Appendix B

Computing in R

B.1 Downloading and installing R and Stan

We do our computing in the open-source package R, a command-based statistical software environment that you can download and operate on your own computer, using RStudio, a free graphical user interface for R. We fit Bayesian regressions in `rstanarm`, an R package that calls Stan, an open-source program written in C++. The `rstanarm` package includes a library of already compiled Stan models for fitting linear and logistic regression, generalized linear models, and a selection of other models that can be called using `stan_glm()` and other functions. Stan itself is more general, allowing the user to program and fit arbitrary Bayesian models.

R and RStudio

To set up R, go to `http://www.r-project.org/` and click on the "download R" link. This will take you to a list of mirror sites. Choose any of these. Now click on the link under "Download and Install R" at the top of the page for your operating system (Linux, Mac, or Windows) and download the binaries corresponding to your system. Follow all the instructions. Default settings should be fine.

Go to the home of RStudio, `http://www.rstudio.com`, click on "Download RStudio," click on "Download RStudio Desktop," and click on the installer for your platform (Windows, Mac, etc.) Then a download will occur.

When the download is done, click on the RStudio icon to start an R session.

To check that R is working, go to the Console window within RStudio. There should be a ">" prompt. Type `2+5` and hit Enter. You should get `[1] 7`. From now on, when we say "type" _____, we mean type _____ into the R console and hit Enter.

You will also want to install some R *packages*, in particular, `foreign` (which allows you to read in files formatted for various other statistics packages, including Stata), `ggplot2` (for building graphs), `knitr` (which allows you to process certain R documentation), `arm` (which has convenient functions for working with some regression models), `rstanarm` (which has functions for fitting Bayesian regression models using simulation), `rstan` (which allows you to fit models more general models in Stan), `bayesplot` (which has functions for model and inference checking), `loo` (which implements fast leave-one-out cross-validation), and `rprojroot` (which has been used in the code for this book to make it easier to work with many folders). Some of the example codes use also other packages which you can see in the beginning of each code file. You can install these packages from RStudio by clicking on the Tools tab and then on Install packages and then entering the names of the packages and clicking Install. When you want to use a package, you load it during your R session as needed, for example by typing `library("foreign")` or `library("arm")`.

Stan and rstanarm

If your only use for Stan is to fit the regression models in this book, it will be enough to install `arm` and `rstanarm` as discussed above, and then begin any R session with,

R code
```
library("arm")
library("rstanarm")
options(mc.cores = parallel::detectCores())
```

This last line allows Stan to be run in parallel on a multiple-core machines. We almost always do our computing by writing scripts, rather than simply typing commands into the R console window; thus, we recommend simply typing the above two lines at the beginning of any of your R scripts that include calls to `stan_glm()`.

For more flexible Bayesian modeling you will need to use Stan itself, for which downloads, documentation, and other information are available at `http://www.mc-stan.org/`. Follow the instructions to set up `rstan`, the R interface to Stan. This will automatically install Stan itself on your computer, which in turn requires a C++ compiler; again, all the necessary instructions are at the rstan set-up page. In any R session where you want to use Stan, start with the sequence,

R code
```
library("rstan")
options(mc.cores = parallel::detectCores())
rstan_options(auto_write = TRUE)
```

This line tells R to allow compiled Stan programs to be saved in the R working directory.

Examples to get started are in the `rstan` and `rstanarm` documentation.

B.2 The basics

Computing is central to modern statistics at all levels, from basic to advanced. If you already know how to program, great. If not, consider this a start.

Try a few things, typing these one line at a time and looking at the results on the console:

R code
```
1/3
sqrt(2)
curve(x^2 + 5, from=-2, to=2)
```

These will return, respectively, `0.3333333`, `1.414214`, and a new graphics window plotting the curve $y = x^2 + 5$.

Finally, quit your R session by closing the RStudio window.

Calling functions and getting help

Open R and play around, using the assignment function ("`<-`"). To start, type the following lines into your script.R file and copy-and-paste them into the R window:

R code
```
a <- 3
print(a)
b <- 10
print(b)
a + b
a*b
exp(a)
10^a
log(b)
log10(b)
a^b
round(3.435, 0)
round(3.435, 1)
round(3.435, 2)
```

R is based on *functions*, which include mathematical operations (`exp()`, `log()`, `sqrt()`, and so forth) and lots of other routines (`print()`, `round()`, ...).

The function `c()` combines things together into a vector. For example, type `c(4,10,-1,2.4)` in the R console or type the following:

```
x <- c(4,10,-1,2.4)                                    R code
print(x)
```

The function `seq()` creates an equally-spaced sequence of numbers; for example, `seq(4,54,10)` returns the sequence from 4, 14, 24, 34, 44, 54. The `seq()` function works with non-integers as well: try `seq(0,1,0.1)` or `seq(2,-5,-0.4)`. For integers, `a:b` is shorthand for `seq(a,b,1)` if `b` $>$ `a`, or `seq(b,a,-1)` if `b` $<$ `a`. Let's try a few more commands:

```
c(1, 3, 5)                                             R code
1:5
c(1:5, 1, 3, 5)
c(1:5, 10:20)
seq(2, 10, 2)
seq(1,9,2)
```

You can get help on any function using "?" in R. For example, type `?seq`. This should open a window with a help file for `seq()`. R help files typically have more information than you'll know what to do with, but if you scroll to the bottom of the page you'll find some examples that you can cut and paste into your console.

Whenever you are trying out a new function, we recommend using "?" to view the help file and running the examples at the bottom to see what happens.

Sampling and random numbers

Here's how to get a random number, uniformly distributed between 0 and 100:

```
runif(1, 0, 100)                                       R code
```

And now 50 more random numbers:

```
runif(50, 0, 100)                                      R code
```

Suppose we want to pick one of three colors with equal probability:

```
color <- c("blue", "red", "green")                     R code
sample(color, 1)
```

Suppose we want to sample with unequal probabilities:

```
color <- c("blue", "red", "green")                     R code
p <- c(0.5, 0.3, 0.2)
sample(color, 1, prob=p)
```

Or we can do it all in one line, which is more compact but less readable:

```
sample(c("blue","red","green"), 1, prob=c(0.5,0.3,0.2))   R code
```

Data types

Numeric data. In R, numbers are stored as *numeric* data. This includes many of the examples above as well as special constants such as `pi`.

Big and small numbers. R recognizes scientific notation. A million can be typed in as `1000000` or `1e6`, but not as `1,000,000`. (R is particular about certain things. Capitalization matters, "`,`" doesn't belong in numbers, and spaces usually aren't important.) Scientific notation also works for small numbers: `1e-6` is `0.000001` and `4.3e-6` is `0.0000043`.

Infinity. Type these into R, one line at a time, and see what happens:

R code
```
 1/0
-1/0
 exp(1000)
 exp(-1000)
 1/Inf
 Inf + Inf
-Inf - Inf
 0/0
 Inf - Inf
```

Those last two operations return `NaN` (Not a Number); type `?Inf` for more on the topic. In general we try to avoid working with infinity but it is convenient to have `Inf` for those times when we accidentally divide by 0 or perform some other illegal mathematical operation.

Missing data. In R, `NA` is a special keyword that represents missing data. For more information, type `?NA`. Try these commands in R:

R code
```
NA
2 + NA
NA - NA
NA / NA
NA * NA
c(NA, NA, NA)
c(1, NA, 3)
10 * c(1, NA, 3)
NA / 0
NA + Inf
is.na(NA)
is.na(c(1, NA, 3))
```

The `is.na()` function tests whether or not the argument is `NA`. The last line operates on each element of the vector and returns a vector with three values that indicate whether the corresponding input is NA.

Character strings. Let's sample a random color and a random number and put them together:

R code
```
color <- sample(c("blue","red","green"), 1, prob=c(0.5,0.3,0.2))
number <- runif(1, 0, 100)
paste(color, number)
```

Here's something prettier:

R code
```
paste(color, round(number,0))
```

`TRUE`, `FALSE`, *and* `ifelse`

Try typing these:

R code
```
2 + 3 == 4
2 + 3 == 5
1 < 2
2 < 1
```

In R, the expressions `==`, `<`, `>` are *comparisons* and return a logical value, `TRUE` or `FALSE` as appropriate. Other comparisons include `<=` (less than or equal), `>=` (greater than or equal), and `!=` (not equal).

Comparisons can be used in combination with the `ifelse()` function. The first argument takes a logical statement, the second argument is an expression to be evaluated if the statement is true, and the third argument is evaluated if the statement is false. Suppose we want to pick a random number between 0 and 100 and then choose the color red if the number is below 30 or blue otherwise:

R code
```
number <- runif(1, 0, 100)
color <- ifelse(number<30, "red", "blue")
```

Loops

A key aspect of computer programming is *looping*—that is, setting up a series of commands to be performed over and over. Start by trying out the simplest possible loop:

R code
```
for (i in 1:10){
  print("hello")
}
```

Or:

R code
```
for (i in 1:10){
  print(i)
}
```

Or:

R code
```
for (i in 1:10){
  print(paste("hello", i))
}
```

The curly braces define what is repeated in the loop. The spaces and line breaks are not necessary—one could just as well do `for(i in 1:10)print(paste("hello",i))`—but they improve readability.

Here's a loop of random colors:

R code
```
for (i in 1:10){
  number <- runif(1, 0, 100)
  color <- ifelse(number<30, "red", "blue")
  print(color)
}
```

B.3 Reading, writing, and looking at data

Your working directory

Choose a *working directory* on your computer where you will do your R work. Suppose your working directory is `c:/myfiles/stat/`. Then you should put all your data files in this directory, and all the files and graphs you save in R will appear here too. To set your working directory in RStudio, click on the Session tab and then on Set Working Directory and then on Choose Directory and then navigate from there.

RStudio has several subwindows: a text editor, the R console, a graphics window, and a help window. It's generally best to type your commands into the RStudio text editor, select the lines you want to run, and run them by pressing Ctrl-Enter. When your session is over, you can save the contents of the text editor into a plain-text file with a name such as `todays_work.R` that you can save in your working directory.

Now go to the R console and type `getwd()`. This shows your current R working directory.

Change your working directory by typing `setwd("c:/myfiles/stat/")`, or whatever you would like to use. In RStudio you can also choose the working directory using menu `Session -> Set Working Directory`.

Then type `getwd()` in the R console. This should return your working directory (for example, `c:/myfiles/stat/`).

The code for the book uses `rprojroot` package, which makes it easy to run code from different folders without need to change the working directory to a specific folder. It is sufficient to set the working directory to the main demo folder or any of the subfolders.

Reading data

Let's read some data into R. The file `heads.csv` has data from a coin-flipping experiment done in a previous class. Each student flipped a coin 10 times and we have a count of the number of students who saw exactly 0, 1, 2, . . . , 10 heads. The data file is in the directory `Coins` from the files at the website `http://www.stat.columbia.edu/~gelman/regression/`. Start by going to this location, finding the directory, downloading the file, and saving it as `heads.csv` in your working directory (for example, `c:/myfiles/stat/`).

Now read the file into R:

R code
```
heads <- read.csv("heads.csv")
```

Typing the name of any object in R displays the object itself. So type `heads` and look at what comes out.

What if you have tabular data separated by spaces and tabs, rather than columns? For example, `mile.txt` from the folder `Mile`, again reachable from `http://www.stat.columbia.edu/~gelman/regression/`. You just use the `read.table()` function:

R code
```
mile <- read.table("mile.txt", header=TRUE)
mile[1:5,]
```

The `header=TRUE` argument is appropriate here because the first line of the file mile.txt is a "header," that is, a list of column names. If the file had just data with no header, we would simply call `read.table("mile.txt")` with no header argument.

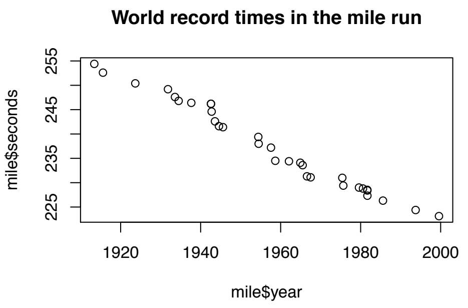
Writing data

You can save data into a file using `write` instead of `read`. For example, to write the R object `heads` into a comma-separated file `output1.csv`, we would type `write.csv(heads,"output1.csv")`. To write it into a space-separated file output2.txt, it's just `write.table(heads,"output2.txt")`.

Examining data

At this point, we should have two variables in our R environment, `heads` and `mile`. We can see what we have in our session by clicking on the Environment tab in the RStudio window.

Data frames, vectors, and subscripting. Most of the functions used to read data return a data structure called a *data frame*. You can see this by typing `class(heads)`. Each column of a data frame is a vector. We can access the first column of `heads` by typing `heads[,1]`. Data frames are indexed using two vectors inside "`[`" and "`]`"; the two vectors are separated by a comma. The first vector indicates which rows you are interested in and the second vector indicates what columns you are interested in. For example, `heads[6,1]` shows the number of heads observed and `heads[6,2]` shows the number of students that observed that number of heads. Leaving it blank is shorthand for including all. Try:



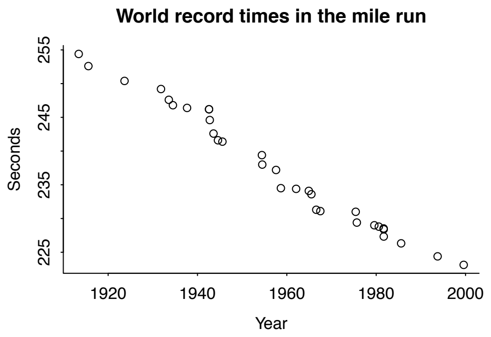


Figure B.1 *World record times (in minutes) in the mile run since 1900. The left plot was made with the basic function call,* `plot(mile$year, mile$record, main="World record times in the mile run")`. *The right plot was made with more formatting:* `par(mar=c(3,3,3,1), mgp=c(2,.5,0), tck=-.01); plot(mile$year, mile$record, bty="l", main="World record times in the mile run", xlab="Year", ylab="Seconds")`.

R code
```
heads[6,]
heads[1:3,]
heads[,1]
heads[,1:2]
heads[,]
```

To find the number of columns in a data frame, use the function `length()`. To find the number of rows, use `nrow()`. We can also find the names of the columns by using `names()`. Try these:

R code
```
length(heads)
nrow(heads)
names(heads)
```

B.4 Making graphs

Graphing data

Scatterplots. A scatterplot shows the relation between two variables. The data frame called `mile` in the folder `Mile` contains the world record times in the mile run since 1900 as four columns, `yr`, `month`, `min`, and `sec`. For convenience we create the following derived quantities in R:

R code
```
mile$year <- mile$yr + mile$month/12
mile$seconds <- mile$min*60 + mile$sec
```

Figure B.1 plots the world record time (in seconds) against time. We can create scatterplots in R using `plot`. Here is the code to make the basic graph:

R code
```
plot(mile$year, mile$seconds, main="World record times in the mile run")
```

And here is a slightly prettier version:

R code
```
par(mar=c(3,3,3,1), mgp=c(2,.5,0), tck=-.01)
plot(mile$year, mile$seconds, bty="l",
     main="World record times in the mile run", xlab="Year", ylab="Seconds")
```

The `par` function sets graphical parameters, in this case reducing the blank border around the graph, placing the labels closer to the axes, and reducing the size of the tick marks, compared to the default settings in R. In addition, in the call to `plot`, we have set the box type to `l`, which makes an “L-shaped” box for the graph rather than fully enclosing it.

We want to focus on the basics, so for the rest of this section we will show simple `plot` calls that won't make such pretty graphs. But we thought it woud be helpful to show one example of a pretty graph, hence the code just shown above. The folder `Mile` includes also an example of making a pretty graph using the `ggplot2` package.

Fitting a line to data. We can fit a regression line predicting world record time from the date as follows:

R code
```
fit <- stan_glm(seconds ~ year, data=mile)
```

R code
```
print(fit)
```

Here is the result:

R output
```
stan_glm
 family:       gaussian [identity]
 formula:      seconds ~ year
 observations: 32
 predictors:   2
------
            Median MAD_SD
(Intercept) 1006.1   23.3
year          -0.4    0.0

Auxiliary parameter(s):
      Median MAD_SD
sigma 1.4    0.2
```

You'll learn later how to interpret all these results. All that you need to know now is that the estimated coefficients are 1006.1 and -0.4; that is, the fitted regression line is $y = 1006.1 - 0.4\text{year}$. It will help to have more significant digits on this slope, so we type `print(fit, digits=2)` to get this:

R output
```
            Median  MAD_SD
(Intercept) 1006.15   23.33
year          -0.39    0.01

Auxiliary parameter(s):
      Median MAD_SD
sigma 1.42   0.19
```

The estimated line is $y = 1006.15 - 0.39\text{year}$.

We can add the straight line to the scatterplot by adding the following line after the call to `plot`:

R code
```
curve(1006.14 - 0.39*x, add=TRUE)
```

The first argument is the equation of the line as a function of x. The second argument, `add=TRUE`, tells R to draw the line onto the existing scatterplot.

And we can graph this line by itself using the following R code:

R code
```
curve(1006.15 - 0.39*x, from=min(mile$year), to=max(mile$year))
```

The `from` and `to` arguments specify the range of values of x over which the curve is plotted. The result is displayed in Figure B.2.

Multiple graphs on a page

Visualizations can be much more powerful using *small multiples*: repeated graphs on a similar theme. There are various ways to put multiple graphs on a page in R; one way uses the `par` function with its `mfrow` option, which tells R to lay out graphs in a grid, row by row.

We illustrate in Figure B.3 with a simple example plotting random numbers:

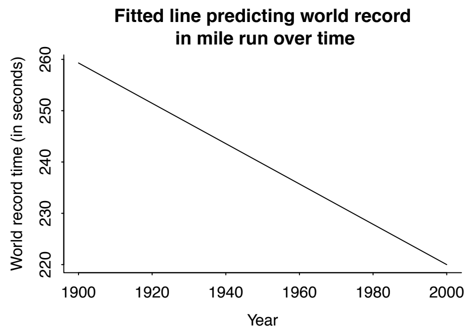


Figure B.2 *Fitted line predicting world record in the mile run given year (data shown in Figure B.1), plotted using the code,* `curve(1006.15 - 0.39*x, from=min(mile$year), to=max(mile$year))`.

R code

```
par(mfrow=c(5,4))
for (i in 1:5){
  for (j in 1:4){
    x <- rnorm(10)
    y <- rnorm(10)
    plot(x,y)
  }
}
```

The actual code we used to make the graphs is more complicated because we included code to label the graphs, put them on a common scale, and size them to better fit on the page, but the above code gives the basic idea.

B.5 Working with messy data

Reading in survey data, one question at a time

Data on the heights, weights, and incomes of a random sample of Americans are available from the Work, Family, and Well-Being survey conducted by Catherine Ross in 1990. We downloaded the data file, `06666-0001-Data.txt`, and the codebook `06666-0001-Codebook.txt` from the Inter-university Consortium for Political and Social Research. Information on the survey is at `http://dx.doi.org/10.3886/ICPSR06666` and can be downloaded if you create an account with the ICPSR.

We saved the files under the names `wfw90.dat` and `wfwcodebook.txt` in the directory `HeightWeight`.

Figure B.4 shows the first ten lines of the data, and Figure B.5 shows the relevant portion of the codebook. Our first step is to save the data file `wfwcodebook.txt` in our working directory. We then want to extract the responses to the questions of interest. To do this we first create a simple function, to read columns of data, making use of R's function `read.fwf` (read in fixed width format).

Copy the following into the R console and then you will be able to use our function for reading one variable at a time from the survey. The following code is a bit tricky so you're not expected to understand it; you can just copy it in and use it.

R code

```
read.columns <- function (filename, columns) {
  start <- min(columns)
  length <- max(columns) - start + 1
  if (start==1)
    return(read.fwf(filename, widths=length))
```

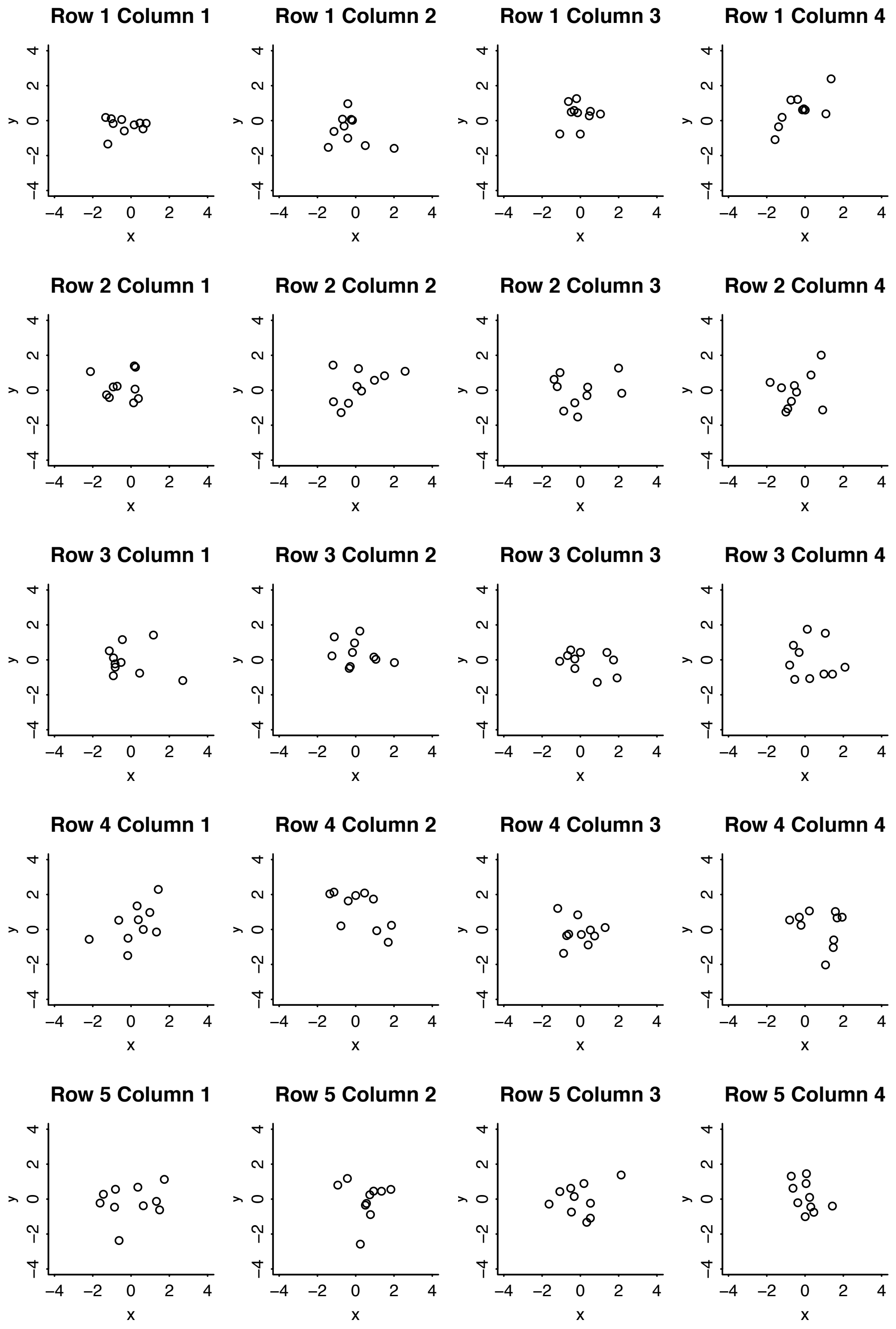


Figure B.3 *Example of a grid of graphs of random numbers produced in R. Each graph plots 10 pairs of numbers randomly sampled from the 2-dimensional normal distribution, and the display has been formatted to make 20 plots visible on a single page with common scales on the x and y-axes and customized plot titles.*

```
100022  31659123     121222113121432 22  2 3 411179797979797 1  4 503100100...
100081  486 2122     111222141122221222  2 1 997979797979797 1  4  01 25 25...
100091   1371123     1232122111113111314 1 0                          30100...
100101  15684222     133122121113232 22  1 0                          10 40...
100111  25371122     122222111111421222  2 2 4 6979797979797 1  2 853 30 95...
100202   2389013     1111221412   22 314 2 0                         100100...
100281   7884021     2232132422   42 22  2 0                          80 60...
100351  15684221     233223242112212 32  2 0                          75100...
100571  88341221     243233321113452 12  2 0                          90 98...
100641  15684223     122112211113432 22  2 0                         100 75...
```

Figure B.4 *First ten lines of the file* `wfw90.dat`*, which has data from the Work, Family, and Well-Being survey.*

```
    HEIGHT     144-146   F3.0     Q.46 HEIGHT IN INCHES
    WEIGHT     147-149   F3.0     Q.47 WEIGHT
. . .
    EARN1      203-208   F6.0     Q.61  PERSONAL INCOME - EXACT AMOUNT
    EARN2      209-210   F2.0     Q.61  PERSONAL INCOME - APPROXIMATION
    SEX        219       F1.0     Q.63  GENDER OF RESPONDENT
. . .
    HEIGHT
    46. What is your height without shoes on?
        __________ ft.  __________in.
    WEIGHT
    47. What is your weight without clothing?
        __________ lbs.
. . .
    61a. During 1989, what was your personal income from your own wages,
    salary, or other sources, before taxes?
    EARN1
    $ __________--> (SKIP TO Q-62a)
    DON’T KNOW . . . 98
    REFUSED  . . . . 99
```

Figure B.5 *Selected rows of the file* `wfwcodebook.txt`*, which first identifies the columns in the data corresponding to each survey question and then gives the question wordings.*

```
  else
    return(read.fwf(filename, widths=c(start-1, length))[,2])
}
```

Now we extract the data that we are interested in.

R code

```
height_feet <- read.columns("wfw90.dat", 144)
height_inches <- read.columns("wfw90.dat", 145:146)
weight <- read.columns("wfw90.dat", 147:149)
income_exact <- read.columns("wfw90.dat", 203:208)
income_approx <- read.columns("wfw90.dat", 209:210)
sex <- read.columns("wfw90.dat", 219)
```

The data did not come in a convenient comma-separated or tab-separated format, so we used the function `read.columns()` to read the coded responses, one question at a time.

Cleaning data within R

We now must put the data together in a useful form, doing the following for each variable of interest:

1. Look at the data
2. Identify errors or missing data
3. Transform or combine raw data into summaries of interest.

We start with height, typing: `table(height_feet, height_inches)`. Here is the result:

R output
```
height_feet   0   1   2   3   4   5   6   7   8   9  10  11  98  99
          4   0   0   0   0   0   0   0   0   0   1   3  17   0   0
          5  66  56 144 173 250 155 247 127 174 105 145  90   0   0
          6 129  59  46  20   8   5   1   0   0   0   1   0   0   0
          7   0   0   0   0   0   0   0   1   0   0   0   0   0   0
          9   0   0   0   0   0   0   0   0   0   0   0   0   2   6
```

Most of the data look fine, but there are some people with 9 feet and 98 or 99 inches (missing data codes) and one person who is 7 feet 7 inches tall (probably a data error). We recode these problem cases as missing:

R code
```
height_inches[height_inches>11] <- NA
height_feet[height_feet>=7] <- NA
```

And then we define a combined height variable:

R code
```
height <- 12*height_feet + height_inches
```

We do the same thing for sex:

R code
```
table(sex)
```

which simply yields:

R output
```
sex
   1    2
 749 1282
```

No problems. But we prefer to have a more descriptive name, so we define a new variable, `female`:

R code
```
female <- sex - 1
```

This *indicator variable* equals 0 for men and 1 for women.

Next, we type `table(weight)` and get the following:

R output
```
weight
 80  85  87  89  90  92  93  95  96  98  99 100 102 103 104 105 106 107 108 110
  1   1   1   1   1   1   1   2   2   3   1  12   5   4   3  16   1   5   7  46
111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130
  4  15   5   5  42   5   4  21   4  72   4  14  20  11  61  11   3  25   8 106
131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
  4  16   9   5  85   9  10  15   4  94   1  12   2   4  74   2   7   8   5 121
151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170
  2   4   8   7  49   3   6  14   1  88   1   8   4   9  65   2   2   8   2  81
171 172 173 174 175 176 178 180 181 182 183 184 185 186 187 188 189 190 192 193
  2  10   4   2  58   5   4  78   3   4   2   4  62   1   5   1   3  46   1   3
194 195 196 197 198 199 200 201 202 203 205 206 207 208 209 210 211 212 214 215
  4  26   3   2   3   2  57   1   2   2  11   2   3   2   3  36   1   2   3  10
217 218 219 220 221 222 223 225 228 230 231 235 237 240 241 244 248 250 255 256
  1   1   1  21   2   1   1  13   2  17   1   3   1  13   1   1   1  10   3   1
260 265 268 270 275 280 295 312 342 998 999
  2   3   1   3   1   3   1   1   1   6  36
```

Everything looks fine until the end. 998 and 999 must be missing data, which we duly code as such:

R code
```
weight[weight>500] <- NA
```

Coding the income responses is more complicated. The variable `income_exact` contains exact responses for income (in dollars per year) for those who answered the question. Typing `table(is.na(income_exact))` reveals that 1380 people answered the question (that is, `is.na(income_exact)` is `FALSE` for these respondents), and 651 did not answer (`is.na` was `TRUE`). These nonrespondents were asked the second, discrete income question, `income_approx`, which gives incomes in round numbers (in thousands of dollars per year) for people who were willing to answer in this way. A careful look at the codebook reveals that an `income_approx` code of 1 corresponds to people who did not supply an exact income value but did say it was more than $100 000. We code these people as having incomes of 150 000, which is approximately the average income of the over-100 000 group from the exact income data, as calculated by `mean(income_exact[income_exact>100000],na.rm=TRUE)`, which yields the value 166 600. The `income_approx` data also appear to have several values indicating ambiguity or missingness, which we code as NA.

We create a combined income variable as follows:

R code
```
income_approx[income_approx>=90] <- NA
income_approx[income_approx==1] <- 150
income <- ifelse(is.na(income_exact), 1000*income_approx, income_exact)
```

The new `income` variable still has 237 missing values (out of 2031 respondents in total) and is imperfect in various ways, but we have to make some choices when working with real data.

Looking at the data

If you stare at the table of responses to the weight question you can see more. People typically round their weight to the nearest 5 or 10 pounds, and so we see a lot of weights reported as 100, 105, 110, and so forth, but not so many in between. Beyond this, people appear to like round numbers: 57 people report weights of 200 pounds, compared to only 46 and 36 people reporting 190 and 210, respectively.

Similarly, if we go back to reported heights we see some evidence that the reported numbers do not correspond exactly to physical heights: 129 people report heights of exactly 6 feet, compared to 90 people at 5 feet 11 inches and 59 people at 6 feet 1 inch. Who are these people? Let's look at the breakdown of height and sex:

R code
```
table(female, height)
```

Here's the result:

R output
```
       height
female  57  58  59  60  61  62  63  64  65  66  67  68  69  70  71  72  73  74
     0   0   0   0   3   2   4   3  14  13  47  43  81  77 119  82 125  56  44
     1   1   3  17  63  54 140 170 236 142 200  84  93  28  26   8   4   3   2
       height
female  75  76  77  78  82
     0  19   8   5   1   1
     1   1   0   0   0   0
```

The extra 6-footers (72 inches tall) are just about all men. But there appear to be too many women of exactly 5 feet tall and an excess of both men and women who report being exactly 5 feet 6 inches.

B.6 Some programming

Working with vectors

In R, a vector is a list of items. These items can include numerics, characters, or logicals. A single value is actually represented as a vector with one element. Here are some vectors:

- (1, 2, 3, 4, 5)
- (3, 4, 1, 1, 1)
- (“A”, “B”, “C”)

Here’s the R code to create these:

R code
```
x <- 1:5
y <- c(3, 4, 1, 1, 1)
z <- c("A", "B", "C")
```

And here’s a random vector of 5 random numbers between 0 and 100:

R code
```
u <- runif(5, 0, 100)
```

Mathematical operations on vectors are done componentwise. Take a look:

R code
```
x
y
x + y
1000*x + u
```

There are scalar operations on vectors:

R code
```
1 + x
2 * x
x / 3
x^4
```

We can summarize vectors in various ways, including the sum and the average (called the “mean” in statistics jargon):

R code
```
sum(x)
mean(x)
```

We can also compute weighted averages if we know the weights. We illustrate with a vector of 3 elements:

R code
```
x <- c(100, 200, 600)
w1 <- c(1/3, 1/3, 1/3)
w2 <- c(0.5, 0.2, 0.3)
```

In the above code, the vector of weights `w1` has the effect of counting each of the three items equally; vector `w2` counts the first item more. Here are the weighted averages:

R code
```
sum(w1*x)
sum(w2*x)
```

Or suppose we want to weight in proportion to population:

R code
```
N <- c(310e6, 112e6, 34e6)
sum(N*x)/sum(N)
```

Or, equivalently,

R code
```
N <- c(310e6, 112e6, 34e6)
w <- N/sum(N)
sum(w*x)
```

The `cumsum()` function does the cumulative sum. Try this:

R code
```
a <- c(1, 1, 1, 1, 1)
cumsum(a)
a <- c(2, 4, 6, 8, 10)
cumsum(a)
```

Subscripting

Vectors can be indexed by using brackets, "`[ ]`". Within the brackets we can put in a vector of elements we are interested in either as a vector of numbers or a logical vector. When using a vector of numbers, the vector can be arbitrary length, but when indexing using a logical vector, the length of the vector must match the length of the vector you are indexing. Try these:

R code
```
a <- c("A", "B", "C", "D", "E", "F", "G", "H", "I", "J")
a[1]
a[2]
a[4:6]
a[c(1,3,5)]
a[c(8,1:3,2)]
a[c(FALSE, FALSE, FALSE, TRUE, TRUE, TRUE, FALSE, FALSE, FALSE, FALSE)]
```

As we have seen in some of the previous examples, we can perform mathematical operations on vectors. These vectors have to be the same length, however. If the vectors are not the same length, we can subset the vectors so they are compatible. Try these:

R code
```
x <- c(1, 1, 1, 2, 2)
y <- c(2, 4, 6)
x[1:3] + y
x[3:5] * y
y[3]^x[4]
x + y
```

The last line runs but produces a warning. These warnings should not be ignored since it isn't guaranteed that R would carry out the operation as you intended.

Writing your own functions

You can write your own function. Most of the functions we will be writing will take in one or more vectors and return a vector. Below is an example of a simple function that triples the value provided:

R code
```
triple <- function(x) {
  return(3*x)
}
```

For example, to call this function, type `triple(c(1,2,3,5))`. This function has one argument, `x`. The body of the function is within the curly braces and the arguments of the function are available for use within the braces. In our example function, we multiply `x` by 3 and we return it back to the user. If we wanted to have more than one argument, we could do something like this:

R code
```
new_function <- function(x, y, a, b) {
  return(a*x+b*y)
}
```

Optimization

Finding the peak of a parabola. Figure B.6 shows the parabola $y = 15 + 10x - 2x^2$. As you can see, the peak is at $x = 2.5$. How can we find this solution systematically (and without using calculus, which would be cheating)? Finding the maximum of a function is called an *optimization* problem. Here's how we do it in R.

1. Graph the function, in this case, `curve(15+10*x-2*x^2,from=___,to=___)`, entering numbers in the blanks. Play around with the "from" and "to" arguments until the maximum appears.

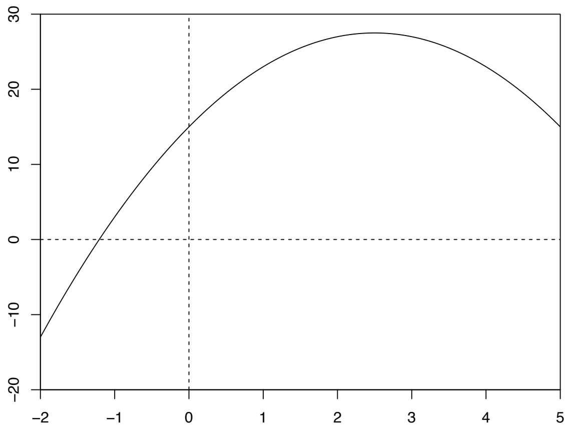


Figure B.6 *The parabola $y = 15 + 10x - 2x^2$, plotted in R using* `curve(15 + 10*x - 2*x^2, from=-2, to=5)`*. The maximum is at $x = 2.5$.*

2. Write it as a function in R:

R code
```
parabola <- function(x) {
  return(15 + 10*x - 2*x^2)
}
```

3. Call `optimize()`. We can find the maximum of a function in R through the `optimize()` function which takes the function to optimize as the first argument, the interval to optimize over as the second argument, and an optional argument indicating whether or not you are searching for the function's maximum. For the example above, suppose we are interested in maximizing over the range from $x = -100$ to $x = 100$. Then we can call:

R code
```
optimize(parabola, interval=c(-100, 100), maximum=TRUE)
```

   This returns two values, x and $f(x)$. The value labeled `maximum` is the x at which the function is optimized and the `objective` is its corresponding $f(x)$ value.

4. Check the solution on the graph to see that it makes sense.

Restaurant pricing. Suppose you own a small restaurant and are trying to decide how much to charge for dinner. For simplicity, suppose that dinner will have a single price, and that your marginal cost per dinner is \$11. From a marketing survey, you have estimated that, if you charge \$$x$ for dinner, the average number of customers per night you will get is $5000/x^2$. How much should you charge, if your goal is to maximize expected net profit?

Your exepected net profit is the expected number of customers times net profit per customer; that is, $(5000/x^2) * (x - 11)$. To get a sense of where this is maximized, we can first make a graph:

R code
```
net_profit <- function(x){
  return((5000/x^2)*(x-11))
}
curve(net_profit(x), from=10, to=100, xlab="Price of dinner",
  ylab="Net profit per night")
```

From a visual inspection of this curve, the peak appears to be around $x = 20$. There are two ways we can more precisely determine where net profit is maximized.

First, the brute-force approach. The optimum is clearly somewhere between 10 and 100, so let's just compute the net profit at a grid of points in this range:

R code
```
x <- seq(10, 100, 0.1)
y <- net_profit(x)
```

The maximum value of net profit is then simply `max(y)`, which equals 113.6, and we can find the value of x where profit is maximized:

R code
```
x[y==max(y)]
```

It turns out to be 22, which is `x[121]`, the 122th element of x. Above, we are subscripting the vector `x` with a logical vector `y==max(y)`, which is a vector of 900 `FALSE`'s and one `TRUE` at the maximum.

We can also use the `optimize()` function:

R code
```
optimize(net_profit, interval=c(10,100), maximum=TRUE)
```

The argument `interval` gives the range over which the optimization is computed, and we set `maximum=TRUE` to maximize, rather than minimize, the net profit. Here is what the function returns:

R output
```
$maximum
[1] 22

$objective
[1] 113.6
```

Alternatively we can perform the optimization in Stan. We first write the following Stan program and save it in the file `restaurant.stan`:[1]

Stan code
```
parameters {
  real<lower=0,upper=100> x;
}
mode {
  target += (5000/x^2)*(x-11);
}
```

Then, in R:

R code
```
resto <- stan_model("restaurant.stan")
fit <- optimizing(resto)
print(fit)
```

The result:

R output
```
$par
       x
22.0

$value
[1] 113.6

$return_code
[1] 0
```

Again, the function returns 113.6 at the input value $x = 22.0$. If the return code had not been zero, that would have indicated a problem with the optimization.

[1]Code for this example appears in the folder `Restaurant`.

B.7 Bibliographic note

The books by Becker, Chambers, and Wilks (1988), Venables and Ripley (2002), Wickham (2014), and Wickham and Grolemund (2017) provide thoughtful overviews of R, and its predecessor S, from different perspectives.

Stan is introduced by Gelman, Lee, and Guo (2015) from a users' perspective and Carpenter et al. (2017) from a developers' perspective. Much more documentation on R and Stan is available at `http://www.r-project.org/` and `http://www.mc-stan.org/`.