 10.500000 3.1464265  6
8 11.833333 2.7141604  6
```

Each row in the output gives the mean richness, standard deviation, and number of observations per transect. In a later chapter we discuss graphic tools to visualise these values.

4.2 The **sapply** and **lapply** Functions

To calculate the mean, minimum, maximum, standard deviation, and length of the full series, we still need to use `mean (Veg$R)`, `min (Veg$R)`, `max (Veg$R)`, `sd (Veg$R)`, and `length (Veg$R)`. This is laborious if we wish to calculate the mean of a large number of variables such as all the numerical variables of the vegetation data. We specifically say "numerical" as one cannot calculate the mean of a factor. There are 20 numerical variables in the vegetation dataset, columns 5–25 of the data frame `Veg`. However, we do not need to type in the `mean` command 20 times. R provides other functions similar to the `tapply` to address this situation: the `lapply` and the `sapply`. The use of `sapply` and its output is given below:

```
> sapply(Veg[, 5:9], FUN= mean)

       R      ROCK    LITTER        ML  BARESOIL
9.965517 20.991379 22.853448  1.086207 17.594828
```

To save space, we only present the results of the first five variables. It is important to realise that `tapply` calculates the mean (or any other function) for subsets of observations of a variable, whereas `lapply` and `sapply` calculate the mean (or any other function) of one or more variables, using *all* observations.

The word FUN stands for function, and must be written in capitals. Instead of the mean, you can use any other function as an argument for `FUN`, and you can write your own functions. So what is the difference between `sapply` and `lapply`? The major differences lie in the presentation of output, as can be seen in the following example.

```
> lapply(Veg[, 5:9], FUN= mean)
$R
[1] 9.965517
$ROCK
[1] 20.99138
```

```
$LITTER
[1] 22.85345
$ML
[1] 1.086207
$BARESOIL
[1] 17.59483
```

The output of `lapply` is presented as a list, whereas `sapply` gives it as a vector. The choice depends on the format in which you would like the output.

The variable that contains the data in `lapply` and `sapply` needs to be a data frame. This will not work:

```
> sapply(cbind(Veg$R, Veg$ROCK, Veg$LITTER, Veg$ML,
                Veg$BARESOIL), FUN = mean)
```

It will produce one long vector of data, because the output of the `cbind` command is not a data frame. It can easily be changed to a data frame:

```
> sapply(data.frame(cbind(Veg$R, Veg$ROCK, Veg$LITTER,
         Veg$ML, Veg$BARESOIL)), FUN = mean)
       X1        X2        X3        X4        X5
 9.965517 20.991379 22.853448  1.086207 17.594828
```

Note that we have lost the variable labels. To avoid this, make a proper data frame (Chapter 2) before running the `sapply` function. Alternatively, use the `colnames` function after combining the data with the `cbind` function.

Do Exercise 1 in Section 4.6. This is an exercise in the use of the `tapply`, `sapply`, and `lapply` functions with a temperature dataset.

4.3 The **summary** Function

Another function that gives basic information on variables is the `summary` command. The argument can be a variable, the output from a `cbind` command, or a data frame. It is run by the following commands.

```
> Z <-cbind(Veg$R, Veg$ROCK, Veg$LITTER)
> colnames(Z) <- c("R", "ROCK", "LITTER")
> summary(Z)
```

```
        R                  ROCK             LITTER
Min.     : 5.000   Min.     : 0.00   Min.     : 5.00
1st Qu. : 8.000    1st Qu. : 7.25    1st Qu. :17.00
Median  :10.000    Median  :18.50    Median  :23.00
Mean    : 9.966    Mean    :20.99    Mean    :22.85
3rd Qu. :12.000    3rd Qu. :27.00    3rd Qu. :28.75
Max.    :18.000    Max.    :59.00    Max.    :51.00
```

The summary command gives the minimum, first quartile, median, mean, third quartile, and maximum value of the variable. An alternative R code gives the same result:

```
> summary(Veg[ , c("R","ROCK","LITTER")])
```

or

```
> summary(Veg[ , c(5, 6, 7)])
```

Output is not presented here.

4.4 The table Function

In Exercises 1 and 7 in Section 2.4, we introduced the deer data from Vicente et al. (2006). The data were from multiple farms, months, years, and sexes. One of the aims of the study was to find a relationship between length of the animal and the number of *E. cervi* parasites. It may be the case that this relationship changes with respect to sex, year, month, farm, or even year and month. To test this, one needs to include interactions in the statistical models. However, problems may be encountered if there are no sampled females in some years, or if some farms were not sampled in every year. The table function can be used to learn how many animals per farm were sampled, as well as the number of observations per sex and year. The following code imports the data, and shows the results.

```
> setwd("c:/RBook/")
> Deer <- read.table(file="Deer.txt", header= TRUE)
> names (Deer)
[1] "Farm"     "Month"    "Year"     "Sex"     "clas1_4"
[6] "LCT"      "KFI"      "Ecervi"   "Tb"
```

```
> str(Deer)
```

```
[1] "Farm"     "Month"    "Year"     "Sex"     "clas1_4"
[6] "LCT"      "KFI"      "Ecervi"   "Tb"
```

```
> str(Deer)
```

```
'data.frame' : 1182 obs. of 9 variables:
 $ Farm      : Factor w/ 27 levels"AL","AU","BA",..: 1...
 $ Month     : int 10 10 10 10 10 10 10 10 10 10 ...
 $ Year      : int 0 0 0 0 0 0 0 0 0 0 ...
 $ Sex       : int 1 1 1 1 1 1 1 1 1 1 ...
 $ clas1_4   : int 4 4 3 4 4 4 4 4 4 4 ...
 $ LCT       : num 191 180 192 196 204 190 196 200 19 ...
 $ KFI       : num 20.4 16.4 15.9 17.3 NA ...
 $ Ecervi    : num 0 0 2.38 0 0 0 1.21 0 0.8 0 ...
 $ Tb        : int 0 0 0 0 NA 0 NA 1 0 0 ...
```

Farm has been coded as AL, AU, and so on, and is automatically imported as a factor. The other variables are all vectors of numerical or integer values. The number of observations per farm is obtained by

```
> table(Deer$Farm)
 AL   AU   BA   BE   CB   CRC   HB   LCV   LN   MAN   MB
 15   37   98   19   93    16   35     2   34    76   41
 MO   NC   NV   PA   PN    QM   RF    RÑ   RO   SAL  SAU
278   32   35   11   45    75   34    25   44     1    3
 SE   TI   TN VISO   VY
 26   21   31   15   40
```

At one farm, 278 animals were sampled and, at others, only one. This dataset typically requires a mixed effects modelling[2] approach in which "farm" is used as a random effect (see Zuur et al., 2009). This method can cope with unbalanced designs. However, the inclusion of a sex/year interaction term[3] in such models for these data will give an error message. This is because both sexes were not measured in every year, as can be seen from the following contingency table. (The labels 0, 1, 2, 3, 4, 5, and 99 in the horizontal direction refer to 2000, 2001, 2002, 2003, 2004, 2005, and 1999, respectively. In the vertical direction 1 and 2 indicate sex).

```
> table(Deer$Sex, Deer$Year)
     0  1   2   3  4  5 99
1  115 85 154  75 78 34 21
2   76 40 197 123 60 35  0
```

In 1999, animals of only one sex were measured. We recommend always using the table command before including interactions between two categorical variables in regression type models.

[2] A mixed effects model is an extension of linear regression.

[3] A sex/year interaction term allows the effect of sex to differ over the years.

Do Exercise 2 in Section 4.6. This is an exercise in using the `table` function with a temperature dataset.

4.5 Which R Functions Did We Learn?

Table 4.1 shows the R functions that were introduced in this chapter.

Table 4.1 R functions introduced in this chapter

Function	Purpose	Example
`tapply`	Apply FUN on y for each level of x	`tapply (y, x, FUN = mean)`
`sapply`	Apply FUN on each variable in y	`sapply (y, FUN = mean)`
`lapply`	Apply FUN on each variable in y	`tapply (y, FUN = mean)`
`sd`	Calculate the standard deviation of y	`sd (y)`
`length`	Determine the length of y.	`length (y)`
`summary`	Calculate general information	`summary (y)`
`table`	Calculate a contingency table	`table (x, y)`

4.6 Exercises

Exercise 1. The use of the `tapply`, `sapply`, and `lapply` functions to calculate mean temperature per month.

The file *temperature.xls* contains temperature observations made at 31 locations along the Dutch coastline. The data were collected and provided by the Dutch institute RIKZ (under the monitoring program MWTL; Monitoring Waterstaatkundige Toestand des Lands). Sampling began in 1990, and the final measurements in the spreadsheet were taken in December 2005, a period of 16 years. Sampling frequency was 0–4 times per month, depending on the season.

Calculate a one-time series of monthly averages using data from all stations. The end result should be a variable of dimension 16 × 12. Also calculate the standard deviation and number of observations per month.

Exercise 2. The use of the `table` function for the temperature data.

Using the data in Exercise 1, determine the number of observations per station. How many observations were made per year? How many observations were made at each station per year?

Chapter 5
An Introduction to Basic Plotting Tools

We have demonstrated the use of R tools for importing data, manipulating data, extracting subsets of data, and making simple calculations, such as mean, variance, standard deviation, and the like. In this chapter, we introduce basic graph plotting tools. If you are interested in only simple graphing, this chapter will suffice; however, to construct more sophisticated graphs, or to add more complicated embellishments such as tick marks, or specialized fonts and font sizes, to basic graphs, you will need the more advanced plotting techniques presented in Chapters 7 and 8.

A discussion of elementary plotting tools may seem out of place at this stage, rather than being included in the sections on graphing beginning with Chapter 7. However, when teaching the material presented in this book, we became aware that, after discussing the relatively pedestrian material of the first four sections, the course participants were eagerly awaiting the lively, more visual, and easier, plotting tools. Therefore, we present a first encounter with graphing here, which allows the presentation of the more complex subjects in the next chapter with the aid of active tools such as the `plot` function.

5.1 The `plot` Function

This section uses the vegetation data introduced in Chapter 4. Recall that these are grassland data from a monitoring program conducted in two temperate communities in Yellowstone National Park and the National Bison Range, USA. To quantify biodiversity, species richness was calculated. In a statistical analysis, we may want to model richness as a function of `BARESOIL` (or any of the other soil and climate variables). Suppose we want to make a plot of species richness versus the substrate variable "exposed soil," denoted by `BARESOIL`. The R commands to create such a graph is

```
> setwd("c:/RBook/")
> Veg <- read.table(file = "Vegetation2.txt",
                    header = TRUE)
> plot(Veg$BARESOIL, Veg$R)
```

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Table 5.1 R functions introduced in this chapter

Function	Purpose	Example
`plot`	Plots *y* versus *x*	`plot(y, x, xlab="X label", xlim=c(0, 1), pch=1, main="Main", ylim=c(0, 2), ylab="Y label", col=1)`
`lines`	Adds lines to an existing graph	`lines(x, y, lwd=3, lty=1, col=1)`
`order`	Determines the order of the data	`order(x)`
`loess`	Applies LOESS smoothing	`M<-loess(y~x)`
`fitted`	Obtains fitted values	`fitted(M)`

killed along a road in Portugal using generalised additive mixed modelling techniques. In this exercise, we use the `plot` command to visualise a segment of the data. Open the file *Amphibian_road_Kills.xls*, prepare a spreadsheet, and import the data into R.

The variable, TOT_N, is the number of dead animals at a sampling site, OLIVE is the number of olive groves at a sampling site, and D Park is the distance from each sampling point to the nearby natural park. Create a plot of TOT_N versus D_park. Use appropriate labels. Add a smoothing curve. Make the same plot again, but use points that are proportional to the value of OLIVE (this may show whether there is an OLIVE effect).

Chapter 6
Loops and Functions

When reading this book for the first time, you may skip this chapter, as building functions[1] and programming loops[2] are probably not among the first R procedures you want to learn, unless these subjects are your prime interests. In general, people perceive these techniques as difficult, hence the asterisk in the chapter title. Once mastered, however, these tools can save enormous amounts of time, especially when executing a large number of similar commands.

6.1 Introduction to Loops

One of R's more convenient features is the provision for easily making your own functions. Functions are useful in a variety of scenarios. For example, suppose you are working with a large number of multivariate datasets, and for each of them you want to calculate a diversity index. There are many diversity indices, and new ones appear regularly in the literature. If you are lucky, the formula for your chosen diversity index has already been programmed by someone else, and, if you are very lucky, it is available in one of the popular packages, the software code is well documented, fully tested, and bug free. But if you cannot find software code for the chosen diversity index, it is time to program it yourself!

If you are likely to use a set of calculations more than once, you would be well advised to present the code in such a way that it can be reused with minimal typing. Quite often, this brings you into the world of functions and loops (and conditional statements such as the `if` command).

The example presented below uses a dataset on owls to produce a large number of graphs. The method involved is repetitive and time consuming, and a procedure that will do the hard work will be invaluable.

[1] A function is a collection of codes that performs a specific task.

[2] A loop allows the program to repeatedly execute commands. It does this by iteration (iteration is synonymous with repetition).

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Developing this procedure requires programming and some logical thinking. You will need to work like an architect who draws up a detailed plan for building a house. You should definitely not begin entering code for a function or loop until you have an overall design.

You also must consider how foolproof your function needs to be. Do you intend to use it only once? Should it work next year on a similar dataset (when you have forgotten most settings and choices in your function)? Will you share it with colleagues?

Functions often go hand in hand with loops, as they both help to automate commands.

Suppose you have 1000 datasets, and for each dataset you need to make a graph and save it as a jpeg. It would take a great deal of time to do this manually, and a mechanism that can repeat the same (or similar) commands any number of times without human intervention would be invaluable. This is where a loop comes in. A plan for the 1000 datasets could be

```
For i is from 1 to 1000:
        Extract dataset i
        Choose appropriate labels for the graph for dataset i
        Make a graph for dataset i
        Save the graph for dataset i
End of loop
```

Note that this is not R code. It is merely a schematic overview, which is the reason that we put the text in a box and did not use the "$>$" symbol and the `Courier New` font that we have been using for R code. The sketch involves a loop, meaning that, once the code is syntax correct, R executes 1000 iterations, with the first iteration having $i = 1$, the second iteration $i = 2$, and in the final iteration $i = 1000$. In each iteration, the commands inside the loop are executed.

This plan has only four steps, but, if we want to do more with the data, it may make sense to group certain commands and put them in a function. Suppose we not only want a graph for each dataset, but also to calculate summary statistics and apply a multivariate analysis. We will very quickly end up with 10–15 commands inside the loop, and the code becomes difficult to manage. In such a scenario, using functions can keep the code simple:

```
For i is from 1 to 1000:
        Extract dataset i
        Execute a function to calculate summary statistics for dataset i.
        Execute a function to make and save a graph for dataset i.
        Execute a function that applies multivariate analysis on dataset i.
End of loop
```

Each function is a small collection of commands acting on individual datasets. Each function works independently, unaffected by what happens elsewhere, and does only what it has been told to do. There is a mechanism in place to allow only the dataset into the function and to return information for this dataset. Once programmed, the function should work for any dataset. Program it once, and, if all goes according to plan, you never have to think about it again.

Just as a house can be designed to be built in different ways, your plan can take more than one approach. In the sketch above, we created a loop for *i* from 1 to 1000, which, in each iteration, extracts data and passes the data to a function. You can also do it the other way around:

```
Execute a function to calculate summary statistics for each dataset.
Execute a function to make and save a graph for each dataset.
Execute a function to apply multivariate analysis on each dataset.
```

Each function will contain a loop in which the data are extracted and subjected to a series of relevant commands. The building of the code depends entirely on personal programming style, length of the code, type of problem, computing time required, and so on.

Before addressing the creation of functions, we focus on loops.

6.2 Loops

If you are familiar with programming languages like FORTRAN, C, C++, or MATLAB,[3] you are likely to be familiar with loops. Although R has many tools for avoiding loops, there are situations where it is not possible. To illustrate a situation in which a loop saves considerable time, we use a dataset on begging behaviour of nestling barn owls. Roulin and Bersier (2007) looked at nestlings' response to the presence of the mother and the father. Using microphones inside, and a video camera outside, the nests, they sampled 27 nests, studying vocal begging behaviour when the parents bring prey. A full statistical analysis using mixed effects modelling is presented in Roulin and Bersier (2007) and also in Zuur et al. (2009).

For this example, we use "sibling negotiation," defined as the number of calls by the nestlings in the 30-second interval immediately prior to the arrival of a parent, divided by the number of nestlings. Data were collected between 21.30 hours and 05.30 hours on two consecutive nights. The variable `ArrivalTime` indicates the time at which a parent arrived at the perch with prey.

Suppose that you have been commissioned to write a report on these data and to produce a scatterplot of sibling negotiation versus arrival time for each nest, preferably in jpeg format. There are 27 nests, so you will need to produce,

[3] These are just different types of programming languages, similar to R.

and save, 27 graphs. This is not an uncommon type of task. We have been involved in similar undertakings (e.g., producing multiple contour plots for > 75 bird species in the North Sea). Keep in mind that they may ask you to do it all again with a different plotting character or a different title! Note that R has tools to plot 27 scatterplots in a single graph (we show this in Chapter 8), but assume that the customer has explicitly asked for 27 separate jpeg files. This is not something you will not want to do manually.

6.2.1 Be the Architect of Your Code

Before writing the code, you will need to plan and produce an architectural design outlining the steps in your task:

1. Import the data and familiarise yourself with the variable names, using the `read.table`, `names`, and `str` commands.
2. Extract the data of one nest and make a scatterplot of begging negotiation versus arrival time for this subset.
3. Add a figure title and proper labels along the *x*- and *y*-axes. The name of the nest should be in the main header.
4. Extract data from a second nest, and determine what modifications to the original graph are needed.
5. Determine how to save the graph to a jpeg file.
6. Write a loop to extract data for nest *i*, plot the data from nest *i*, and save the graph to a jpeg file with an easily recognized name.

   If you can implement this algorithm, you are a good architect!

6.2.2 Step 1: Importing the Data

The following code imports the data and shows the variable names and their status. There is nothing new here in terms of R code; the `read.table`, `names`, and `str` commands were discussed in Chapters 2 and 3.

```
> setwd("C:/RBook/")
> Owls <- read.table(file = "Owls.txt", header = TRUE)
> names(Owls)
[1] "Nest"               "FoodTreatment"
[3] "SexParent"          "ArrivalTime"
[5] "SiblingNegotiation" "BroodSize"
[7] "NegPerChick"
> str(Owls)
'data.frame':   599 obs. of  7 variables:
 $ Nest              : Factor w/ 27 levels ...
```

```
 $ FoodTreatment     : Factor w/ 2 levels ...
 $ SexParent         : Factor w/ 2 levels ...
 $ ArrivalTime       : num 22.2 22.4 22.5 22.6 ...
 $ SiblingNegotiation: int 4 0 2 2 2 2 18 4 18 0 ...
 $ BroodSize         : int 5 5 5 5 5 5 5 5 5 5 ...
 $ NegPerChick       : num 0.8 0 0.4 0.4 0.4 0.4 ...
```

The variables `Nest`, `FoodTreatment`, and `SexParent` are defined using alphanumerical values in the ascii file, and therefore R considers them (correctly) as factors (see the output of the `str` command for these variables).

6.2.3 Steps 2 and 3: Making the Scatterplot and Adding Labels

To extract the data from one nest, you first need to know the names of the nests. This can be done with the `unique` command

```
> unique(Owls$Nest)
 [1] AutavauxTV        Bochet        Champmartin
 [4] ChEsard           Chevroux      CorcellesFavres
 [7] Etrabloz          Forel         Franex
[10] GDLV              Gletterens    Henniez
[13] Jeuss             LesPlanches   Lucens
[16] Lully             Marnand       Moutet
[19] Murist            Oleyes        Payerne
[22] Rueyes            Seiry         SEvaz
[25] StAubin           Trey          Yvonnand
27 Levels: AutavauxTV Bochet Champmartin ... Yvonnand
```

There are 27 nests, and their names are given above. Extracting the data of one nest follows the code presented in Chapter 3:

```
> Owls.ATV <- Owls[Owls$Nest=="AutavauxTV", ]
```

Note the comma after `Owls$Nest = = "AutavauxTV"` to select rows of the data frame. We called the extracted data for this nest `Owls.ATV`, where ATV refers to the nest name. The procedure for making a scatterplot such as that needed to show arrival time versus negotiation behaviour for the data in `Owls.ATV` was discussed in Chapter 5. The code is as follows.

```
> Owls.ATV <- Owls[Owls$Nest == "AutavauxTV", ]
> plot(x = Owls.ATV$ArrivalTime,
       y = Owls.ATV$NegPerChick,
       xlab = "Arrival Time", main = "AutavauxTV"
       ylab = "Negotiation behaviour)
```

You will be plotting the variable `ArrivalTime` versus `NegPerChick` from the data frame `Owls.ATV`, hence the use of the $ sign. The resulting graph is presented in Fig. 6.1. So far, the procedure requires no new R code.

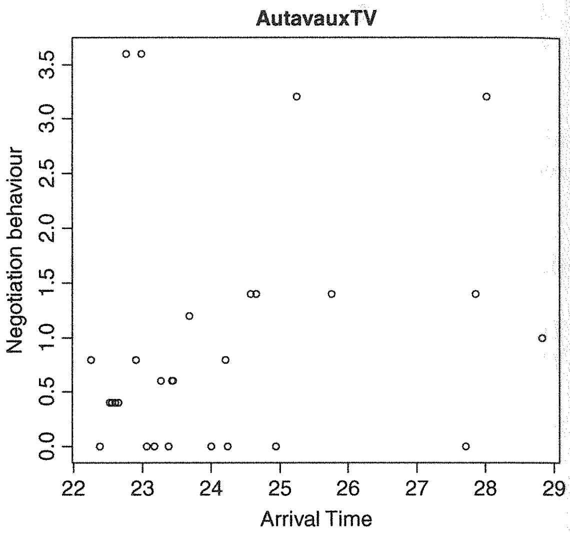


Fig. 6.1 Scatterplot of arrival time (*horizontal axis*) versus average negotiation behaviour per visit (*vertical axis*) for a single nest (AutavauxTV). Time is coded from 22 (22.00) to 29 (4.00). Measurements were conducted on two consecutive nights

6.2.4 Step 4: Designing General Code

To investigate the universality of the code, go through the same procedure for data from another nest. The code for the second nest requires only a small modification; where you entered `AutavauxTV`, you now need `Bochet`.

```
> Owls.Bot <- Owls[Owls$Nest == "Bochet", ]
> plot(x = Owls.Bot$ArrivalTime,
       y = Owls.Bot$NegPerChick,
       xlab = "Arrival Time",
       ylab = "Negotiation behaviour", main = "Bochet")
```

The graph is not shown here. Note that we stored the data from this particular nest in the data frame `Owls.Bot`, where "Bot" indicates "Bochet." If you were to make the same graph for another nest, you need only replace the main title and the name of the data frame and the actual data (the loop will do this for us).

The question is, in as much as you must do this another 25 times, how can you minimise the typing required? First, change the name of the data frame to something more abstract. Instead of `Owls.ATV` or `Owls.Bot`, we used `Owls.i`. The following construction does this.

```
> Owls.i <- Owls[Owls$Nest == "Bochet", ]
> plot(x = Owls.i$ArrivalTime,
       y = Owls.i$NegPerChick, xlab = "Arrival Time",
       ylab = "Negotiation behaviour", main = "Bochet")
```

Instead of a specific name for the extracted data, we used a name that can apply to any dataset and pass it on to the `plot` function. The resulting graph is not presented here. The name "Bochet" still appears at two places in the code, and they need to be changed each time you work with another dataset. To minimise typing effort (and the chance of mistakes), you can define a variable, `Nest.i`, containing the name of the nest, and use this for the selection of the data and the main header:

```
> Nest.i <- "Bochet"
> Owls.i <- Owls[Owls$Nest == Nest.i, ]
> plot(x = Owls.i$ArrivalTime, y = Owls.i$NegPerChick,
      xlab = "Arrival Time", main = Nest.i,
      ylab = "Negotiation behaviour")
```

In order to make a plot for another nest, you only need to change the nest name in the first line of code, and everything else will change accordingly.

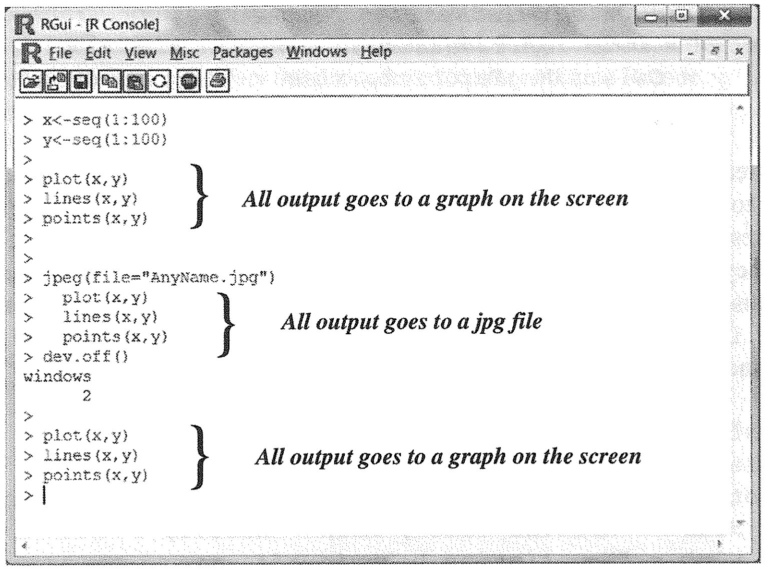
6.2.5 Step 5: Saving the Graph

You now need to save the graph to a jpeg file (see also the help file of the `jpeg` function):

1. Choose a file name. This can be anything, for example, `'' AnyName.jpg''`.
2. Open a jpeg file by typing `jpeg(file = '' AnyName.jpg'')`.
3. Use the `plot` command to make graphs. Because you typed the `jpeg` command, R will send all graphs to the jpeg file, and the graphic output will not appear on the screen.
4. Close the jpeg file by typing: `dev.off()`.

You can execute multiple graphing commands in Step 3 (e.g., `plot`, `lines`, `points`, `text`) and the results of each will go into the jpeg file, until R executes the `dev.off` (device off) command which closes the file. Any graphing command entered after the `dev.off` command will not go into the jpeg file, but to the screen again. This process is illustrated in Fig. 6.2.

At this point, you should consider where you want to save the file(s), as it is best to keep them separate from your R working directory. In Chapter 3 we discussed how to set the working directory with the `setwd` command. We set it to "C:/AllGraphs/" in this example, but you can easily modify this to your own choice.



```
> x<-seq(1:100)
> y<-seq(1:100)
>
> plot(x,y)
> lines(x,y)
> points(x,y)
>
>
> jpeg(file="AnyName.jpg")
>   plot(x,y)
>   lines(x,y)
>   points(x,y)
> dev.off()
windows
      2
>
> plot(x,y)
> lines(x,y)
> points(x,y)
> |
```

All output goes to a graph on the screen

All output goes to a jpg file

All output goes to a graph on the screen

Fig. 6.2 Summary of the jpeg and dev.off commands. The results of all graphing commands between the jpeg and dev.off commands are sent to a jpg file. The *x*- and *y*-coordinates were arbitrarily chosen

The final challenge is to create a file name that automatically changes when we change the name of the nest (the variable Nest.i). You will need a file name that consists of the nest name (e.g., Bochet) and the file extension jpg. To connect "Bochet" and ".jpg" with no separation between these two strings (i.e., "Bochet.jpg") use the paste command:

```
> paste(Nest.i, ".jpg", sep = "")
[1] "Bochet.jpg"
```

The output of the paste command is a character string that can be used as the file name. You can store it in a variable and use it in the jpeg command. We called the variable YourFileName in the code below, and R sends all graphic output created between the jpeg and dev.off commands to this file.

```
> setwd("C:/AllGraphs/")
> Nest.i <- "Bochet"
> Owls.i <- Owls[Owls$Nest == Nest.i, ]
> YourFileName <- paste(Nest.i, ".jpg", sep="")
> jpeg(file = YourFileName)
> plot(x = Owls.i$ArrivalTime, y = Owls.i$NegPerChick,
     xlab = "Arrival Time", main = Nest.i,
     ylab = "Negotiation behaviour")
> dev.off()
```

Once this code has been executed, you can open the file *Bochet.jpg* in your working directory with any graphic or photo editing package. The help file for the jpeg function contains further information on increasing the size and quality of the jpeg file. Alternative file formats are obtained with the functions bmp, png, tiff, postscript, pdf, and windows. See their help files for details.

6.2.6 Step 6: Constructing the Loop

You still have to modify the variable Nest.i 27 times, and, each time, copy and paste the code into R. Here is where Step 6 comes in, the loop. The syntax of the loop command in R is as follows.

```
for (i in 1 : 27) {
     do something
     do something
     do something
   }
```

"Do something" is not valid R syntax, hence the use of a box. Note that the commands must be between the two curly brackets { and }. We used 27 because there are 27 nests. In each iteration of the loop, the index *i* will take one of the values from 1 to 27. The "do something" represent orders to execute a specific command using the current value of *i*. Thus, you will need to enter into the loop the code for opening the jpeg file, making the plot, and closing the jpeg file for a particular nest. It is only a small extension of the code from Step 5.

On the first line of the code below, we determined the unique names of the nests. On the first line in the loop, we set Nest.i equal to the name of the *i*th nest. So, if *i* is 1, Nest.i is equal to ′′AutavauxTV′′; $i = 2$ means that Nest.i =′′Bochet′′; and, if *i* is 27, Nest.i equals′′Yvonnand′′ The rest of the code was discussed in earlier steps. If you run this code, your working directory will contain 27 jpeg files, exactly as planned.

```
> AllNests <- unique(Owls$Nest)
> for (i in 1:27){
  Nest.i <- AllNests[i]
  Owls.i <- Owls[Owls$Nest == Nest.i, ]
  YourFileName <- paste(Nest.i, ".jpg", sep = "")
  jpeg(file = YourFileName)
  plot(x = Owls.i$ArrivalTime, y = Owls.i$NegPerChick,
       xlab = "Arrival Time",
       ylab = "Negotiation behaviour", main = Nest.i)
  dev.off()
  }
```

Do Exercise 1 in Section 6.6. This is an exercise in creating loops, using a temperature dataset.

6.3 Functions

The principle of a *function* may be new to many readers. If you are not familiar with it, envision a function as a box with multiple holes on one side (for the input) and a single hole on the other side (for the output). The multiple holes can be used to introduce information into the box; the box will act as directed upon the information and feed the results out the single hole. When a function is running properly, we are not really interested in knowing how it obtains the results. We have already used the `loess` function in Chapter 5. The input consisted of two variables and the output was a list that contained, among other things, the fitted values. Other examples of existing functions are the `mean`, `sd`, `sapply`, and `tapply`, among others.

The underlying concept of a function is sketched in Fig. 6.3. The input of the function is a set of variables, A, B, and C, which can be vectors, matrices, data frames, or lists. It then carries out the programmed calculations and passes the information to the user.

The best way to learn how to use a function is by seeing some examples.

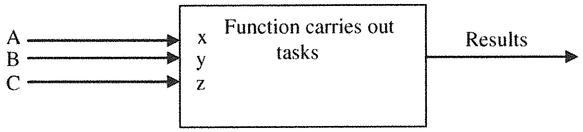


Fig. 6.3 Illustration of the principle of a function. A function allows for the input of multiple variables, carries out calculations, and passes the results to the user. According to the order in which the variables are entered, A, B, and C are called x, y, and z within the function. This is called positional matching

6.3.1 Zeros and NAs

Before executing a statistical analysis, it is important to locate and deal with any missing values, as they may present some difficulties. Certain techniques, such as linear regression, will remove any case (observation) containing a missing value. Variables with many zeros cause trouble as well, particularly in multivariate analysis. For example, do we say that dolphins and elephants are similar because they are both absent on the moon? For a discussion on double zeros in multivariate analysis, see Legendre and Legendre (1998). In univariate analysis, a response variable with many zeros can also be problematical (See the Zero Inflated Data chapter in Zuur et al., 2009).

We recommend creating a table that gives the number of missing values, and the number of zeros, per variable. A table showing the number of missing values (or zeros) per case is also advisable. The following demonstrates using R code to create the tables, but before continuing, we suggest that you do Exercise 2 in Section 6.6, as it guides you through the R code in this section.

Our example uses the vegetation data from Chapter 4. We imported the data with the `read.table` command, and used the `names` command to see the list of variables:

```
> setwd("C:/RBook/")
> Veg <- read.table(file = "Vegetation2.txt",
                    header = TRUE)
> names(Veg)
 [1] "TransectName" "Samples"      "Transect"
 [4] "Time"         "R"            "ROCK"
 [7] "LITTER"       "ML"           "BARESOIL"
[10] "FallPrec"     "SprPrec"      "SumPrec"
[13] "WinPrec"      "FallTmax"     "SprTmax"
[16] "SumTmax"      "WinTmax"      "FallTmin"
[19] "SprTmin"      "SumTmin"      "WinTmin"
[22] "PCTSAND"      "PCTSILT"      "PCTOrgC"
```

The first four variables contain transect name, transect number, and time of survey. The column labelled R contains species richness (the number of species) per observation. The remaining variables are covariates.

Suppose you want a function that takes as input a data frame that contains the data, and calculates the number of missing values in each variable. The syntax of such a function is

```
NAPerVariable <- function(X1) {
  D1 <- is.na(X1)
  colSums(D1)
}
```

If you type this code into a text editor and paste it into R, you will see that nothing happens. The code defines a function with the name `NAPerVariable`, but it does not execute the function. This is done with the command

```
> NAPerVariable(Veg[,5:24])
       R     ROCK   LITTER        ML  BARESOIL  FallPrec
       0        0        0         0         0         0
 SprPrec  SumPrec  WinPrec  FallTmax   SprTmax   SumTmax
       0        0        0         0         0         0
 WinTmax FallTmin  SprTmin   SumTmin   WinTmin   PCTSAND
       0        0        0         0         0         0
 PCTSILT  PCTOrgC
       0        0
```

We omitted the first four columns of the data frame `Veg`, as these contain the transect and time information. There appear to be no missing values in the listed variables. Take a closer look at what is going on inside the function. The first, and only, argument of the function is `X1`. We assume that the variables are in columns and the observations in rows. The command `is.na(X1)` creates a Boolean matrix of the same dimension as `X1`, with the value `TRUE` if the corresponding element of `X1` is a missing value and `FALSE` if not. The `colSums` function is an existing R function that takes the sum of the elements in each column (variable). Normally, `colSums` is applied to a data matrix with numbers, but if it is applied to a Boolean matrix, it converts a `TRUE` to 1, and a `FALSE` to 0. As a result, the output of `colSums(D1)` is the number of missing values per variable.

If you replace the `colSums` command with the `rowSums` command, the function gives the number of missing values per observation.

6.3.2 Technical Information

There are a few aspects of the function that we need to address: first, the names of the variables used inside the function. Note that we used `X1` and `D1`. You may wonder why the code inside the function runs at all, as `X1` seems to come out of the blue. The application here is called *positional matching*. The first and, in this case, only, argument in `NAPerVariable`, is a subset of the data frame `Veg`. Inside the function, these data are allocated to `X1`, because `X1` is the first variable in the argument of the function. Hence, `X1` contains columns 5 – 24 of the data frame `Veg`.

The principle of positional matching was illustrated in Fig. 6.1. The external variables A, B, and C are called *x*, *y*, and *z* within the function. R knows that *x* is A, because both are the first argument in the call to the function. We have already seen this type of action with the arguments in the `plot`, `lines`,and `loess` functions. The reason for changing the variable designations is that you should not use names within a function that also exist outside the function. If you make a programming mistake, for example, if you use `D1 <- is.na(X)` instead of `D1 <- is.na(X1)`, R will look first inside the function for the values of `X`. If it does not find this variable inside the function, it will look outside the function. If such a variable exists outside the function, R will happily use it without telling you. Instead of calculating the number of missing values in the variable `Veg`, it will show you the number of missing values in `X`, whatever `X` may be. The convention of using different, or new, names for the variables inside a function applies to all variables, matrices, and data frames used in the function.

A second important aspect of functions is the form in which the resulting information is returned to the user. FORTRAN and C++ users may assume that this is done via the arguments of the function, but this is not the case. It is the information coded for on the final line of the function that is returned. The function `NAPerVariable` has `colSums(D1)` on the last line, so this is the information provided. If you use

```
> H <- NAPerVariable(Veg[ , 4 : 24])
```

`H` will contain the number of missing values in vector format. If the final line of the function is a list, then `H` will be a list as well. In an example presented later in this chapter, we see that this is useful for taking back multiple variables (see also Chapter 3).

As always, you should document your code well. Add comments (with the # symbol) to the function, saying that the data must be in an "observation by variable" format, and that it calculate the number of missing values per column.

You should also ensure that the function will run for every possible dataset that you may enter into it in the future. Our function, for example, will give an error message if the input is a vector (one variable) instead of a matrix; `colSums` only works if the data contain multiple columns (or at least are a matrix). You need to document this, provide an understandable error message, or extend the function so that it will run properly if the input consists of a vector.

6.3.3 A Second Example: Zeros and NAs

The red king crab *Paralithodes camstchaticus* was introduced to the Barents Sea in the 1960 s and 1970 s from its native area in the North Pacific. The leech *Johanssonia arctica* deposits its eggs into the carapace of this crab. The leech is a vector for a trypanosome blood parasite of marine fish, including cod. Hemmingsen et al. (2005) examined a large number of cod for trypanosome infections during annual cruises along the coast of Finnmark in North Norway. We use their data here. The data included the presence or absence of the parasite in fish as well as the number of parasites per fish. Information on the length, weight, age, stage, sex, and location of the host fish was recorded. The familiar `read.table` and `names` functions are used to import the data and show the variable names:

```
> setwd("c:/RBook/")
> Parasite <- read.table(file = "CodParasite.txt",
                header = TRUE)
> names(Parasite)
[1] "Sample"     "Intensity"  "Prevalence" "Year"
[5] "Depth"      "Weight"     "Length"     "Sex"
[9] "Stage"      "Age"        "Area"
```

Because we already copied and pasted the function `NAPerVariable` into R in Section 6.3.1, there is no need to do this again. To obtain the number of missing values per variable, type

```
> NAPerVariable(Parasite)
Sample  Intensity Prevalence        Year        Depth
     0         57          0           0            0
Weight     Length        Sex       Stage          Age
     6          6          0           0            0
  Area
     0
```

There are 57 missing values in the variable Intensity, and 6 in each of the variables Length and Weight.

In a statistical analysis, we would model the number of parasites as a function of year and length or weight, sex, and location of host fish. This is typically done with generalised linear modelling for count data. Problems may occur if the response variable is zero inflated (too many zeros). Therefore, we need to determine how many zeros are in each variable, especially in Intensity. Our first attempt is the function

```
ZerosPerVariable <- function(X1)  {
  D1 = (X1 == 0)
  colSums(D1)
}
```

It is similar to the earlier function NAPerVariable, except that D1 is now a matrix with values TRUE if an element of X1 equals 1, and FALSE otherwise. To execute the function, use

```
> ZerosPerVariable(Parasite)
Sample  Intensity Prevalence        Year        Depth
     0         NA        654           0            0
Weight     Length        Sex       Stage          Age
    NA         NA         82          82           84
  Area
     0
```

There are 654 fish with no parasites, and 82 observations with a value of 0 for Sex. The fact that Sex and Stage have a certain number of observations equal to 0 is a matter of coding; these are nominal variables. So it is not a problem. There are NAs for the variables Intensity, Weight, and Length. This is because the colSums function gives NA as output if there is an NA anywhere in the variable. The help file of colSums (obtained by typing ?colSums) shows that the option na.rm = TRUE can be added. This leads to:

```
ZerosPerVariable <- function(X1)  {
  D1 = (X1 == 0)
  colSums(D1, na.rm = TRUE)
}
```

Missing values are now ignored because of the na.rm = TRUE option. To execute the new function, we use

```
> ZerosPerVariable(Parasite)
Sample  Intensity Prevalence        Year        Depth
     0        654        654           0            0
Weight     Length        Sex       Stage          Age
     0          0         82          82           84
  Area
     0
```

The output now shows no observations with weight or length equal to 0, and this makes sense. The fact that both Intensity and Prevalence have 654 zeros also makes sense; absence is coded as 0 in the variable Prevalence.

6.3.4 A Function with Multiple Arguments

In the previous section, we created two functions, one to determine the number of missing values per variable and another to find the number of zeros per variable. In this section, we combine them and tell the function to calculate the sum of the number of observations equal to zero or the number of observations equal to NA. The code for the new function is given below.

```
VariableInfo <- function(X1, Choice1)  {
   if (Choice1 == "Zeros"){ D1 = (X1 == 0)  }
   if (Choice1 == "NAs")  { D1 <- is.na(X1)}
   colSums(D1, na.rm = TRUE)
}
```

The function has two arguments: X1 and Choice1. As before, X1 should contain the data frame, and Choice1 is a variable that should contain either the value "Zeros" or "NAs." To execute the function, use

```
> VariableInfo(Parasite, "Zeros")
Sample  Intensity Prevalence        Year        Depth
     0        654        654           0            0
Weight     Length        Sex       Stage          Age
     0          0         82          82           84
  Area
     0
```

For the missing values, we can use

```
> VariableInfo(Parasite, "NAs")
Sample   Intensity Prevalence        Year       Depth
     0          57          0           0           0
Weight      Length        Sex       Stage         Age
     6           6          0           0           0
  Area
     0
```

As you can see, the output is the same as in the previous section. So, the function performs as we intended. We can also allocate the output of the function to a variable in order to store it.

```
> Results <- VariableInfo(Parasite, "Zeros")
```

If you now type `Results` into the console, you will get the same numbers as above. Figure 6.4 gives a schematic overview of the function up to this point. The function takes as input the data frame `Parasite` and the character string `"Zeros"`, and internally calls them `X1` and `Choice1`, respectively. The function then performs its calculations and the final result is stored in `D1`. Outside the function, the results are available as `Results`. Once everything is perfectly coded and bug free, you can forget about `X1`, `Choice1`, and `D1`, and what is going on inside the function; all that matters is the input and the results.

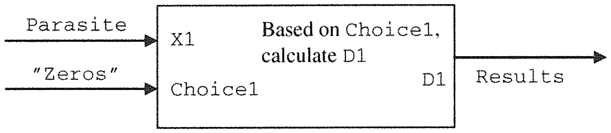


Fig. 6.4 Illustration of the function to calculate the number of zeros or the number of missing values of a dataset. Due to positional matching, the data frame `Parasite` and the argument "`Zeros`" are called `X1` and `Choice1` within the function

The only problem is that our current function is not robust against user error. Suppose you make a typing mistake, spelling "Zeros" as "zeroos":

```
> VariableInfo(Parasite, "zeroos")
Error in inherits(x, "data.frame"): object "D1" not
found
```

The variable `Choice1` is equal to the nonexistent "zeroos", and therefore none of the commands is executed. Hence, `D1` has no value, and an

error message is given on the last line. Another possible mistake is to forget to include a value for the second argument:

```
> VariableInfo(Parasite)
Error in VariableInfo(Parasite): argument "Choice1" is
missing, with no default
```

The variable `Choice1` has no value; the code crashes at the first line. The challenge in making a function is anticipating likely errors. Here, we have seen two silly (but common) mistakes, but the function can be written to provide a safety net for these types of errors.

6.3.5 *Foolproof Functions*

To make a foolproof function, you have to give it to hundreds of people and ask them all to try it and report any errors, or apply it on hundreds of datasets. Even then, you may be able to crash it. But there are a few common things you can do to make it as stable as possible.

6.3.5.1 Default Values for Variables in Function Arguments

The variable `Choice1` can be given a default value so that if you forget to enter a value for `Choice1`, the function will do the calculations for the default value. This is done with

```
VariableInfo <- function(X1, Choice1 = "Zeros") {
  if (Choice1 == "Zeros"){ D1 = (X1 == 0) }
  if (Choice1 == "NAs")  { D1 <- is.na(X1)}
  colSums(D1, na.rm = TRUE)
}
```

The default value is now "Zeros." Executing this function without specifying a value for `Choice1` produces valid output. To test it, type

```
> VariableInfo(Parasite)

Sample   Intensity Prevalence        Year       Depth
     0         654        654           0           0
Weight      Length        Sex       Stage         Age
     0           0         82          82          84
  Area
     0
```

To calculate the number of missing values, use as before:

```
> VariableInfo(Parasite, "NAs")
```

In this case, the second `if` command in the function is executed. The output of this command is not shown here. Don't forget to write a help file to document the default value!

6.3.5.2 Misspelling

We also want a function that executes the appropriate code, depending on the value of `Choice1`, and gives a warning message if `Choice1` is not equal to "Zeros" or "NAs". The following code does just that.

```
VariableInfo <- function(X1, Choice1 = "Zeros") {
   if (Choice1 == "Zeros"){ D1 = (X1 == 0) }
   if (Choice1 == "NAs")  { D1 <- is.na(X1)}
   if (Choice1 != "Zeros" & Choice1 != "NAs") {
       print("You made a typo")} else {
             colSums(D1, na.rm = TRUE)}
}
```

The third `if` statement will print a message if `Choice1` is not equal to either "Zeros" or "NAs". If one of these conditions is TRUE, then the `colSums` command is executed. To see it in action, type:

```
> VariableInfo(Parasite, "abracadabra")
```

```
[1] "You made a typo"
```

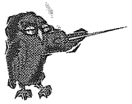
Note that internally the function is doing the following steps.

If A then blah blah
If B then blah blah
If C then blah blah, ELSE blah blah

A professional programmer will criticise this structure, as each `if` statement is inspected by R, even if the argument is "Zero" and only the first `if` statement is relevant. In this case, this does not matter, as there are only three `if` statements which won't take much time, but suppose there are 1000 `if` statements, only one of which needs to be executed. Inspecting the entire list is a waste of time. The help file for the `if` command, obtained by `?if`, provides some tools to address this situation. In the "See also" section, there is a link to the `ifelse` command. This can be used to replace the first two commands in the function:

```
> ifelse(Choice1 == "Zeros", D1 <- (X1 == 0),
                             D1 <- is.na(X1))
```

If the value of `Choice1` is equal to "Zeros", then the *D1* <-(*X1* == *0*) command is executed, and, in all other situations, it is *D1* <- *is.na*(*X1*). Not exactly what we had in mind, but it illustrates the range of options available in R. In Section 6.4, we demonstrate the use of the `if else` construction to avoid inspecting a large number of if statements.



Do Exercise 2 in Section 6.6 on creating a new categorical variable with the `ifelse` command, using the owl data.

6.4 More on Functions and the `if` Statement

In the following we discuss passing multiple arguments out of a function and the `ifelse` command, with the help of a multivariate dataset. The Dutch government institute RIKZ carried out a marine benthic sampling program in the summer of 2002. Data on approximately 75 marine benthic species were collected at 45 sites on nine beaches along the Dutch coastline. Further information on these data and results of statistical analyses such as linear regression, generalised additive modelling, and linear mixed effects modelling, can be found in Zuur et al. (2007, 2009).

The data matrix consists of 45 rows (sites) and 88 columns (75 species and 13 explanatory variables). You could apply multivariate analysis techniques to see which species co-occur, which sites are similar in species composition, and which environmental variables are driving the species abundances. However, before doing any of this, you may want to start simply, by calculating a diversity index and relating this index to the explanatory variables.

A diversity index means that, for each site, you will characterise the 75 species with a single value. There are different ways of doing this, and Magurran (2004) describes various diversity indices. We do not want to engage in a discussion of which is better. You only need to develop an R function that takes as input an observation-by-species matrix, potentially with missing values, and a variable that tells the function which diversity index to calculate. To keep it simple, we limit the code to three indices. Interested readers can extend this R function and add their own favourite diversity indices. The three indices we use are:

1. Total abundance per site.
2. Species richness, defined as the number of different species per site.
3. The Shannon index. This takes into account both the presence/absence nature of the data and the actual abundance. It is defined by

$$H_i = -\sum\nolimits_i^m p_{ij} \times \log_{10} p_{ij}$$

p_{ij} is calculated by

$$p_{ij} = \frac{Y_{ij}}{\sum_{j=1}^{n} Y_{ij}}$$

where p_{ij} is the proportion of a particular species j at site i, and m (in the first equation) is the total number of species. The total number of species is n.

6.4.1 Playing the Architect Again

Just as with the previous example presented in this chapter, begin by making a sketch of the tasks to be carried out.

1. Import the data and investigate what you have in terms of types of variables, variable names, dimension of the data, and so on.
2. Calculate total abundance for site 1. Repeat this for site 2. Automate this process, making the code as general as possible. Use elegant and efficient coding.
3. Calculate the different number of species for site 1. Repeat this process for site 2. Automate this process, and make the code as general as possible.
4. Do the same for the Shannon index.
5. Combine the code, and use an `if` statement to choose between the indices. Use elegant coding.
6. Put all the code in a function and allow the user to specify the data and the diversity index. The function should return the actual index and also indicate which diversity index was chosen (as a string).

In the following, we transform this sketch into fully working R code.

6.4.2 Step 1: Importing and Assessing the Data

Import the RIKZ data, separate the species data from the environmental data, and determine the size of the data with the following R code.

```
> Benthic <- read.table("C:/RBook/RIKZ.txt",
                        header = TRUE)
> Species <- Benthic[ , 2:76]
> n <- dim(Species)
> n
[1] 45 75
```

The first column in the data frame `Benthic` contains labels, columns 2–76 contain species data, and columns 77–86 are the explanatory variables. The species data are extracted and stored in the data frame `Species`. Its dimension is 45 rows and 75 columns, and these values are obtained and stored in `n` using the `dim` command. To save space, results of the `names` and `str` command are not shown here; all variables are coded numerically.

6.4.3 Step 2: Total Abundance per Site

Calculate the sum of all species at site 1 by using

```
> sum(Species[1, ], na.rm = TRUE)

[1] 143
```

The total number of species at site 1 is 143. The same can be done for site 2:

```
> sum(Species[2, ], na.rm = TRUE)

[1] 52
```

To avoid typing this command 45 times, construct a loop that calculates the sum of all species per site. Obviously, we need to store these values. The following code does this.

```
> TA <- vector(length = n[1])
> for (i in 1:n[1]){
    TA[i] <- sum(Species[i, ], na.rm = TRUE)
  }
```

The vector `TA` is of length 45 and contains the sum of all species per site:

```
> TA

 [1] 143  52  70 199 67 944 241 192 211 48 35
[12]   1  47  38  10  1  47  73   8  48  6 42
[23]  29   0  43  33 34  67  46   5   7  1  1
[34] 102 352   6  99 27  85   0  19  34 23  0
[45]  11
```

Three sites have no species at all, whereas at one site the total abundance is 944. Note that you must define `TA` as a vector of length 45 before constructing the loop or `TA[i]` will give an error message (see the code above). You also need to ensure that the index i in the loop is indeed between 1 and 45; `T[46]` is not defined. Instead of using `length = 45` in the vector command, we used length = n[1]; remember that the task was to make the code as general as possible. The loop is what we call the brute force approach, as more elegant programming, producing identical results, is given by:

```
> TA <- rowSums(Species, na.rm = TRUE)
> TA

 [1] 143  52 70 199 67 944 241 192 211 48 35
[12]   1  47 38  10  1  47  73   8  48  6 42
[23]  29   0 43  33 34  67  46   5   7  1  1
[34] 102 352  6  99 27  85   0  19  34 23  0
[45]  11
```

The rowSums command takes the sum for each row. Note that this requires only one line of coding and also involves less computing time (albeit for such a small dataset the difference is very small), and is preferable to the loop.

6.4.4 Step 3: Richness per Site

The number of species at site 1 is given by

```
> sum(Species[1, ] > 0, na.rm = TRUE)

[1] 11
```

There are 11 different species at site 1. Species[1,] > 0 creates a Boolean vector of length 75 with elements TRUE and FALSE. The function sum converts the value TRUE to 1, and FALSE to 0, and adding these values does the rest.

For site 2, use

```
> sum(Species[2, ] > 0, na.rm = TRUE)

[1] 10
```

To calculate the richness at each site, create a loop as for total abundance. First define a vector Richness of length 45, then execute a loop from 1 to 45. For each site, richness is determined and stored.

```
> Richness <- vector(length = n[1])
> for (i in 1:n[1]){
```

```
   Richness[i] <- sum(Species[i, ] > 0, na.rm = TRUE)
  }
> Richness

 [1] 11 10 13 11 10 8  9 8 19 17 6  1 4 3 3
[16]  1  3  3  1  4 3 22 6  0  6 5  4 1 6 4
[31]  2  1  1  3  4 3  5 7  5  0 7 11 3 0 2
```

The elegant approach uses the rowSums command and gives the same result:

```
> Richness <- rowSums(Species > 0, na.rm = TRUE)
> Richness

 [1] 11 10 13 11 10 8  9 8 19 17 6  1 4 3 3
[16]  1  3  3  1  4 3 22 6  0  6 5  4 1 6 4
[31]  2  1  1  3  4 3  5 7  5  0 7 11 3 0 2
```

6.4.5 Step 4: Shannon Index per Site

To calculate the Shannon index, we need only three lines of elegant R code that include the equations of the index:

```
> RS <- rowSums(Species, na.rm = TRUE)
> prop <- Species / RS
> H <- -rowSums(prop * log10(prop), na.rm = TRUE)
> H

 [1]  0.76190639  0.72097224  0.84673524
 [4]  0.53083926  0.74413939  0.12513164
 [7]  0.40192006  0.29160667  1.01888185
[10]  0.99664096  0.59084434  0.00000000
                    < Cut to reduce space>
```

We could have used code with a loop instead. The calculation can be done even faster with the function "diversity", which can be found in the vegan package in R. This package is not part of the base installation; to install it, see Chapter 1. Once installed, the following code can be used.

```
> library(vegan)
> H <- diversity(Species)
> H
```

```
        1         2         3         4         5
1.7543543 1.6600999 1.9496799 1.2223026 1.7134443
        6         7         8         9        10
0.2881262 0.9254551 0.6714492 2.3460622 2.2948506
       11        12        13        14        15
1.3604694 0.0000000 0.4511112 0.5939732 0.9433484
       16        17        18        19        20
0.0000000 0.7730166 0.1975696 0.0000000 0.8627246
                 < Cut to reduce space>
```

Note that the values are different. The diversity help file shows that this function uses the natural logarithmic transformation, whereas we used the logarithm with base 10. The diversity help file gives instructions for changing this when appropriate.

A limitation of using the vegan package is that this package must be installed on the computer of the user of your code.

6.4.6 Step 5: Combining Code

Enter the code for all three indices and use an if statement to select a particular index.

```
> Choice <- "Richness"
> if (Choice == "Richness") {
     Index <- rowSums(Species >0, na.rm = TRUE)}
> if (Choice == "Total Abundance") {
     Index <- rowSums(Species, na.rm = TRUE)  }
> if (Choice=="Shannon")  {
     RS <- rowSums(Species, na.rm = TRUE)
     prop <- Species / RS
     Index <- -rowSums(prop*log10(prop), na.rm = TRUE)}
```

Just change the value of Choice to'' Total Abundance'' or" Shannon'' to calculate the other indices.

6.4.7 Step 6: Putting the Code into a Function

You can now combine all the code into one function and ensure that the appropriate index is calculated and returned to the user. The following code does this.

```
Index.function <- function(Spec, Choice1){
  if (Choice1 == "Richness")  {
```

```
     Index <- rowSums(Spec > 0, na.rm = TRUE)}
  if (Choice1 == "Total Abundance")  {
     Index <- rowSums(Spec, na.rm = TRUE)  }
  if (Choice1 == "Shannon") {
     RS <- rowSums(Spec, na.rm = TRUE)
     prop <- Spec / RS
     Index <- -rowSums(prop * log10(prop),
                       na.rm = TRUE)}
  list(Index = Index, MyChoice = Choice1)
  }
```

The if statement ensures that only one index is calculated. For small datasets, you could calculate them all, but for larger datasets this is not good practice. Before executing the code, it may be wise to ensure that none of the variables within the function also exists outside the function. If they do, remove them with the rm command (see Chapter 1), or quit and restart R. We renamed all input variables so that no duplication of variable names is possible. In order to execute the function, copy the code for the function, paste it into the console, and type the command:

```
> Index.function(Species, "Shannon")

$Index

 [1] 0.76190639 0.72097224 0.84673524 0.53083926
 [5] 0.74413939 0.12513164 0.40192006 0.29160667
 [9] 1.01888185 0.99664096 0.59084434 0.00000000
[13] 0.19591509 0.25795928 0.40969100 0.00000000
[17] 0.33571686 0.08580337 0.00000000 0.37467654
[21] 0.37677792 1.23972435 0.62665477 0.00000000
[25] 0.35252466 0.39057516 0.38359186 0.00000000
[29] 0.58227815 0.57855801 0.17811125 0.00000000
[33] 0.00000000 0.12082909 0.08488495 0.43924729
[37] 0.56065567 0.73993117 0.20525195 0.00000000
[41] 0.65737571 0.75199627 0.45767851 0.00000000
[45] 0.25447599

$MyChoice

[1] "Shannon"
```

Note that the function returns information from of the final command, which in this case is a list command. Recall from Chapter 2 that a list allows us to combine data of different dimensions, in this case a variable with 45 values and also the selected index.

Is this function perfect? The answer is no, as can be verified by typing

```
> Index.function(Species, "total abundance")
```

The error message produced by R is

```
Error in Index.function(Species, "total abundance"):
   object "Index" not found
```

Note that we made a typing error in not capitalizing “total abundance”. In the previous section, we discussed how to avoid such errors. We extend the function so that it inspects all `if` statements and, if none of them is executed, gives a warning message. We can use the `if else` command for this.

```
Index.function <- function(Spec,Choice1){
  if (Choice1 == "Richness") {
    Index <- rowSums(Spec > 0, na.rm = TRUE) } else
  if (Choice1 == "Total Abundance") {
    Index <- rowSums(Spec, na.rm = TRUE) } else
  if (Choice1 == "Shannon") {
    RS <- rowSums(Spec, na.rm = TRUE)
    prop <- Spec / RS
    Index <- -rowSums(prop*log(prop),na.rm=TRUE)} else {
       print("Check your choice")
       Index <- NA }
  list(Index = Index, MyChoice = Choice1)}
```

R will look at the first `if` command, and, if the argument is `FALSE`, it will go to the second `if` statement, and so on. If the variable `Choice1` is not equal to “Richness”, “Total Abundance”, or “Shannon”, the function will execute the command,

```
print("Check your choice")
Index <- NA
```

You can replace the text inside the `print` command with anything appropriate. It is also possible to use the `stop` command to halt R. This is useful if the function is part of a larger calculation process, for example, a bootstrap procedure. See the help files on `stop`, `break`, `geterrmessage`, or `warning`. These will help you to create specific actions to deal with unexpected errors in your code.

Table 6.1 R functions introduced in this chapter

Function	Purpose	Example
`jpeg`	Opens a jpg file	`jpeg(file = "AnyName.jpg")`
`dev.off`	Closes the jpg file	`dev.off()`
`function`	Makes a function	`z <- function(x, y){ }`
`paste`	Concatenates variables as characters	`paste("a", "b", sep = " ")`
`if`	Conditional statement	`if (a) { x<-1 }`
`ifelse`	Conditional statement	`ifelse(a, x<-1, x<-2)`
`if elseif`	Conditional statement	`if (a) { x<-1 } elseif (b) { x<-2 }`

6.5 Which R Functions Did We Learn?

Table 6.1 shows the R functions that were introduced in this chapter.

6.6 Exercises

Exercise 1. Using a loop to plot temperature per location.
In Section 6.2, sibling negotiation behaviour was plotted versus arrival time for each nest in the owl data. A graph for each nest was created and saved as a jpg file. Do the same for the temperature data; see Exercise 4.1 for details. The file *temperature.xls* contains temperature observations made at 31 locations (denoted as stations in the spreadsheet) along the Dutch coastline. Plot the temperature data versus time for each station, and save the graph as a jpg file.

Exercise 2. Using the `ifelse` command for the owl data.
The owl data were sampled on two consecutive nights. If you select the data from one nest, the observations will cover both nights. The two nights differed as to the feeding regime (satiated or deprived). To see observations from a single night, select all observations from a particular nest and food treatment. Use the `ifelse` and `paste` functions to make a new categorical variable that defines the observations from a single night at a particular nest. Try rerunning the code from Exercise 1 to make a graph of sibling negotiation versus arrival time for observations of the same nest and night.

Exercise 3. Using the `function` and `if` commands with the benthic dataset.
In this exercise we provide the steps for the function that was presented in Section 6.4: the calculation of diversity indices. Read the introductory text in Section 6.4 on diversity indices. Import the benthic data and extract columns 2–76; these are the species.

Calculate total abundance at site 1. Calculate total abundance at site 2. Calculate total abundance at site 3. Calculate the total abundance at site 45. Find a function that can do this in one step (sum per row). Brute force may work as well (`loop`), but is less elegant.

Calculate the total number of *different* species in site 1 (species richness). Calculate species richness for site 2. Do the same for sites 3 and 45. Find a function that can do this in one step.

Create a function using the code for all the diversity indices. Make sure that the user can choose which index is calculated. Ensure that the code can deal with missing values.

If you are brave, add the Shannon index. Apply the same function to the vegetation data.

Chapter 7
Graphing Tools

Chapter 5, the `plot` function was introduced. We demonstrated elementary scatterplots, modifying plotting characters, and adding *x*- and *y*-labels and a main title. In this chapter, we introduce more graphing tools. Not all of them are among our favourites. For example, we have never used pie charts or bar charts. However, these graphs seem to be on the shortlist of so many scientists that we find it necessary to include them in this book. They are discussed in Sections 7.1 and 7.2. Tools to detect outliers—the boxplot and Cleveland dotplot—are presented in Sections 7.3 and 7.4, respectively. We also demonstrate graphs illustrating the mean with lines added to represent the standard error. Scatterplots are further discussed in Section 7.5. Multipanel scatterplots are discussed in Sections 7.6 and 7.7, and advanced tools to display multiple graphs in a single window are presented in Section 7.8.

7.1 The Pie Chart

7.1.1 Pie Chart Showing Avian Influenza Data

We demonstrate the pie chart using the avian influenza dataset from Exercise 1 in Section 3.7. Recall that the data represent the numbers of confirmed human cases of Avian Influenza A/(H5N1) reported to the World Health Organization (WHO). The data for several countries were taken from the WHO website at www.who.int and are reproduced only for educational purposes. We exported the data in the Excel file, *BidFlu.xls*, to a tab-separated ascii file with the name *Birdflucases.txt*. The following code imports the data and presents the usual information.

```
> setwd("C:/RBook/")
> BFCases <- read.table(file = "Birdflucases.txt",
                       header = TRUE)
> names(BFCases)
 [1] "Year"       "Azerbaijan"  "Bangladesh"
 [4] "Cambodia"   "China"       "Djibouti"
```

A.F. Zuur et al., *A Beginner's Guide to R*, Use R,
DOI 10.1007/978-0-387-93837-0_7, © Springer Science+Business Media, LLC 2009