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# Introduction to R

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The materials presented here teach spatial data analysis and modeling with *R*. *R* is a widely used programming language and software environment for data science. *R* also provides unparalleled opportunities for analyzing spatial data for spatial modeling.

If you have never used *R*, or if you need a refresher, you should start with our [Introduction to R \(pdf\)](#)

There are two version of this website, the “[raster](#)” version and the “[terra](#)” version. The “[raster](#)” version is well established and more elaborate. If in doubt, go there.

The version using the “[terra](#)” package is new, and under development. It is particularly useful for those who are interested in switching from the *raster* to the *terra* package, for faster processing and for remote sensing.

# 1 Introduction to R

## 1.1 Introduction

*R* is perhaps the most powerful computer environment for data analysis that is currently available. *R* is both a computer *language*, that allows you to write instructions, and a *program* that responds to these instructions. *R* has core functionality to read and write files, manipulate and summarize data, run statistical tests and models, make fancy plots, and many more things like that. This core functionality is extended by hundreds of packages (plug-ins). Some of these packages provide more advanced generic functionality, others provide cutting-edge methods that are only used in highly specialized analysis.

Because of its versatility, *R* has become very popular across data analysts in many fields, from agronomy to bioinformatics, ecology, finance, geography, pharmacology and psychology. You can read about it in this article in [Nature](#) or in the [New York Times](#). So you probably should learn *R* if you want to do modern data analysis, be a successful researcher, collaborate, get a [high paying job](#), ... If you are not that much into *data analysis* but want to learn programming for more general tasks, I would suggest that you learn [python](#) instead.

This document provides a concise introduction to *R*. It emphasizes what you need to know to be able to use the language in any context. There is no fancy statistical analysis here. We just present the basics of the *R* language itself. We do not assume that you have done any computer programming before (but we do assume that you think it is about time you did). Experienced *R* users obviously need not read this. But the material may be useful if you want to refresh your memory, if you have not used *R* much, or if you feel confused.

When going through the material, it is very important to follow [Norman Matloff's](#) advice: "*When in doubt, try it out!*". That is, copy the examples shown, and then make modifications to test if you can predict what will happen. Only then will you really understand what is going on. You are learning a language, and you will have to use it a lot to become good at it. And you just have to accept that for a while you will be stumbling.

To work with *R* on your own computer, you need to [download](#) the program and install it. I recommend that you also install [R-Studio](#). R-Studio is a separate program that makes *R* easier to use. Here is a [video](#) that shows how to work in R-Studio.

If you have trouble with the material presented here, you could consult additional resources to learn *R*. There are many free resources on the web, including [R for Beginners](#) by Emmanuel Paradis and this [tutorial](#) by Kelly Black that is similar to the one you are reading now. Or consult this [brief overview](#) by Ross Ihaka (one of the originators of *R*) from his [Information Visualization](#) course. You can also pick up an introductory *R* book such as [A Beginner's Guide to R](#) by Zuur, Ieno and Meesters, [R in a nutshell](#) by Joseph Adler, and Norman Matloff's [The Art of R Programming](#). Another on-line resources you might try is Datacamp's [Introduction to R](#).

There is also a lot of very good material on [rstatistics.net](#)

If you want to take it easy, or perhaps learn about *R* while you commute on a packed train, you could watch some [Google Developers videos](#).

If none of this appeals to you, and you already are experienced with *R*, or you have done a lot of programming with other languages, skip all of this and have a look at Hadley Wickham's [Advanced R](#).

## Installing the R and R Studio software

### Windows

#### *Install R*

[Download](#) the latest R installer (.exe) for Windows. Install the downloaded file as any other windows app.

#### *Install RStudio*

Now that R is installed, you need to download and install RStudio. First [download](#) the installer for Windows. Run the installer (.exe file) and follow the instructions.

### Mac

#### *Install R*

First [download](#) the latest release (“R-version.pkg”) of R Save the .pkg file, double-click it to open, and follow the installation instructions. Now that R is installed, you need to download and install RStudio.

#### *Install RStudio*

First [Download] the the version for Mac. After downloading, double-click the file to open it, and then drag and drop it to your applications folder.

### Linux

#### *Install R*

Go to [this web page](#) and open the folder based on your linux distribution and follow the instructions in the ‘readme’.

#### *Install RStudio*

It is difficult to provide a single guideline for different linux distributions. Please follow the general steps [provided here](#) and download the installer for the linux distribution you are using and install it.

Ubuntu users can follow the instructions in this [discussion on stackoverflow](#) to avoid complexity in installing some of the `spatial` packages, particularly `rgdal`.

## 1.2 Basic data types

This chapter briefly discusses the basic data types that are used in *R*. Here we mainly show how to create data of these types. There is much more on how to manipulate data in the following chapters. The most important basic (or “primitive”) data types are the “numeric” and “character” types. Additional types are the “integer”, which can be used to represent whole numbers; the “logical” and the “factor”. These are all discussed below.

## Numeric and integer values

Let's create a variable `a` that is a vector of one number.

```
a <- 7
```

To do this yourself, type the code in an R console. Or, if you use R-Studio, use 'File / New File / R script' and type it in the new script. Then press "Run" or "Ctrl-Enter" (Apple-Enter on a Mac) to run the line (make sure your cursor is on the line that you want to run).

The "arrow" `<-` was used to **assign** the value `7` to variable `a`. You can pronounce the above as "a becomes 7".

It is also possible to use the `=` sign.

```
a = 7
```

Although you can use `=`, `<-` is preferred, because the arrow clearly indicates the assignment action, and because `=` is also used in another context (to pass arguments to functions).

The name `a` is entirely arbitrary. We could have used `x`, `varib`, `fruit` or any other name that would help us recognize it. There are a few restrictions: variable names cannot start with a number, and they cannot contain spaces or "special" characters, such as `*` (which is used for multiplication).

To check the value of `a`, we can ask *R* to show or print it.

```
show(a)
## [1] 7
print(a)
## [1] 7
```

This is also what happens if you simply type the variable name.

```
a
## [1] 7
```

In *R*, all basic values are stored as a *vector*, a one-dimensional array of  $n$  values of a certain type. Even a single number is a vector (of length 1). That is why *R* shows that the value of `a` is `[1] 7`. Because `7` is the first element in vector `a`.

We can use the `class` function to find out what type of object `a` is (what class it belongs to).

```
class(a)
## [1] "numeric"
```

*numeric* means that `a` is a real (decimal) number. Its value is equivalent to `7.000`, but trailing zeros are not printed by default. In a few cases it can be useful, or even necessary, to use integer (whole number) values. To create a vector with a single integer you can either use the `as.integer` function, or append an `L` to the number.

```
a <- as.integer(7)
class(a)
## [1] "integer"
a <- 7L
class(a)
## [1] "integer"
```

To create a vector of several numbers, the `c` (combine) function can be used.

```
b <- c(1.25, 2.9, 3.0)
b
## [1] 1.25 2.90 3.00
```

But to create a regular sequence it is easier to use `:`.

```
d <- 5:9
d
## [1] 5 6 7 8 9
```

You can also use the `:` to create a sequence in descending order.

```
6:2
## [1] 6 5 4 3 2
```

The `seq` function provides more flexibility. For example it allows for step sizes different than one. In this case we go from 3 to 12, taking steps of 3. Try some variations!

```
e <- seq(from=6, to=12, by=3)
e
## [1] 6 9 12
```

To go in descending order the `by` argument needs to be negative.

```
seq(from=12, to=0, by=-4)
## [1] 12 8 4 0
```

You can also reverse the order of a sequence, after making the sequence, using the `rev` function.

```
s <- seq(from=0, to=12, by=4)
s
## [1] 0 4 8 12
r <- rev(s)
r
## [1] 12 8 4 0
```

We will discuss *functions* like `seq` in more detail later. But, in essence, a *function* is a named procedure that performs a certain task. In this case the name is `seq`, and the task is to create a sequence of numbers. The exact specification of the sequence is modified by the *arguments* that are provided to `seq`, in this case: `from`, `to`, and `by`. If you are unsure what a function does, or which arguments are available, then read the function's help page. You can get to the help page for `seq` by typing `?seq` or `help(seq)`, and likewise for all other functions in *R*.

The `rep` (for repeat) function provides another way to create a vector of numbers. You can repeat a single number, or a sequence of numbers.

```
rep(9, times=5)
## [1] 9 9 9 9 9
rep(5:7, times=3)
## [1] 5 6 7 5 6 7 5 6 7
rep(5:7, each=3)
## [1] 5 5 5 6 6 6 7 7 7
```

## Character values

A character variable is used to represent letters, codes, or words. Character values are often referred to as a 'string'.

```
x <- 'Yi'
y <- 'Wong'
class(x)
## [1] "character"
x
## [1] "Yi"
```

To distinguish a character value from a variable name, it needs to be quoted. 'x' is a character value, but x is a variable! Double-quoted "Yi" is the same as single-quoted 'Yi', but you cannot mix the two in one value: "Yi' is not valid. But you can enclose one type of quote inside a pair of the other type. For example, you can do "Yi's dog" or 'Wong said "hello" and left'.

One of the most common mistakes for beginners is to forget the quotes.

```
Yi
## Error in eval(expr, envir, enclos): object 'Yi' not found
```

The error occurs because R tries to print the value of variable Yi, but there is no such variable. So remember that any time you get the error message object 'something' not found, the most likely reason is that you forgot to quote a character value. If not, it probably means that you have misspelled, or not yet created, the variable that you are referring to.

Keep in mind that R is case-sensitive: a is not the same as A. In most computing contexts, a and A are **entirely** different and, for most intents and purposes, **unrelated** symbols.

Now let's create variable countries holding a character vector of five elements.

```
countries <- c('China', 'China', 'Japan', 'South Korea', 'Japan')
class(countries)
## [1] "character"
countries
## [1] "China" "China" "Japan" "South Korea" "Japan"
```

The function length tells us how long the vector is (how many elements it has).

```
length(countries)
## [1] 5
```

If you want to know the number of characters of each element of the vector, you can use nchar.

```
nchar(countries)
## [1] 5 5 5 11 5
```

nchar returns a vector of integers with the same length as x (5). Each number is the number of characters of the corresponding element of countries. This is an example of why we say that most functions in R are *vectorized*. This means that you normally do not need to tell R to compute things for each individual element in a vector.

It is handy to know that letters (a constant value, like pi) returns the alphabet (LETTERS returns them in uppercase), and toupper and tolower can be used to change case.

```
z <- letters
z
## [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n" "o" "p" "q" "r" "s"
## [20] "t" "u" "v" "w" "x" "y" "z"
up <- toupper(z)
```

Perhaps the most commonly used function for string manipulation is `paste`. This function is used to concatenate strings. For example:

```
girl <- "Mary"
boy <- "John"
paste(girl, "likes", boy)
## [1] "Mary likes John"
```

By default, `paste` uses a space to separate the elements. You can change that with the `sep` argument.

```
paste(girl, "likes", boy, sep = " ~ ")
## [1] "Mary ~ likes ~ John"
```

Sometimes you do not want any separator. You can then use `sep=""` or the `paste0` function.

By using the “collapse” argument, we can concatenate all values of a vector into a single element.

```
paste(countries, collapse=' -- ')
## [1] "China -- China -- Japan -- South Korea -- Japan"
```

We’ll leave more advanced manipulation of strings for later, but here are two more important functions. To get a part of a string use ‘`substr`’.

```
substr('Hello World', 1, 5)
## [1] "Hello"
substr('Hello World', 7, 11)
## [1] "World"
```

To replace characters in a string use `gsub` or `sub`.

```
gsub('l', '!!!', 'Hello World')
## [1] "He!!!!o Wor!!d"
gsub('Hello', 'Bye bye', 'Hello World')
## [1] "Bye bye World"
```

To find elements that fit a particular pattern use `grep`. It returns the index of the matching elements in a vector.

```
d <- c('az20', 'az21', 'az22', 'ba30', 'ba31', 'ba32')
i <- grep('b', d)
i
## [1] 4 5 6
d[i]
## [1] "ba30" "ba31" "ba32"
```

Which elements of `d` include the character “2”?

```
grep('2', d)
## [1] 1 2 3 6
```

Which elements of `d` *end* with the character “2”? “\$” has a special meaning.

```
grep('2$', d)
## [1] 3 6
```

Which elements of `d` *start* with the character “b”? “^” has a special meaning.

```
grep('^b', d)
## [1] 4 5 6
```

## Logical values

A logical (or Boolean) value is either `TRUE` or `FALSE`. They are used very frequently in *R* and in computer programming in general.

```
z <- FALSE
z
## [1] FALSE
class(z)
## [1] "logical"
z <- c(TRUE, TRUE, FALSE)
z
## [1] TRUE TRUE FALSE
```

`TRUE` and `FALSE` can be abbreviated to `T` and `F`, but that is very bad practice. This is because it is possible to change the value of `T` and `F` to something else which would be extraordinarily confusing. In contrast, `TRUE` and `FALSE` are constants that cannot be changed.

Logical values are often the result of a computation. For example, here we ask if the values of `x` are larger than 3, which is `TRUE` for values 4 and 5

```
x <- 5
x > 3
## [1] TRUE
```

Likewise we can test for equality using two equal signs `==` (not `=` which would be an assignment!). `<=` means “smaller or equal”.

```
x == 3
## [1] FALSE
x <= 2
## [1] FALSE
```

Logical values can be treated as numerical values. `TRUE` is equivalent to 1 and `FALSE` to 0.

```
y <- TRUE
y + 1
## [1] 2
```

However, if you go the other way, only zero is equivalent to `FALSE` while any number that is not zero, is `TRUE`

```
as.logical(0)
## [1] FALSE
as.logical(1)
## [1] TRUE
as.logical(2.5)
## [1] TRUE
```



## Factors

A factor is a nominal (categorical) variable with a set of known possible values called `levels`. They can be created using the `as.factor` function. In *R* you typically need to convert (cast) a character variable to a factor to identify groups for use in statistical tests and models.

```
f1 <- as.factor(countries)
f1
## [1] China      China      Japan      South Korea Japan
## Levels: China Japan South Korea
```

But numbers can also be used. For example, they may simply indicate group membership.

```
f2 <- c(5:7, 5:7, 5:7)
f2
## [1] 5 6 7 5 6 7 5 6 7
f2 <- as.factor(f2)
f2
## [1] 5 6 7 5 6 7 5 6 7
## Levels: 5 6 7
```

Dealing with factors can be tricky. For example `f2` created above is not what it may seem. We see numbers 5, 6 and 7, but these are now just labels to identify groups. They cannot be used in algebraic expressions.

We can convert factors to something else. Here we use `as.integer`. If you want a number with decimal places, you can use `as.numeric` instead.

```
f2
## [1] 5 6 7 5 6 7 5 6 7
## Levels: 5 6 7
as.integer(f2)
## [1] 1 2 3 1 2 3 1 2 3
```

The result of `as.integer(f2)` may have been surprising. But it should not be, as there is no direct link between a category with label “5” and the number 5. In this case, “5” is simply the label of the first category and hence it gets converted to the integer 1. Nevertheless, we can get the numbers back as there is an established link between the character symbol ‘5’ and the number 5. So we first create characters from the factor values, and then numbers from the characters.

```
fc2 <- as.character(f2)
fc2
## [1] "5" "6" "7" "5" "6" "7" "5" "6" "7"
as.integer(fc2)
## [1] 5 6 7 5 6 7 5 6 7
```

This is different from `as.integer(f2)`, which returned the indices of the factor values. It has no way of knowing if you want factor level 6 to represent the number 6.

At this point it is OK if you are confused about factors and *why* you might do such things as conversion from and to them.

## Missing values

All basic data types can have “missing values”. These are represented by the symbol `NA` for “not available”. For example, we can have vector ‘`m`’

```
m <- c(2, NA, 5, 2, NA, 2)
m
## [1] 2 NA 5 2 NA 2
```

Note that `NA` is *not* quoted.

Properly treating missing values is very important. The first question to ask when they appear is whether they should be missing (or did you make a mistake in the data manipulation?). If they should be missing, the second question becomes how to treat them. Can they be ignored? Should the records with `NA`s be removed?

## Time

Representing time is a somewhat complex problem. There are different calendars, hours, days, months, and leap years to consider. As a basic introduction, here is simple way to create date values.

```
d1 <- as.Date('2015-4-11')
d2 <- as.Date('2015-3-11')
class(d1)
## [1] "Date"
d1 - d2
## Time difference of 31 days
```

And there are more advanced classes as well that capture date and time.

```
as.POSIXlt(d1)
## [1] "2015-04-11 UTC"
as.POSIXct(d1)
## [1] "2015-04-10 17:00:00 PDT"
```

See <http://www.stat.berkeley.edu/~s133/dates.html> for more info.

## 1.3 Basic data structures

In the previous chapter we saw the most basic data types in *R*: vectors of numeric, integer, character, factor and boolean values. These were all stored as a `vector`. A vector is a one dimensional structure. In this chapter we look at additional, multi-dimensional, data structures that can store basic data: the `matrix`, `data.frame` and `list`.

### Matrix

A vector is a one-dimensional array. A two-dimensional array can be represented with a matrix. Here is how you can create a matrix with two rows and three columns.

```
matrix(ncol=3, nrow=2)
##      [,1] [,2] [,3]
## [1,]  NA  NA  NA
## [2,]  NA  NA  NA
```

The matrix above did not have any values: all values were `missing` (`NA`). Let’s make a matrix with values 1 to 6.

```
matrix(1:6, ncol=3, nrow=2)
##      [,1] [,2] [,3]
## [1,]  1   3   5
## [2,]  2   4   6
```

Note that by default the values are distributed column-wise. To go row-wise you can use the `byrow=TRUE` argument.

```
matrix(1:6, ncol=3, nrow=2, byrow=TRUE)
##      [,1] [,2] [,3]
## [1,]  1   2   3
## [2,]  4   5   6
```

This can also be achieved by switching the number of columns and rows and using the `t` (transpose) function.

```
m <- matrix(1:6, ncol=2, nrow=3)
t(m)
##      [,1] [,2] [,3]
## [1,]  1   2   3
## [2,]  4   5   6
```

It is common to create a matrix by column-binding and/or row-binding vectors using `cbind` and `rbind`. These are two of the most commonly used functions in *R* so pay close attention!

```
a <- c(1,2,3)
b <- 5:7
```

column binding

```
m1 <- cbind(a, b)
m1
##      a b
## [1,] 1 5
## [2,] 2 6
## [3,] 3 7
```

row binding

```
m2 <- rbind(a, b)
m2
##      [,1] [,2] [,3]
## a      1   2   3
## b      5   6   7
```

You can use `cbind` and `rbind` also to combine matrices, as long as the number of rows or columns of the two objects are the same.

```
m3 <- cbind(b, b, a)
m <- cbind(m1, m3)
m
##      a b b b a
## [1,] 1 5 5 5 1
## [2,] 2 6 6 6 2
## [3,] 3 7 7 7 3
```

We can get some of the structural properties of a matrix with functions such as `nrow`, `ncol`, `dim` and `length`.

```
nrow(m)
## [1] 3
ncol(m)
## [1] 5
# dimensions of m (nrow, ncol)
dim(m)
## [1] 3 5
# number of cells, or nrow(m) * ncol(m)
length(m)
## [1] 15
```

Columns have (variable) names that can be changed.

```
# get the column names
colnames(m)
## [1] "a" "b" "b" "b" "a"
# set the column names
colnames(m) <- c('ID', 'X', 'Y', 'v1', 'v2')
m
##           ID X Y v1 v2
## [1,]    1 5 5  5  1
## [2,]    2 6 6  6  2
## [3,]    3 7 7  7  3
```

Likewise there are row names, but these are less important.

```
rownames(m) <- paste0('row_', 1:nrow(m))
m
##           ID X Y v1 v2
## row_1    1 5 5  5  1
## row_2    2 6 6  6  2
## row_3    3 7 7  7  3
```

A matrix can only store a single data type. If you try to mix character and numeric values, all values will become character values (as the other way around may not be possible).

```
cbind(vchar=c('a', 'b'), vnumb=1:2)
##           vchar vnumb
## [1,]    "a"    "1"
## [2,]    "b"    "2"
```

You can see that 1 and 2 are character values because they are quoted. You could not use them in algebra without first converting them back to numbers. Note that the column names were set by providing them to `cbind`

A matrix is a two dimensional array. Higher dimensional arrays can also be created. See `help(array)`, but these data structures are not that commonly used, so we do not discuss them here.

## List

A `list` is a very flexible container to store data. Each element of a list can contain any type of *R* object, e.g. a vector, matrix, data.frame, another list, or more complex data types.

A simple list:

```
list(1:3)
## [[1]]
## [1] 1 2 3
```

It shows that the first element `[[1]]` contains a vector of 1, 2, 3

Here is one with two data types.

```
e <- list(c(2,5), 'abc')
e
## [[1]]
## [1] 2 5
##
## [[2]]
## [1] "abc"
```

List elements can be named.

```
names(e) <- c('first', 'last')
e
## $first
## [1] 2 5
##
## $last
## [1] "abc"
```

And a more complex list.

```
m <- matrix(1:6, ncol=3, nrow=2)
f <- list(e, m, 'abc')
f
## [[1]]
## [[1]]$first
## [1] 2 5
##
## [[1]]$last
## [1] "abc"
##
##
## [[2]]
##      [,1] [,2] [,3]
## [1,]    1    3    5
## [2,]    2    4    6
##
## [[3]]
## [1] "abc"
```

Note that the first element of list `f` is itself a list of two elements.

## Data frame

The `data.frame` is the workhorse for statistical data analysis in *R*. It is rectangular like a matrix, but unlike matrices a `data.frame` can have columns (variables) of different data types. A `data.frame` is what you get when you read spreadsheet-like data into *R* with functions like `read.table` or `read.csv`. We'll show that in a later chapter. We can also create a `data.frame` with some simple code.

```
# four vectors
ID <- as.integer(1:4)
name <- c('Ana', 'Rob', 'Liu', 'Veronica')
sex <- as.factor(c('F', 'M', 'M', 'F'))
score <- c(10.2, 9, 13.5, 18)

d <- data.frame(ID, name, sex, score, stringsAsFactors=FALSE)
d
##   ID      name sex score
## 1  1     Ana   F  10.2
## 2  2     Rob   M   9.0
## 3  3     Liu   M  13.5
## 4  4  Veronica F  18.0
```

I used the argument `stringsAsFactors=FALSE` to avoid converting the character variable `name` to a factor. `d` is a `data.frame`, but individual columns can be of any class. Note that the length of a `data.frame` is defined as the number of variables (columns), while the length of a matrix is defined as the number of cells! This is because a matrix is a special kind of vector, while a `data.frame` is a special kind of list in which each element has the same size.

```
class(d)
## [1] "data.frame"
length(d)
## [1] 4
```

Because a `data.frame` is a special kind of list, you can do with a `data.frame` what you can do with a list.

```
is.list(d)
## [1] TRUE
names(d)
## [1] "ID"      "name"    "sex"     "score"
```

But in other ways, a `data.frame` is also similar to a matrix (which normal lists are not).

```
nrow(d)
## [1] 4
dim(d)
## [1] 4 4
colnames(d)
## [1] "ID"      "name"    "sex"     "score"
```

## 1.4 Indexing

There are multiple ways to access or replace values in vectors or other data structures. The most common approach is to use “indexing”. This is also referred to as “slicing”.

Note that brackets [ ] are used for indexing, whereas parentheses ( ) are used to call a function.

### Vector

Here are some examples that show how elements of vectors can be obtained by indexing.

```
b <- 10:15
b
## [1] 10 11 12 13 14 15
```

Get the first element of a vector

```
b[1]
## [1] 10
```

Get the first second element of a vector

```
b[2]
## [1] 11
```

Get elements 2 and 3

```
b[2:3]
## [1] 11 12
# this is the same as
b[c(2,3)]
## [1] 11 12
```

Now a more advanced example, return all elements except the second

```
b[c(1,3:6)]
## [1] 10 12 13 14 15
# or the simpler:
b[-2]
## [1] 10 12 13 14 15
```

You can also use an index to change values

```
b[1] <- 11
b
## [1] 11 11 12 13 14 15
b[3:6] <- -99
b
## [1] 11 11 -99 -99 -99 -99
```

An important characteristic of R’s vectorization system is that shorter vectors are ‘recycled’. That is, they are repeated until the necessary number of elements is reached. This applies in many circumstances, and is very practical when you are aware of it. It may, however, also lead to undetected errors, when this was not intended to happen.

Here you see recycling at work. First we assign a single number to the first three elements of b, so the number is used three times. Then we assign two numbers to a sequence of 3 to 6, such that both numbers are used twice.

```

b[1:3] <- 2
b
## [1] 2 2 2 -99 -99 -99
b[3:6] <- c(10,20)
b
## [1] 2 2 10 20 10 20

```

## Matrix

Consider matrix m.

```

m <- matrix(1:9, nrow=3, ncol=3, byrow=TRUE)
colnames(m) <- c('a', 'b', 'c')
m
##      a b c
## [1,] 1 2 3
## [2,] 4 5 6
## [3,] 7 8 9

```

Like vectors, values of matrices can be accessed through indexing. There are different ways to do this, but it is generally easiest to use two numbers in a double index, the first for the row number(s) and the second for the column number(s).

```

# one value
m[2,2]
## b
## 5
# another one
m[1,3]
## c
## 3

```

You can also get multiple values at once.

```

# 2 columns and rows
m[1:2,1:2]
##      a b
## [1,] 1 2
## [2,] 4 5

# entire row
m[2, ]
## a b c
## 4 5 6

# entire column
m[ ,2]
## [1] 2 5 8

```

Or use the column names for sub-setting.

```

#single column
m[, 'b']
## [1] 2 5 8
# two columns
m[, c('a', 'c')]

```

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```
##      a c
## [1,] 1 3
## [2,] 4 6
## [3,] 7 9
```

Instead of indexing with two numbers, you can also use a single number. You can think of this as a “cell number”. Cells are numbered column-wise (i.e., first the rows in the first column, then the second column, etc.). Thus,

```
m[2,2]
## b
## 5
# is equivalent to
m[5]
## [1] 5
```

Note that

```
m[ ,2]
## [1] 2 5 8
```

returns a vector. This is because a single-column matrix can be simplified to a vector. In that case the matrix structure is ‘dropped’. This is not always desirable, and to keep this from happening, you can use the `drop=FALSE` argument.

```
m[ , 2, drop=FALSE]
##      b
## [1,] 2
## [2,] 5
## [3,] 8
```

Setting values of a matrix is similar to how you would do that for a vector, except that you now need to deal with two dimensions.

```
# one value
m[1,1] <- 5
m
##      a b c
## [1,] 5 2 3
## [2,] 4 5 6
## [3,] 7 8 9
# a row
m[3,] <- 10
m
##      a b c
## [1,] 5 2 3
## [2,] 4 5 6
## [3,] 10 10 10
# two columns, with recycling
m[,2:3] <- 3:1
m
##      a b c
## [1,] 5 3 3
## [2,] 4 2 2
## [3,] 10 1 1
```

There is a function to get (or set) the values on the diagonal.

```
diag(m)
## [1] 5 2 1
diag(m) <- 0
m
##           a b c
## [1,]    0 3 3
## [2,]    4 0 2
## [3,]   10 1 0
```

## List

Indexing lists can be a bit confusing as you can both refer to the elements of the list, or the elements of the data (perhaps a matrix) in one of the list elements. Note the difference that double brackets make. `e[3]` returns a list (of length 1), but `e[[3]]` returns what is inside that list element (a matrix in this case)

```
m <- matrix(1:9, nrow=3, ncol=3, byrow=TRUE)
colnames(m) <- c('a', 'b', 'c')
e <- list(list(1:3), c('a', 'b', 'c', 'd'), m)
```

We can access data inside a list element by combining double and single brackets. By using the double brackets, the list structure is dropped.

```
e[2]
## [[1]]
## [1] "a" "b" "c" "d"
e[[2]]
## [1] "a" "b" "c" "d"
```

List elements can have names.

```
names(e) <- c('zzz', 'xyz', 'abc')
```

And the elements can be extracted by their name, either as an index, or by using the `$` (dollar) operator.

```
e$xyz
## [1] "a" "b" "c" "d"
e[['xyz']]
## [1] "a" "b" "c" "d"
```

The `$` can also be used with `data.frame` objects (a special list, after all), but not with matrices.

## Data.frame

Indexing a `data.frame` can generally be done as for matrices and for lists.

First create a `data.frame` from matrix `m`.

```
d <- data.frame(m)
class(d)
## [1] "data.frame"
```

You can extract a column by column number.

```
d[,2]
## [1] 2 5 8
```

Here is an alternative way to address the column number in a `data.frame`.

```
d[2]
##  b
## 1 2
## 2 5
## 3 8
```

Note that whereas `[2]` would be the second *element* in a `matrix`, it refers to the second *column* in a `data.frame`. This is because a `data.frame` is a special kind of list and not a special kind of matrix.

You can also use the column name to get values. This approach also works for a `matrix`.

```
d[, 'b']
## [1] 2 5 8
```

But with a `data.frame` you can also do

```
d$b
## [1] 2 5 8
# or this
d[['b']]
## [1] 2 5 8
```

All these return a vector. That is, the complexity of the `data.frame` structure was dropped. This does not happen when you do

```
d['b']
##  b
## 1 2
## 2 5
## 3 8
```

or

```
d[, 'b', drop=FALSE]
##  b
## 1 2
## 2 5
## 3 8
```

Why should you care about this `drop` business? Well, in many cases `R` functions want a specific data type, such as a `matrix` or `data.frame` and report an error if they get something else. One common situation is that you think you provide data of the right type, such as a `data.frame`, but that in fact you are providing a `vector`, because the structure dropped.

## Which, %in% and match

Sometimes you do not have the indices you need, and so you need to find them. For example, what are the indices of the elements in a vector that have values above 15?

```
x <- 10:20
i <- which(x > 15)
x
## [1] 10 11 12 13 14 15 16 17 18 19 20
i
```

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```
## [1] 7 8 9 10 11
x[i]
## [1] 16 17 18 19 20
```

Note, however, that you can also use a logical vector for indexing (values for which the index is TRUE are returned).

```
x <- 10:20
b <- x > 15
x
## [1] 10 11 12 13 14 15 16 17 18 19 20
b
## [1] FALSE FALSE FALSE FALSE FALSE FALSE TRUE TRUE TRUE TRUE TRUE
x[b]
## [1] 16 17 18 19 20
```

A very useful operator that allows you to ask whether a set of values is present in a vector is `%in%`.

```
x <- 10:20
j <- c(7,9,11,13)
j %in% x
## [1] FALSE FALSE TRUE TRUE
which(j %in% x)
## [1] 3 4
```

Another handy similar function is `match`:

```
match(j, x)
## [1] NA NA 2 4
```

telling us that the third value in `j` is equal to the second value in `x` and that the fourth value in '`j`' is equal to the fourth value in `x`.

`match` is asymmetric: `match(j, x)` is not the same as `match(x, j)`.

```
match(x, j)
## [1] NA 3 NA 4 NA NA NA NA NA NA
```

This tells us that the second value in `x` is equal to the third value in '`j`', etc.

## 1.5 Algebra

Vectors and matrices can be used to compute new vectors (matrices) with simple and intuitive algebraic expressions.

### Vector algebra

We have two vectors, `a` and `b`

```
a <- 1:5
b <- 6:10
```

Multiplication works element by element. That is `a[1] * b[1]`, `a[2] * b[2]`, etc

```
d <- a * b
a
## [1] 1 2 3 4 5
b
## [1] 6 7 8 9 10
d
## [1] 6 14 24 36 50
```

The examples above illustrate a special feature of *R* not found in most other programming languages. This is that you do not need to ‘loop’ over elements in an array (vector in this case) to compute new values. It is important to use this feature as much as possible. In other programming languages you would need to do something like the ‘for-loop’ below to achieve the above (for-loops do exist in *R* and are discussed in a later chapter).

You can also multiply with a single number.

```
a * 3
## [1] 3 6 9 12 15
```

In the examples above the computations used either vectors of the same length, or one of the vectors had length 1. But be careful, you can use algebraic computations with vectors of different lengths, as the shorter ones will be “recycled”. *R* only issues a warning if the length of the longer vector is not a multiple of the length of the shorter object. This is a great feature when you need it, but it may also make you overlook errors when your data are not what you think they are.

```
a + c(1,10)
## Warning in a + c(1, 10): longer object length is not a multiple of shorter
## object length
## [1] 2 12 4 14 6
```

No warning here:

```
1:6 + c(0,10)
## [1] 1 12 3 14 5 16
```

## Logical comparisons

Recall that `==` is used to test for equality

```
a == 2
## [1] FALSE TRUE FALSE FALSE FALSE
f <- a > 2
f
## [1] FALSE FALSE TRUE TRUE TRUE
```

`&` is Boolean “AND”, and `|` is Boolean “OR”.

```
a
## [1] 1 2 3 4 5
b
## [1] 6 7 8 9 10
b > 6 & b < 8
## [1] FALSE TRUE FALSE FALSE FALSE
# combining a and b
b > 9 | a < 2
## [1] TRUE FALSE FALSE FALSE TRUE
```

“Less than or equal” is  $\leq$ , and “more than or equal” is  $\geq$ .

```
b >= 9
## [1] FALSE FALSE FALSE TRUE TRUE
a <= 2
## [1] TRUE TRUE FALSE FALSE FALSE
b >= 9 | a <= 2
## [1] TRUE TRUE FALSE TRUE TRUE
b >= 9 & a <= 2
## [1] FALSE FALSE FALSE FALSE FALSE
```

## Functions

There are many functions that allow us to do vectorized algebra. For example:

```
sqrt(a)
## [1] 1.000000 1.414214 1.732051 2.000000 2.236068
exp(a)
## [1] 2.718282 7.389056 20.085537 54.598150 148.413159
```

Not all functions return a vector of the same length. The following functions return just one or two numbers:

```
min(a)
## [1] 1
max(a)
## [1] 5
range(a)
## [1] 1 5
sum(a)
## [1] 15
mean(a)
## [1] 3
median(a)
## [1] 3
prod(a)
## [1] 120
sd(a)
## [1] 1.581139
```

If you cannot guess what `prod` and `sd` do, look it up in the help files (e.g. `?sd`)

## Random numbers

It is common to create a vector of random numbers in data analysis, and also to create example data to demonstrate how a procedure works. To get 10 numbers sampled from the uniform distribution between 0 and 1 you can do

```
r <- runif(10)
r
## [1] 0.3506256 0.3939491 0.9509510 0.1066483 0.9347601 0.3461621 0.5330606
## [8] 0.5387943 0.7147179 0.4057905
```

For Normally distributed numbers, use `rnorm`

```
r <- rnorm(10, mean=10, sd=2)
r
## [1] 7.950903 10.646013 12.087225 11.466181 9.091726 8.688436 9.928155
## [8] 12.138323 9.032050 9.757980
```

If you run the functions above, you will get different numbers. After all, they are random numbers! Well, computer generated numbers are not truly random, but ‘pseudo-random’. To be able to exactly reproduce examples or data analysis we often want to assure that we take exactly the same “random” sample each time we run our code. To do that we use `set.seed`. This function initializes the random number generator to a specific point. This is illustrated below.

```
set.seed(12)
runif(3)
## [1] 0.06936092 0.81777520 0.94262173
runif(4)
## [1] 0.26938188 0.16934812 0.03389562 0.17878500
runif(5)
## [1] 0.641665366 0.022877743 0.008324827 0.392697197 0.813880559

set.seed(12)
runif(3)
## [1] 0.06936092 0.81777520 0.94262173
runif(5)
## [1] 0.26938188 0.16934812 0.03389562 0.17878500 0.64166537

set.seed(12)
runif(3)
## [1] 0.06936092 0.81777520 0.94262173
runif(5)
## [1] 0.26938188 0.16934812 0.03389562 0.17878500 0.64166537
```

Note that each time `set.seed` is called, the same sequence of (pseudo) random numbers will be generated. This is a very important feature, as it allows us to exactly reproduce results that involve random sampling. The seed number is arbitrary; a different seed number will give a different sequence.

```
set.seed(12)
runif(3)
## [1] 0.06936092 0.81777520 0.94262173
runif(5)
## [1] 0.26938188 0.16934812 0.03389562 0.17878500 0.64166537
```

## Matrices

Computation with matrices is also ‘vectorized’. For example, with matrix `m` you can do `m * 5` to multiply all values of `m` with 5, or do `m^2` or `m * m` to square the values of `m`.

```
# set up an example matrix
m <- matrix(1:6, ncol=3, nrow=2, byrow=TRUE)
m
##      [,1] [,2] [,3]
## [1,]  1   2   3
## [2,]  4   5   6

m * 2
##      [,1] [,2] [,3]
```

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```
## [1,] 2 4 6
## [2,] 8 10 12

m^2
##      [,1] [,2] [,3]
## [1,] 1 4 9
## [2,] 16 25 36
```

We can also do math with a matrix and a vector. Note, again, that computation with matrices in *R* is column-wise, and that shorter vectors are recycled.

```
m * 1:2
##      [,1] [,2] [,3]
## [1,] 1 2 3
## [2,] 8 10 12
```

You can multiply two matrices.

```
m * m
##      [,1] [,2] [,3]
## [1,] 1 4 9
## [2,] 16 25 36
```

Note that this is “cell by cell” multiplication. For ‘matrix multiplication’ in the mathematical sense, you need to use the `%*%` operator.

```
m %*% t(m)
##      [,1] [,2]
## [1,] 14 32
## [2,] 32 77
```

## 1.6 Read and write files

In most cases, the first step in data analysis is to read in a file with data. This can be pretty complicated due to the variations in file format. Here we discuss reading matrix-like (data.frame/spreadsheet) data structures, which is the most common case and relatively painless.

Although it is possible to directly read Excel files, we do not discuss that here.

To read a file into R, you need to know its name. That is, you need to know the full path (directory) name and the name of the file itself. Wrong path names often create confusion. On Windows, it is easy to copy the path from the top bar in Windows Explorer. On a Mac you can select the file and type Command + Option + C to copy the path to the clipboard.

Below I try to assign a Windows style full path and file name to a variable `f` so that we can use it.

```
f <- "C:\projects\research\data\obs.csv"
## Error: '\p' is an unrecognized escape in character string starting "'C:\p"
```

Yikes, an error! The problem is the use of backslashes. In R (and elsewhere), the backslash is the “escape” symbol, which is followed by another symbol to indicate a special character. For example, “\t” represents a “tab” and “\n” is the symbol for a new line (hard return). This is illustrated below.

```
txt <- "Here is an example:\nA new line has started!\nAnd another one...\n"
message(txt)
```

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```
## Here is an example:  
## A new line has started!  
## And another one...
```

So for path delimiters we need to use either the forward-slash "/" or an escaped back-slash "\\ ". Both of the following are OK.

```
f1 <- "C:/projects/research/data/obs.csv"  
f2 <- "C:\\projects\\research\\data\\obs.csv"
```

The values of `f1` and `f2` are just names. A file with that name may, or may not, actually exist. We can find out with the `file.exists` function.

```
file.exists(f1)  
## [1] FALSE
```

To make what you see here reproducible, we'll first create files from some example data.

```
d <- data.frame(id=1:10, name=letters[1:10], value=seq(10,28,2))  
d  
##      id name value  
## 1     1    a     10  
## 2     2    b     12  
## 3     3    c     14  
## 4     4    d     16  
## 5     5    e     18  
## 6     6    f     20  
## 7     7    g     22  
## 8     8    h     24  
## 9     9    i     26  
## 10    10   j     28
```

Now we write the values in data.frame `d` to disk. In this section, I show how to write to simple “text” files using two different (but related) functions: `write.csv` and `write.table`. It is also possible to read Excel files (with the `read_excel` function from the `readxl` package) and many other file types but that is not shown here.

```
write.csv(d, 'test.csv', row.names=FALSE)  
write.table(d, 'test.dat', row.names=FALSE)
```

`write.csv` is a derived from `write.table`. The main difference between the two is that in `write.csv` the field separator is a comma (“csv” stands for “comma separated values”), while in `write.table` the default is a tab (the `\t` character).

Now we have two files on disk.

```
file.exists('test.csv')  
## [1] TRUE  
file.exists('test.dat')  
## [1] TRUE
```

As we only specified a file name, but not a path, the files are in our working directory. We can use `getwd`(get working directory) to see where that is.

```
getwd()  
## [1] "C:/github/rspatial/web/base/source/intr/_R"
```

The working directory is the 'default' location where *R* will look for files and write files. To get the full path name for one of the files we created, we can use `file.path`.

```
file.path(getwd(), 'test.csv')
## [1] "C:/github/rspatial/web/base/source/intr/_R/test.csv"
```

As this is a '.csv' (comma separated values) file we can read it with `read.csv`.

```
d <- read.csv('test.csv', stringsAsFactors=FALSE)
head(d)
##   id name value
## 1  1   a    10
## 2  2   b    12
## 3  3   c    14
## 4  4   d    16
## 5  5   e    18
## 6  6   f    20
```

Sometimes values are delimited by other characters. In that case you can try `read.table`. `read.table` has an argument `sep` (separator) to indicate the field delimiter. Here we do not use that, because the default (whitespace, tab) works fine.

```
d <- read.table('test.dat', stringsAsFactors=FALSE)
head(d)
##   V1  V2  V3
## 1 id name value
## 2  1   a    10
## 3  2   b    12
## 4  3   c    14
## 5  4   d    16
## 6  5   e    18
```

Note that `read.table` did not automatically recognize the header row with the variable names. Instead, the variable names have become the first records, and new dummy variable names `V1`, `V2` and `V3` were assigned. To fix that, we use the `header` argument:

```
d <- read.table('test.dat', header=TRUE, stringsAsFactors=FALSE)
head(d)
##   id name value
## 1  1   a    10
## 2  2   b    12
## 3  3   c    14
## 4  4   d    16
## 5  5   e    18
## 6  6   f    20
```

`read.table` can also read csv files; you just need to tell it that the field delimiter is a comma.

```
d <- read.table('test.dat', sep=',', stringsAsFactors=FALSE)
```

In the examples above, I used `stringsAsFactors=FALSE`. This is not required, but it is helpful. Otherwise, all character variables are converted to factors, which in many cases is a nuisance. If `read.table` fails, there are other options, such as `readLines`.

```
d <- readLines('test.csv')
class(d)
## [1] "character"
```

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```
d
## [1] "\"id\", \"name\", \"value\"" "1, \"a\", 10"
## [3] "2, \"b\", 12" "3, \"c\", 14"
## [5] "4, \"d\", 16" "5, \"e\", 18"
## [7] "6, \"f\", 20" "7, \"g\", 22"
## [9] "8, \"h\", 24" "9, \"i\", 26"
## [11] "10, \"j\", 28"
```

But this makes it more difficult to process the data. You may need to do something like:

```
x <- sapply(d, function(i){ unlist(strsplit(i, ',')) }, USE.NAMES=FALSE)
t(x)
##      [,1]      [,2]      [,3]
## [1,] "\"id\""  "\"name\""  "\"value\""
## [2,] "1"       "\"a\""     "10"
## [3,] "2"       "\"b\""     "12"
## [4,] "3"       "\"c\""     "14"
## [5,] "4"       "\"d\""     "16"
## [6,] "5"       "\"e\""     "18"
## [7,] "6"       "\"f\""     "20"
## [8,] "7"       "\"g\""     "22"
## [9,] "8"       "\"h\""     "24"
## [10,] "9"      "\"i\""     "26"
## [11,] "10"     "\"j\""     "28"
```

And then some. (sapply is explained later on).

For some files, readLines is the way to go. For example, you may want to read 'html' files if you are scraping a website. We can read this very page:

```
webpage <- readLines("http://rspatial.org/intr/6-files.html", warn=FALSE)
#show some of the first lines:
webpage[150:155]
## [1] "</pre></div>"
## [2] "</div>"
## [3] "<p>Now we write the values in data.frame <code class=\"docutils literal_
↳notranslate\"><span class=\"pre\">d</span></code> to disk. In this section, I"
## [4] "show how to write to simple â\200etextâ\200\235 files using two different (but
↳"
## [5] "related) functions: <code class=\"docutils literal notranslate\"><span class=
↳pre\">write.csv</span></code> and <code class=\"docutils literal notranslate\">
↳<span class=\"pre\">write.table</span></code>. It is also"
## [6] "possible to read Excel files (with the <code class=\"docutils literal_
↳notranslate\"><span class=\"pre\">read_excel</span></code> function from the"
```

Another relevant function in this context is list.files. That shows you which files are present in your working directory (or another path of choice) and perhaps all other subdirectories (when using the argument recursive=TRUE). By doing something like ff <- list.files(pattern = 'csv\$') you can get a vector of all files with names that end with "csv" (that is what the \$ sign is for).

Before writing files (e.g. with write.csv, write.table, or writeLines), you may want to use dir.exists to assure that the path you are using exists and perhaps use dir.create if it does not.

File names need to be the full file name, including the path, unless you are reading from or writing to the working directory. You can set the working directory with setwd. For example: setwd("C:/projects/research/).

## 1.7 Data exploration

After reading data from a file (see the previous chapter), the next thing to do is to look at some summary statistics. This is in the first place just to check your data. Very often you discover some strange values that are not quite right. Careful inspection of your data after you read it is very important. It can help avoid a lot of trouble later on when you are trying to explain odd results!

Sometimes you can correct errors in *R* but in other cases you first need to fix the data file. Fixing a data file can be the way to go if you are dealing with your own primary data. However when you are working with a file provided by someone else it is generally better to not change the file, but to correct things via *R* code, if possible. That leaves an exact trail of what you have done, and allows you to apply the same corrections to a new version of the data.

Inspecting your data is also important to understand it better, and such “exploratory data analysis” can be an important step before doing the specific analyses of interest. There are many general and specialized tools for this, and here we only cover some of the very basic tools.

### Summary and table

Consider `data.frame d`

```
d <- data.frame(id=1:10,
  name=c('Bob', 'Bobby', '???', 'Bob', 'Bab', 'Jim', 'Jim', 'jim', '', 'Jim'),
  score1=c(8, 10, 7, 9, 2, 5, 1, 6, 3, 4),
  score2=c(3, 4, 5, -999, 5, 5, -999, 2, 3, 4), stringsAsFactors=FALSE)
d
##   id  name score1 score2
## 1  1  Bob      8      3
## 2  2 Bobby    10      4
## 3  3   ???     7      5
## 4  4  Bob     9    -999
## 5  5  Bab     2      5
## 6  6  Jim     5      5
## 7  7  Jim     1    -999
## 8  8  jim     6      2
## 9  9      3      3
## 10 10  Jim     4      4
```

`d` is very small and we can simply look at the values in `d` to see if they look all-right. But with real data you may have 100s or 1000s of rows and many columns, making it very hard, if not impossible, to spot errors by eye-balling.

The summary function is an easy way to start, at least for numeric variables.

```
summary(d)
##      id          name          score1          score2
## Min.   : 1.00   Length:10   Min.    : 1.00   Min.    : -999.00
## 1st Qu.: 3.25   Class :character 1st Qu.: 3.25   1st Qu.:  2.25
## Median : 5.50   Mode  :character Median : 5.50   Median :  3.50
## Mean   : 5.50          Mean  : 5.50   Mean   : -196.70
## 3rd Qu.: 7.75          3rd Qu.: 7.75 3rd Qu.:  4.75
## Max.   :10.00          Max.   :10.00 Max.    :  5.00
```

The minimum value of variable `score2` is `-999`. That was probably used in data entry to indicate a missing value. These should be changed to `NA`.

```
# which values in score2 are -999?
i <- d$score2 == -999
# set these to NA
```

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```
d$score2[i] <- NA
summary(d)
##           id           name           score1           score2
##  Min.      : 1.00   Length:10   Min.      : 1.00   Min.      :2.000
##  1st Qu.: 3.25   Class :character  1st Qu.: 3.25   1st Qu.:3.000
##  Median : 5.50   Mode  :character  Median : 5.50   Median :4.000
##  Mean    : 5.50                   Mean    : 5.50   Mean    :3.875
##  3rd Qu.: 7.75                   3rd Qu.: 7.75   3rd Qu.:5.000
##  Max.    :10.00                   Max.    :10.00   Max.    :5.000
##                                     NA's    :2
```

The two steps used above: `i <- d$score2 == -999` and `d$score2[i] <- NA` are usually done in a single line: `d$score2[d$score2 == -999] <- NA`.

For character (and integer) variables it can be useful to use `unique` and `table`:

```
unique(d$name)
## [1] "Bob" "Bobby" "???" "Bab" "Jim" "jim" ""
table(d$name)
##
##      ??? Bab Bob Bobby jim Jim
##      1  1  1  2  1  1  3
```

Often you will discover slight variations in spelling that need to be corrected. In this case, let's assume that 'Bobby' and 'Bab' should both be 'Bob'. We replace 'Bab' and 'Bobby' with 'Bob'.

```
d$name[d$name %in% c('Bab', 'Bobby')] <- 'Bob'
table(d$name)
##
##      ??? Bob jim Jim
##      1  1  4  1  3
```

'jim' should be "Jim". It is easy enough to replace as done above. But what if there were many cases like that? It would be easy to make all character values lower- or uppercase with `d$name <- toupper(d$name)` but I want to keep the normal name capitalization of the first letter only. So let's assure that all names start with an uppercase letter.

```
# get the first letters
first <- substr(d$name, 1, 1)
# get the remainder
remainder <- substr(d$name, 2, nchar(d$name))
# assure that the first letter is upper case
first <- toupper(first)
# combine
name <- paste0(first, remainder)
# assign back to the variable
d$name <- name
table(d$name)
##
##      ??? Bob Jim
##      1  1  4  4
```

The question marks in name should probably also be replaced with NA.

```
d$name[d$name == '???'] <- NA
table(d$name)
```

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```
##  
##      Bob Jim  
##    1  4  4
```

You can force `table` to also count the NA values:

```
table(d$name, useNA='ifany')  
##  
##      Bob  Jim <NA>  
##    1  4  4  1
```

Note that there is one 'empty' value.

```
d$name[9]  
## [1] ""
```

That should also be a missing value in this case.

```
d$name[d$name == ''] <- NA  
table(d$name, useNA='ifany')  
##  
##      Bob  Jim <NA>  
##    4  4  2
```

You can also use `table` to make a contingency table of two variables.

```
table(d[ c('name', 'score2')])  
##      score2  
## name  2 3 4 5  
##   Bob 0 1 1 1  
##   Jim 1 0 1 1
```

## Quantile, range, and mean

Other useful functions include `quantile`, `range`, and `mean`.

```
quantile(d$score1)  
##    0%   25%   50%   75%  100%  
##  1.00  3.25  5.50  7.75 10.00  
range(d$score1)  
## [1]  1 10  
mean(d$score1)  
## [1] 5.5
```

Note that in some functions you may need to use `na.rm=TRUE` if there are NA values. Otherwise, as soon as there is a single NA value in a computation, the results becomes NA. This is very common in *R* — so keep that in mind if all your results are NA.

```
quantile(d$score2)  
## Error in quantile.default(d$score2): missing values and NaN's not allowed if 'na.rm  
→' is FALSE  
range(d$score2)  
## [1] NA NA  
quantile(d$score2, na.rm=TRUE)  
##    0%   25%   50%   75%  100%
```

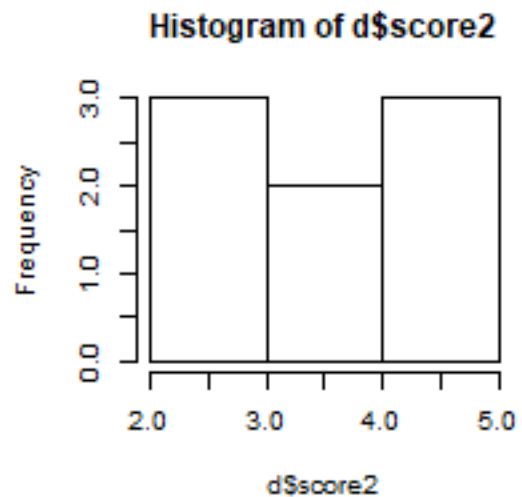
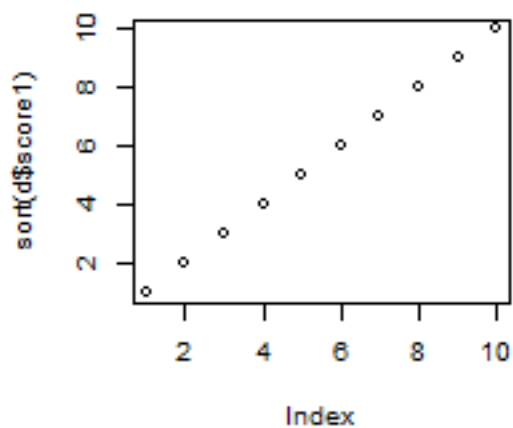
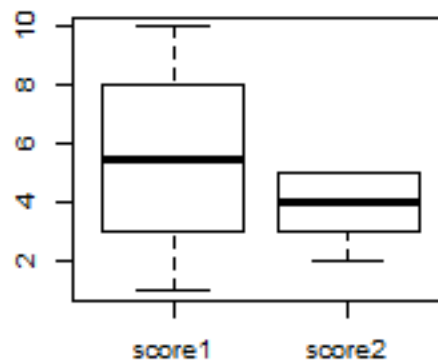
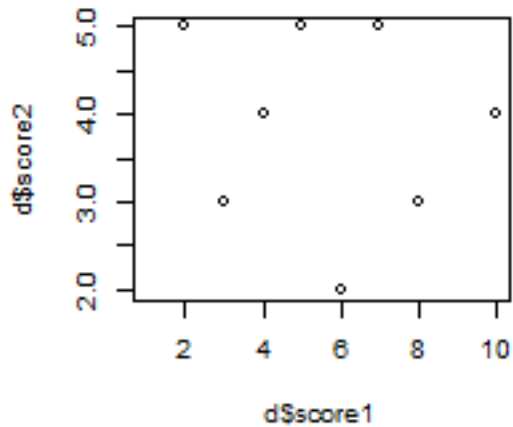
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```
##      2      3      4      5      5
range(d$score2, na.rm=TRUE)
## [1] 2 5
```

In this data exploration phase it is very useful to make plots. We'll discuss plotting in a later chapter, but here are four example plots. Note how `par(mfrow=c(2,2))` sets up the canvas for two rows and columns, that is for four plots.

```
par(mfrow=c(2,2))
plot(d$score1, d$score2)
boxplot(d[, c('score1', 'score2')])
plot(sort(d$score1))
hist(d$score2)
```



## 1.8 Functions

We now have used many functions that come with *R*. For example `c`, `matrix`, `read.csv`, and `sum`. Functions are always used ('called') by typing their name, followed by parenthesis. In most, but not all, cases you supply 'arguments' within the parenthesis. If you do not type the parenthesis the function is not called. Instead, either the function definition or some of type of reference to it is shown.

### Existing functions

To see the content of a function, type its name:

```
nrow
## function (x)
## dim(x) [1L]
## <bytecode: 0x000000001862ef80>
## <environment: namespace:base>
```

We see that `nrow` has a single argument called `x`. It calls another function, `dim` to which it provides the same argument (`x`) and returns its first element (`1L`) (recall that adding `L` ('literal') is a way to create an integer). Can you guess how `ncol` is implemented? (See for yourself if you are right!). Now, let's see what `dim` looks like.

```
dim
## function (x) .Primitive("dim")
```

It is a 'primitive' (low level) *R* function that we cannot easily learn more about. Well, you could, by looking at the source code of *R* — but that is way out of scope of this tutorial.

To run (instead of inspect) `nrow` we add parentheses:

```
nrow()
## Error in nrow(): argument "x" is missing, with no default
```

But this fails, because the function requires a valid argument, like this:

```
m <- matrix(1:6, nrow=2, ncol=3, byrow=TRUE)
nrow(m)
## [1] 2
```

Note `nrow(m)` and that this is equivalent to

```
nrow(x=m)
## [1] 2
```

because the first argument of `nrow` is called `x`.

### Writing functions

*R* comes with thousands of functions for you to use. Nevertheless, it is often necessary to write your own functions. For example, you may want to write a function to:

- more clearly describe and isolate a particular task in your data analysis workflow.
- re-use code. Rather than repeating the same steps several times (e.g. for each of 200 cases you are analysing), you can write a function that gets called 200 times. This should lead to faster development of scripts and to fewer mistakes. And if there is a mistake it only needs to be fixed in one place.



- create a function that is an argument to another function (!). This is quite commonly done when using ‘apply’ type functions (see next chapter).

Writing your own functions is not difficult. The below is a very simple function. It is called `f`. This is an entirely arbitrary name. You can also call it `myFirstFunction`. It takes no arguments, and always returns ‘hello’.

```
f <- function() {
  return('hello')
}
```

Look carefully how we assign a function to name `f` using the `function` keyword followed by parenthesis that enclose the arguments (there are none in this case). The *body* of the function is enclosed in braces (also known as “curly brackets” or “squiggly brackets”).

Now that we have the function, we can inspect it, and use it.

```
#inspect
f
## function() {
##   return('hello')
## }
## <environment: 0x000000001ff140c0>
#use 2 times
f()
## [1] "hello"
f()
## [1] "hello"
```

`f` is a very boring function. It takes no arguments and always returns the same result. Let’s make it more interesting.

```
f <- function(name) {
  x <- paste('hello', name)
  return(x)
}

f('Jasmin')
## [1] "hello Jasmin"
```

Note the `return` statement. This indicates that variable `x` (which is only known inside of the function) is returned to the caller of the function. Simply typing `x` would also suffice, and ending the function with `paste('hello', name)` would also do! So the below is equivalent but shorter, at the expense of being less explicit.

```
f <- function(name) {
  paste('hello', name)
}

f('Sviatoslav')
## [1] "hello Sviatoslav"
```

Here is a function that returns a sequence of letters. The length is determined by argument `n`.

```
frs <- function(n) {
  s <- sample(letters, n, replace=TRUE)
  r <- paste0(s, collapse='')
  return(r)
}
```

Because the function uses randomization, I use `set.seed` to always get the same result (as we discussed [here](#)).

```
set.seed(0)
frs(5)
## [1] "nydga"
frs(5)
## [1] "bwknr"
x <- frs(10)
x
## [1] "sauujvnjgi"
```

Now an example of a functions that manipulates numbers. This function squares the sum of two numbers.

```
sumsquare <- function(a, b) {
  d <- a + b
  dd <- d * d
  return(dd)
}
```

We can now use the sumsquare function. Note that it is vectorized (each argument can be more than one number)

```
sumsquare(1,2)
## [1] 9
x <- 1:3
y <- 5
sumsquare(x,y)
## [1] 36 49 64
```

You can name the arguments when using a function; that often makes your intentions clearer.

```
sumsquare(a=1, b=2)
## [1] 9
```

But the names must match

```
sumsquare(a=1, d=2)
## Error in sumsquare(a = 1, d = 2): unused argument (d = 2)
```

And both arguments need to be present

```
sumsquare(1:5)
## Error in sumsquare(1:5): argument "b" is missing, with no default
```

Unless we redefine the function with default arguments that will be used if a value for the argument is not provided.

```
sumsquareD <- function(a=0, b=1) {
  d <- a + b
  dd <- d * d
  return(dd)
}

sumsquareD(1:5, 2)
## [1] 9 16 25 36 49
```

As both arguments have a default value, we can call sumsquareD without providing arguments

```
sumsquareD()
## [1] 1
```

Or with a single argument

```
sumsquareD(5)
## [1] 36
```

Above the value 5 was assigned to argument `a` because the argument was matched “by position”. If we only wanted to provide a value for `b`, we need to match “by name”.

```
sumsquareD(b=3)
## [1] 9
```

Just another example, a function to compute the number of unique values in a vector:

```
nunique <- function(x) {
  length(unique(x))
}

data <- c('a', 'b', 'a', 'c', 'b')
nunique(data)
## [1] 3
```

Of course, these were toy examples, but if you understand these, you should be able to write much longer and more useful functions. It can be difficult to “debug” (find errors in) a function. It is often best to first write the sequence of commands that you need outside a function, and only when it all works, wrap that code inside of a function block (`function( ) { }`).

## Ellipses (...)

Ellipses `...` are a special argument to many functions. It allows to pass optional additional arguments and/or arguments that are passed on to other functions. Consider these two functions (this is a bit advanced).

```
f1 <- function(x, y=10) {
  x * y
}

# f2 calls f1
f2 <- function(x, ...) {
  f1(x, ...)
}

f2(5)
## [1] 50
f2(5, y=5)
## [1] 25
```

Even though `f2` does not have an argument `y` it can be provided and it is passed on to `f1`. This call returns an error :

```
f2(5, z=5)
## Error in f1(x, ...): unused argument (z = 5)
```

because `f1` does not have an argument `z`.

## Functions overview

A list of much used functions that we discuss in this introduction to *R*:

`c`, `cbind`, `rbind` `length`, `dim`, `nrow`, `ncol`

`sum`, `mean`, `prod`, `sqrt`

`apply`, `sapply`, `tapply`, `aggregate` `rowSums`, `rowMeans`

`merge`, `reshape`

Also see this [cheatsheet](#)

## 1.9 Apply

The “apply family” of functions (`apply`, `tapply`, `lapply` and others) and related functions such as `aggregate` are central to using *R*. They provide an concise, elegant and efficient approach to apply (sometimes referred to as “to map”) a function to a set of cases, be they rows or columns in a matrix or `data.frame`, or elements in a list.

### apply

Consider matrix `m`

```
m <- matrix(1:15, nrow=5, ncol=3)
m
##      [,1] [,2] [,3]
## [1,]    1    6   11
## [2,]    2    7   12
## [3,]    3    8   13
## [4,]    4    9   14
## [5,]    5   10   15
```

### apply

Computation with matrices is ‘vectorized’. For example you can do `m * 5` to multiply all values of `m` with 5 or do `m^2` or `m * m` to square the values of `m`. But often we need to compute values for the margins of a matrix, that is, a single value for each row or column. The `apply` function can be used for that:

```
# sum values in each row
apply(m, 1, sum)
## [1] 18 21 24 27 30

# get mean for each column
apply(m, 2, mean)
## [1] 3 8 13
```

Note that the `apply` uses at least three arguments: a matrix, a 1 or 2 indicating whether the computation is for rows or for columns, and a function that computes a new value (or values) for each row or column. You can read more about this in the help file of the function (type `?apply`). In most cases you will also add the argument `na.rm=TRUE` to remove NA (missing) values as any computation that includes an NA value will return NA. In this case we used existing basic functions `mean` and `sum` but we could also supply a function that we wrote ourselves.

Note that `apply` (and related functions such as `tapply` and `sapply`) are ways to avoid writing a loop. In the `apply` examples above you could have written a loop to do the computations row by row (or column by column) but using `apply` is more compact and efficient.

The rowSums and colSums functions are (fast) shorthand functions for apply( , , sum)

```
rowSums(m)
## [1] 18 21 24 27 30
```

## tapply

tapply can be used to compute a summary statistic, e.g. a mean value, for groups of rows in a data.frame. You need one column that indicates the group, and then you can compute, for example, the mean value for that group.

```
colnames(m) <- c('v1', 'v2', 'v3')
d <- data.frame(name=c('Yi', 'Yi', 'Yi', 'Er', 'Er'), m, stringsAsFactors=FALSE)
d$v2[1] <- NA
d
##   name v1 v2 v3
## 1  Yi  1 NA 11
## 2  Yi  2  7 12
## 3  Yi  3  8 13
## 4  Er  4  9 14
## 5  Er  5 10 15
```

Imagine that you would like to compute the average value of v1, v2 and v3 for each individual (name). You can use tapply for that.

```
tapply(d$v1, d$name, mean)
## Er Yi
## 4.5 2.0
tapply(d$v1, d$name, max)
## Er Yi
## 5 3
tapply(d$v2, d$name, mean)
## Er Yi
## 9.5 NA
tapply(d$v2, d$name, mean, na.rm=TRUE)
## Er Yi
## 9.5 7.5
```

## aggregate

aggregate is similar to tapply but more convenient if you want to compute a summary statistic for multiple variables. It does have the annoying problem that the second argument cannot be a vector:

```
aggregate(d[, c('v1', 'v2', 'v3')], d$name, mean, na.rm=TRUE)
## Error in aggregate.data.frame(d[, c("v1", "v2", "v3")], d$name, mean, : 'by' must
  ↳ be a list
```

You can fix that in two ways

```
aggregate(d[, c('v1', 'v2', 'v3')], d[, 'name', drop=FALSE], mean, na.rm=TRUE)
##   name  v1  v2  v3
## 1  Er 4.5 9.5 14.5
## 2  Yi 2.0 7.5 12.0
# or
aggregate(d[, c('v1', 'v2', 'v3')], list(d$name), mean, na.rm=TRUE)
##   Group.1  v1  v2  v3
```

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```
## 1      Er 4.5 9.5 14.5
## 2      Yi 2.0 7.5 12.0
```

As explained before, this is why the first one works: when you extract a single column from a `matrix` or `data.frame`, the structure (class) “drops” to a simpler form, it becomes a vector. `drop=FALSE` stops that from happening.

## sapply and lapply

To iterate over a list, we can use `lapply` or `sapply`. The difference is that `lapply` always returns a list while `sapply` tries to simplify the result to a vector or matrix.

```
names <- list('Antoinette', 'Mary', 'Duncan', 'Obalaya', 'Jojo')
nchar('Jim')
## [1] 3

lapply(names, nchar)
## [[1]]
## [1] 10
##
## [[2]]
## [1] 4
##
## [[3]]
## [1] 6
##
## [[4]]
## [1] 7
##
## [[5]]
## [1] 4
sapply(names, nchar)
## [1] 10 4 6 7 4
```

In all cases (`t`) (`s`) (`l`) `apply` and `aggregate` (and many more functions) we provided some data and a function, such as `mean` or `nchar`. You can also provide your own custom function. For example

```
shortname <- function(name) {
  if (nchar(name) < 5) {
    name <- toupper(name)
    return(name)
  } else {
    name <- substr(name,1,5)
    return(name)
  }
}

sapply(names, shortname)
## [1] "Antoi" "MARY" "Dunca" "Obala" "JOJO"
```

More examples: <https://nsaunders.wordpress.com/2010/08/20/a-brief-introduction-to-apply-in-r/>

## 1.10 Flow control

Most programs have two general control-flow features: iteration and alternation. Iteration is done via “loops”, alternation via “if-then-else” branches.

### Looping

Loops are typically used to repeat the same code a number of times for a set of cases. For example, compute the average grade for each student.

In *R* we avoid loops wherever we can, as they tend to be slower than ‘vectorized’ computation. We also generally prefer functions like `apply` (see the previous chapter), as this is more concise. At first code using for-loops may seem easier to read, but after using *R* for a while, the reverse is true in most cases. Nevertheless, there are cases where loops are much easier to write and clearer to read than using vectorized approaches.

There are two types of loops: ‘for-loops’ and ‘while-loops’. A ‘for-loop’ repeats the same code a predefined number of times. A ‘while-loop’ continues until a certain condition has been met (and is therefore prone to the dreaded “infinite loop” that never finishes!)

### for-loops

Here is a basic *for-loop* that does not do anything useful. The trick is that in the parenthesis after `for`, you define a sequence of values. This sets the number of repetitions (the length of the sequence) and potentially provides a value that changes what is done in each loop.

Note that the braces `{ }` are used to open and close a ‘block’ of code.

```
for (i in 1:3) {
  print('hi')
}
## [1] "hi"
## [1] "hi"
## [1] "hi"
```

Now let’s do something with `i`. You normally do not use `print` inside a loop. I am only doing that here to illustrate what is going on.

```
j <- 0
for (i in 1:3) {
  print(i)
  j <- j + i
}
## [1] 1
## [1] 2
## [1] 3
j
## [1] 6
```

The loop above was used to sum the values 1, 2, and 3. Of course, it would have been easier to use `sum(1:3)`.

Another example.

```
for (i in 1:3) {
  txt <- paste('the square of', i, 'is', i * i)
  print(txt)
}
```

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```
## [1] "the square of 1 is 1"  
## [1] "the square of 2 is 4"  
## [1] "the square of 3 is 9"
```

The example below is a bit more complex. It shows how iterator `i` is typically used in a loop (to get a single case from a collection of cases and compute a new value for that case).

```
s <- 0  
a <- 1:6  
b <- 6:1  
  
# initialization of output variables  
res <- vector(length=length(a))  
  
# i goes from 1 to 6 (the length of b)  
for (i in 1:length(b)) {  
  s <- s + a[i]  
  res[i] <- a[i] * b[i]  
}  
s  
## [1] 21  
res  
## [1] 6 10 12 12 10 6
```

Again, for this simple problem, it would have been simpler to do `s <- sum(a)` and `res <- a * b`.

## break and next

Sometimes you want to include a condition to either “break out” of a for loop, or to skip the remainder of the for block and go to the next iteration. How to do that is illustrated below:

```
for (i in 1:10) {  
  if (i %in% c(1,3,5,7)) {  
    next  
  }  
  if (i > 8) {  
    break  
  }  
  print(i)  
}  
## [1] 2  
## [1] 4  
## [1] 6  
## [1] 8
```



## while-loops

“while-loops” are not nearly as common as “for-loops”. Here is an example.

```
i <- 0
while (i < 4) {
  print(paste(i, 'and counting ...'))
  i <- i + 1
}
## [1] "0 and counting ..."
## [1] "1 and counting ..."
## [1] "2 and counting ..."
## [1] "3 and counting ..."
```

And one that is less predictable, as it depends on the value of a random number.

```
set.seed(1)
i <- 0
while(i < 0.5) {
  i <- runif(1)
  print(i)
}
## [1] 0.2655087
## [1] 0.3721239
## [1] 0.5728534
```

You can also combine while with break.

```
set.seed(1)
while(TRUE) {
  i <- runif(1)
  print(i)
  if (i > 0.5) {
    break
  }
}
## [1] 0.2655087
## [1] 0.3721239
## [1] 0.5728534
```

## Branching

Branching is an important mechanism in computer programs. A branch allows you to execute some code if certain conditions are met, and do something else in other cases. This is illustrated below. Note that the braces { } are used to open and close a ‘block’ of code.

We have two variables, x and y

```
x <- 5
y <- 10
```

We want to change y, depending on the value of x.

We need to branch our R code using one or more conditional statements (if, then, else) and some boolean logic (a statement that can evaluate to TRUE or FALSE).

```

if (x == 5) {
  y <- 15
}
Y
## [1] 15

```

We tested for one condition,  $x==5$ . If this condition evaluated to `TRUE`, the code within the block, `{ y <- 15 }` is executed. If it evaluates to `FALSE`, the code within the block is ignored. Note that the expression within the parenthesis `if()`, or `else()` should always evaluate to a single value of either `TRUE` or `FALSE` (not to `NA` or to multiple values).

Here is a more complex example, where we evaluate three cases.  $x > 20$  ( $x$  is larger than 20),  $x >= 5 \ \& \ x < 10$  ( $x$  is in between 5 and 10, including 5, but not 10), and all other cases.

```

if (x > 20) {
  y <- y + 2
} else if (x > 5 & x < 10) {
  y <- y - 1
} else {
  y <- x
}
Y
## [1] 5

```

If we have a boolean variable

```
b <- TRUE
```

You can do

```

if (b == TRUE) {
  print('hello')
}
## [1] "hello"

```

But it is more elegant to do

```

if (b) {
  print('hello')
}
## [1] "hello"

```

Now combining the previous chapter with this one, a for loop with an if/else branch:

```

a <- 1:5
f <- vector(length=length(a))
for (i in 1:length(a)) {
  if (a[i] > 2) {
    f[i] <- a[i] / 2
  } else {
    f[i] <- a[i] * 2
  }
}
f
## [1] 2.0 4.0 1.5 2.0 2.5

```

## 1.11 Data preparation

A very large part of research work can consist of data gathering, cleaning, combining and formatting. You may spend much more time on data preparation than on analysis, modeling or visualization. R provides some tools to make this process easier; but doing this well also requires that you carefully consider your options. See Wickham (2014) for a discussion. Two very important functions in this context are `reshape` and `merge`. Sorting of data can also be helpful.

### reshape

`reshape` allows you to rearrange data from a *wide* to a *long* form and vice versa. This can be a very important step to simplify data analysis. In the *wide* form, each variable is a column and each case (e.g. individual) is a single row. This is the common ‘spreadsheet’ approach. In the *long* form there is column that indicates the variable name and a column that has its value. Other columns identify the cases, and these can be repeated many times. The long form can be much easier for use in data analysis than the wide form. In many cases you may want to go from one form to the other and back.

The function to go between *wide* and *long* form is called `reshape`. Unfortunately `reshape` is rather difficult to use. There is only one function to go from wide to long and vice versa, creating confusion about what arguments to use when. It is also poorly documented, and its error messages are bewildering. (There is a package called `reshape` that you can use instead. But in this Introduction I want to stick with base R idiom.)

There is a good example of how to use `reshape` [here](#). And I will re-use that and expand on it.

### wide to long

Get some example data on student’s performance in different subjects. Note how you can read a text on a web server (http address).

```
dd <- read.csv('https://stats.idre.ucla.edu/stat/data/hsb2.csv')
d <- dd[1:3, c(1:2, 8:9)]
d
##      id female write math
## 1   70      0   52   41
## 2  121      1   59   53
## 3   86      0   33   54
```

This is a “wide” form dataset. To go to a long form, you need to provide an argument `varying` that indicates the variables that are combined into one new variable. `v.names` is the name of this new variable.

```
wvars <- c("write", "math")
x <- reshape(d, varying=wvars, v.names="score", direction = "long")
x
##           id female time score
## 70.1     70      0    1    52
## 121.1  121      1    1    59
## 86.1     86      0    1    33
## 70.2     70      0    2    41
## 121.2  121      1    2    53
## 86.2     86      0    2    54
```

`x` has two new variables “time”, and “score”. As you can see, “score” has the values for “write” and “math” in the `d`. The “time” variable identifies which is which. “write” is identified with a 1, and “math” is identified with a 2. To have clear labels rather than such numbers, you can use the `times` argument; and add the `timevar` argument to

rename “time” to something more meaningful. Note that the argument names are based on the idea that the data refer to different measurements over time. But this is not always the case.

```
x <- reshape(d, varying=wvars, v.names="score", times=wvars, timevar = "subject",  
↳direction = "long")  
x  
##      id female subject score  
## 70.write  70      0  write  52  
## 121.write 121      1  write  59  
## 86.write  86      0  write  33  
## 70.math   70      0  math   41  
## 121.math 121      1  math   53  
## 86.math   86      0  math   54
```

The row names also identify how the records were created. To get rid of the row names do

```
rownames(x) <- NULL  
x  
##      id female subject score  
## 1  70      0  write  52  
## 2 121      1  write  59  
## 3  86      0  write  33  
## 4  70      0  math   41  
## 5 121      1  math   53  
## 6  86      0  math   54
```

Variables “id” and “female” were unchanging, but they were duplicated because two variables (“write” and “math”) were combined into one (“subject”)

## long to wide

To go from long to wide we need to use “idvar” and “timevar”. “idvar” identifies the variables that identify a single case (e.g. a single person, or other observational unit). In contrast, “timevar” indicates the variable that has the identifiers that become variables in the wide format. The remaining variable should have the values that match these new variables.

```
w <- reshape(x, idvar=c("id", "female"), timevar = "subject", direction = "wide")  
w  
##      id female score.write score.math  
## 1  70      0      52      41  
## 2 121      1      59      53  
## 3  86      0      33      54
```

Note that w is identical to d, except for the last two column names that now have “score.” prepended to them. We can change that like this:

```
cn <- colnames(w)  
cn <- gsub("score.", "", cn)  
colnames(w) <- cn  
w  
##      id female write math  
## 1  70      0     52   41  
## 2 121      1     59   53  
## 3  86      0     33   54
```

## merge

A common situation is to have multiple data.frames with data for the same cases (e.g., individuals, fields, countries, ...). Such data.frames may need to be joined such that they can be analyzed. For example here we have a and b:

```
a <- dd[, 1:3]
# random sample of 100 records)
set.seed(1)
b <- dd[sample(nrow(dd), 100), c(1, 7:10)]
```

a has 200 records. It has a unique identifier for each student and information about their sex (female or not) and race (4 groups).

```
dim(a)
## [1] 200 3
head(a)
##   id female race
## 1  70      0   4
## 2 121      1   4
## 3  86      0   4
## 4 141      0   4
## 5 172      0   4
## 6 113      0   4
table(a$female)
##
##  0  1
## 91 109
table(a$race)
##
##  1  2  3  4
## 24 11 20 145
```

b has the same unique identifier as a (but only for 100 students) and it has the grades for four subjects.

```
dim(b)
## [1] 100 5
head(b)
##   id read write math science
## 68 107  47   39   47      42
## 167 156  50   59   53      61
## 129  91  50   49   56      47
## 162  74  57   50   50      51
##  43 168  52   54   57      55
##  14 104  54   63   57      55
```

Imagine we were interested in differences in reading by sex or race. We would need to combine a and b. That, fortunately, is very simple, because we have the merge function.

```
ab <- merge(a, b, by='id')
head(ab)
##   id female race read write math science
## 1  3      0   1  63   65   48      63
## 2  6      1   1  47   41   46      40
## 3  8      1   1  39   44   52      44
## 4  9      0   1  48   49   52      44
## 5 12      0   1  37   44   45      39
## 6 13      1   1  47   46   39      47
```

Always check the dimensions of the result

```
dim(ab)
## [1] 100  7
```

In this case we expected 100 records (the lower number of the two; a had 200 records, but b only 100). Sometimes you get fewer than expected, suggesting that the identifiers do not match. In other cases you might want to keep *all* records, and create missing values where these are not available. You can do that like this:

```
ab <- merge(a, b, by='id', all.x=TRUE)
dim(ab)
## [1] 200  7
head(ab)
##   id female race read write math science
## 1  1     1    1  NA   NA   NA     NA
## 2  2     1    1  NA   NA   NA     NA
## 3  3     0    1  63   65   48     63
## 4  4     1    1  NA   NA   NA     NA
## 5  5     0    1  NA   NA   NA     NA
## 6  6     1    1  47   41   46     40
```

Note that the “x” in `all.x` refers to the first argument, hence a in this case. In other cases you might need to say `all.y=TRUE` or `all=TRUE`. Consider these extreme cases (with no matching records):

```
merge(a[1:3,], b[1:3, ], by='id')
## [1] id      female race   read   write  math   science
## <0 rows> (or 0-length row.names)
merge(a[1:3,], b[1:3, ], by='id', all.x=T)
##   id female race read write math science
## 1  70     0    4  NA   NA   NA     NA
## 2  86     0    4  NA   NA   NA     NA
## 3 121     1    4  NA   NA   NA     NA
merge(a[1:3,], b[1:3, ], by='id', all.y=T)
##   id female race read write math science
## 1  91     NA   NA  50   49   56     47
## 2 107     NA   NA  47   39   47     42
## 3 156     NA   NA  50   59   53     61
merge(a[1:3,], b[1:3, ], by='id', all=T)
##   id female race read write math science
## 1  70     0    4  NA   NA   NA     NA
## 2  86     0    4  NA   NA   NA     NA
## 3  91     NA   NA  50   49   56     47
## 4 107     NA   NA  47   39   47     42
## 5 121     1    4  NA   NA   NA     NA
## 6 156     NA   NA  50   59   53     61
```

Now that we have ab we can compute what we needed:

```
tapply(ab$read, ab$female, mean, na.rm=TRUE)
##      0      1
## 53.43902 52.20339
tapply(ab$read, ab$race, mean, na.rm=TRUE)
##      1      2      3      4
## 49.69231 56.00000 45.00000 54.22535
```

## sort

It is often useful to sort data to make it easier to inspect it. R has a sort function but that is only for vectors. For matrices or data.frames you need to use the `order` function.

`sort` is straightforward:

```
x <- sample(10)
x
## [1] 10 8 2 5 4 7 6 9 3 1
sort(x)
## [1] 1 2 3 4 5 6 7 8 9 10
```

Now consider `order`:

```
i <- order(x)
i
## [1] 10 3 9 5 4 7 6 2 8 1
x[i]
## [1] 1 2 3 4 5 6 7 8 9 10
```

`order` returns a vector that allows you to sort. The first value of `i` is 7. This means that `x[7]` should be the lowest number in `x`. The next number is `x[6]` followed by `x[3]` and `x[2]` and so forth.

Consider data.frame `x`:

```
set.seed(0)
x <- a[sample(nrow(a), 10), ]
x
##      id female race
## 142  90      1    4
##  68 107      0    4
## 167 156      1    4
## 129  91      1    4
## 162  74      1    4
##  43 168      0    4
##  14 104      0    4
## 187 158      1    4
##  51  27      0    2
##  85  58      0    4
```

Here is how you can use `order` to sort it by one column (“id” in this case):

```
oid <- order(x$id)
y <- x[oid, ]
y
##      id female race
##  51  27      0    2
##  85  58      0    4
## 162  74      1    4
## 142  90      1    4
## 129  91      1    4
##  14 104      0    4
##  68 107      0    4
## 167 156      1    4
## 187 158      1    4
##  43 168      0    4
```

Or by multiple columns. In this case, we want to sort first by “race”, then by “female” and then by “id”:

```
oid <- order(x$race, x$female, x$id)
x[oid, ]
##      id female race
## 51    27      0    2
## 85    58      0    4
## 14   104      0    4
## 68   107      0    4
## 43   168      0    4
## 162   74      1    4
## 142   90      1    4
## 129   91      1    4
## 167  156      1    4
## 187  158      1    4
```

## 1.12 Graphics

With R you can make beautiful plots. You have a lot of control over what you want your plots to look like. But all the control is via code, and this does make things pretty complicated at times.

Moreover, there are entirely different approaches to make plots. Here we only discuss scatter-plots with the “base” package. The next chapter shows other basic plot types. The chapter thereafter shows how you can make plots with additional packages `lattice` and `ggplot`. It is very useful to learn about “base” plotting first before you get into the more complicated (and sometimes, but not always more fancy) approaches. There are many websites with cool examples.

Here we use the `cars`, `InsectSprays` and `iris` data sets that come with R.

`cars` has two variables: the speed of cars and the distances taken to stop (data recorded in the 1920s), see `?cars`

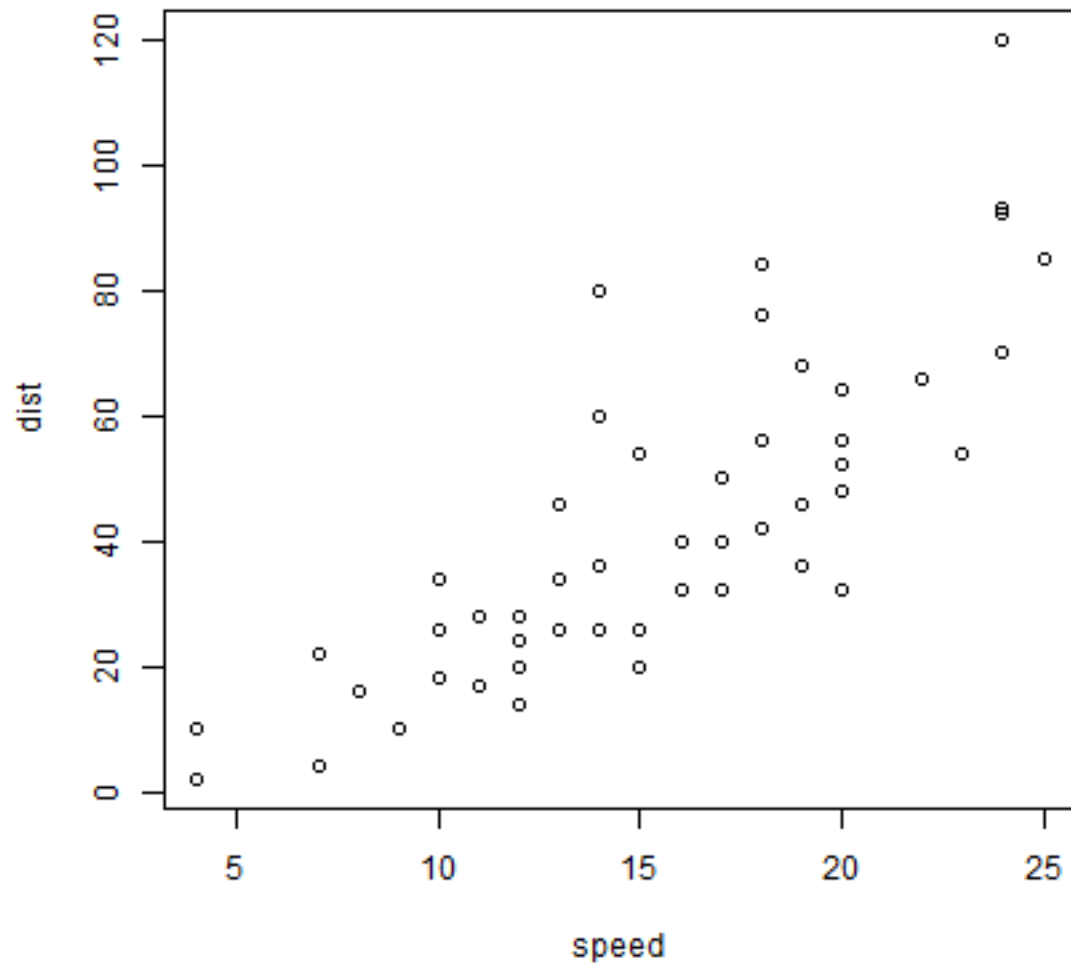
### Scatter plots

```
data(cars)
head(cars)
##   speed dist
## 1     4    2
## 2     4   10
## 3     7    4
## 4     7   22
## 5     8   16
## 6     9   10
```

As we only have two variables, we can simply do

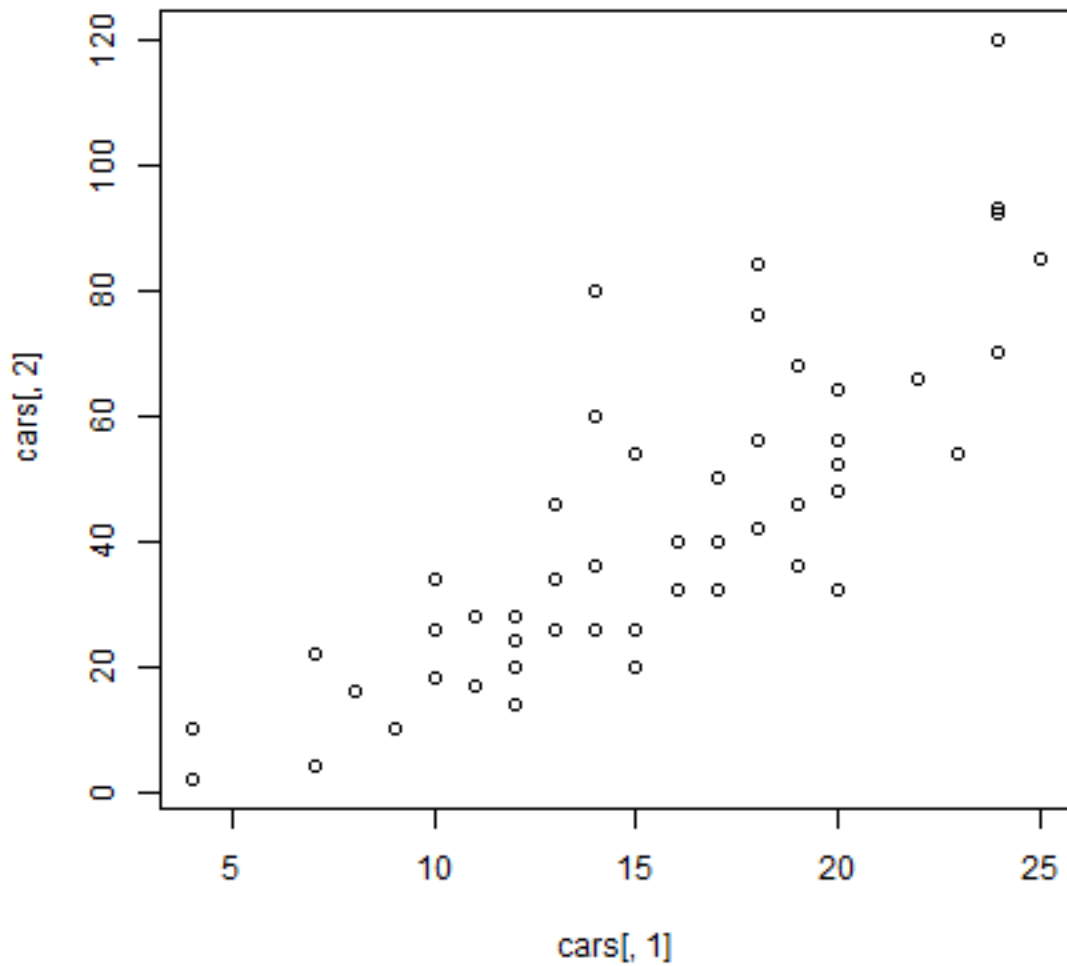
```
plot(cars)
```





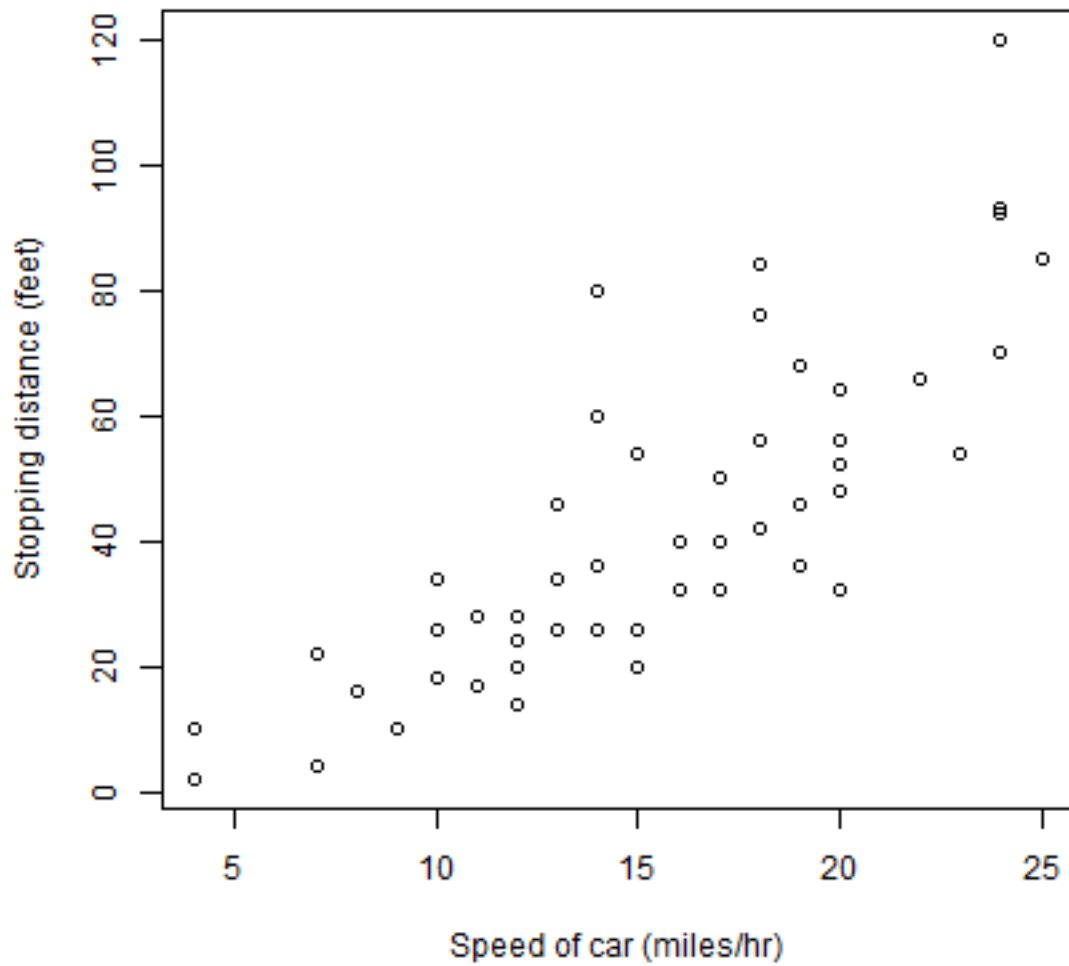
But to be more explicit:

```
plot(cars[,1], cars[,2])
```



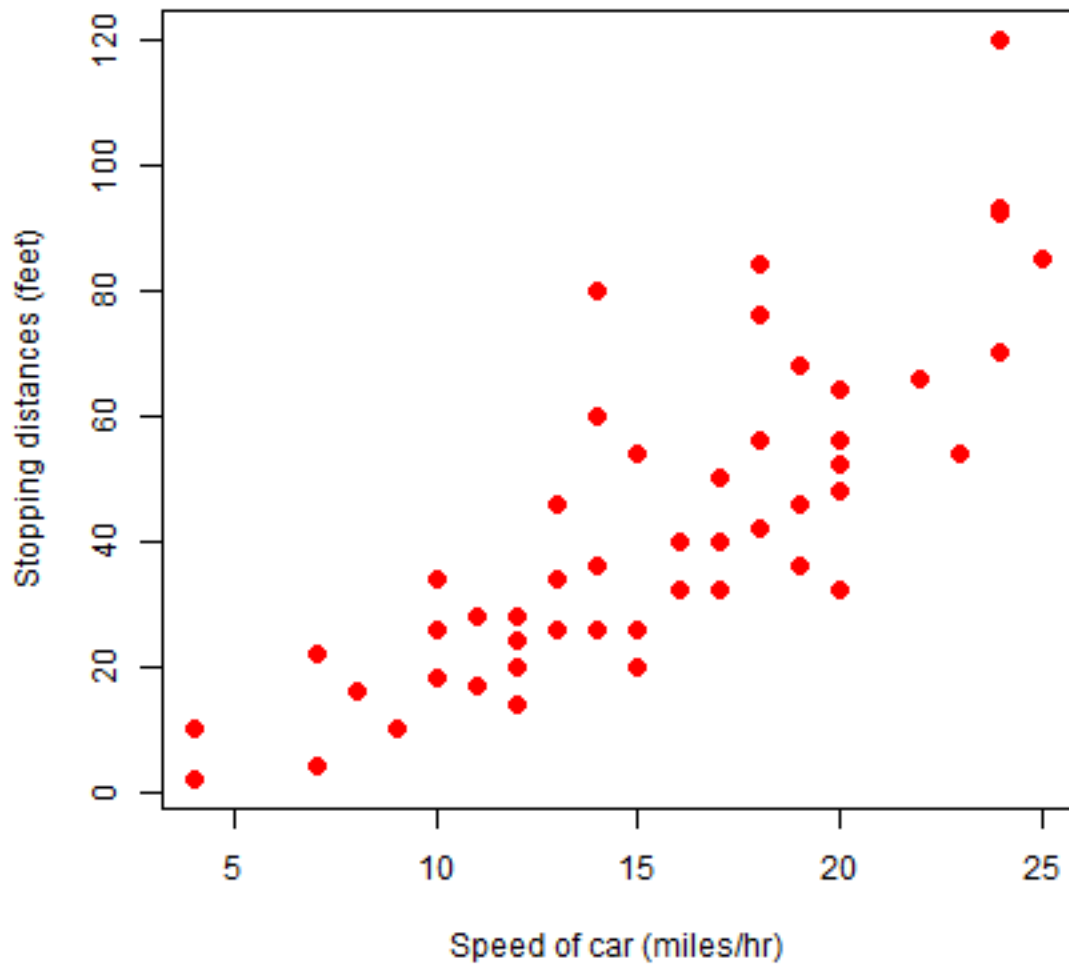
And now to embellish, add axes labels.

```
plot(cars[,1], cars[,2], xlab='Speed of car (miles/hr)', ylab='Stopping distance_  
→ (feet)')
```



Different symbols (pch is the symbol type, cex is the size).

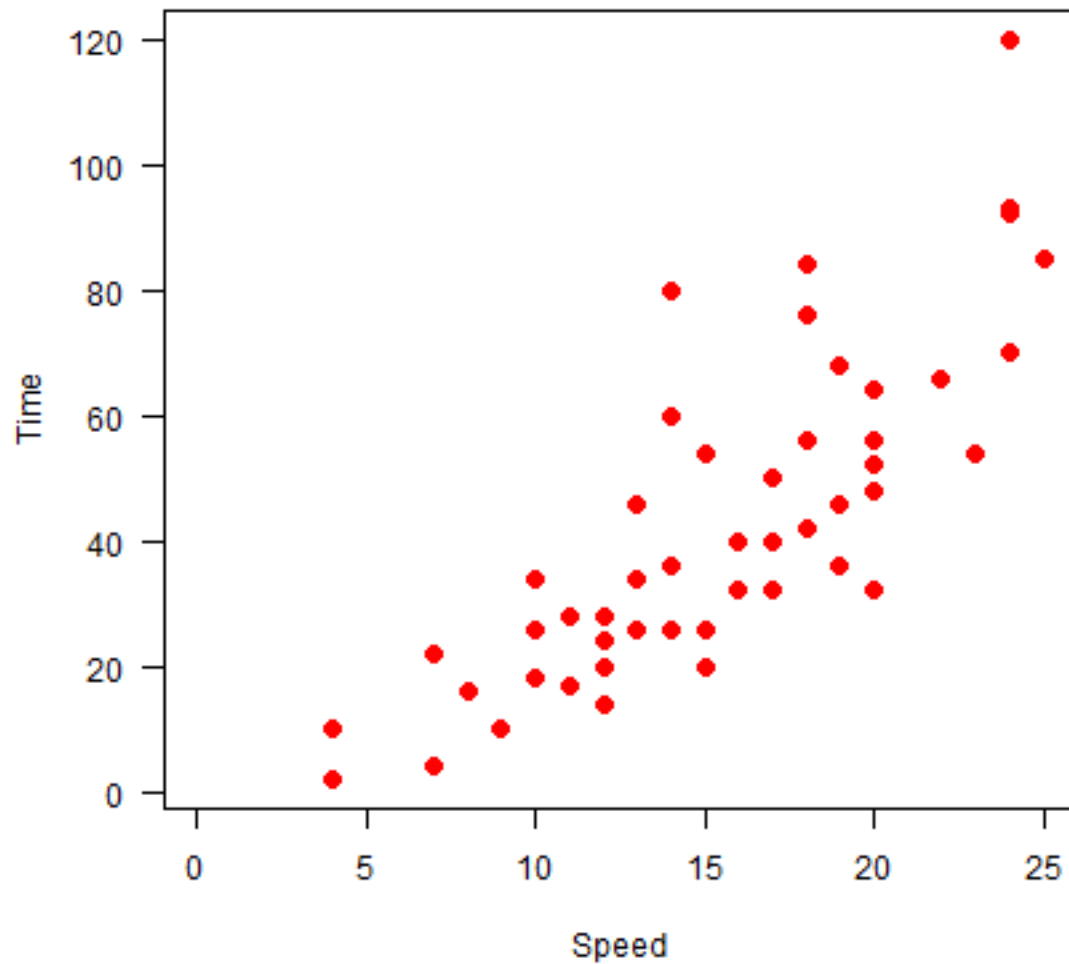
```
plot(cars, xlab='Speed of car (miles/hr)', ylab='Stopping distances (feet)', pch=20, cex=2, col='red')
```



`cex` is the *magnification factor*. The default value is 1.

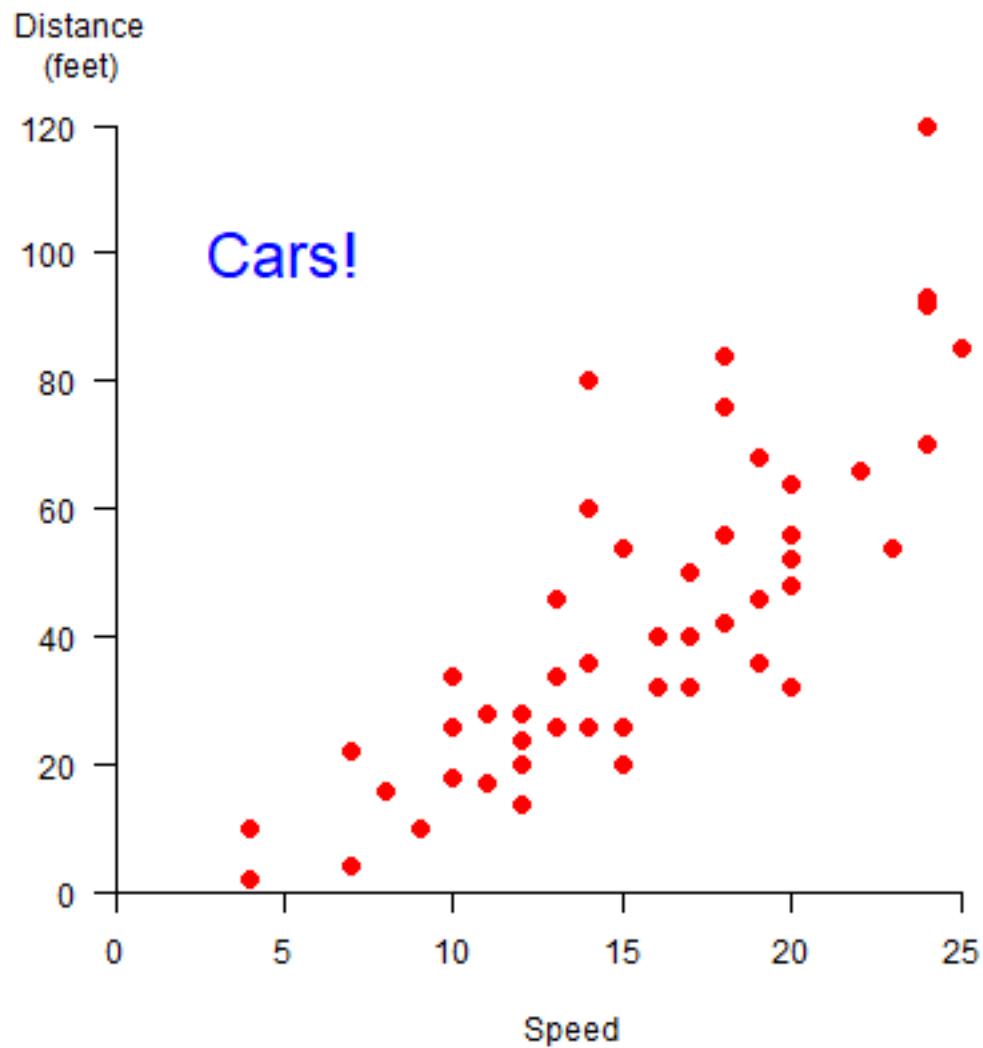
Let's change some things about the axes. Use `xlim` and `ylim` to set the start and end of an axis. `las=1` changes the orientation of the y-axis labels to horizontal.

```
plot(cars, xlab='Speed', ylab='Time', pch=20, cex=2, col='red', xlim = c(0,25), las=1)
```



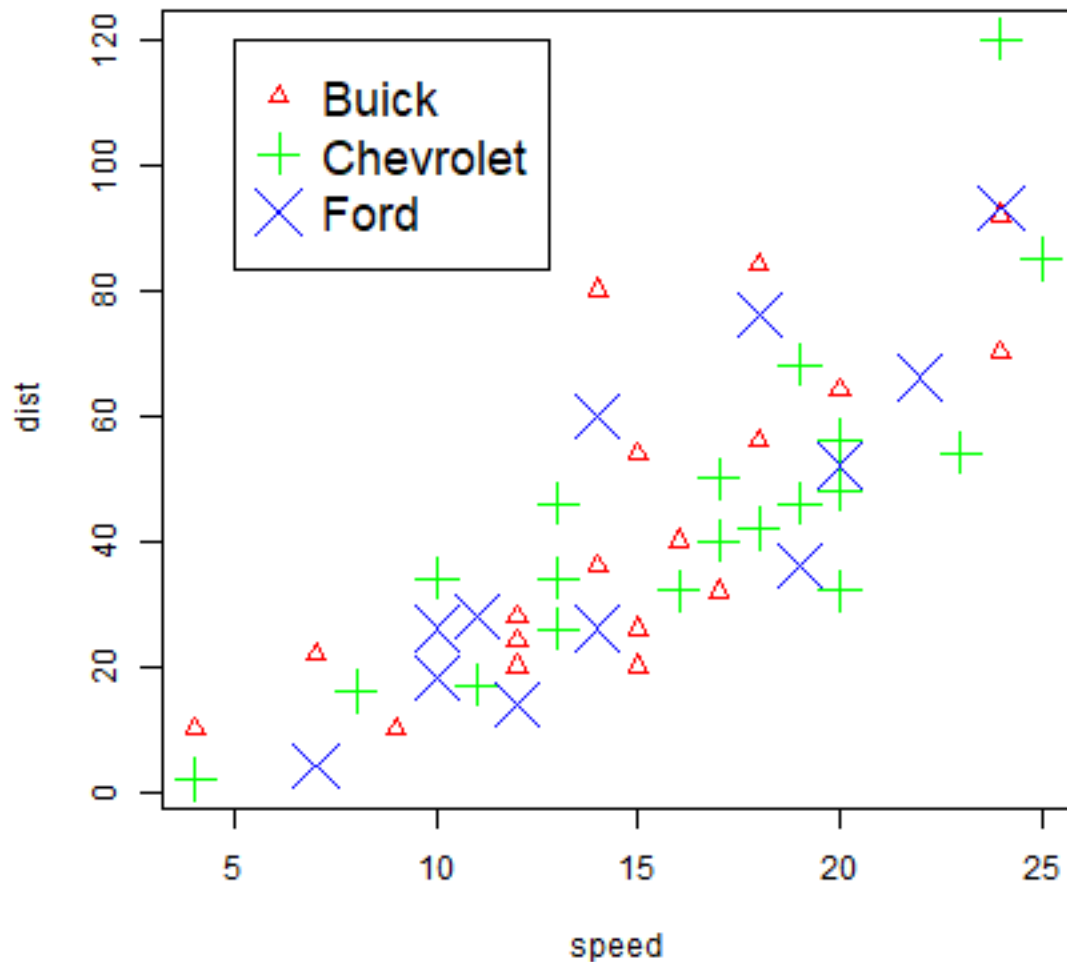
Here we do not draw axes at first, and then add the lower (1) and left (2) axis, to avoid drawing the clutter from the unnecessary “upper” and “right” axis. Arguments `xaxs="i"` and `yaxs="i"` force the axis to touch at  $(0, 0)$ .

```
plot(cars, xlab='Speed', ylab='', pch=20, cex=2, col='red', xlim = c(0,27), ylim=c(0,
↪125), axes=FALSE, xaxs="i", yaxs="i")
axis(1)
axis(2, las=1)
text(5, 100, 'Cars!', cex=2, col='blue')
par(xpd=NA)
text(-1, 133, 'Distance\n(feet)')
```



We can change the symbols using another variable. Let's say we have three car brands and that we want to vary the symbol type, color, and size by brand (typically one of these changes should suffice to distinguish them!).

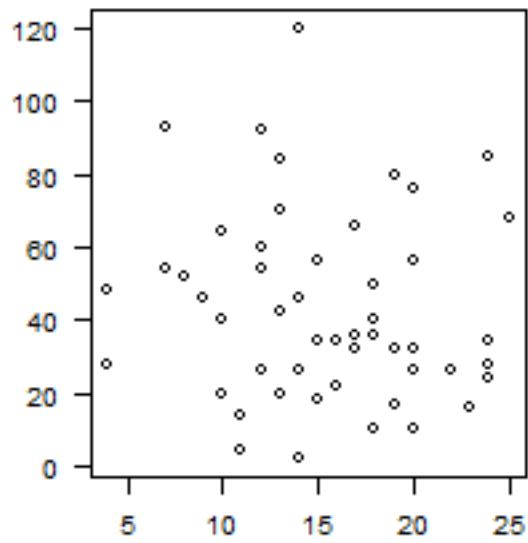
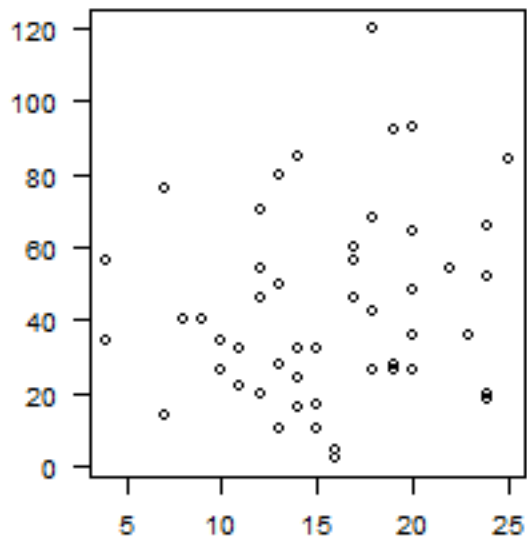
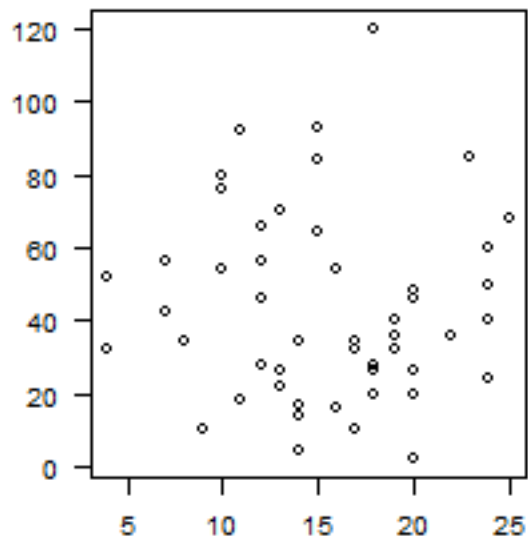
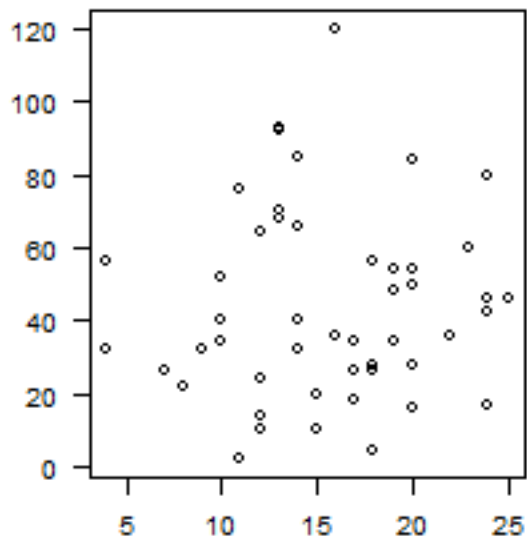
```
set.seed(0)
brands <- c('Buick', 'Chevrolet', 'Ford')
b <- sample(brands, nrow(cars), replace=TRUE)
i <- match(b, brands)
plot(cars, pch=i+1, cex=i, col=rainbow(3)[i])
j <- 1:length(brands)
legend(5, 120, brands, pch=(j+1), pt.cex=j, col=rainbow(3), cex=1.5)
```



The important step is the use of `match`, that creates for each character string a matching number that can be used to set the character type desired.

As you have seen above, `plot` takes many variables. Several other parameters influencing your plot, can be set with `par`. See `?par` for details. Here I use it to create 4 subplots (`mfcrow=c(2,2)` with non-default margins (`mar=c(2,3,1.5,1.5)`).

```
par(mfrow=c(2,2), mar=c(2,3,1.5,1.5))
for (i in 1:4) {
  plot(sample(cars[,1]), sample(cars[,2]), xlab='', ylab='', las=1)
}
```



### Some other base plots

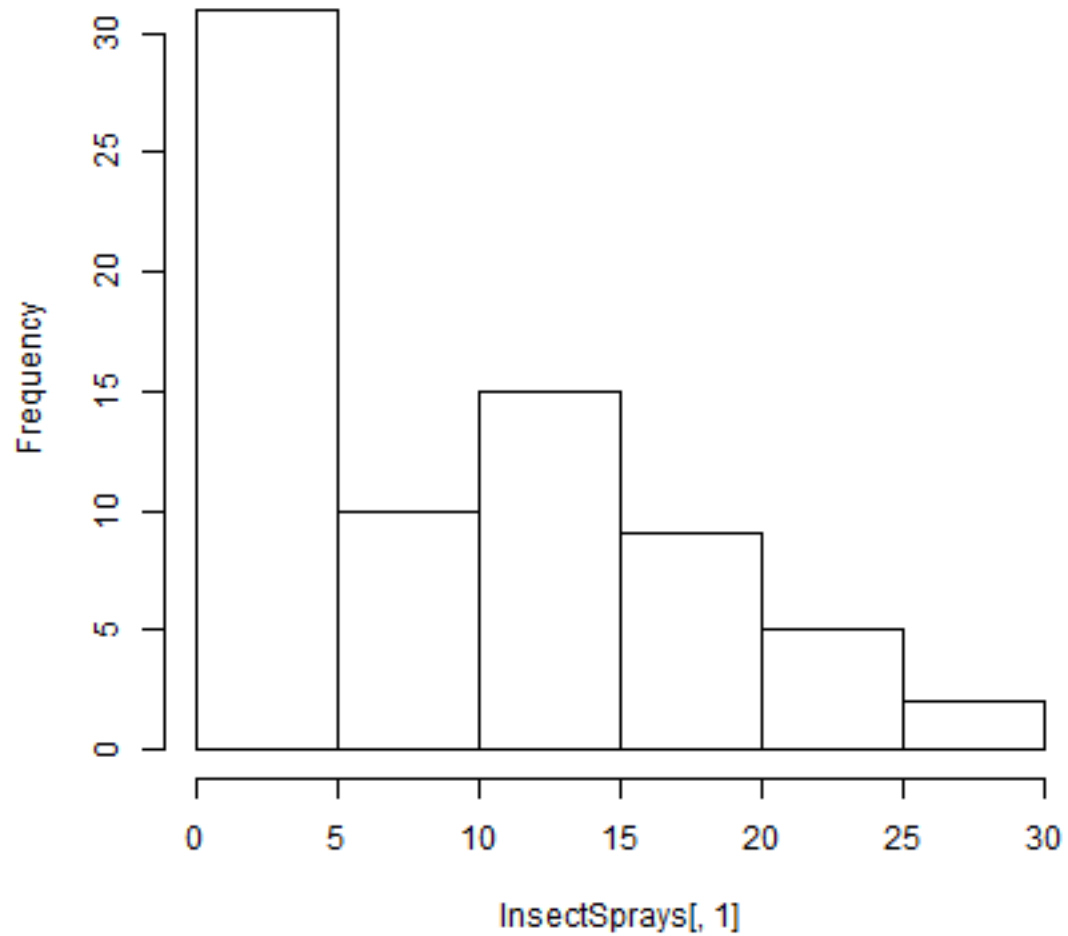
Now consider the `InsectSprays` dataset

```
head(InsectSprays)
##   count spray
## 1    10    A
## 2     7    A
## 3    20    A
## 4    14    A
## 5    14    A
## 6    12    A
```

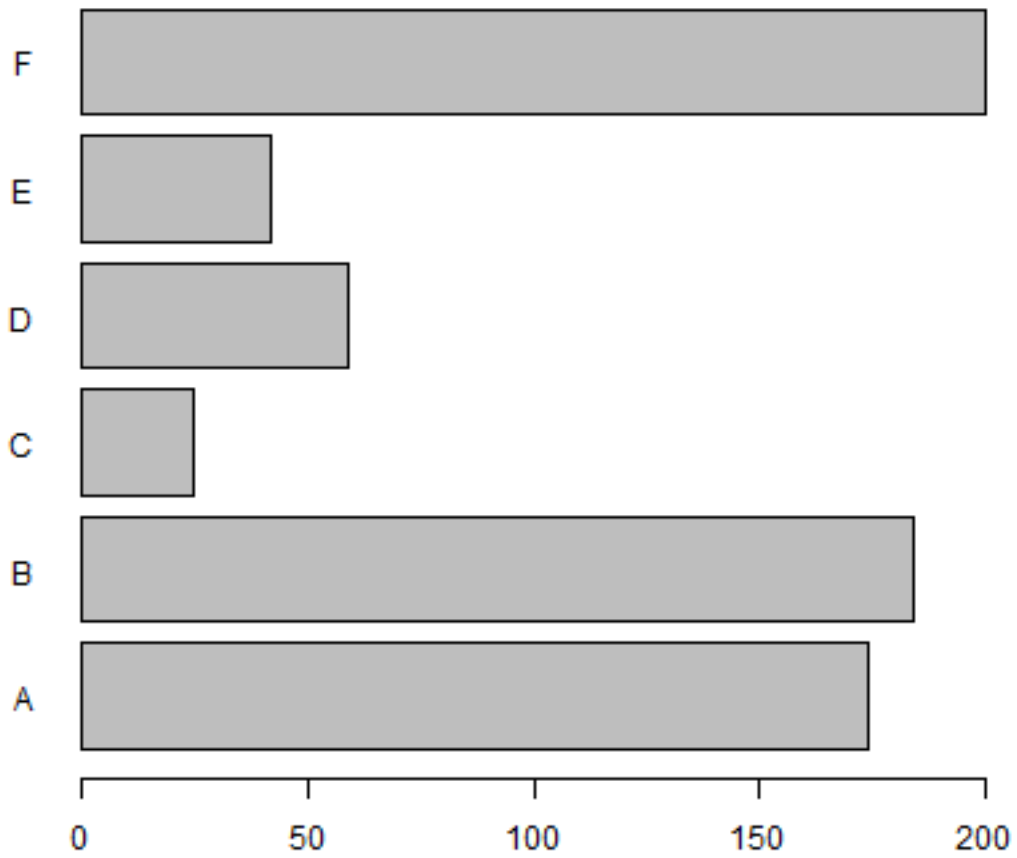
```
hist(InsectSprays[,1])
```



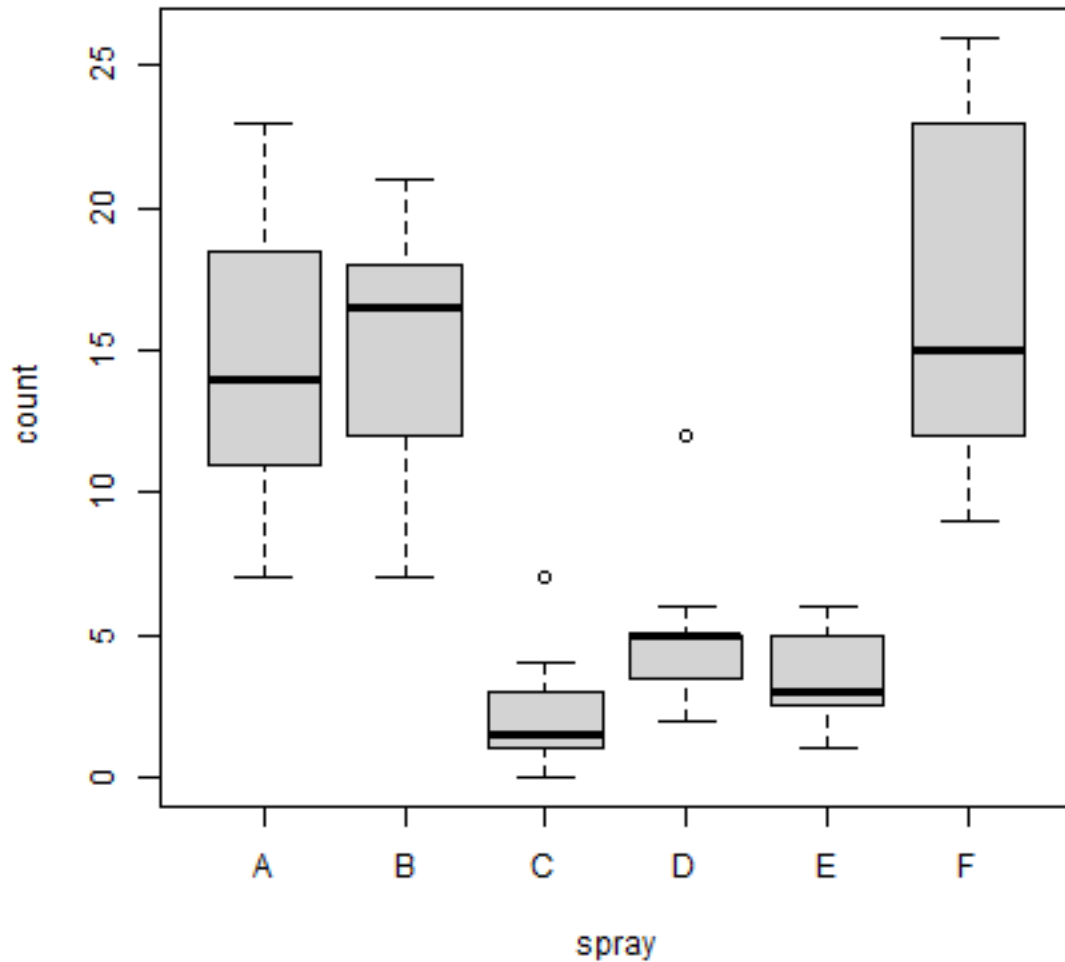
## Histogram of InsectSprays[, 1]



```
x <- aggregate(InsectSprays[,1,drop=F], InsectSprays[,2,drop=F], sum)
barplot(x[,2], names=x[,1], horiz=T, las=1)
```



```
boxplot(count ~ spray, data = InsectSprays, col = "lightgray")
```



## Exploring the iris data set

Now let's have a look at the 'iris' dataset. It has 150 observations of 5 variables for 3 species of iris.

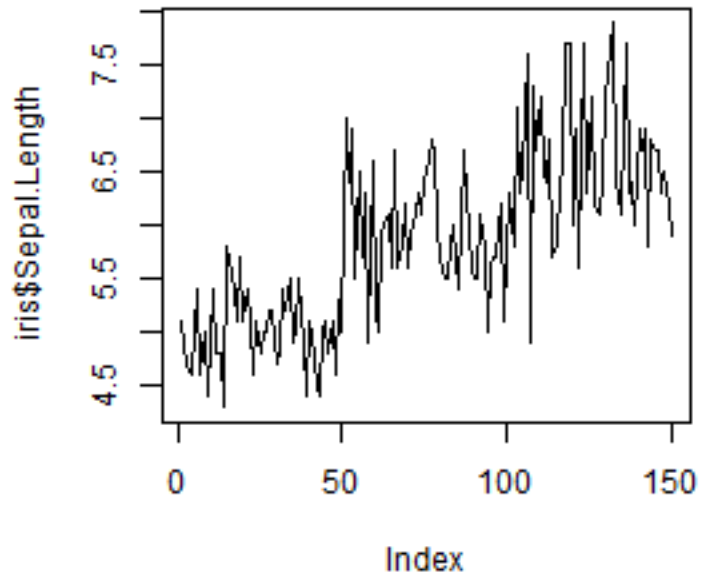
```
data(iris)
str(iris)
## 'data.frame': 150 obs. of 5 variables:
## $ Sepal.Length: num 5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
## $ Sepal.Width : num 3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
## $ Petal.Length: num 1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
## $ Petal.Width : num 0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
## $ Species : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 .
↪...
```

Default plot characteristics are not satisfactory most of the time. You may want different heading, labels of x and y axis or different color of lines/points/bars. There is a large number of graphical parameters to set these. Here are some examples.

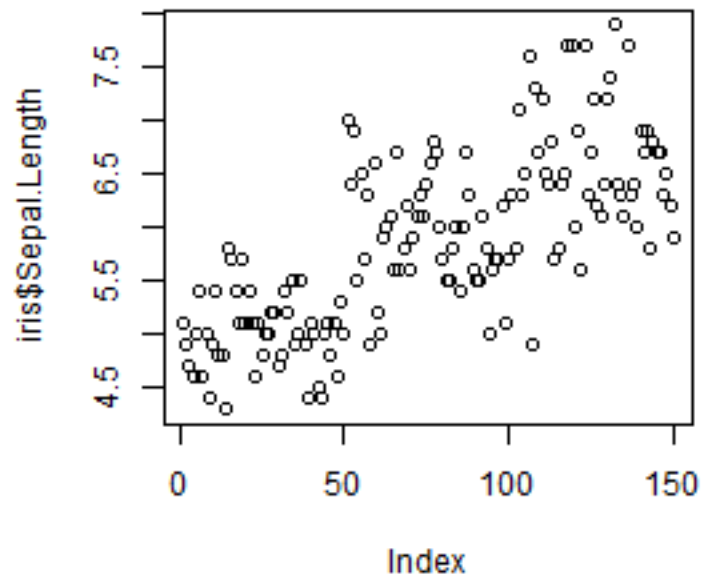
## Scatter plot

Note how the scatter plot type is controlled by `type` parameter.

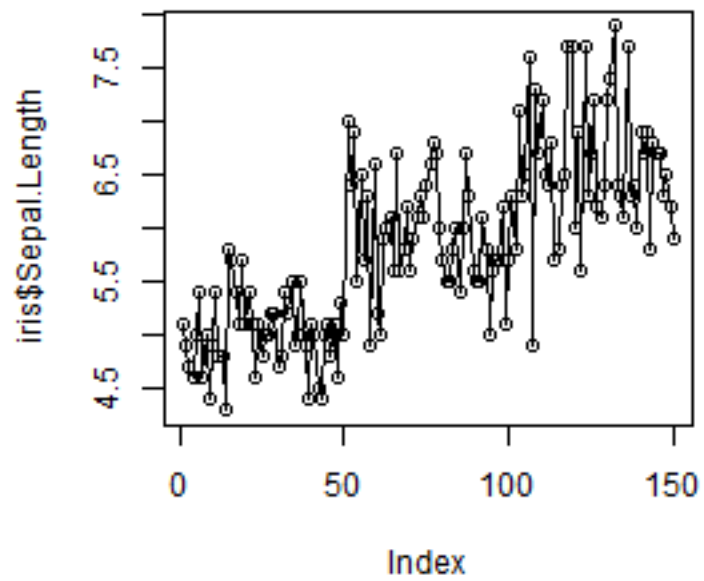
```
plot(iris$Sepal.Length, type = 'l')
```



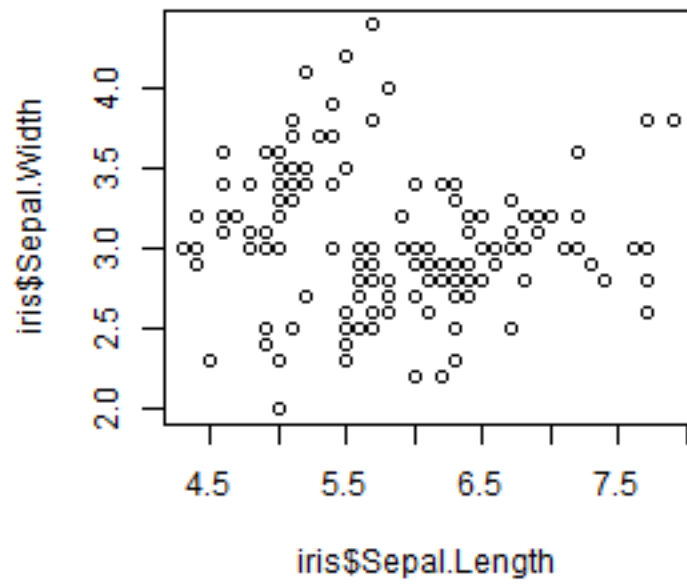
```
plot(iris$Sepal.Length, type = 'p')
```



```
plot(iris$Sepal.Length, type = 'o')
```



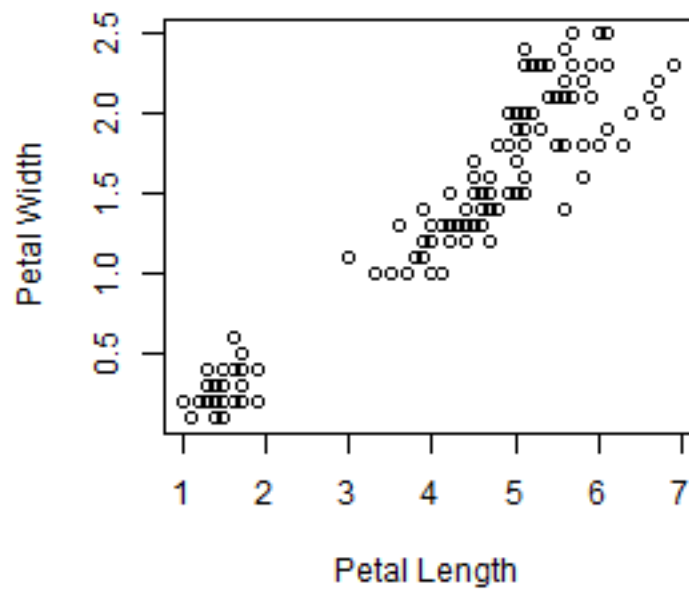
```
plot(iris$Sepal.Length, iris$Sepal.Width, type = 'p')
```



#### Titles and axis labels

```
plot(iris$Petal.Length, iris$Petal.Width, main = "Edgar Anderson's Iris Data",  
     xlab = "Petal Length", ylab = "Petal Width")
```

## Edgar Anderson's Iris Data



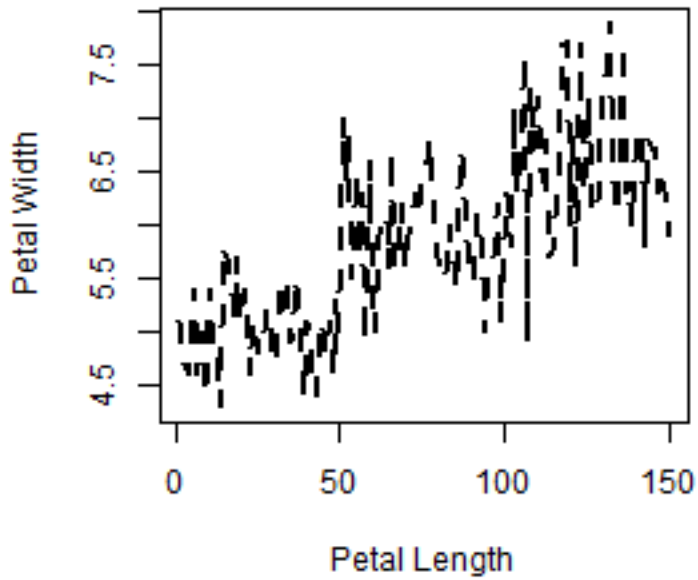
The font size can be changed by `cex.main` and `cex.lab` argument. Try setting `cex.lab = 2` to increase the font size of the axes. `cex.axis` controls the size of axis tick values.

### Plotting characters

You can use `lty` to change the line type, and `pch` to choose a point type.

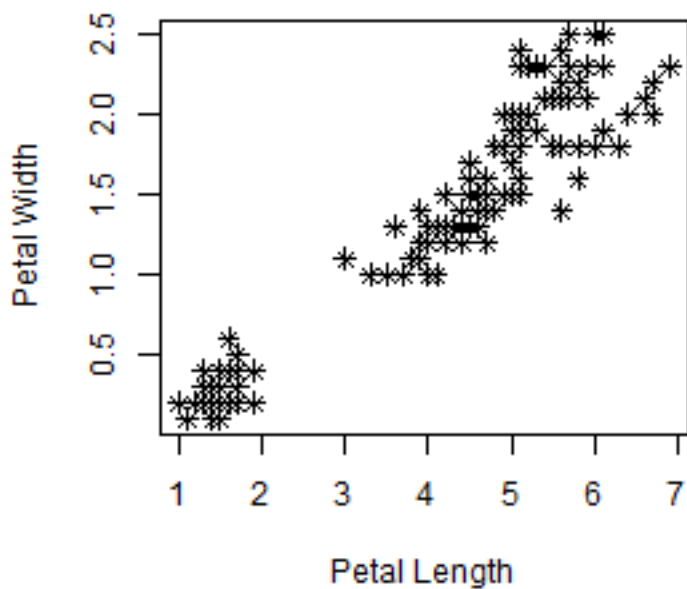
```
plot(iris$Sepal.Length, type = 'l', lty = 2, lwd = 2,  
     main = "Edgar Anderson's Iris Data", xlab = "Petal Length", ylab = "Petal Width")
```

**Edgar Anderson's Iris Data**



```
plot(iris$Petal.Length, iris$Petal.Width, pch = 8,  
     main = "Edgar Anderson's Iris Data", xlab = "Petal Length", ylab = "Petal Width")
```

**Edgar Anderson's Iris Data**



There are many choices for pch. You can use `example("pch")`, or do `plot(1:25, pch=1:25)` to see the

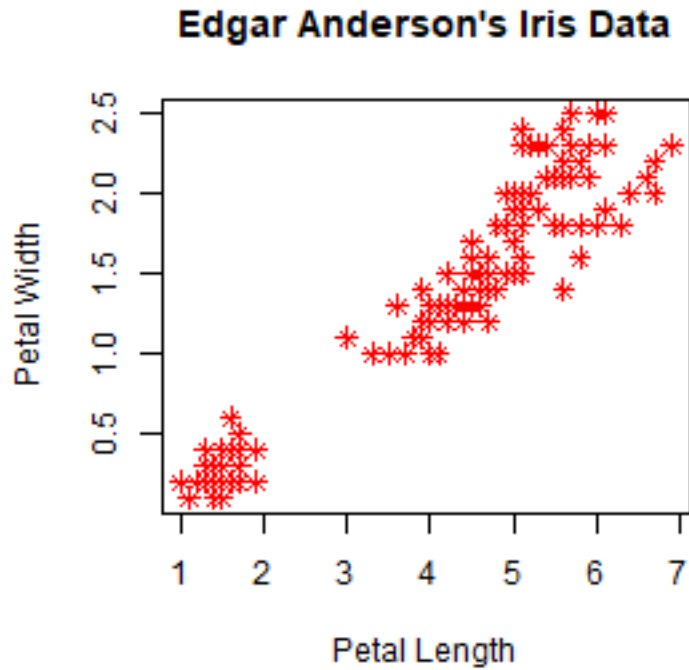


some plotting characters. Instead of a code, you can also specify the character like in `pch="&".`

The size of a point character (`pch`) can be controlled with `cex` argument.

## Colors

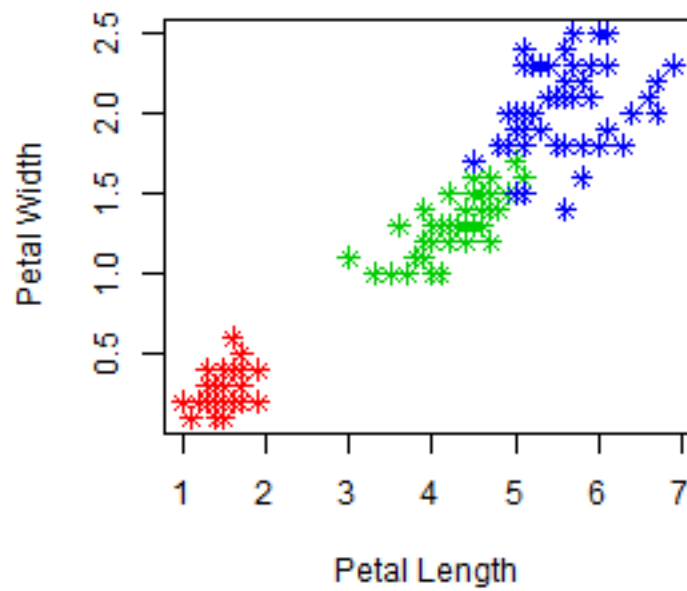
```
plot(iris$Petal.Length, iris$Petal.Width, pch = 8, col = 'red',  
     main = "Edgar Anderson's Iris Data", xlab = "Petal Length", ylab = "Petal Width")
```



We can link a color to a value.

```
mycolor <- c("red", "green3", "blue")[as.factor(iris$Species)]  
  
plot(iris$Petal.Length, iris$Petal.Width, pch = 8, col = mycolor,  
     main = "Edgar Anderson's Iris Data", xlab = "Petal Length", ylab = "Petal Width")
```

## Edgar Anderson's Iris Data



Note that the length of `col` vector should be equal to the number of items you are plotting.

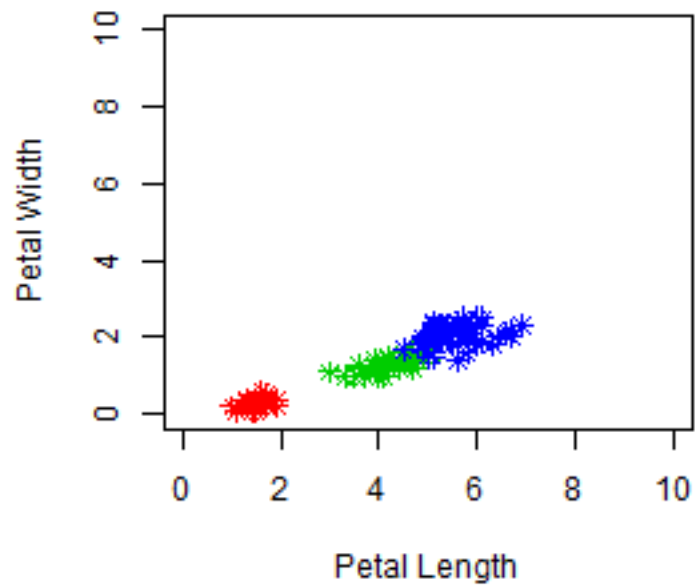
You can use `colors()` to see a list of named colors.

### Axes

To change the range of an axis you can use `xlim` and/or `ylim` argument(s).

```
plot(iris$Petal.Length, iris$Petal.Width, pch = 8, col = mycolor,  
     main = "Edgar Anderson's Iris Data", xlab = "Petal Length", ylab = "Petal Width",  
     xlim = c(0,10), ylim= c(0,10))
```

## Edgar Anderson's Iris Data

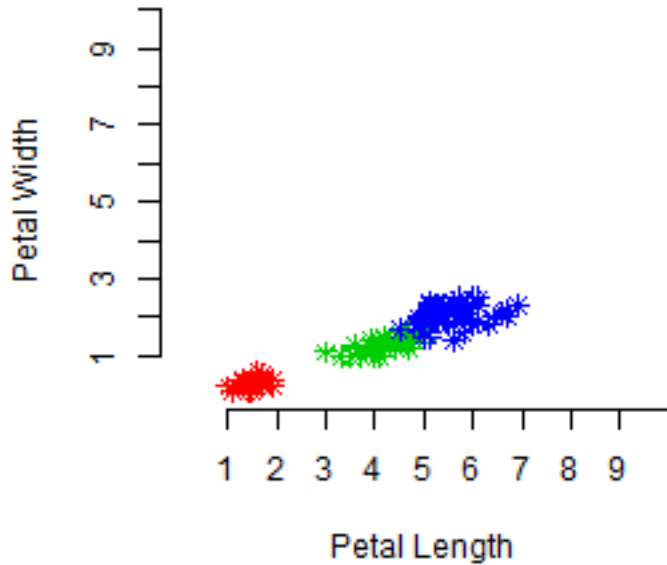


You can also set `xlim` and `ylim` with `range`. Try `xlim = range(iris$Petal.Length)`.

Use `axis` function to change the tick position and annotations (axes labels). First you need to turn off the default axes.

```
plot(iris$Petal.Length, iris$Petal.Width, pch = 8, col = mycolor,  
     main = "Edgar Anderson's Iris Data", xlab = "Petal Length", ylab = "Petal Width",  
     xlim = c(0,10), ylim = c(0,10), axes = FALSE)  
  
axis(1, at = 1:10, lab = c(1:10))  
axis(2, at = 1:10, lab = c(1:10))
```

## Edgar Anderson's Iris Data



### Interacting with plots

You can use `identify()` to identify a particular point in the plot. Try `identify(iris$Petal.Length, iris$Petal.Width)`. You can left click with the mouse to identify multiple points. Once complete use ESC to end the process.

You can use `locator()` to find out the coordinates at a particular position on a graph. Try `locator()`. You can left click with the mouse any number of times within the axes and use ESC to end the process. A list of X and Y coordinates of the positions clicked will be returned. You can retain this information by assigning a variable to `locator` before starting it: `loc <- locator()`. The coordinates will be stored as `loc$x` and `loc$y`. `locator` is particularly useful to add additional information to the graph. See the following example.

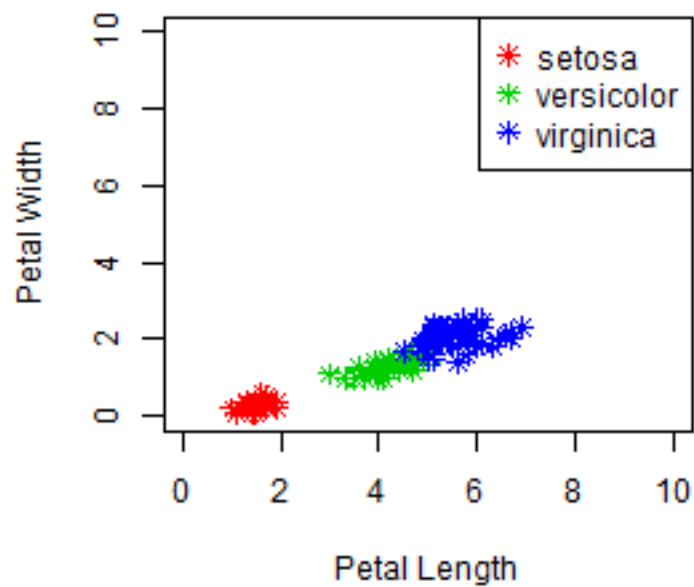
### Legend

We use a different color to represent each species of iris. We can create a legend for this information using `legend` function.

```
plot(iris$Petal.Length, iris$Petal.Width, pch = 8, col = mycolor,
     main = "Edgar Anderson's Iris Data", xlab = "Petal Length", ylab = "Petal Width",
     xlim = c(0,10), ylim= c(0,10))

legend('topright', legend = unique(iris$Species), col = c("red", "green3", "blue"), pch_
↵ = 8)
```

## Edgar Anderson's Iris Data



To make a legend with no border use `btty = 'n'`.

###Add text

Often we want include additional text in the plot. `locator` can be used to find the approximate x and y coordinates where you want to place the text. Use `loc <- locator()`.

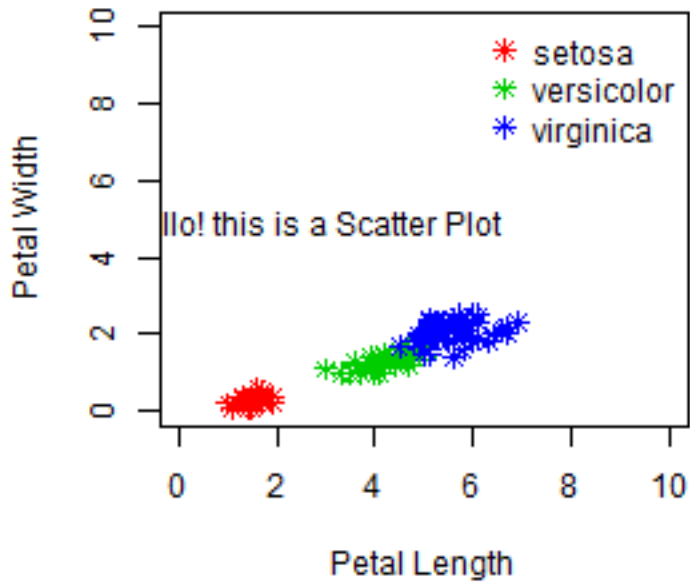
```
loc <- list()
loc$x <- 2.75
loc$y <- 4.94

plot(iris$Petal.Length, iris$Petal.Width, pch = 8, col = mycolor,
     main = "Edgar Anderson's Iris Data", xlab = "Petal Length", ylab = "Petal Width",
     xlim = c(0,10), ylim= c(0,10))

legend('topright', legend = unique(iris$Species), col = c("red", "green3", "blue"),
      pch = 8, btty = 'n')

text(loc$x, loc$y, labels = "Hello! this is a Scatter Plot")
```

## Edgar Anderson's Iris Data



### Multiple plots

To combine multiple plots in one image you can use `layout()` or `par()`. For example, 4 plots can be combined with `layout(matrix(1:4, 2, 2))` or `par(mfrow=c(2,2))`.

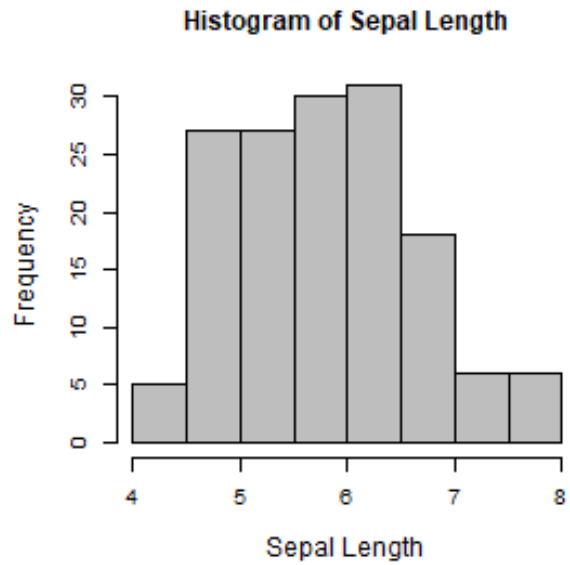
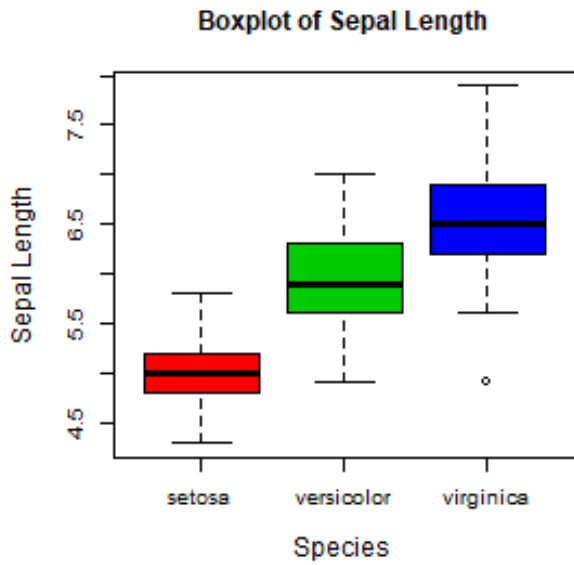
```
par(mfrow=c(2,2))

boxplot(iris$Sepal.Length~iris$Species, main = "Boxplot of Sepal Length",
        xlab = "Species", ylab = "Sepal Length", col = c("red","green3","blue"),
        cex.lab = 1.25)

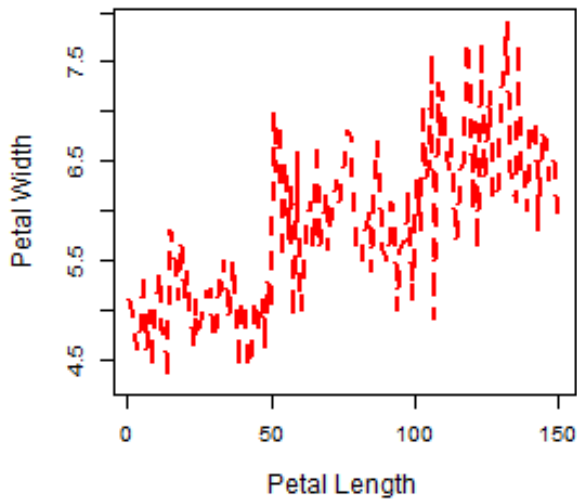
hist(iris$Sepal.Length, main = "Histogram of Sepal Length",
     xlab = "Sepal Length", ylab = "Frequency", col = c("grey"), cex.lab = 1.25)

plot(iris$Sepal.Length, type = 'l', lty = 2, lwd = 2, col = 'red',
     main = "Variation with of Petal Width and Petal Length",
     xlab = "Petal Length", ylab = "Petal Width", cex.lab = 1.25)

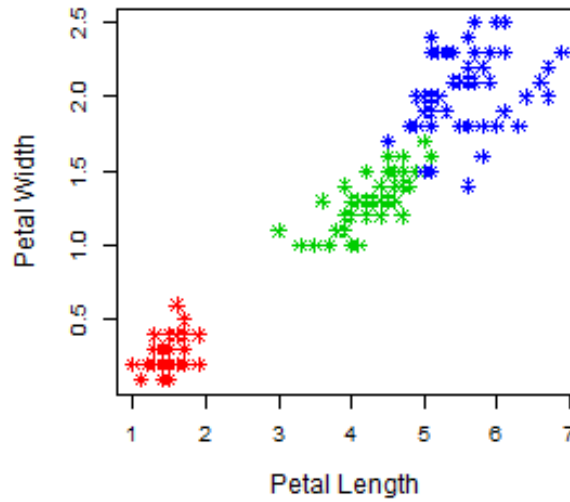
plot(iris$Petal.Length, iris$Petal.Width, pch = 8, col = mycolor,
     main = "Scatter plot of Petal Width and Petal Length",
     xlab = "Petal Length", ylab = "Petal Width", cex.lab = 1.25)
```



**Variation with of Petal Width and Petal Length**



**Scatter plot of Petal Width and Petal Length**



## Saving plots

You can directly write a plot to a file such as pdf or png. To save any of the above plots in a pdf file called `theplot.pdf` you first open the pdf device, then do the plotting and use `dev.off()` when done.

```
pdf("theplot.pdf")
boxplot(iris$Sepal.Length~Species, main = "Boxplot of Sepal Length",
        xlab = "Species", ylab = "Sepal Length", col = c("red", "green3", "blue"))
dev.off()
```

For plotting to an image file, you can use png and other formats. To set the device size (dimensions and resolution), you can use a few parameters

```
png(filename = "myplot.png", width = 200, height = 300, units = "cm", res = 300)

boxplot(iris$Sepal.Length~iris$Species, main = "Boxplot of Sepal Length",
        xlab = "Species", ylab = "Sepal Length", col = c("red", "green3", "blue"))

dev.off()
```

You should now have a file called “myplot.png” in your working directory.

## Summary

### Some different plot types

+ <code>`plot( )`</code>	Scatter plot, and general plotting
+ <code>`hist( )`</code>	Histogram
+ <code>`stem( )`</code>	Stem-and-leaf
+ <code>`boxplot( )`</code>	Boxplot
+ <code>`qqnorm( )`</code>	Normal probability plot
+ <code>`mosaicplot( )`</code>	Mosaic plot

### Add elements to a plot

+ <code>`points( )`</code>	Add points
+ <code>`lines( )`</code>	Add lines
+ <code>`text( )`</code>	Add text
+ <code>`abline( )`</code>	Add lines
+ <code>`legend( )`</code>	Add legend

### Important graphical parameters

+ <code>`par( )`</code>	Set parameters for plotting
+ <code>`cex`</code>	Font size
+ <code>`col`</code>	Color of plotting symbols
+ <code>`lty`</code>	Line type
+ <code>`lwd`</code>	Line width
+ <code>`mar`</code>	Inner margins
+ <code>`mfrow`</code>	Multiple figures per image
+ <code>`oma`</code>	Outer margins
+ <code>`pch`</code>	Plotting symbol
+ <code>`xlim`</code>	Min and max of X axis range
+ <code>`ylim`</code>	Min and max of Y axis range

## Resources

Additional resources you may want to consult are the R demo for different types of plots: `demo("graphics")` and the help for plot (`?plot`).

There is also a comprehensive [gallery of plots](#)



## 1.13 Statistical models

There are many type of statistical models. Here we show how to make simple regression models with *R*. Other modeling approaches tend to use similar syntax.

The most common way to specify a regression model in *R* is by creating a formula. For example  $y \sim x$  means  $y$  is a function of  $x$ .  $y \sim a + b$  means that  $y$  is a function of  $a$  and  $b$ .

Let's use the cars data that come with *R*. This dataset has measurements on the distance needed to stop given the speed a car was driven when the driver stepped on the breaks. We use the `lm` (linear model) function.

```
head(cars)
##   speed dist
## 1     4    2
## 2     4   10
## 3     7    4
## 4     7   22
## 5     8   16
## 6     9   10
m <- lm(dist ~ speed, data=cars)
m
##
## Call:
## lm(formula = dist ~ speed, data = cars)
##
## Coefficients:
## (Intercept)      speed
##   -17.579      3.932
```

Note that the data is provided by data.frame `cars`, and that the names in formula are column names in this data frame. The functions returned a model (`lm`) object. When printed it shows the coefficients of the regression model ( $\text{dist} = -17.579 + 3.932 * \text{speed}$ ). `m` has quite a bit more information, but that is not shown, by default.

There are several functions that can be used to extract this information.

```
summary(m)
##
## Call:
## lm(formula = dist ~ speed, data = cars)
##
## Residuals:
##   Min       1Q   Median       3Q      Max
## -29.069  -9.525  -2.272   9.215  43.201
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -17.5791     6.7584  -2.601  0.0123 *
## speed        3.9324     0.4155   9.464 1.49e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 15.38 on 48 degrees of freedom
## Multiple R-squared:  0.6511, Adjusted R-squared:  0.6438
## F-statistic: 89.57 on 1 and 48 DF,  p-value: 1.49e-12
anova(m)
## Analysis of Variance Table
##
## Response: dist
```

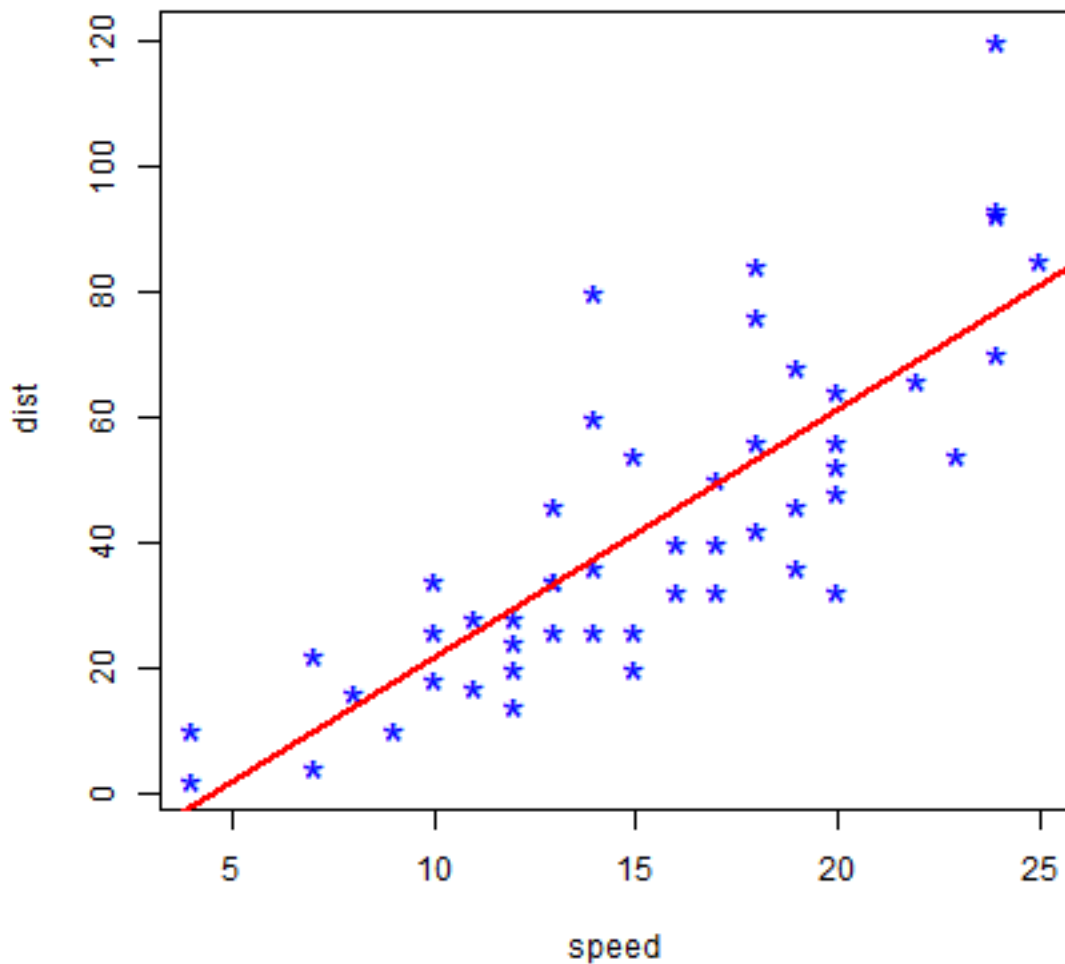
(continues on next page)

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```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## speed      1  21186 21185.5  89.567 1.49e-12 ***
## Residuals 48  11354   236.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
residuals(m) [1:10]
##          1          2          3          4          5          6          7          8
## 3.849460 11.849460 -5.947766 12.052234  2.119825 -7.812584 -3.744993  4.255007
##          9         10
## 12.255007 -8.677401
```

You can use `abline` to draw a simple regression line like this.

```
plot(cars, col='blue', pch='*', cex=2)
abline(m, col='red', lwd=2)
```

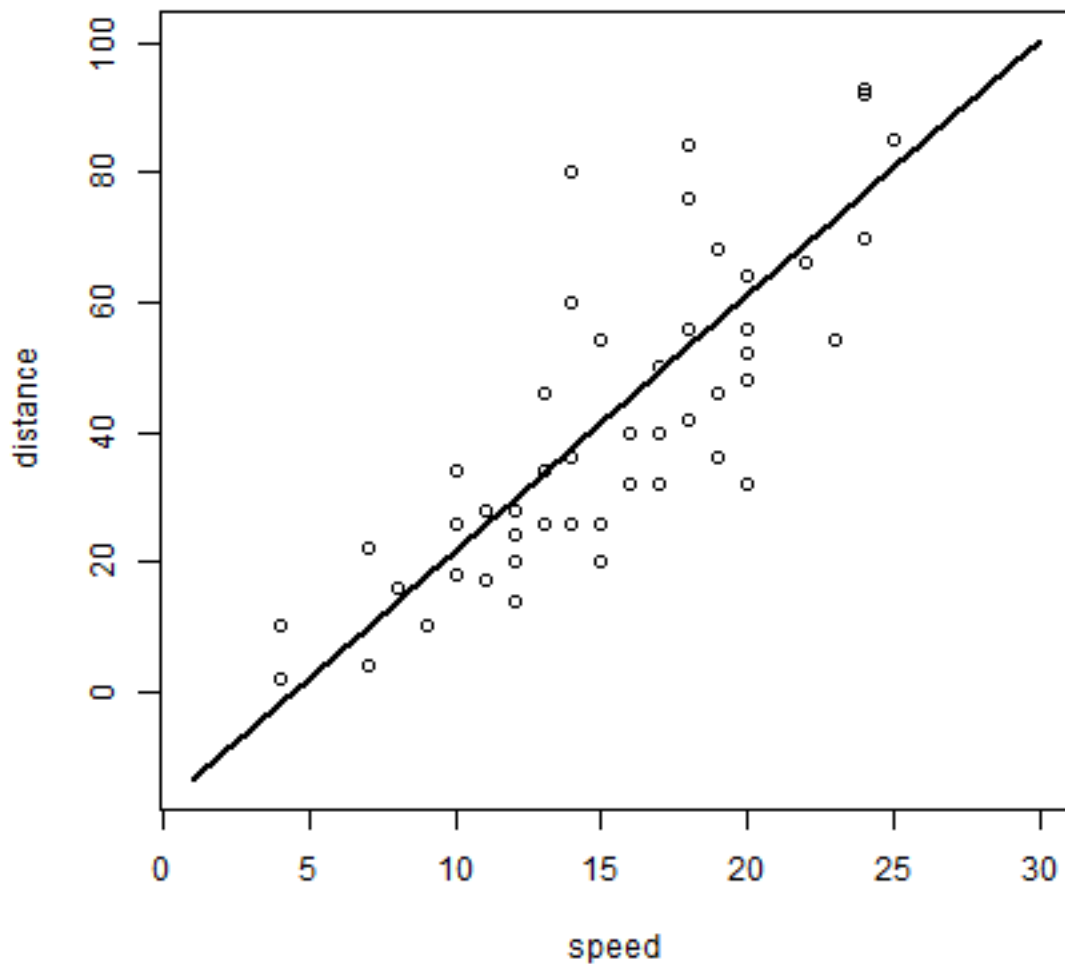


More generally, you can use the `predict` function to use the model to predict values of  $y$  for any  $x$ .

```

p <- predict(m, data.frame(speed=1:30))
p
##           1           2           3           4           5           6           7
## -13.646686  -9.714277  -5.781869  -1.849460   2.082949   6.015358   9.947766
##           8           9          10          11          12          13          14
##  13.880175  17.812584  21.744993  25.677401  29.609810  33.542219  37.474628
##          15          16          17          18          19          20          21
##  41.407036  45.339445  49.271854  53.204263  57.136672  61.069080  65.001489
##          22          23          24          25          26          27          28
##  68.933898  72.866307  76.798715  80.731124  84.663533  88.595942  92.528350
##          29          30
##  96.460759 100.393168
plot(1:30, p, xlab='speed', ylab='distance', type='l', lwd=2)
points(cars)

```



The `glm` (generalized linear models) function can do what `lm` can, but it is much more versatile. For example you can also use it for logistic regression. In logistic regression the response variable is normally binomial (0 or 1) or at least between 0 and 1. I create such a variable here (was the stopping distance above 40 or not?).

```
cars$above40 <- cars$dist > 40
```

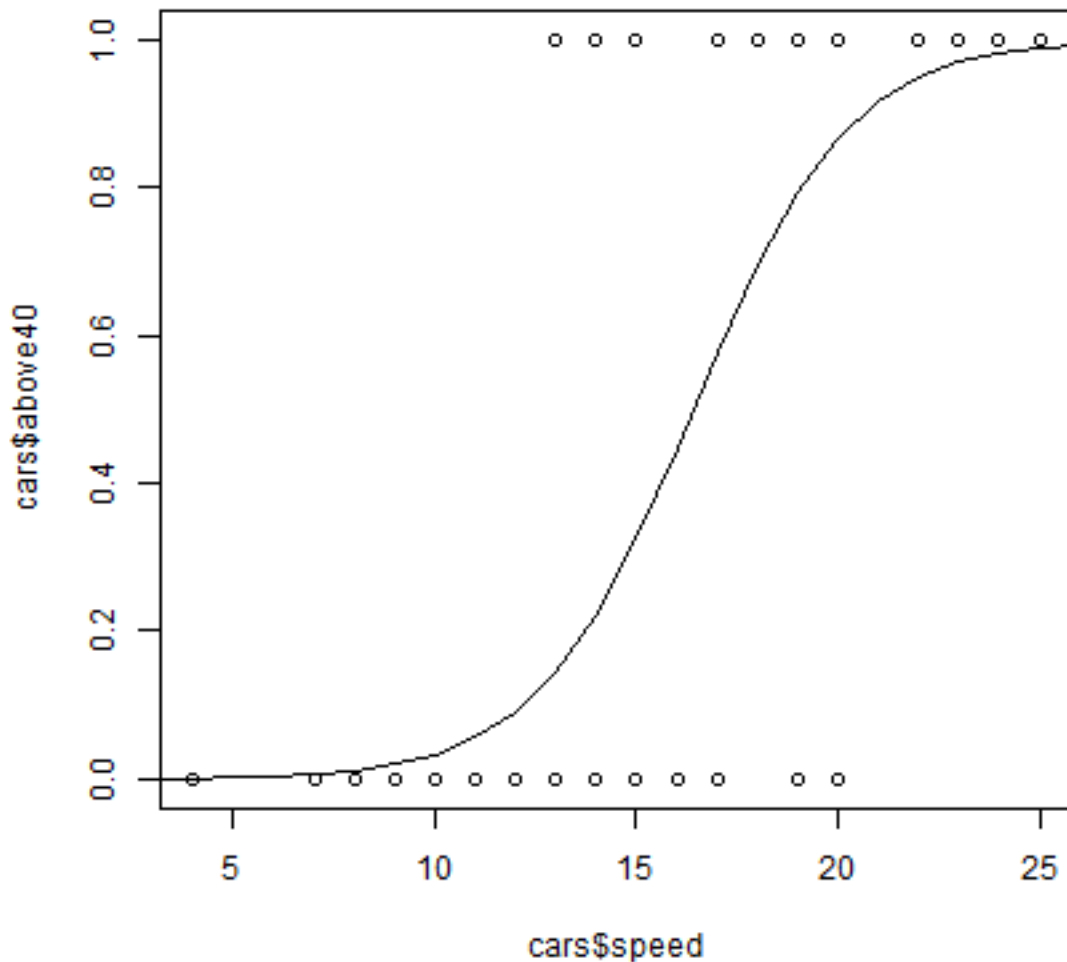
Now we can use this variable in a glm model. By stating that family='binomial' we indicate that we want logistic regression. (The default is family=gaussian which indicates standard (normal) regression.

```
mlog <- glm(above40 ~ speed, data=cars, family='binomial')
mlog
##
## Call:  glm(formula = above40 ~ speed, family = "binomial", data = cars)
##
## Coefficients:
## (Intercept)      speed
##      -8.553      0.521
##
## Degrees of Freedom: 49 Total (i.e. Null);  48 Residual
## Null Deviance:      68.59
## Residual Deviance: 36.37    AIC: 40.37
```

Because a logistic model operates with logistically transformed numbers, we need to tell the predict function that we want the predicted values on the original scale (type='response').

```
p <- predict(mlog, data.frame(speed=1:30), type='response')
```

```
plot(cars$speed, cars$above40)
lines(1:30, p)
```



For a more in-depth discussion of regression models with R [go here](#).

## 1.14 Miscellaneous

### Packages

Packages are collections of *R* functions. Typically around a related set of tasks. *R* comes with a standard “base” set of packages. Others are available for download and installation. These packages are developed by (groups of) individuals independently of the “core R” development team. Most of these packages are developed by volunteers, who write them to support their research or other work. For that reason they are highly variable in design and quality. There is also a lot of overlap between packages and it can take a while to find the ones you need to best accomplish a task.

To install a package, you can do `install.packages("package")`; replace “package” with the name of an actual package. For example `install.packages("raster")`.

You can install multiple packages at the same time like this: `install.packages(c("randomForest",`

```
"raster", "gstat"))
```

The directory where packages are stored is called the library. Once installed, a package needs to be loaded into the session (taken out of the library) to be used. You do that with the `library` function. For example:

```
library(raster)
```

If the package is not installed, you get an error message like this

```
Error in library(raster) : there is no package called 'raster'
```

So you install a package only once (for each R version), or once in a while (to get updates), but you load a package every time you start a new R session (script) that needs it.

It is very important to stay up to date with R and the packages, as they improve every day... You should update the main R program every 6 months and update your packages more regularly, perhaps once a month. To update all your packages you can run `update.packages()`

## Piping

It has become quite common to use the `%>%` “piping” operator in R, from the defined in the `magrittr` package. We do not use it in our tutorials, but we show it here so that you can understand it when you come across it.

In this example we have vector `v`. We want to change it into a `data.frame` with 10 rows and 3 columns, use `apply` to get the mean values per row, and show the first few results

```
v <- 1:30
```

The classic approach to this is

```
m <- matrix(v, nrow=10)
d <- as.data.frame(m)
a <- apply(d, 1, mean)
head(a)
## [1] 11 12 13 14 15 16
```

The above can also be written as nested function calls

```
head(apply(as.data.frame(matrix(v, nrow=10)), 1, mean))
## [1] 11 12 13 14 15 16
```

Nested function calls can be difficult to read, as they need to be read from the inside parentheses going out, but it can be hard to keep track of the parentheses.

The “piped” approach goes like this

```
library(magrittr)
x <- v %>%
  matrix(nrow=10) %>%
  as.data.frame %>%
  apply(MARGIN=1, FUN=mean)

head(x)
## [1] 11 12 13 14 15 16
```

Or on one line

```
v %>% matrix(nrow=10) %>% as.data.frame %>% apply(MARGIN=1, FUN=mean) %>% head
## [1] 11 12 13 14 15 16
```

Note that we start with an object `v` that gets passed to the first function (`as.data.frame`) as its first argument. The output of that function becomes the first argument of the next function and so on.

Compared to nested function calls, the benefit of this approach is that the operation sequence is read from left-to-right (not from the inside and out). Compared with non-nested function calls, the benefit of this approach is that there are fewer variables created.

## How to write a good script?

Read and follow [this style guide](#).

Only use a path name at the very top of your script. After that, all path names should be relative.

Do not copy and paste the same code into a single script (or multiple scripts), perhaps with minor changes. Rather, write general purpose functions to put code together. You can store these functions in a separate `.R` file and access them via `source('myfunctions.R')`; and then reuse them. If you have a few of these, you might want to put them into your own R package. Even if the functions are only for your own use.

## 1.15 Help!

How to get help when you are stuck? How to find and fix errors? That is the hardest part for beginners. You can start by checking the list of [frequently used functions](#). And, there is always [Google](#)... Any question you may have as a beginner has been asked and answered before. Often on [Stackoverflow](#).

But at first it is hard to find the right search terms, and to distinguish between good answers, and “solutions” that just pull you down further into the hole you are in.

When asking a question about how to do something in *R*, it is very important to simplify it as much as possible, and focus on the nucleus of the problem only. That is, do not show a long script where all kinds of things happen that are OK. Show a short script that gets you up to the point where you are stuck. Such a script should be reproducible and self-contained.

Reproducible means that anyone can run it in *R* and get the same results. So you need to include `set.seed`. Self-contained means that it should not point to files you only have. You could make these available, but why complicate things? Just create some data with code or use a data set that comes with *R* (e.g. “cars”, “iris”, but there are many). See the examples in the *R* help files for 1000s of ideas of how you can do this.

For more discussion see [this posting guide](#) and [this discussion](#)

## 2 Spatial data with “raster”

see <https://rspatial.org/raster/index.html>

## 3 Spatial data with “terra”

see <https://rspatial.org/terra/index.html>