# Introduction to Programming and Statistical Modelling in R

Course Website: http://isites.harvard.edu/icb/icb.do?keyword=k91599

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# Contents

**R set up script for this manual**

We will run this course with R>2.15 and RStudio 0.97.

To ensure you have all of the packages needed to run this course, either

1. install course R package (available on the course website)
2. source the following commands into your R session

```
pkgs<-list("lme4","xtable","xlsx","RODBC","Hmisc",
           "SAScii","R2HTML","BiocInstaller","plyr",
           "RColorBrewer","lattice","ggplot2","googleVis",
           "network","igraph","vcd","MASS","survival",
           "venneuler", "gplots", "ggmap", "knitr",
           "markdown","tm", "wordcloud", "ade4", "gmodels",
           "XML", "XLConnect", "scatterplot3d", "manipulate",
           "KernSmooth", "foreign")


Biocpkgs<-c("parallel", "annotate")

checkPkg<- function(x) {
             print(x)
             if (!x%in%installed.packages()[,1])
               install.packages(x)
             }

checkBioCPkg<- function(x) {
               print(x)
               require(BiocInstaller)
               if (!x%in%installed.packages()[,1])
                 biocLite(x)
               }

lapply(pkgs, checkPkg)
lapply(Biocpkgs,checkBioCPkg)

search()
```

This script checked to see if you have installed each package on your computer. If it is installed, its loads the package into your R session. If it is not installed, it downloads the package from CRAN or Bioconductor and installed it.

The function search lists the packages that are loaded into your current R session. We'll talk more about packages, how to install them and how to load them during the course.

# Chapter 1

# Getting started with R

## 1.1 R Software: Obtaining R and RStudio

R can be downloaded from the website: http://cran.r-project.org/. R is available for all platforms: Unix/Linux, Windows and Mac. In this course we will also use RStudio an interface to R. RStudio can be obtained from www.rstudio.org). RStudio is available as a desktop program for all platforms Unix/Linux, Windows and Mac. There is more information about installing R in Chapter **??**.

If you don't want to install R on your own machine, or tie up your own machine, with a memory or CPU intensive task. You can run R through web server or even in the Cloud. Its really simple to run R jobs in the Amazon cloud as described in Section 5.11 and these can be run through the RStudio interface, which looks exactly as it does on the desktop version.

In this course, we will concentrate on the Windows implementation of R. The differences between the platforms are minor, so most of the material (R, RStudio) is applicable to the other platforms.

## 1.2 First R Encounter

When you start R, and see the prompt $>$ , it may appear as if nothing is happening. But this prompt is now awaiting commands from you. This can be daunting to the new user, however it is easy to learn a few commands and get started

```
demo()
```

Note we place **round brackets** after all functions ALWAYS.

If the brackets are empty () it runs the function with default parameters. To specify a parameters these are inserted into the brackets. For example to run a demo on a specific topics we give that parameters to demo

```
demo(graphics)
demo(nlm)
```

Demo will run through each example, hit return to view each, once it is done you will see the command prompt $>$ again.

***Note if a command is not complete on one line (missing close bracket or quote), R will use continuation prompt '+'***

To find out more about parameters and options for the function demo, lets look at help for demo. To get help simply use the command help or type a question mark ? before the command

```
help(demo)
`?`(demo)
```

### 1.2.1 Interupting and Quiting R

If you wish to interupt a job, press the ESC key in windows or MacOS or click on the "stop sign" (its red). On linux press ctrl-C which interupts R without terminating it.

If you wish to exit R, you can click on the red X in the upper corner of the window frame (Windows), press CMD-q (MacOS) or Ctrl-D (Linux). On all platforms, you can type

```
q()
```

It will ask you if you wish to save the workspace image, and gives you three choices y/n/c.

- y Save workspace and exit
- n Don't save workspace, but still exit
- c Cancel, returning to R session (command prompt) and don't exit

We'll talk more about the workspace later, for now just press **c** but at least you know how to exit should you wish to.

### 1.2.2 Use Arrows to key browse command history

Note you can recover or browser previous commands using the up and down arrow keys.

To demonstrate this, use the function `rnorm` to generate random numbers from a normal distribution. Repeat this a *several times* (hint: the up arrow key is useful). To learn more about rnorm, type ?rnorm

```
rnorm(5)
rnorm(5)
rnorm(10)
rnorm(10, mean = 5, sd = 2)
```

If you wish to generate the same set of random numbers each time, you could *set.seed(10)*

You can view previous expressions entered into the R session using the function history. By default only 25 expresssion are show, if you wish to see more type the number as an argument to the function history.

```
history()
history(50)
```

Browsing, saving and searching is discussed in more detail later in section refsec:history. In Rstudio you can also view expression history in the **history** tab on top right panel (see section refsec:RStudioHistory for further details.

## 1.3 Getting started: R as a big calculator

Type the following into an R session (or copy and paste from this document).

```
2 + 2
2 * 2
2 * 100/4
2 * 100/4 + 2
2 * 100/(4 + 2)
2^10
11%%2  #modulus
log(2)
log(2, base = 2)
```

Each of these are called "expressions". When you type an expression into R, R evaluates the code and prints the results. The result is not stored or saved to a file. In order to manuiplate expressions we need to assign the result of an expression to a variable.

## 1.4 Assignment

Even in the simple use of R as a calculator, it is useful to store intermediate results.Lets store the value of (`tmpVal=log(2)` in a *symbolic variable* `tmpVal`.

```
tmpVal <- log(2)
print(tmpVal)

## [1] 0.6931

tmpVal

## [1] 0.6931

exp(tmpVal)

## [1] 2
```

Note when you assign a value to such a variable, there is no immediate visible result. We need to `print(tmpVal)` or just type `tmpVal` in order to see what value was assigned to `tmpVal`

- In summary elementary commands are either:
  - *expressions* are evaluated, printed and value lost;
  - *assignments* evaluate expressions, passes value to a variable, but not automatically printed

```
2 * 5^2

## [1] 50
```

```
x <- 2 * 5^2
print(x)

## [1] 50
```

- Variables can be assigned using the assignment operators: `'<-', '=', '->'`

  `'<-'` is the most popular assignment operator, and `'='` is a recent addition.

  It is `'<-'` (less than and a minus symbol)

  There is no space between $<$ and $-$.

  When assigning a value spaces are ignored so `'z<-3'` is equivalent to `'z  <-  3'`

```
  y <- 2*5^2    # Spaces are disregarded
  z<-2*5^2
  2*5^2  -> z   # Using the -> operator is equivalent
  print(y)

## [1] 50

  y==z

## [1] TRUE
```

- Note '=' and '==' have very different uses in R. == is a binary operator, which test for equality (A==B determines if A 'is equal to' B ).

## 1.5 Basic operators

We already saw that == tests for equality or a match between 2 objects. Other operators are:

### 1.5.1 Comparison operators

- equal: ==
- not equal: !=
- greater/less than: $>$ $<$
- greater/less than or equal: >= <=

```
1 == 1

## [1] TRUE
```

### 1.5.2 Logical operators

- AND &

  Returns TRUE if both comparisons return TRUE.

```
x <- 1:10
y <- 10:1
x > y & x > 5

##  [1] FALSE FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE
```

- OR |

  Returns TRUE where at least one comparison returns TRUE.

```
x == y | x != y

##  [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

- NOT !

  The '!' sign returns the negation (opposite) of a logical vector.

```
!x > y

##  [1]  TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE
```

  These return a logical vector of TRUE or FALSE and can be useful for filtering (we will see this later)

## 1.6 Help with functions and features

There are many resources for help on functions (or commands) in R.

### 1.6.1 R functions

Within R, you can find help on any command (or find commands) using the following:

- help or ?

  If you know the command type help or ?

```
## help or ? will open a help page
help(lm)

# ?matrix
`?`(matrix)
```

- apropos

  If you know part of the function name you can perform a search of all command to retrieve a list of functions with a partial match. It is not case sensitive

  The functions find() or apropos() will perform a search for a commands that partial match the input argument

```
apropos("fish")

## [1] "fisher.test"

apropos("Fisher")

## [1] "fisher.test"
```

- Example

  Almost all functions have an example, use the command to get an example of how to use the function

```
## The function example will run example of a command
example(rep)
```

  This will run all the examples included with the help for a particular function. If we want to run particular examples, we can highlight the commands in the help window and submit them by typing $Ctrl^V$

- help.search or ??

  If you don't know the command and want to do a keyword search for it. For example we wished to find the command to perform a Student's t-test, we could perform a search of function help pages

```
help.search("Student")
help.start()
`?`(`?`(Student))
```

  Note using the double question mark ?? or the command help.search are equivalent.

- RSiteSearch

  The function RSiteSearch performs a key words search of R-help mailing list archives, help pages, vignettes or task views at the website at `http://search.r-project.org` which is maintained by Jonathan Baron and the School of Arts and Sciences of the University of Pennsylvania.

```
RSiteSearch("Student's t-test")
```

`help.search` will open a html web browser or a MSWindows help browser (depending on the your preferences) in which you can browse and search R documentation.

### 1.6.2 Web resources for R help

There is a large R community who are incredibly helpful. There is a mailing list for R, Bioconductor and almost every R project. It is useful to search the archives of these mailing lists. Frequently you will find someone encountered the same problem as you, and previously asked the R mailing list for help (and got a solution!).

- The R search engine `http://www.Rseek.org`
- R bloggers website `http://www.r-bloggers.com/`

In addition, there numerous useful resources for learning R on the web including the R project `http://www.r-project.org` and its mailing lists but also I recommend the following:

- Emmanuel Paradis has an excellent beginners guide to R available from `http://cran.r-project.org/doc/contrib/Paradis-rdebuts_en.pdf`
- There is an introduction to R classes and objects on the R website `http://cran.r-project.org/doc/manuals/R-intro.html`
- also see Tom Guirkes manual at `http://manuals.bioinformatics.ucr.edu/home/R_BioCondManual`
- Tom Short's provides a useful short R reference card at `http://cran.r-project.org/doc/contrib/Short-refcard.pdf`

### 1.6.3 Transitioning from SAS or SPSS

If you come from a SAS or SPSS background, the following maybe useful to you

- In the December 2009 issue of the R Journal. Transitioning to R: Replicating SAS, STATA, and SUDAAN Analysis Techniques in Health Policy Data. Anthony Damico `http://journal.r-project.org/archive/2009-2/RJournal_2009-2_Damico.pdf`
- SAS and R. A blog devoted to examples of tasks (and their code) replicated in SAS and R `http://sas-and-r.blogspot.com/`
- R for SAS and SPSS Users. Download a free 80 page document, `http://rforsasandspssusers.com/`
  R for SAS and SPSS Users which contains over 30 programs written in all three languages.

## 1.7 Quiz

- Find a function that will calculate the mean and standard deviation.
- Get help on the function *rnorm*. What is the default mean and standard deviation of the random normal distribution from which numbers are sampled?
- Draw 10, 100, 1000 number from a random normal distributionand assign these to the objects r10, r100 and r1000 respectively.
  - What is the mean of each?
  - How would you draw the same random number each time?
- Are each of the following TRUE or FALSE

  Q1

```
z <- 1:11
Z <- 2:22
z == Z
```

  Q2

```
a <- LETTERS[1:5]
b <- c("a", "b", "c", "d", "e")
a == b
a[1] %in% b  # x%in%y tests if x is a member of y
```

  Q3

```
a <- 1:5
b <- a%%2  #%% is modulus
b == TRUE
```

## 1.8 A few important points on R

- `R` is case sensitive, i.e. `myData` and `Mydata` are different names

```
x
```

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

```
y
```

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

```
Z <- 20
x == z
```

```
##  [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

```
x == Z
```

```
##  [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

- Comments can be put anywhere. To comment text, insert a hashmarh `#`. Everything following it to end of the line is commented out (ignored, not evaluated).

```
print(y)  # Here is a comment
```

- Quotes, you can use both " double or ' single quotes, as long as they are matched.
- For names, normally all alphanumeric symbols are allowed plus `'.'` and `'_'` Start names with a character [Aa-Zz] not a numeric character [0-9]. Avoid using single characters or function names t, c, q, diff, mean, plot etc.
- Arguments (parameters) to a function calls f(x), PROC are enclosed in round brackets. Even if no arguments are passed to a function, the round brackets are required.

```
print(x)
getwd()
```

- Commands can be grouped together with braces (`'{'` and `'}'`). They can be separate by semi-colon ; or on different lines

```
{
    a <- 1
    b <- 3
    c <- "What the connection between the Students t-test and Guinness?"
    print(a + b + 2)
    print(c(a, b) + 2)
    print(length(c))
    print(nchar(c))
}
```

```
## [1] 6
## [1] 3 5
```

```
## [1] 1
## [1] 61
```

- Note on brackets. It is very important to use the correct brackets.

| Bracket | Use |
|---|---|
| `()` | To set priorities 3*(2+4). Function calls f(x) |
| `[]` | Indexing in vectors, matrices, data frames |
| `{}` | Creating new functions. Grouping commands `{mean(x); var(x)}` |
| `[[]]` | Indexing of lists |

- Missing values called represented by NA. For more on missing values see section 3.5.4.
- Inf and -Inf are positive and negative infite values respectively

```
1/0

## [1] Inf

-1/0

## [1] -Inf
```

- Sometimes a computation will create a value that doesn't make sense returning an 'NaN' value. 'NaN' is 'Not A Number'

```
0/0

## [1] NaN
```

-

## 1.9 Working with R

When you begin your first project in R, you will need to know how to organize your R files and save your R scripts and output.

### 1.9.1 Defining a working directory

The first thing to do when starting an R session, is to ensure that you will be able to find your data and also that your output will be saved to a useful location on your computer hard-drive. Therefore, set a "working directory"

Within R Studio, you can define a RStudio project folder is a great way to start a new project. It aids with managing R code, data and results.

However even if you don't use the project option or are accessing R through the default or another interface, you still will need to be able to set a current working directory (in which all your output files are saved).

When I create a new working directory for an R project, I try to include a project Name and Date in the folder name eg colonJan13.

Within this folder I incrementally name scripts for example S001prepData.R, S0002transform.R, S003analysis.R, S004results.R etc. I also create a simple file which gives a brief description of each. We have a lot more tips on scriting in R in section 5.12

There are numerous way to define the working directory in R. To change directory:

1. In the classic R interface. Use the file menu, to change directory File $->$ Change dir
2. If you start R by clicking on an R icon. You may wish to change the default start location by right mouse clicking on the R icon on the desktop/start menu and changing the "Start In" property. For example make a folder 'C:/work', and make this as a "Start in" folder
3. In RStudio Tools $->$ Set Working Directory
4. Or in RStudio click on the Files tab (on the bottom right panel). Use the File browser window to view the contents of a directory and navigate to the directory you wish to set as your home directory.
   - click on the triple dot icon on the top right. Navigate to the correct directory
   - Once you are in the correct directory and see your data files click on the More (blue cog-wheel), and select "Set as Working Directory"

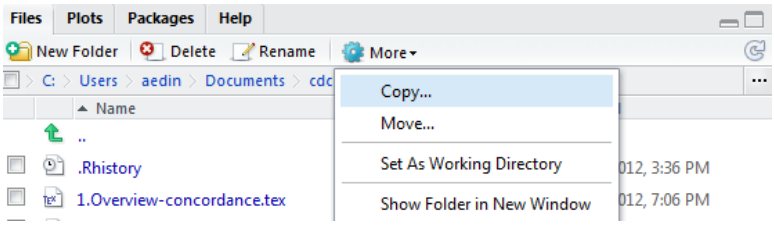



Figure 1.1: Viewing Files and Setting wkdir
Note the triple dot icon on the far right and the blue cog wheel

5. The commands to set the working directory.

```
# What is my current directory
getwd()
```

To change the directory:

```
# Set working directory
setwd("C:/work/colonJan13")
```

To see folders or files in the working directory, use the command *dir()* (or browse the files using the Files Browser panel in RStudio)

```
dir()
dir(pattern = ".txt")
```

*Important side note:* R doesn't like windows a back slash (\) that separate folders in a file path. Indeed it will return a rather cryptic error

```
> setwd("C:\Users\aedin\Documents\Rwork")
Error: "\U" used without hex digits
in character string starting "C:\U"
```

There are a couple of ways to prevent this, either replace backslash (\) with forward (/) slash or double back slash (\\) The first back slash tells R to treat the character literally, it is called an escape character which invokes an alternative interpretation on subsequent characters.

```
setwd("C:/Users/aedin/Documents/Rwork")
setwd("C:\\Users\\aedin\\Documents\\Rwork")
```

Using all those slashes can be rather tedious. A nicer way to make scripts work across platform is to define directories in a more generic way.

The R command *file.path* will automatically add in the correct "slashes" for windows, mac or Linux

```
file.path("~", "Documents", "Rwork")

## [1] "~/Documents/Rwork"
```

Here the tilde symbol (~ ) which is the shortcut to your home drive (on any operating system). These is more details about using these shortcuts in chapter 5.8.1

### 1.9.2 Navigating folders in R

If you are setting a working directory within a script, you may need to check a folder exisits or create a new one. These can be achieved with the command file.exists and dir.create respectively

```
# check if the directory or file exisits
file.exists("colonJan13")
# Create a directoryfolder
dir.create("colonJan13")
setwd("colonJan13")
```

To create a full directory or more complex directory path. A path can be relative to the current location, in this case two dots mean "the directory above"

```
setwd("../../RWork/colonJan13")
```

Or you can specific a full directory path. For cross-platform compatibility, its best to use file.path() to create paths. for example to set move the working directory to a folder called Project1 within the current directory;

```
wkdir <- getwd()
subdir <- "Project1"
newdirPath <- file.path(wkdir, subdir)
```

```r
# If directory doesn't exist create it
if (!file.exists(newdirPath)) dir.create(newdirPath)
setwd(newdirPath)
```

### 1.9.3 Saving, Loading R workspace and history

To finish up today, we will save our R session and history

1. Saving a R objects
   One can either save one or more R object in a list to a file using *save()* or save the entire R session (workspace) using *save.image()*.

```
save(women, file = "women.RData")
save.image(file = "entireL2session.RData")
```

   To load this into R, start a new R session and use the *load()*

```
rm(women)
ls(pattern = "women")
load("women.RData")
ls(pattern = "women")
```

2. Saving R history
   R records the commands history of each R session. To view most recent R commands in a session

```
history()
help(history)
history(100)
```

   To search for a particular command, for example ”save”

```
history(pattern = "save")
```

   To save the commands in an R session to a file, use *savehistory()*

```
savehistory(file = "L2.Rhistory")
```

3. Note you can also browse and search history in RStudio, really easily in the history window. A really nice feature of this window is the ease of sending command either to the console (to execute code again) or to Source (to a text file or script you are writing in the editor)

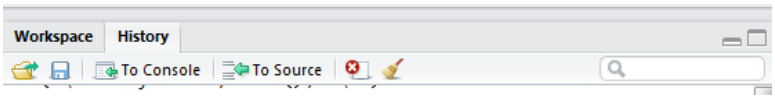



Figure 1.2: Browsing history in RStudio

You can easily save or search command history, send commands to the R console or a source (script) file

4. Default saving of RData and Rhistory
   By default, when you quit *q()* an R session, it will ask if you wish to save the R workspace image. If you select yes, it will create two file in the current working directory, there are .RData and .Rhistory. These are hidden system files, unless you choose to ”Show Hidden Files” in the folder options. There are output files are the same as running save.image(file=”.RData”) and savehistory(file=”.Rhistory”) respectively.

# Chapter 2

# R Interfaces: Using R and RStudio

## 2.1 R Software: Obtaining `R` and `RStudio`

`R` can be downloaded from the website: `http://cran.r-project.org/`. `R` is available for all platforms: Unix/Linux, Windows and Mac. When you download R, its default editor and console are relatively basic (we describe it below). In this course we will call R using RStudio which provides a richer interface to R. RStudio can be obtained from `www.rstudio.org`). RStudio is available as a desktop program for all platforms Unix/Linux, Windows and Mac.

I have additional online notes which give a very detailed description on downloading and installing R (and Bioconductor).

When you download R, it will not over-write an existing installation of R, instead you get multiple version of R, eg R2.14, R.15 etc. To get rid of an older version of R, simple uninstall it, each release is stored its in own structure and is independent of previous releases. This has the advantage of easily calling an older version of R (maybe to repeat an old analysis) but had the disadvanatge that when a new version of R is released, the install is a longer process, as you have to install R and the packages that you require. More about those later in this chapter. For now, lets look at the basic R software you have installed.

## 2.2 The default `R` interface

After downloading R, click on the R icon. It will open the basic R interface. The windows or macOS the R interface will pretty similar. The linux interface had fewer options and can be initaed using the command

verbatim R -g Tk

- On the menu bar, there are the menus:
  - File - load script, load/save session (workspace) or command history. **Change Directory**
  - Edit - Cut/Paste. GUI preferences
  - View
  - Misc - stop computations, list/remove objects in session
  - Packages - allows one to install new, update packages

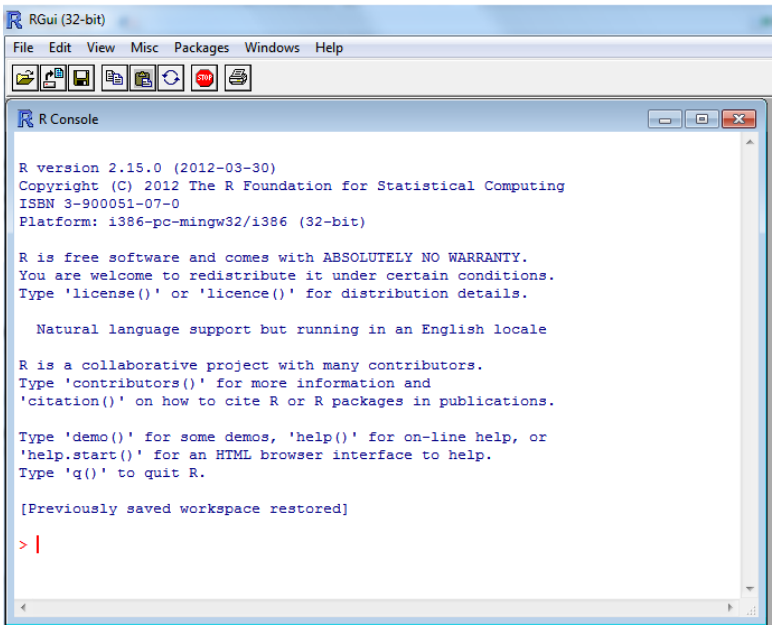



Figure 2.1: R interface
R interface with windows installation of R

  - Windows
  - Help - **An essential resource!**
- The *icons* below will allow one to
  - open script (.R file),
  - load image (previous R session, .RData file)
  - save .R script
  - copy and paste
  - stop a computation (this can be an important button, but the ESC also works!)
  - print.

### 2.2.1 Default R Console

The main window that you see in the R Console. This is where you type R commands. Note it says type demo() or help() or q() to view example R in code, to see R help or to quit R respectively.

Within the R console, you can

- Type at the prompt > symbol.
- If the prompt instead show the continuation prompt is '+', it means the command you typed is incomplete and R is waiting for it to complete (usually its missing a closing quote or bracket)
- Use up and down arrow keys to scroll through previous commands. This is useful if you would like to repeat a previous command
- R also includes basic automatic completions for function names and filenames. Type the "tab" key to see a list of possible completions for a function or filenames.

### 2.2.2 Default R Editor

- Within R, one can open an editor using the menu command *File -> New script*
- Can type commands in the editor
- Highlight the commands and type `Ctrl^R` to submit the commands for R evaluation
- Evaluation of the commands can be stopped by pressing the `Esc` key or the `Stop` button
- Saving (`Ctrl^S`) and opening saved commands (`Ctrl^O`)
- Can open a new editor by typing `Ctrl^N`

### 2.2.3 R Shortcuts

Keyboard Shortcuts for traditional R GUI

- Ctrl + A: gets you to the beginning of the line
- Ctrl + E: gets you to the end
- Ctrl + K: wipes everything to the right of your cursor
- Esc: kills the current comment and takes you back to ¿
- Up Arrow: brings back last command you typed
- Down Arrow: brings back the next command (Up and down basically scrolls up and down through your history)

Keyboard shortcuts for RStudio are listed online at `http://www.rstudio.org/docs/using/keyboard_shortcuts`.

## 2.3 RStudio Interface

RStudio is a free and open source integrated development environment for R. Those familiar with MatLab will recognize the layout as its pretty similar. RStudio have a brief 2 minute guide to the interface on their website `http://rstudio.org/` which I recommend watching.

On start-up R Studio brings up a window with 3 or 4 panels. If you only see 3 panels, click on **File** –> **New** –> **New R Script**.

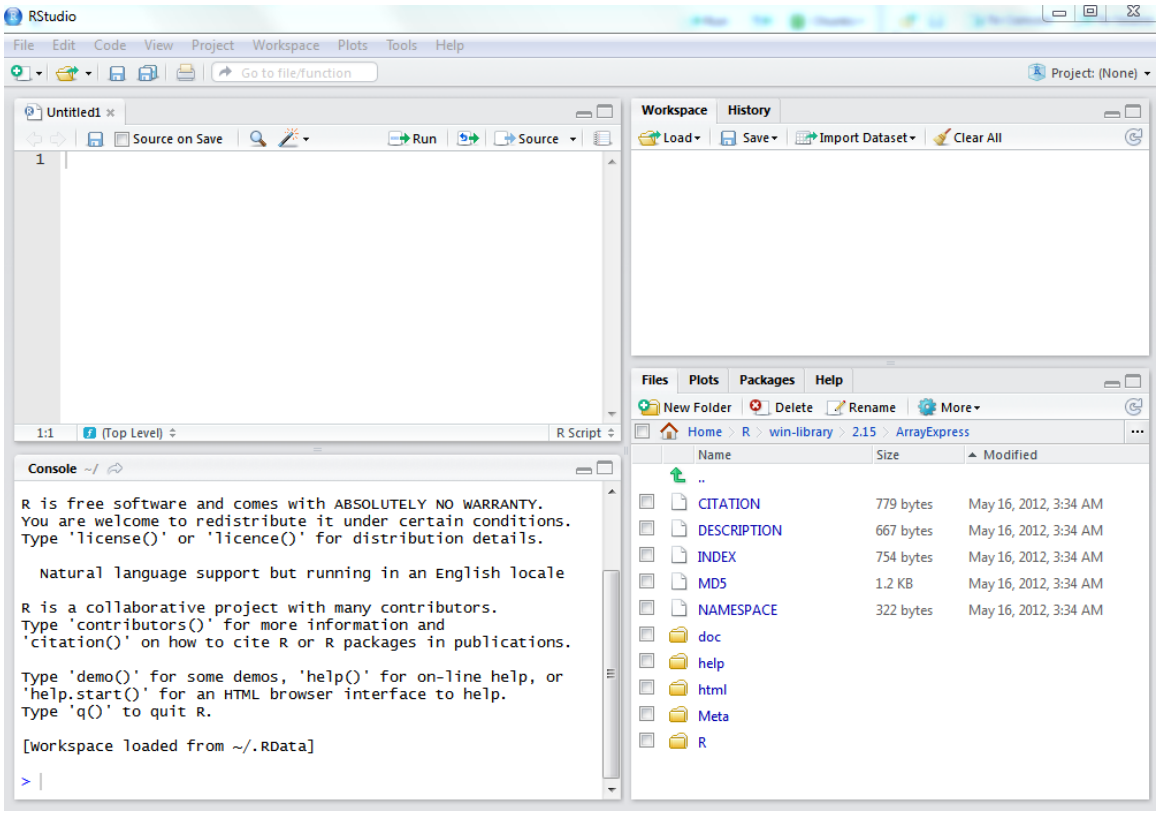



Figure 2.2: RStudio interface
RStudio v0.96 interface with 4 panels

The first thing to notice, is that the bottom left panel "console" is the exact same as the standard R console. RStudio just loads your local version of R. You can specify a different version of R (if you have multiple versions of R running on your machine) by clicking on `Tools -> Options` and selecting R version.

### 2.3.1 R Console

RStudio has a nice console features

- start typing a command, for example `fi`, press the TAB key, it will suggest function that begin with `fi`
- Select `fis` for *fisher.test*. Type

```
fisher.test(
```

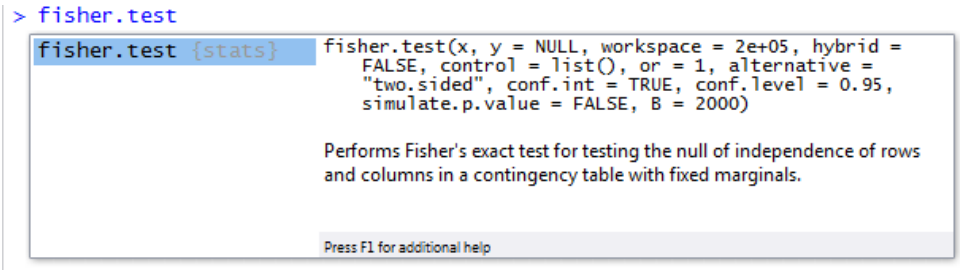



Figure 2.3: Pressing Tab to reveal function help
Tab not only auto-completes, but also suggests parameters and input to the function. Note it says press F1 for further help on this function

and then press the TAB key. You will notice it bring up help on each parameter, you can browse these and it will help you get familiar with R.

- Press **F1**, it will bring up a **help** document about the function in the help panel (right bottom)
- Press **F2**, it will show the **source code** for function

There are many useful keyboard shortcuts in RStudio for a full list of these see `http://rstudio.org/docs/using/keyboard_shortcuts`

### 2.3.2 R Editor

The top left panel is an editor which can be used to edit R scripts (.R), plain text (.txt), html web files or Sweave (rnw) or markdown (md), the latter two of these can be converted to pdf files. There are several nice features to this text editor which we will describe during the course. But for now note, that it highlights R code, and that the code is searchable (click Control-F to search)

In the menu **code**, you can set preferences to highlight, indent or edit code.

### 2.3.3 R Workspace, history

On the top right there is a tab menu workspace and history. We will talk about these in detail.

- Workspace list the objects in the current R session. You can load, save or "Clear All" object for a workspace
- Note that under the workspace panel there is the option to **Import Dataset**
- The history panel lists all of the command that have been typed or input in the console. There are options to load, save, search or delete history
- One can easily repeat a command by highlighting one or more line(s) and sending these **To Console**
- One can easily copy a command to a new R script or text file, by highlighting one or more line(s) and sending these **To Source**

### 2.3.4 Files, Plots, Packages, Help

On the bottom right there is a tab menu Files, Plots, Packages and Help.

- **Files** is a file browser, which allows you to create a new folder, rename a folder or delete a folder. Click on the triple dot icon (...) on the far right on the menu to browse folders. Under the More menu you can set your current working directory (more about that below). If you double click on a text, .R, Sweave or html file it will automatically open in the Editor.
- The **Plots** window displays plots generated in R. Simply type the following command into the Console window

```
plot(1:10)
plot(rnorm(10), 1:10)
```

  It will create 2 plots. Use the arrows keys to browse plots, click on zoom, export or delete to manage plots.
- **Packages** list all of the packages installed in your computer. The packages with tick marked are those loaded in your current R session. Click on a package name to view help on that package. Note you can **install packages or check for updates**. You can also search for a package or search package descriptions using the search window.
- The **Help** menu provides an extensive R help. The arrows button go forward or back through recent help pages you have viewed. You can go home (house icon), print or open help in new window. You can search help, use the search window. Help can also be browsed through main menu bar at the open of the page

### 2.3.5 Projects, SVN in RStudio

RStudio provides an easy approach to managing projects. In the main menu there is a **Projects** menu which which will create folder for your project and retain all data files and command history for your project. It is also possible to set up a backup subversion management control system for your code as RStudio will directly communicate with your SVN or github account.

## 2.4 Example Datasets in R

Both the R core installation and contributed R package contain data sets, which are useful example data when learning R. To list all available data sets:

```
data()
```

To load a dataset, for example, the dataset women which gives the average heights and weights for 15 American women aged 30-39.

```
data(women)
ls()
ls(pattern = "w")
```

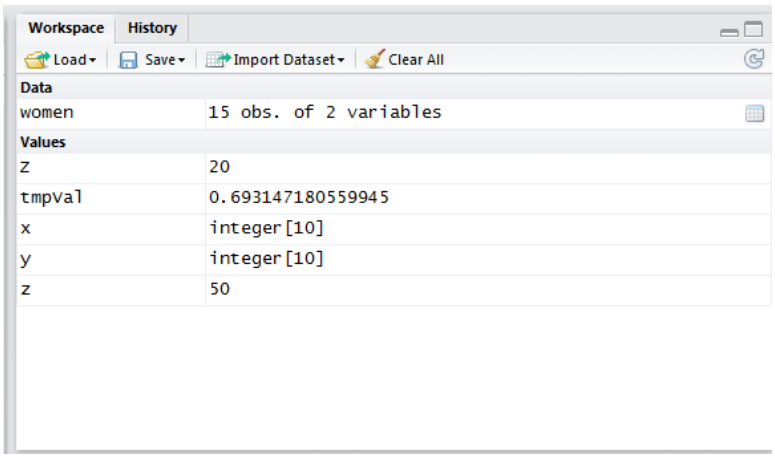



Figure 2.4: RStudio Viewing objects in R workspace
The Workspace windows lists the object currently in the R workspace. You can click on each item to view or edit it. Note women is a data table with dimensions 15 rows x 2 columns, you can click on the table icon to view it. Z and y are a single value (50). x and y are integer vectors of length 10.

## 2.5 R Packages

By default, R is packaged with a small number of essential packages, however as we saw there are many contributed R packages.

1. Some packages are loaded by default with every `R` session. The libraries included in the Table are loaded on the `R` startup.

Table 2.1: Preloaded packages

| Package | Description |
|---|---|
| **base** | Base R functions |
| **datasets** | Base R datasets |
| **grDevices** | Graphics devices for base and grid graphics |
| **graphics** | R functions for base graphics |
| **methods** | Formally defined methods and classes for R objects, plus other programming tools |
| **stats** | R statistical functions. |
| **utils** | R utility functions |

2. To see which packages are currently loaded, use

```
search()
sessionInfo()
```

3. To see which packages are installed on your computer, issue the command

```
library()
```

Within **RStudio installed packages can be view in the Package Tab of the lower right panel**. You can tick or select a library to load it in R.

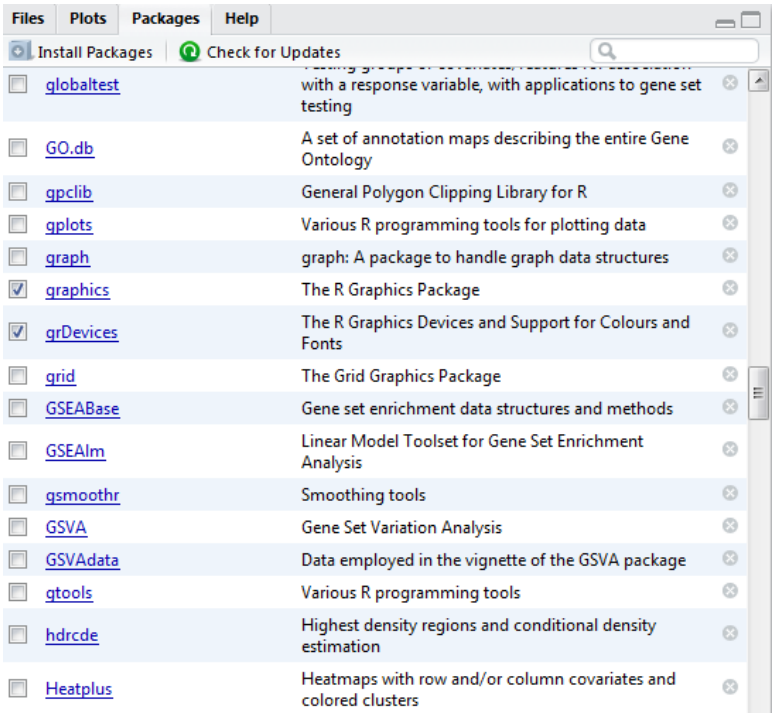



Figure 2.5: RStudio- Viewing the list of all packages that are Installed loaded into a workspace
The list is all installed packages. A tick marked indicates its loaded into the current R session. Clicking on the package name will open help for that package

You will very likely want to install additional packages or libraries.

## 2.6 Installing new R libraries

There are several thousand R packages and >500 Bioconductor packages (also called libraries) available. These are not installed by default, so we have to select and install additional packages that will be of use to us. Not all of them, actually a small subset, will be useful to us. R users are free to selected which libraries to install.

### 2.6.1 Installing packages in R

Install packages using the basic R GUI using the drop-down menu `Packages` or command line (*install.packages*). First Click on "Packages" and "Set CRAN mirror" and choose an available mirror (choose one close by, it'll be faster hopefully). Then If you know the name of the package you want to install, or if you want to install all the available packages, click on "install Packages"

Open a CMD shell and type

```
R CMD INSTALL  packageName.tar.gz.
```

You can open a CMD shell from RStudio *Tools −> Shell* or type 'cmd' to run cmd.exe into the Start box on windows

### 2.6.2 Installing packages using RStudio

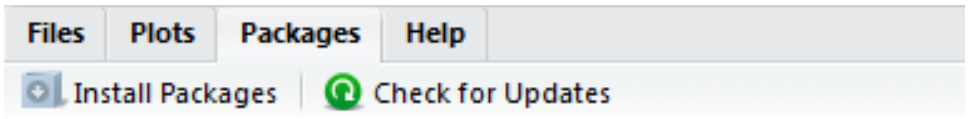



Figure 2.6: Click on Install Packages

This will open an install window:

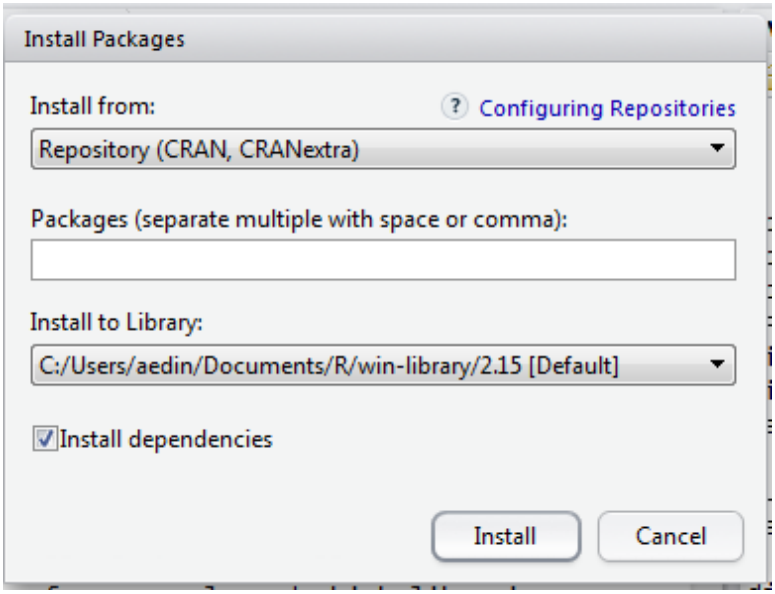



Figure 2.7: Type the name of the package. Unfortunately RStudio does not display a list of all available packages

On windows, sometimes I have encountered problems with program installation using RStudio. This is normally when R tried to write to a folder but doesn't have write permission to this folder. To check this

1. Run RStudio as administrator
2. Or check you have write permission to the path where it will write the files (use the following R function to list your RStudio Paths) ¡¡rsPref, eval=FALSE¿¿= .rs.defaultUserLibraryPath() Path where RStudio installs packages .rs.rpc.get$_p ackage_i nstall_c ontext()Otherusef ulRStudioconf igurationinf o@$

### 2.6.3 Commands to install packages

```
# Installing and updating R libraries
install.packages("lme4")
update.packages("lme4")
```

Installation of all packages takes some time and space on your computer. If the name of the package is not known, you could use task-views help or archives of the mailing list to pinpoint one. Also look on the R website Task views description of packages (see Additional Notes in Installation which I have provided).

To list all of the packages installed on your computer.

```
library()  # List all installed packages
installed.packages()
```

/subsectionCreating an Install R packages script Its useful to create an install package script, to automate package installation when you wish to update R to a new version.

The easiest way to do this is to take the list of currently install package and send to them to a script, similar to that at the start of this manual in section

```
## before upgrading, save the list of current packages
pkgs <- installed.packages()[, 1]
write(pkgs, file = "MyPkgList.txt")

## To upgrade, download and install the new version of R
pkgs <- scan("MyPkgList.txt", what = "tt")
lapply(pkgs[1:2], install.packages)
```

Note if you have Bioconductor packages, the install is different. See the online manual on installing Bioconductor packages, and then use biocLite rather than install.packages to install Bioconductor packages.

### 2.6.4 Package help

To get an information on a package, type

```
library(help = lme4)
```

Many packages, particular those in Bioconductor have vignette documents which provide a case studies or tutorial on the functions in a package

To see if a package has a vignette, either browse the package help in the Rstudio help window, or online using help.search

```
## list vignettes associated with the package lme4
vignette(package = "lme4")

## open the vignette with the title Theory
vignette("Theory", package = "lme4")
```

### 2.6.5 Load package into workspace

Once you have installed a package, you do NOT need to re-install it. To load the library in your current R session use the commands

```
library(lme4)  # Load a package
## Or the alternative
require(lme4)
```

To list all packages loaded in the current R session

```
sessionInfo()
search()
```

You can unload the loaded package pkg by

```
search()
detach(package:lme4)
search()
```

NOTE: Packages are often inter-dependent, and loading one may cause others to be automatically loaded.

## 2.7 Customizing R Start-up

### 2.7.1 R Studio Environment

To customize your R environment, you can change options through RStudio File -> Tools -> Options

### 2.7.2 Rprofile

In addition you can specify preferences for either a site or local installation in Rprofile.site. On Windows, this file is in the `C:\Program Files\R\R-x.y.z\etc` directory where x.y.z is the version of R. Or you can also place a .Rprofile file in the directory that you are going to run R from or in the user home directory.

At startup, R will source the Rprofile.site file. It will then look for a .Rprofile file in the current working directory. If it doesn't find it, it will look for one in the user's home directory.

There are two special functions you can place in these files. .First( ) will be run at the start of the R session and .Last( ) will be run at the end of the session. These can be used to load a set of libraries that you use most.

```
# Sample Rprofile.site file

# Things you might want to change options(papersize='a4')
# options(editor='notepad') options(pager='internal')
```

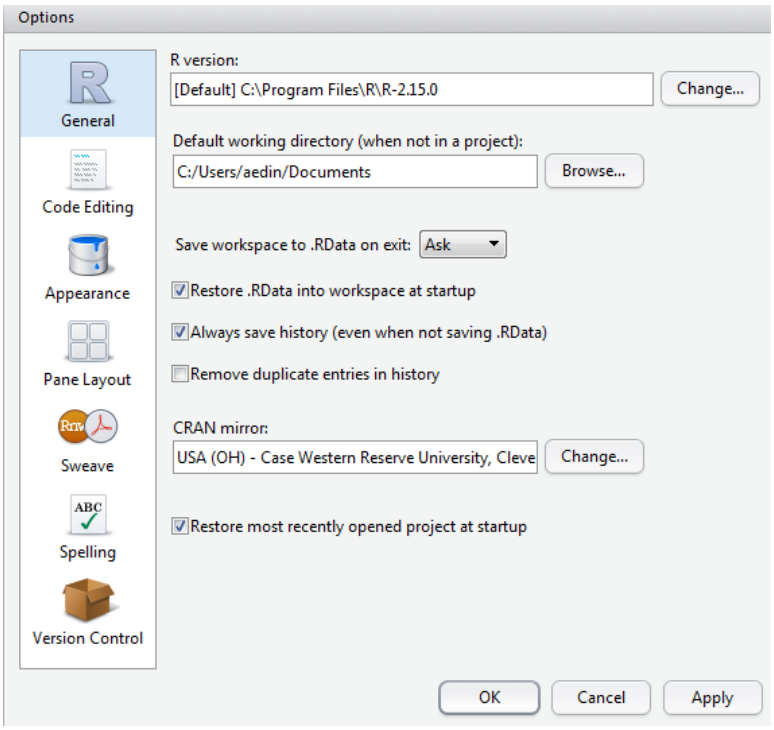



Figure 2.8: Options in RStudio
Within the options window you can change the version of R, your default directory and SVN preferences

```
# R interactive prompt options(prompt='> ') options(continue='+ ')

# General options
options(tab.width = 2)
options(width = 100)
options(digits = 5)


.First <- function() {
    library(lme4)
    library(xtable)
    cat("\nWelcome at", date(), "\n")
}

.Last <- function() {
    cat("\nGoodbye at ", date(), "\n")
}
```

For more help on this see `http://www.statmethods.net/interface/customizing.html`

# Chapter 3

# Objects in R

1. Everything (variable, functions etc) in R is an *object*
2. Every object has attributes one of which is *class*

## 3.1 Using ls and rm to managing R Objects

R creates and manipulates *objects*: variables, matrices, strings, functions, etc. *objects* are stored by name during an R session.

During a R session, you may create many objects, if you wish to list the objects you have created in the current session use the command

```
objects()
ls()
```

The collection of objects is called *workspace*.

If you wish to delete (remove) objects, issue the commands:

```
rm(x, y, z, junk)
```

where `x, y, junk` were the objects created during the session.

Note `rm(list=ls())` will remove everything. Use with caution

## 3.2 Types of R objects

Objects can be thought of as a container which holds data or a function. The most basic form of data is a single element, such as a single numeric or a character string. However one can't do statistics on single numbers! Therefore there are many other objects in R.

### 3.2.1 vector

A `vector` is an ordered collection of numerical, character, complex or logical objects. Vectors are collection of *a*tomic (same data type) components or modes. For example

```
# Numeric
vec1 <- 1:10
vec1

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


# Character
vec2 <- LETTERS[1:10]
vec2

##  [1] "A" "B" "C" "D" "E" "F" "G" "H" "I" "J"


# logical
vec3 <- vec2 == "D"
vec3

##  [1] FALSE FALSE FALSE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE
```

In each case above, these vectors have 10 elements, and are of length=10.

### 3.2.2 Matrix

A `matrix` is a multidimensional collection of data entries of the *s*ame type. Matrices have two dimensions. It has rownames and colnames.

```
mat1 <- matrix(vec1, ncol = 2, nrow = 5)
print(mat1)

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

dim(mat1)

## [1] 5 2
```

```r
colnames(mat1) <- c("A", "B")
rownames(mat1) <- paste("N", 1:5, sep = "")
print(mat1)
```

```
##    A  B
## N1 1  6
## N2 2  7
## N3 3  8
## N4 4  9
## N5 5 10
```

### 3.2.3 list

A `list` is an ordered collection of objects that can be of different modes (e.g. numeric vector, array, etc.).

```r
a <- 20
newList1 <- list(a, vec1, mat1)
print(newList1)
```

```
## [[1]]
## [1] 20
##
## [[2]]
##  [1]  1  2  3  4  5  6  7  8  9 10
##
## [[3]]
##    A  B
## N1 1  6
## N2 2  7
## N3 3  8
## N4 4  9
## N5 5 10
##
```

```r
newList1 <- list(a = a, myVec = vec1, mat = mat1)
print(newList1)
```

```
## $a
## [1] 20
##
## $myVec
##  [1]  1  2  3  4  5  6  7  8  9 10
##
## $mat
##    A  B
```

```
## N1 1  6
## N2 2  7
## N3 3  8
## N4 4  9
## N5 5 10
##
```

### 3.2.4 data.frame

Though a `data.frame` is a restricted list with class `data.frame`, it maybe regarding as a matrix with columns that can be of different modes. It is displayed in matrix form, rows by columns. (Its like an excel spreadsheet)

```
df1 <- as.data.frame(mat1)
df1
```

```
##    A  B
## N1 1  6
## N2 2  7
## N3 3  8
## N4 4  9
## N5 5 10
```

### 3.2.5 factor

A `factor` is a vector of categorical variables, it can be ordered or unordered.

```
charVec <- rep(LETTERS[1:3], 10)
print(charVec)
```

```
##  [1] "A" "B" "C" "A" "B" "C" "A" "B" "C" "A" "B" "C" "A" "B" "C" "A"
## [17] "B" "C" "A" "B" "C" "A" "B" "C" "A" "B" "C" "A" "B" "C"
```

```
table(charVec)  # Tabulate charVec
```

```
## charVec
##  A  B  C
## 10 10 10
```

```
fac1 <- factor(charVec)
print(fac1)
```

```
##  [1] A B C A B C A B C A B C A B C A B C A B C A B C A B C A B C
## Levels: A B C
```

```r
attributes(fac1)

## $levels
## [1] "A" "B" "C"
##
## $class
## [1] "factor"
##

str(fac1)

##  Factor w/ 3 levels "A","B","C": 1 2 3 1 2 3 1 2 3 1 ...

levels(fac1)

## [1] "A" "B" "C"
```

The order of the levels of these categories is not important, but sometimes the order of the factor is important

### 3.2.6 ordered factor

By default the levels are ordered according to the alphabetical order of the categories.

But this may not be appropriate where factor order in important. For example if we have a survey response scale of good to poor. Or we are looking at a gradient such as tumor grade 1 to 3. In these cases, the order is important.

For example, we have a variable of socio-economic status from low to high. By default alphabetical ordering, ”high” is the lowest and ”low” is the highest level. In order to fix the ordering we need to use levels argument to indicate the correct ordering of the categories.

```r
facA <- sample(c("low", "medium", "high"), 10, replace = TRUE)
fac1 <- factor(facA)
str(fac1)

##  Factor w/ 3 levels "high","low","medium": 2 2 2 3 3 3 1 2 1 3

levels(fac1)

## [1] "high"   "low"    "medium"


fac2 <- factor(facA, levels = c("low", "medium", "high"))
fac2

##  [1] low    low    low    medium medium medium high   low    high
## [10] medium
## Levels: low medium high
```

```
fac3 <- factor(facA, levels = c("low", "medium", "high"),
    ordered = TRUE)
fac3
```

```
##  [1] low    low    low    medium medium medium high   low    high
## [10] medium
## Levels: low < medium < high
```

```
# To convert an unordered factor to an ordered factor you can use
# the function ordered
ordered(fac2)
```

```
##  [1] low    low    low    medium medium medium high   low    high
## [10] medium
## Levels: low < medium < high
```

### 3.2.7 array

An array in R can have one, two or more dimensions. I find it useful to store multiple related data.frame (for example when I jack-knife or permute data). Note if there are insufficient objects to fill the array, R recycles (see below)

```
array(1:24, dim = c(2, 4, 3))
```

```
## , , 1
##
##      [,1] [,2] [,3] [,4]
## [1,]    1    3    5    7
## [2,]    2    4    6    8
##
## , , 2
##
##      [,1] [,2] [,3] [,4]
## [1,]    9   11   13   15
## [2,]   10   12   14   16
##
## , , 3
##
##      [,1] [,2] [,3] [,4]
## [1,]   17   19   21   23
## [2,]   18   20   22   24
##
```

```r
array(1:23, dim = c(2, 4, 3))
```

```
## , , 1
##
##      [,1] [,2] [,3] [,4]
## [1,]    1    3    5    7
## [2,]    2    4    6    8
##
## , , 2
##
##      [,1] [,2] [,3] [,4]
## [1,]    9   11   13   15
## [2,]   10   12   14   16
##
## , , 3
##
##      [,1] [,2] [,3] [,4]
## [1,]   17   19   21   23
## [2,]   18   20   22    1
##
```

```r
array(1:23, dim = c(2, 4, 3), dimnames = list(paste("Patient",
    1:2, sep = ""), LETTERS[1:4], c("X", "Y", "Z")))
```

```
## , , X
##
##          A B C D
## Patient1 1 3 5 7
## Patient2 2 4 6 8
##
## , , Y
##
##           A  B  C  D
## Patient1  9 11 13 15
## Patient2 10 12 14 16
##
## , , Z
##
##           A  B  C  D
## Patient1 17 19 21 23
## Patient2 18 20 22  1
##
```

## 3.3 Attributes of R Objects

Basic attributes: mode and length

The most basic and fundamental properties of every objects is its `mode`and `length` These are intrinsic attributes of every object. Examples of `mode` are ”logical”, ”numeric”, ”character”, ”list”, ”expression”, ”name/symbol” and ”function”.

Of which the most basic of these are:

- `'character'`: a character string
- `'numeric'`: a real number, which can be an integer or a double
- `'integer'`: an integer
- `'logical'`: a logical (true/false) value

```
# Numeric
x <- 3
mode(x)

## [1] "numeric"


# Charachter
x <- "apple"
mode(x)

## [1] "character"

x <- 3.145
x + 2  # 5.145

## [1] 5.145


# FALSE, logical
x == 2

## [1] FALSE

x <- x == 2
x

## [1] FALSE

mode(x)

## [1] "logical"
```

All R objects have mode

```r
# vectors of different modes Numeric
x <- 1:10
mode(x)

## [1] "numeric"


x <- matrix(rnorm(50), nrow = 5, ncol = 10)
mode(x)

## [1] "numeric"


# Character
x <- LETTERS[1:5]
mode(x)

## [1] "character"


# logical
x <- x == "D"
mode(x)

## [1] "logical"
```

> ***Quick Exercise***
> Repeat above, and find the `length` and `class` of x in each case.

### 3.3.1 Dimension

```r
x <- matrix(5:14, nrow = 2, ncol = 5)
x

##      [,1] [,2] [,3] [,4] [,5]
## [1,]    5    7    9   11   13
## [2,]    6    8   10   12   14

attributes(x)

## $dim
## [1] 2 5
##
```

**In summary**

| Object | Modes | Allow >1 Modes* |
|---|---|---|
| vector | numeric, character, complex or logical | No |
| matrix | numeric, character, complex or logical | No |
| list | numeric, character, complex, logical, function, expression, ... | Yes |
| data frame | numeric, character, complex or logical | Yes |
| factor | numeric or character | No |
| array | numeric, character, complex or logical | No |

*Whether object allows elements of different modes. For example all elements in a vector or array have to be of the same mode. Whereas a list can contain any type of object including a list.

## 3.4 Creating and accessing objects

We have already created a few objects: `x, y, junk`. Will create a few more and will select, access and modify subsets of them.

- Create vectors, matrices and data frames using *seq*, *rep*, *rbind* and *cbind*

```
# Vector
x.vec <- seq(1, 7, by = 2)

# The function seq is very useful, have a look at the help on seq
# (hint ?seq)

names(x.vec) <- letters[1:4]
# Matrices
xMat <- cbind(x.vec, rnorm(4), rep(5, 4))
yMat <- rbind(1:3, rep(1, 3))
z.mat <- rbind(xMat, yMat)
# Data frame
x.df <- as.data.frame(xMat)
names(x.df) <- c("ind", "random", "score")
```

- Accessing elements

  *NOTE* Use square brackets to access elements. The number of elements within the square bracket must equal the dimension of the object.

  1. vector `[1]`
  2. matrix `[1,1]`
  3. array with 3 dimensions `[1,1,1]`

```
# Access first element of 'x.vec'
x.vec[1]

## a
## 1
```

```
# or if you know the name
x.vec["a"]

## a
## 1

# Access an element of 'xMat' in the second row, third column
xMat[2, 3]

## [1] 5

# Display the second and third columns of matrix 'xMat'
xMat[, c(2:3)]

##
## a -1.2081 5
## b -1.2717 5
## c -0.7870 5
## d  0.3818 5

# or
xMat[, -c(1)]

##
## a -1.2081 5
## b -1.2717 5
## c -0.7870 5
## d  0.3818 5
```

Here `-1` means everything except for the first column.

***Quick Exercise*** What does this command do?

```
xMat[xMat[, 1] > 3, ]

##   x.vec
## c     5 -0.7870 5
## d     7  0.3818 5
```

If the object has class data.frame or list, you can use the dollar symbol `$` to access elements. The `$` can only access columns of *data.frame*

```
# Get the vector of 'ind' from 'x.df'
colnames(x.df)

## [1] "ind"    "random" "score"

x.df$ind

## [1] 1 3 5 7

x.df[, 1]

## [1] 1 3 5 7


names(newList1)

## [1] "a"     "myVec" "mat"

newList1$a

## [1] 20
```

## 3.5 Modifying elements

```
# Change the element of 'xMat' in the third row and first column to
# '6'
xMat[3, 1] <- 6
# Replace the second column of 'z.mat' by 0's
z.mat[, 2] <- 0
```

### 3.5.1 Sorting and Ordering items

Frequently we need to re-order the rows/columns of a matrix or see the rank order or a sorted set elements of a vector

The functions *sort* and *order* are designed to be applied on vectors. Sort returns a sorted vector. Order returns an index which can be used to sort a vector or matrix.

```
# Simplest 'sort'
z.vec <- c(5, 3, 8, 2, 3.2)
sort(z.vec)

## [1] 2.0 3.0 3.2 5.0 8.0
```

```
order(z.vec)

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

Sorting the rows of a matrix. We will use an example dataset in R called ChickWeight. First have a look at the ChickWeight documentation (help)

Lets take a subset of the matrix, say the first 36 rows.

```
# ?ChickWeight
ChickWeight[1:2, ]

##   weight Time Chick Diet
## 1     42    0     1    1
## 2     51    2     1    1

chick.short <- ChickWeight[1:36, ]
```

Now order this matrix by time and weight

```
## by just weight
chickOrd <- chick.short[order(chick.short$weight), ]
chickOrd[1:5, ]

##    weight Time Chick Diet
## 26     39    2     3    1
## 13     40    0     2    1
## 1      42    0     1    1
## 25     43    0     3    1
## 14     49    2     2    1


## By both time and weight
chick.srt <- chick.short[order(chick.short$Time, chick.short$weight),
    ]
chick.srt[1:5, ]

##    weight Time Chick Diet
## 13     40    0     2    1
## 1      42    0     1    1
## 25     43    0     3    1
## 26     39    2     3    1
## 14     49    2     2    1
```

### 3.5.2 Sort a matrix by 2 columns,one in decreasing order, the second ascending

There are 2 ways to do this. First is to sort the data in 2 steps

```
x <- matrix(c(2, 1, 1, 3, 0.5, 0.3, 0.5, 0.2), ncol = 2)
# Sort the second column in decreasing order
x1 <- x[order(x[, 2], decreasing = TRUE), ]
# Sort the first column in the partially sorted matrix
x2 <- x1[order(x1[, 1]), ]
```

Or if both columns are numeric, you negatives sort in the reverse order of positives

```
x[order(x[, 1], -x[, 2]), ]

##      [,1] [,2]
## [1,]    1  0.5
## [2,]    1  0.3
## [3,]    2  0.5
## [4,]    3  0.2
```

If the values aren't known to be numeric, convert them to numeric before sorting

```
x[order(xtfrm(x[, 1]), -xtfrm(x[, 2])), ]

##      [,1] [,2]
## [1,]    1  0.5
## [2,]    1  0.3
## [3,]    2  0.5
## [4,]    3  0.2
```

Note with both of these, missing values NA will be appended to the end of the list

```
z.vec <- c(5, NA, 8, 2, 3.2)
order(z.vec)

## [1] 4 5 1 3 2

z.vec[order(z.vec)]

## [1] 2.0 3.2 5.0 8.0  NA

z.vec[order(z.vec, decreasing = TRUE)]

## [1] 8.0 5.0 3.2 2.0  NA
```

### 3.5.3 Creating empty vectors and matrices

To create a empty vector, matrix or data.frame

```
x1 <- numeric()
x2 <- numeric(5)
x1.mat <- matrix(0, nrow = 10, ncol = 3)
```

### 3.5.4 Missing Values

Missing values are assigned special value of 'NA'. If you create a R object with length greater than the number of values, you will get missing values

```
a <- 1:3
length(a) <- 4
a

## [1]  1  2  3 NA
```

```
z <- c(1:3, NA)
z

## [1]  1  2  3 NA

ind <- is.na(z)
ind

## [1] FALSE FALSE FALSE  TRUE
```

To remove missing values from a vector

```
print(z)

## [1]  1  2  3 NA

x <- z[!is.na(z)]
print(x)

## [1] 1 2 3
```

Check to see if a vector has all, any or a certain number of missing values. These create logical vectors which can be used to filter a matrix or data.frame

```
all(is.na(z))

## [1] FALSE
```

```r
any(is.na(z))
```

```
## [1] TRUE
```

```r
sum(is.na(z))
```

```
## [1] 1
```

```r
sum(is.na(z)) > 1
```

```
## [1] FALSE
```

## 3.6 Quick recap

- R Environment, interface, R help and R-project.org and Bioconductor.org website
- installing R and R packages.
- assignment <-, =, ->
- operators ==, !=, <, >, Boolean operators `&`, `|`
- Management of R session, starting session, *getwd()*, *setwd()*, *dir()*
- Listing and deleting objects in memory, *ls()*, *rm()*
- R Objects

| **Object** | **Modes** | **Allow >1 Modes*** |
|---|---|---|
| vector | numeric, character, complex or logical | No |
| matrix | numeric, character, complex or logical | No |
| list | numeric, character, complex, logical, function, expression, ... | Yes |
| data frame | numeric, character, complex or logical | Yes |
| factor | numeric or character | No |
| array | numeric, character, complex or logical | No |

*Whether object allows elements of different modes. For example all elements in a vector or array have to be of the same mode. Whereas a list can contain any type of object including a list.

There are other objects type include *ts* (time series) data time etc. See the R manual for more information. All R Objects have the attributes mode and length.

- Creating objects; *c()*, *matrix()*, *data.frame()*, *seq()*, *rep()*, etc
- Adding rows/columns to a matrix using *rbind()* or *cbind()*
- Sub-setting/Accessing elements in a *vector()*, *matrix()*, *data.frame()*, *list()* by element name or index.

## 3.7 Exercise 1

For this exercise we will work on data from a study which examined the weight, height and age of women. Data from the women Study is available as an R dataset and information about this study can be found by using R help (hint ?women) which we will read directly from the website URL `http://bcb.dfci.harvard.edu/~aedin/courses/R/Women.txt` into the object women

Basic tools for reading and writing data are respectively: *read.table* and *write.table*. We will go into further detail about each later today, but first lets read in this file by typing these commands:

```
myURL <- "http://bcb.dfci.harvard.edu/~aedin/courses/R/Women.txt"
women <- read.table(myURL, sep = "\t", header = TRUE)
```

(Or in RStudio Click on Workspace -> Import Dataset)

**Tasks**

1. Get help on the command *colnames*
2. what is the class of this dataset?
3. How many rows and columns are in the data? (hint try using the functions str, dim, nrow and ncol))
4. Use the *summary()*, to view the mean height and weight of women
5. Compare the result to using the function *colMeans*
6. How many women have a weight under 120?
7. What is the average height of women who weigh between 124 and 150 pounds (hint: need to select the data, and find the mean).
8. Sort the matrix `women` by 'weight' hint use order
9. Give the 5th row the rowname "Lucy"

# Chapter 4

# Reading and writing data to and from R

So far, we have only analyzed data that were already stored in R. Basic tools for reading and writing data are respectively: *read.table* and *write.table*. We will go into further detail about each. First we will talk about reading in simple text documents; comma and tab-delimited format text files, then Excel and import/export from other statistical software.

## 4.1 Importing and reading text files data into RStudio

RStudio has a nice user interface to reading in file. Click on Workspace −> Import Dataset.

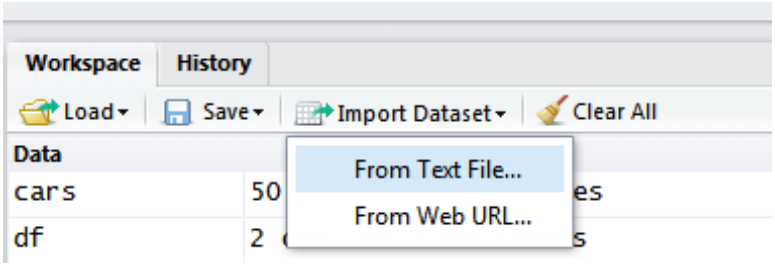



Figure 4.1: which provides an easy approach to read a text from a local directory or directly from a web URL

Enter a file location (either local or on the web), and RStudio will make a ”best guess” at the file format. There are a limited number of options (heading yes or no), separators (comma, space or tab) etc but these should cover the most common data exchange formats (The R interfaces RCommander and RExcel also provide rich support for data import of many different file formats into R)

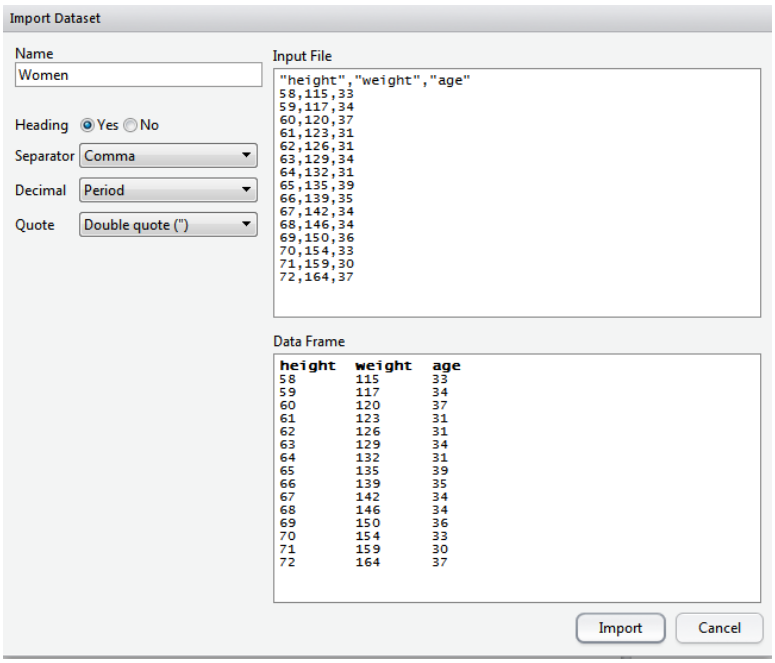



Figure 4.2: The top panel shows the plain text of the file, and the lower panels displays how R is interpreting the data. Black rows are the column headings

## 4.2 Importing data using R command read.table()

If you are calling R from a script, or are using R on a machine in which RStudio is not available, knowledge of commands to read and write files are vital

### 4.2.1 Using read.table() and read.csv()

1. The most commonly used function for reading data is *read.table()*. It will read the data into R as a *data.frame*.

   By Default *read.table()* assumes a file is space delimited and it will fail if the file is in a different format with the error below.

   ```
   Women<-read.table("Women.txt")
   ```

   In order to read files that are tab or comma delimited, the defaults must be changed. We also need to specify that the table has a header row

```
# Tab Delimited
Women <- read.table("Women.txt", sep = "\t", header = TRUE)
Women[1:2, ]

##   height weight age
## 1     58    115  33
## 2     59    117  34
```

```
summary(Women)

##      height          weight          age
##  Min.   :58.0   Min.   :115   Min.   :30.0
##  1st Qu.:61.5   1st Qu.:124   1st Qu.:32.0
##  Median :65.0   Median :135   Median :34.0
##  Mean   :65.0   Mean   :137   Mean   :33.9
##  3rd Qu.:68.5   3rd Qu.:148   3rd Qu.:35.5
##  Max.   :72.0   Max.   :164   Max.   :39.0

class(Women$age)

## [1] "integer"
```

***Note by default, character vector (strings) are read in as factors. To turn this off, use the parameter as.is=TRUE***

2. Important options:

| | |
|---|---|
| header==TRUE | should be set to 'TRUE', if your file contains the column names |
| as.is==TRUE | otherwise the character columns will be read as factors |
| sep="" | field separator character (often comma ',' or tab "" eg: sep=",") |
| na.strings | a vector of strings which are to be interpreted as 'NA' values. |
| row.names | The column which contains the row names |
| comment.char | by default, this is the pound # symbol, use "" to turn off interpretation of commented text. |

```
# Read the help file
help(read.table)
```

Note the defaults for *read.table()*, *read.csv()*, *read.delim()* are different. For example, in *read.table()* function, we specify *header=TRUE*, as the first line is a line of headings among other parameters.

3. *read.csv()* is a derivative of *read.table()* which calls *read.table()* function with the following options so it reads a comma separated file:

```
read.csv(file, header = TRUE, sep = ",", quote="\"", dec=".",
         fill = TRUE, comment.char="", ...)
```

Read in a comma separated file:

```
# Comma Delimited
Women2 <- read.csv("Women.csv")
Women2[1:2, ]

##   height weight age
## 1     58    115  33
## 2     59    117  34
```

4. Reading directly from Website You can read a file directly from the web

```
myURL <- "http://bcb.dfci.harvard.edu/~aedin/courses/R/Women.txt"
read.table(myURL, header = TRUE)[1:2, ]

##   height weight age
## 1     58    115  33
## 2     59    117  34
```

### 4.2.2 Reading compressed data into R

Files compressed via the algorithm used by gzip can be used as connections created by the function gzfile, whereas files compressed by bzip2 can be used via bzfile. Suppose your data is in a compressed gzip or tar.gz file, you can use the R gzfile function to decompress on the fly. Do this:

```
myDataFrame <- read.table(gzfile("myData.gz"), header = T)
```

## 4.3 Exercise 2

The ToothGrowth data are from a study which examined the growth of teeth in guinea pigs (n=10) in response to three dose levels of Vitamin C (0.5, 1, and 2 mg), which was administered using two delivery methods (orange juice or ascorbic acid). Data from the Tooth Growth Study is available as an R dataset and information about this study can be found by using R help (hint ?ToothGrowth)

1. Download the data set "ToothGrowth.xls" which is available on the course website. Save it in your local directory. Open this file "ToothGrowth.xls" in Excel.
2. Export the data as both a comma or tab delimited text files. In Excel select File -> Save as and
   Tab: select the format Text (Tab delimited) (*.txt).
   CSV: select the format CSV (Comma delimited) (*.csv).

1. Load each data file (.txt and .csv) into R
2. How many rows are there is ToothGrowth?
3. what is the mean and SD of Tooth length
4. Does treatment have a significant effect?

### 4.3.1 Importing text files Using scan()

NOTE: *read.table()* is not the right tool for reading large matrices, especially those with many columns. It is designed to read 'data frames' which may have columns of very different classes. Use *scan()* instead.

*scan()* is an older version of data reading facility. Not as flexible, and not as user-friendly as *read.table()*, but useful for Monte Carlo simulations for instance. *scan()* reads data into a *vector* or a *list* from a file.

```
myFile <- "outfile.txt"
# Create a file
cat("Some data", "1 5 3.4 8", "9 11 23", file = myFile, sep = "\n")
exampleScan <- scan(myFile, skip = 1)
print(exampleScan)

## [1]  1.0  5.0  3.4  8.0  9.0 11.0 23.0
```

Note by default *scan()* expects numeric data, if the data contains text, either specify what="text" or give an example what="some text".

Other useful parameters in *scan()* are nmax (number of lines to be read) or n (number of items to be read).

```
scan(myFile, what = "some text", n = 3)

## [1] "Some" "data" "1"
```

### 4.3.2 Parsing each line - Readlines

There are several function in R for parsing large files. You can use the command *readLine* or *readLines* to parse a file line by line.

## 4.4 Writing Data table from R

1. Function *sink()* diverts the output from the console to an external file

```
myPath <- getwd()
sink(file.path(myPath, "sinkTest.txt"))
print("This is a test of sink")
ls()
sin(1.5 * pi)
print(1:10)
sink()
```

2. Writing a data matrix or data.frame using the *write.table()* function *write.table()* has similar arguments to *read.table()*

```
myResults <- matrix(rnorm(100, mean = 2), nrow = 20)
write.table(myResults, file = "results.txt")
```

This will write out a space separated file.

```
df1 <- data.frame(myResults)
colnames(df1) <- paste("MyVar", 1:5, sep = "")
write.table(df1, file = "results2.txt", row.names = FALSE,
    col.names = TRUE)
read.table(file = "results2.txt", head = TRUE)[1:2, ]

##   MyVar1 MyVar2 MyVar3 MyVar4 MyVar5
## 1  2.654  3.149  4.073  1.224 0.8089
## 2  1.260  2.338  2.764  3.020 3.0991
```

3. Important options

| | |
|---|---|
| append = FALSE | create new file |
| sep = ” ” | separator (other useful possibility sep=”,”) |
| row.names = TRUE | may need to change to row.names=FALSE |
| col.names = TRUE | column header |

4. Output to a webpage
The package R2HTML will output R objects to a webpage

### 4.4.1 Other considerations when reading or writing data

It is often useful to create a variable with the path to the data directory, particular if we need to read and/or write more than one dataset. NOTE: use double backslashes to specify the path names, or the forward slash can be used.

```
myPath <- file.path("C://Project1")
file.exists(myPath)

## [1] FALSE


# Set myPath to be current directory
myPath <- file.path(getwd())
```

It is better to expand a path using *file.path()* rather than *paste()* as *file.path()* will expand the path with delimiting characters appropriate to the operating system in use (eg / unix, \, windows etc)

```
myfile <- file.path(myPath, "Women.txt")
```

Use *file.exists()* to test if a file can be found. This is very useful. For example, use this to test if a file exists, and if TRUE read the file or you could ask the R to warn or stop a script if the file does not exist

```
if (!file.exists(myfile)) {
    print(paste(myfile, "cannot be found"))
} else {
    Women <- read.table(myfile, sep = "\t", header = TRUE)
    Women[1:2, ]
}

##   height weight age
## 1     58    115  33
## 2     59    117  34
```

## 4.5 Viewing Data

After you use read.table or other function to import data into you, you will need to quickly review the data to ensure it important correctly

### 4.5.1 head, tail

There are several functions which are useful for this. the functions head and tail will display the first and last 6 rows respectively. These can be used to view parts of a vector, matrix, table, data.frame or function

```
# Data
head(women)

##   height weight age
## 1     58    115  33
## 2     59    117  34
## 3     60    120  37
## 4     61    123  31
## 5     62    126  31
## 6     63    129  34

tail(women)

##    height weight age
## 10     67    142  34
## 11     68    146  34
## 12     69    150  36
## 13     70    154  33
## 14     71    159  30
## 15     72    164  37


# View the head and tail (15 line) of the function cor which
# calculates correlation

head(cor)

##
## 1 function (x, y = NULL, use = "everything", method = c("pearson",
## 2     "kendall", "spearman"))
## 3 {
## 4     na.method <- pmatch(use, c("all.obs", "complete.obs", "pairwise.cor
## 5         "everything", "na.or.complete"))
## 6     if (is.na(na.method))

tail(cor, n = 15)
```

```
##
## 99                    x2 <- rank(x2[ok])
## 100                   y2 <- rank(y2[ok])
## 101                   r[i, j] <- if (any(ok))
## 102                     .Internal(cor(x2, y2, 1L, method == "kendall"))
## 103                   else NA
## 104                 }
## 105             }
## 106             rownames(r) <- colnames(x)
## 107             colnames(r) <- colnames(y)
## 108             if (matrix_result)
## 109                 r
## 110             else drop(r)
## 111         }
## 112     }
## 113 }
```

### 4.5.2 str

The function *str* is very useful, it displays the structure of an R object

```
str(women)

## 'data.frame': 15 obs. of  3 variables:
##  $ height: int  58 59 60 61 62 63 64 65 66 67 ...
##  $ weight: int  115 117 120 123 126 129 132 135 139 142 ...
##  $ age   : int  33 34 37 31 31 34 31 39 35 34 ...

str(1:10)

##  int [1:10] 1 2 3 4 5 6 7 8 9 10

str(cor)

## function (x, y = NULL, use = "everything", method = c("pearson",
##     "kendall", "spearman"))
```

### 4.5.3 The function Summary

The function *summary* can be applied to a vector, factor,matrix,data.frame, list etc. and will be summarized the object. The function will generate a summary specialized for the class of the object.

```
methods(summary)
```

```
##  [1] summary.aov             summary.aovlist
##  [3] summary.aspell*         summary.connection
##  [5] summary.data.frame      summary.Date
##  [7] summary.default         summary.ecdf*
##  [9] summary.factor          summary.glm
## [11] summary.infl            summary.lm
## [13] summary.loess*          summary.manova
## [15] summary.matrix          summary.mlm
## [17] summary.nls*            summary.packageStatus*
## [19] summary.PDF_Dictionary* summary.PDF_Stream*
## [21] summary.POSIXct         summary.POSIXlt
## [23] summary.ppr*            summary.prcomp*
## [25] summary.princomp*       summary.srcfile
## [27] summary.srcref          summary.stepfun
## [29] summary.stl*            summary.table
## [31] summary.tukeysmooth*
##
##    Non-visible functions are asterisked
```

For a vector, data.frame or matrix its provides information data distribution (min, quantile, mean, max etc)

```
summary(1:10)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    1.00    3.25    5.50    5.50    7.75   10.00
```

```
summary(women)
```

```
##      height          weight          age
##  Min.   :58.0   Min.   :115   Min.   :30.0
##  1st Qu.:61.5   1st Qu.:124   1st Qu.:32.0
##  Median :65.0   Median :135   Median :34.0
##  Mean   :65.0   Mean   :137   Mean   :33.9
##  3rd Qu.:68.5   3rd Qu.:148   3rd Qu.:35.5
##  Max.   :72.0   Max.   :164   Max.   :39.0
```

For character vector or factor, it provides a count of the items

```
vec <- sample(c("old", "young"), 20, replace = TRUE)
summary(vec)

##    Length     Class      Mode
##        20 character character

summary(factor(vec))

##   old young
##    10    10
```

### 4.5.4 Table

The function *table* will tabulate the elements of a character vector

```
table(vec)

## vec
##   old young
##    10    10

class(vec)

## [1] "character"
```

I have included a lot more on cross-tabulation and generating summaries on data in chapter 9

## 4.6 Exercise 3

1. Use *read.table()* to read the space separated text file WomenStats.txt directly from the website `http://bcb.dfci.harvard.edu/~aedin/courses/R/WomenStats.txt`, Call this *data.frame* women.
2. Change the rownames to be the letters of the alphabet eg "A", "B" "C" "D" etc
3. Write out this file as a tab delimited file using *write.table()*
4. Read this into R using *read.table()*. What parameters need modifying to read the data as a tab-delimited file?

## 4.7 Importaing Data from other Software

### 4.7.1 Reading data from Excel into R

There are several packages and functions for reading Excel data into R, however I normally export data as a .csv file and use *read.table()*.

However if you wish to directly load Excel data, here are many the options available to you. See the section on "Importing-from-other-statistical-systems" in the webpage `http://cran.r-project.org/doc/manuals/R-data.html` for more information

1. xslx seems to be the simplest option at the moment

```
library(xlsx)
ww <- read.xlsx(file = "Women.xlsx", sheetIndex = 1)
```

   read.xlsx accepts .xls and .xlsx format. You must include a worksheet name or number. It is optional to specify a row or column index to indicate a section of a Worksheet

2. There is also a packages call XLConnect which is similar

```
require(XLConnect)
wb <- loadWorkbook("Women.xlsx", create = TRUE)
WW <- readWorksheet(wb, sheet = 1)
```

   Or you can read direct from a connection, calling the file directly.

```
Ww <- readWorksheetFromFile("Women.xlsx", name = "sheet1")
```

3. RExcel R can be ran from within Excel on Windows using RExcel (`http://rcom.univie.ac.at/`). This add a menu to Excel that allows you to call R functions from within Excel. RExcel is part of the much large Statconn project.

4. `RODBC` library. We are not sure it will not work with .xlsx files. See the vignette for more information

```
library(RODBC)
RShowDoc("RODBC", package = "RODBC")
```

   The following `RODBC` function works under windows, but may have issues under MacOS or Linux as may need to install ODBC drivers.

```
channel<-odbcConnectExcel("ToothGrowth.xls")
#list the spreadsheets
sqlTables(channel)

#read the Excel Sheet ToothGrowth using either:
ToothGrowth<-sqlFetch(channel, "ToothGrowth")
ToothGrowth<-sqlQuery(channel, "select * from [ToothGrowth$]")
ToothGrowth[1:2,]
```

5. The `gdata` library function *read.xls()*

   Perl must be installed on your computer in order for these to work, as it uses the Perl functions 'xls2csv' or 'xls2tab'.

## 4.8 Import/Export from other statistical software

Most binary data files written by statistical software other than `R` such as EpiInfo, Minitab, S-PLUS, SAS, SPSS,Stata and Systat, can be loaded into R using the R package foreign or Hmisc. Details can be found in the `R` manual: R data Import/Export.

### 4.8.1 Reading data from SAS

If you have SAS, you can use Frank Harrell's 'Hmisc' package which has functions sas.get and sasxport.get, and other utility functions such as label,sas.get, contents,describe. For those without a SAS license, package 'foreign' has read.ssd, lookup.xport, and read.xport.

- From SAS, save SAS dataset in transport format

```
libname out xport 'c:/mydata.xpt';
data out.mydata;
set sasuser.mydata;
run;
```

  In R

```
library(Hmisc)
mydata <- sasxport.get("c:/mydata.xpt")
```

- SAScii. Anthony Joseph Damico recently announced SAScii is a new packages to parse SAS input code to read.fwf However although they stated the code below should work, I have been not so successful with it in my hands.

```
require("SAScii")

## Loading required package: SAScii

## Loading required package: stringr
```

```
# Load the 2010 National Health Interview Survey Persons file as an
# R data frame from CDC
NHIS10_personsx_SASInst <- "ftp://ftp.cdc.gov/pub/Health_Statistics/NCHS/Program_Code/NHIS/2010/PERSONSX.sa

NHIS10_personsx_SASInst <- "ftp://ftp.cdc.gov/pub/Health_Statistics/NCHS/Datasets/NHIS/2010/personsx.zip"
```

```
#store the NHIS file as an R data frame!
NHIS10_personsx_df <- read.SAScii(NHIS10_personsx_SASInst, NHIS10_perso

#or store the NHIS SAS import instructions for use in a
#read.fwf function call outside of the read.SAScii function
NHIS10_personsx_sas <- parse.SAScii(NHIS10_personsx_SASInst)

#save the data frame now for instantaneous loading later
save(NHIS10_personsx_df , file = "NHIS10_personsx_data.RData" )
```

- Recently Xin Wei of Roche Pharmaceuticals published a SAS macro called PROC_R that may potentially ease integrating R and SAS (reference Xin Wei PROC_R: A SAS Macro that Enables Native R Programming in the Base SAS Environment J. Stat Software. Vol. 46, Code Snippet 2, Jan 2012) which allows you to put R code within a SAS macro.

```
%include "C:\aedin\sasmacros\Proc_R.sas";
%Proc_R (SAS2R =, R2SAS =);
Cards4;

*****************************
***Please Enter R Code Here***
*****************************

;;;;
%Quit;
```

### 4.8.2 S

PSS

From SPSS, save SPSS dataset in transport format

```
get file='c:\mydata.sav' .
export outfile='c:\mydata.por' .
```

In R

```
library(Hmisc)
mydata <- spss.get("c:/mydata.por", use.value.labels = TRUE)
```

### 4.8.3 Stata or Systat

```
library(foreign)
mydata <- read.dta("c:/mydata.dta")
```

## 4.9 From a Database Connection

There is also support for database connectivity including for mySQL, Oracle and specialized file formats including network Common Data Form (netCDF) etc. See `http://cran.r-project.org/doc/manuals/R-data.html` for more details.

Note installation of RMySQL or ROracle is simple on Linux or Mac, but maybe complex on MSWindows, as there is no binary file. See the ReadMe associated with the package on the R website

## 4.10 Sampling and Creating simulated data

1. *seq* and rep. we have already seen the function seq and rep which generate a sequence or repeat elements.

2. Create data from a specific distribution

   Often we want to sample data from a specific distribution, also sometimes called simulating data. This data is usually used to test some algorithm or function that someone has written. Since the data is simulated, you know where it came from and so what the answer should be from your algorithm or function. Simulated data lets you double-check your work.

   Each distribution has 4 functions associated with it:

   For example, *rnorm( )*, *dnorm( )*, *pnorm( )*, and *qnorm( )* give random normals, the normal density (sometimes called the differential distribution function), the normal cumulative distribution function (CDF), and the inverse of the normal CDF (also called the quantile function), respectively.

   Almost all of the other distributions have similar sets of four functions. The 'r' versions are rbeta, rbinom, rcauchy, rchisq, rexp, rf, rgamma, rgeom, rhyper, rlogis, rlnorm, rmultinom, rnbinom, rnorm, rpois, rsignrank, rt, runif, rweibull, and rwilcox (there is no rtukey because generally only ptukey and qtukey are needed).

   For example, generate 5 observations from a normal distribution with mean 0 and stdev 1, or 10 observation with a mean of 20 and a stdev of 2

```
rnorm(5, 0, 1)

## [1]  0.156133  0.002906  1.747518 -0.924189 -0.445842

rnorm(10, 6, 2)

##  [1] 6.488 8.059 7.217 9.168 4.904 8.448 5.516 4.433 4.003 4.582
```

   For most of the classical distributions, these simple function provide probability distribution functions (p), density functions (d), quantile functions (q), and random number generation (r). Beyond this basic functionality, many CRAN packages provide additional useful distributions. In particular, multivariate distributions as well as copulas are available in contributed packages. See `http://cran.r-project.org/web/views/Distributions.html` and `http://cran.r-project.org/doc/manuals/R-intro.html#Probability-distri` for more information.

3. Sample from existing data

   The second type of simulation you may wish to perform is to bootstrap or permute existing data. In bootstrapping one generally follows the same basic steps

   (a) Resample a given data set a specified number of times

   (b) Calculate a specific statistic from each sample

   (c) Find the standard deviation of the distribution of that statistic

The function *sample()* will resample a given data set with or without replacement

```
sample(1:10)

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

sample(1:10, replace = TRUE)

##  [1] 10  4  8 10  4  1  5  3  8  5
```

You can also add weights to bias selection or probability of selecting of a certain subset. For example bootstrap sample from the same sequence (1:10) with probabilities that favor the numbers 1-5

```
weights <- c(rep(0.25, 5), rep(0.05, 5))
print(weights)

##  [1] 0.25 0.25 0.25 0.25 0.25 0.05 0.05 0.05 0.05 0.05

sample(10, replace = T, prob = weights)

##  [1] 9 5 2 2 1 4 8 5 3 3
```

## 4.11 Exercise 4

1. Create the vector which contains the first 20 letters of the alphabet and the sequence of number 0:200 in increments of 10 (hint use *seq()*).
2. Use *sample()* to randomize the order of the vector.
3. Use the function *cat()* to write this vector to a file called ”myVec.txt”.
4. Use *scan()* to read the first 10 items in the file, what value do you give to the parameter ’what’. Compare running *scan()* with different data types; eg: what=”text”, what=123 and what=TRUE

# Chapter 5

# Introduction to programming and writing Functions in R

## 5.1 Why do we want to write functions?

We have a general knowledge of function use, so how do we write our own functions. In other words, we want to create objects of mode *function*.

1. Why do we want to write functions?
2. Definition of a function: assignment of the form

   ```
   myFunction <- function(arg1, arg2, ...) expression
   ```

   *expression* is an `R` expression using arguments `arg1`, `arg2` to calculate a value. Function returns the value of the expression
3. Call to a function within `R`

   ```
   myFunction(expr1, expr2, ...)
   ```

4. Lets write a short function, a function to calculate the means of a vector.

   ```
   myMean <- function(y1) {
       mean <- sum(y1)/length(y1)
       return(mean)
   }
   ```

   Now Lets test out function

   ```
   testVec <- rnorm(50, 20, 4)
   mean(testVec)

   ## [1] 20.6

   myMean(testVec)

   ## [1] 20.6
   ```

5. A more complex example

   Example of a function 'twosam': takes as arguments two vectors 'y1' and 'y2', calculates the 2-sample t-test statistic (assuming equal variance), and returns the t-statistic

```
twosam <- function(y1, y2) {
    n1 <- length(y1)
    n2 <- length(y2)
    yb1 <- mean(y1)
    yb2 <- mean(y2)
    s1 <- var(y1)
    s2 <- var(y2)
    s <- ((n1 - 1) * s1 + (n2 - 1) * s2)/(n1 + n2 - 2)
    tst <- (yb1 - yb2)/sqrt(s * (1/n1 + 1/n2))
    return(tst)
}
```

## 5.2 Conditional statements (if, ifelse, switch)

### 5.2.1 *if* statement

`if (condition) expr1 else expr2`

`condition` must evaluate to a single logical value, ie either TRUE or FALSE.

```
x <- 9
if (x > 0) sqrt(x) else sqrt(-x)

## [1] 3
```

### 5.2.2 *ifelse* statement

Vectorized version of the if/else construct: *ifelse(condition, expr1, expr2)* function which returns a vector with elements expr1 if condition is true, otherwise it returns expr2.

```
ifelse(x >= 0, sqrt(x), sqrt(-x))

## [1] 3
```

### 5.2.3 *switch* statement

The *switch* function, a generalization of the *if* statement

```
spread <- function(x, type) {
    switch(type, sd = sd(x), mad = mad(x), IQR = IQR(x)/1.349)
}
samp <- rnorm(50)
spread(samp, 2)

## [1] 0.8806

spread(samp, "IQR")

## [1] 1.108
```

Why IQR(x)/1.349 ? In a normal distribution 50% of the data (between 0.25 and 0.75 quartiles). So the distance between the two quartiles IQR(x) = quantile(x,0.75) − quantile(x,0.25). For a normal distribution IQR is qnorm(0.75) - qnorm(0.25) ≈ 1.349. Therefore $IQR/1.349$ is an estimator of the standard deviation of a normal distribution.

## 5.3 Repetitive execution: For and While loops

### 5.3.1 For loops

```
for (i in expr1) expr2
```

where `i` is the loop variable, `expr1` is usually a sequence of numbers, and `expr2` is an expression.

```
for (i in 1:5) print(i^2)

## [1] 1
## [1] 4
## [1] 9
## [1] 16
## [1] 25
```

### 5.3.2 while loops

*while* (condition) expr continues till the *condition* becomes false. Used often in iterative calculations

```
x <- 1
y <- 16
while (x^2 < y) {
    cat(x, "squared is ", x^2, "\n")  # print x and sq(x)
    x <- x + 1
}
```

```
## 1 squared is  1
## 2 squared is  4
## 3 squared is  9
```

A word of caution, it is easy to write a *while()* loop that doesn't terminate, in which case your script may go into a never-ending cycle. Therefore if possible, write a *for()* loop in preference to a *while()* loop.

Iterative for and while loops in R are sometimes memory intensive, and functions such as apply, sweep or aggregate should be should instead. For a comparision of the computational efficiency of For versus apply loops see section 5.8.2

## 5.4 The Apply Functions

1. apply

   *appply()* applies a function over the rows or columns of a matrix. The syntax is

   ```
   apply(X, MARGIN, FUN, ARGs)
   ```

   where X: array, matrix or data.frame; MARGIN: 1 for rows, 2 for columns, c(1,2) for both; FUN: one or more functions; ARGs: possible arguments for function

   For example, lets go back to the example dataset women which we loaded from the web.

```
summary(women)

##      height          weight          age
##  Min.   :58.0   Min.   :115   Min.   :30.0
##  1st Qu.:61.5   1st Qu.:124   1st Qu.:32.0
##  Median :65.0   Median :135   Median :34.0
##  Mean   :65.0   Mean   :137   Mean   :33.9
##  3rd Qu.:68.5   3rd Qu.:148   3rd Qu.:35.5
##  Max.   :72.0   Max.   :164   Max.   :39.0

colMeans(women)

## height weight    age
##  65.00 136.73  33.93

apply(women, 2, mean)

## height weight    age
##  65.00 136.73  33.93
```

```
testEq <- all(rowMeans(women) == apply(women, 1, mean))
print(testEq)

## [1] TRUE

if (testEq) print("rowMeans is equivalent to apply(df, 1, mean)")

## [1] "rowMeans is equivalent to apply(df, 1, mean)"
```

Create a function using apply

```
colSd <- function(df) apply(df, 2, sd)
colSd(women)

## height weight    age
##  4.472 15.499  2.576
```

2. tapply

   *tapply()* is a member of the very important *apply()* functions. It is applied to "ragged" arrays, that is array categories of variable lengths. Grouping is defined by vector.

   The syntax is:

   ```
   tapply(vector, factor, FUN)
   ```

   Example:

   ```
   ageSplit <- ifelse(women$age < 35, "under35", "over35")
   print(ageSplit)

   ##  [1] "under35" "under35" "over35"  "under35" "under35" "under35"
   ##  [7] "under35" "over35"  "over35"  "under35" "under35" "over35"
   ## [13] "under35" "under35" "over35"

   tapply(women$weigh, ageSplit, length)

   ##  over35 under35
   ##       5      10

   tapply(women$weigh, ageSplit, summary)
   ```

```
## $over35
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##     120     135     139     142     150     164
##
## $under35
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##     115     124     130     134     145     159
##
```

3. lapply and sapply
   *lapply()* and *sapply()* are applied to lists. *lapply()* returns a *list* (of the same length as input). *sapply()* is a user-friendly version of lapply by default returning a *vector* or *matrix* if appropriate.
   tapply will

```
myList <- list(ToothGrowth = TG, WomenAge = women$age, beta = exp(-3:3),
    logicalVec = c(TRUE, FALSE, FALSE, TRUE))
# compute the list mean for each list element
res1 <- lapply(myList, length)
print(res1)
print(paste("Class of res1:", class(res1)))

res2 <- sapply(myList, length)
print(res2)
print(paste("Class of res2:", class(res2)))
```

4. for more apply functions see the library plyr

### 5.4.1 Merging Datasets

There are several function for manipulating data, see the plyr library for functions. Also see the function reshape and stack which make it easier to convert a "wide" table into a narrow one.

```
x1 <- data.frame(Case = sample(letters, 10), A1 = rnorm(10),
    B1 = 1:10, C1 = rep(1:5, 2))
x1

##    Case       A1 B1 C1
## 1     f -0.05922  1  1
## 2     d -0.50757  2  2
## 3     g  0.92258  3  3
## 4     i -0.05271  4  4
## 5     x -2.60035  5  5
## 6     a  1.16796  6  1
## 7     v -2.52888  7  2
```

```
## 8      q -0.22759  8  3
## 9      m -0.86923  9  4
## 10     o  0.05612 10  5

x2 <- data.frame(A1 = seq(1, 10, 2), Case = sample(letters,
    10), D1 = rnorm(10, 4), E1 = rep(1:5, 2), B1 = c(rep(c("Non-Smoker",
    "Smoker"), each = 4), NA, NA))
x2

##    A1 Case    D1 E1         B1
## 1   1    k 3.263  1 Non-Smoker
## 2   3    v 3.864  2 Non-Smoker
## 3   5    d 4.993  3 Non-Smoker
## 4   7    z 5.525  4 Non-Smoker
## 5   9    n 2.906  5     Smoker
## 6   1    w 2.989  1     Smoker
## 7   3    r 4.262  2     Smoker
## 8   5    u 4.504  3     Smoker
## 9   7    m 5.215  4       <NA>
## 10  9    p 4.851  5       <NA>

merge(x1, x2, "Case")

##   Case    A1.x B1.x C1 A1.y    D1 E1       B1.y
## 1    d -0.5076    2  2    5 4.993  3 Non-Smoker
## 2    m -0.8692    9  4    7 5.215  4       <NA>
## 3    v -2.5289    7  2    3 3.864  2 Non-Smoker
```

## 5.5 Exercise 5

1. Write a *for* loop printing the consecutive powers of 2, from 0 to 10
2. Write a *while* loop printing the consecutive powers of 2, less than 1000

## 5.6 Functions for parsing text

There are many functions with R for parsing text. We will cover some of this here.

- To search for text within an R vector, use *grep*. It uses the same regular expression patterns as perl is you set perl=TRUE

```
grep("A", LETTERS)

## [1] 1

grep("A", LETTERS, value = TRUE)

## [1] "A"
```

To search for a string begining with 'Ma' or ending in the letters d or v use regular expression pattern seach. Here  means the start and

means the end.

```
poem <- c("Mary", "Had", "a", "little", "lamb")
grep("^Ma", poem, value = TRUE)

## [1] "Mary"

grep("[dv]$", poem, value = TRUE)

## [1] "Had"
```

R has full support regular expresion (see ?regex) synthax. For example to search for words containing the letter a. Here  refers to any alphanumeric character and $+$ means one or more whereas $*$ means zero or more.

```
grep("\\w*a\\w+", poem, value = TRUE)

## [1] "Mary" "Had"  "lamb"

grep("\\w*a\\w*", poem, value = TRUE)

## [1] "Mary" "Had"  "a"    "lamb"
```

- To substitute characters within a string use *sub*

```
sub("B", "A", LETTERS)

##  [1] "A" "A" "C" "D" "E" "F" "G" "H" "I" "J" "K" "L" "M" "N" "O" "P"
## [17] "Q" "R" "S" "T" "U" "V" "W" "X" "Y" "Z"
```

Trim trailing white space

```
str <- "Mary had a little lamb      "
sub(" +$", "", str)  ## spaces only

## [1] "Mary had a little lamb"

sub("\\s+$", "", str, perl = TRUE)  ## Perl-style syntax

## [1] "Mary had a little lamb"
```

- To split a character string use *strsplit*

```
a <- date()
strsplit(a, " ")

## [[1]]
## [1] "Fri"      "Dec"      "14"       "04:03:23" "2012"
##

strsplit(a, "J")

## [[1]]
## [1] "Fri Dec 14 04:03:23 2012"
##

b <- strsplit(a, "11")
class(b)

## [1] "list"

b <- unlist(b)
class(b)

## [1] "character"
```

- For special characters you need to precede them with a double back slash

```
a <- "aedin@jimmy.harvard.edu"
strsplit(a, "\\.")

## [[1]]
## [1] "aedin@jimmy" "harvard"     "edu"
##
```

## 5.7 Programming in R: More advanced

## 5.8 Viewing Code of functions from R packages

Its often useful to view the code of R functions. To see the code, type the name of that code without parenthesis. Take a look closer at a built-in function *IQR*. We see it is simply taking the difference (*diff()*) of the $25\%$ and $75\%$ quantile. We can use the functions body() and args() to see the code and the arguments (parameters) of the function.

```
help(IQR)

## starting httpd help server ...

## done

xx <- sample(1:30, 10)
quantile(xx)

##   0%  25%  50%  75% 100%
##  1.0  5.0 11.0 16.5 22.0

IQR(xx)

## [1] 11.5


args(IQR)

## function (x, na.rm = FALSE, type = 7)
## NULL

body(IQR)

## diff(quantile(as.numeric(x), c(0.25, 0.75), na.rm = na.rm, names = FALSE,
##     type = type))

IQR

## function (x, na.rm = FALSE, type = 7)
## diff(quantile(as.numeric(x), c(0.25, 0.75), na.rm = na.rm, names = FALSE,
##     type = type))
## <bytecode: 0x02d05c8c>
## <environment: namespace:stats>
```

Sometimes, functions don't appear to be "visible". In this case, use *methods* or *getAnywhere* to view the function.

Someone a function may have different version, and may depend on the class of the input object. In this case functions will be called functionname.class. In the case below, mean will call a the function mean.Data or mean.difftime if the input object is a Date, difftime respectivel

```
mean

## function (x, ...)
## UseMethod("mean")
## <bytecode: 0x037e1920>
## <environment: namespace:base>

methods(mean)

## [1] mean.data.frame mean.Date       mean.default    mean.difftime
## [5] mean.POSIXct    mean.POSIXlt
```

Now we can see the code for mean, as we know the full name of the function is mean.default.

```
mean.default

## function (x, trim = 0, na.rm = FALSE, ...)
## {
##     if (!is.numeric(x) && !is.complex(x) && !is.logical(x)) {
##         warning("argument is not numeric or logical: returning NA")
##         return(NA_real_)
##     }
##     if (na.rm)
##         x <- x[!is.na(x)]
##     if (!is.numeric(trim) || length(trim) != 1L)
##         stop("'trim' must be numeric of length one")
##     n <- length(x)
##     if (trim > 0 && n) {
##         if (is.complex(x))
##             stop("trimmed means are not defined for complex data")
##         if (any(is.na(x)))
##             return(NA_real_)
##         if (trim >= 0.5)
##             return(stats::median(x, na.rm = FALSE))
##         lo <- floor(n * trim) + 1
##         hi <- n + 1 - lo
##         x <- sort.int(x, partial = unique(c(lo, hi)))[lo:hi]
##     }
##     .Internal(mean(x))
## }
## <bytecode: 0x037e1568>
## <environment: namespace:base>
```

Some function are "Non visible" that means you can see the code. When you These are hidden in the package namespace. use the function methods, non visible functions are marked by an asterisk.

```
`?`(t.test)
t.test

## function (x, ...)
## UseMethod("t.test")
## <bytecode: 0x030f6f60>
## <environment: namespace:stats>

methods(t.test)

## [1] t.test.default* t.test.formula*
##
##    Non-visible functions are asterisked
```

To view a hidden or non-visible function use "PackageName:::function"

```
stats:::t.test.default
```

To reduce the output and save paper in the manual, we will just view the first 5 and last 10 lines of the function.

```
head((stats:::t.test.default), 5)

##
## 1 function (x, y = NULL, alternative = c("two.sided", "less", "greater"),
## 2     mu = 0, paired = FALSE, var.equal = FALSE, conf.level = 0.95,
## 3     ...)
## 4 {
## 5     alternative <- match.arg(alternative)

print("truncated...")

## [1] "truncated..."

tail((stats:::t.test.default), 10)

##
## 102     names(mu) <- if (paired || !is.null(y))
## 103         "difference in means"
## 104     else "mean"
## 105     attr(cint, "conf.level") <- conf.level
## 106     rval <- list(statistic = tstat, parameter = df, p.value = pval,
## 107         conf.int = cint, estimate = estimate, null.value = mu,
## 108         alternative = alternative, method = method, data.name = dname)
## 109     class(rval) <- "htest"
## 110     return(rval)
## 111 }
```

There are some functions that you will not be able to see using these commands. These are most likely written in object orientated R (called S4). Much of Bioconductor's functions are written in S4. However a full discussion of S4 functions is beyond the scope of this course.

### 5.8.1 Making scripts work across your computers or platforms

I work on several computers, each have fairly different directory structures. But by setting a consistent directory structure within the home directory I can sync code between computers and have them run properly on each one since where I run my R projects have similar directory structures.

The R command *file.path* will automatically add in the correct "slashes" for windows, mac or Linux

```
file.path("home", "projects", "Dec01")

## [1] "home/projects/Dec01"
```

The command *path.expand* will expand a path name. You can combine it with the tilde symbol ( ~ ) which is the shortcut to your home drive (on any operating system)

```
path.expand("~")
myhome <- path.expand("~")
newdir <- file.path(path.expand("~"), "Rwork", " colonJan13")
setwd(newdir)
```

*Advanced Side Note: What is your system home directory*
Your system HOME (~ ) is set by your operating system. To view or change it, type

```
Sys.getenv("HOME")

## [1] "C:/Users/aedin/Documents"
```

Here "pathName" is the directory you wish to set as your new home directory

```
Sys.setenv(HOME = "pathName")
```

### 5.8.2 Efficient For Loop in R (Use apply)

sapply and lapply will repeat a function over a list

```
myList <- list(WomenMat = women, WomenAge = women$age, beta = exp(-3:3),
    logicalVec = c(TRUE, FALSE, FALSE, TRUE))
# compute the list mean for each list element
res1 <- lapply(myList, length)
print(res1)
print(paste("Class of res1:", class(res1)))

res2 <- sapply(myList, length)
print(res2)
print(paste("Class of res2:", class(res2)))
```

Note apply is much more computational efficient that a for loop. But if you can use built in functions like rowMeans or colMeans these are quicker still

```
myMA <- matrix(rnorm(1000000), 100000, 10, dimnames=
  list(1:100000, paste("C", 1:10, sep="")))

results <- NULL
system.time(for(i in seq(along=myMA[,1]))
   results <- c(results, mean(myMA[i,])))

##    user  system elapsed
##   24.25    0.48   24.88


results <- numeric(length(myMA[,1]))
system.time(for(i in seq(along=myMA[,1]))
  results[i] <- mean(myMA[i,]))

##    user  system elapsed
##    2.08    0.00    2.07



system.time(myMAmean <- apply(myMA, 1, mean))

##    user  system elapsed
##    1.75    0.00    1.74

system.time(myMAmean <- rowMeans(myMA))

##    user  system elapsed
##       0       0       0


system.time(myMAsd <- apply(myMA, 1, sd))

##    user  system elapsed
##    3.50    0.00    3.51


system.time(myMAsd <- sqrt((rowSums((myMA-rowMeans(myMA))^2)) / (length(myMA

##    user  system elapsed
##    0.03    0.00    0.03
```

### 5.8.3 Handling missing values

```
a <- c(1:10, NA, NA)
a <- c(1:10, NA, NA)
summary(a)

##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    1.00    3.25    5.50    5.50    7.75   10.00       2

mean(a)

## [1] NA

mean(a, na.rm = TRUE)

## [1] 5.5
```

## 5.9 Exercise 6: Parsing Real Data - World Population Data from Wikipedia

We demonstrated how to get data tables a URL. This means we can retrieve data from most any table on the web. The function *readHTMLTable* is very flexible for this. Please retrieve the table entitled "Estimated world population at various dates (in millions)" (Table 13) from `http://en.wikipedia.org/wiki/World_population`.

```
require(XML)

## Loading required package: XML

worldPop <- readHTMLTable("http://en.wikipedia.org/wiki/World_population")
names(worldPop)

##  [1] "NULL"
##  [2] "toc"
##  [3] "NULL"
##  [4] "World population milestones (USCB estimates)"
##  [5] "The 10 countries with the largest total population:"
##  [6] "10 most densely populated countries (with population above 1 million)"
##  [7] "Countries ranking highly in terms of both total population (more than 15 million p
##  [8] "NULL"
##  [9] "UN (medium variant  2010 revision) and US Census Bureau (December 2010) estimates
## [10] "UN 2008 estimates and medium variant projections (in millions)[97]"
## [11] "World historical and predicted populations (in millions)[101][102]"
## [12] "World historical and predicted populations by percentage distribution[101][102]"
## [13] "Estimated world and regional populations at various dates (in millions)"
## [14] "Starting at 500 million"
## [15] "Starting at 375 million"
## [16] "NULL"
## [17] "NULL"
## [18] "NULL"
## [19] "NULL"

worldPop <- worldPop[[13]]  # Just look at Table 13
```

1. First tidy the data. The data are factors, its easier to edit data that are character. Apply as.character to each column
2. Remove rows with dates before 1750. Remove the additional header in row 32.
3. Remove column 9 notes
4. Use the *sub* to remove the comma in the data values
5. convert the data to numeric
6. In what year did the population of Europe, Africa and Asia exceed 500 million?
7. Bonus: Plot the population growth of the World, Africa or Europe since 1750. Given this plot, would you guess that the the population of the World, Africa or Europe would be more likely to double again before the end of 21st century?

### 5.9.1 Writing functions: More on arguments

We are equipped now with all basic tools we need for writing functions. We include a few tips on arguments to functions.

1. Function arguments: Default values In many cases arguments have default values. For example the *qnorm(x, mean = 0, SD = 1,lower.tail = TRUE, log.p = FALSE )* has default values for the mean, standard deviation, cdf calculation and probabilities on the original scale.

```
prob <- c(0.5, 0.9, 0.95, 0.975, 0.99)
args(qnorm)
qnorm(prob)
qnorm(prob, 2)
qnorm(prob, mean = 2, sd = 1)
```

2. Function arguments: order is important

   - The argument sequence may begin in the unnamed, positional form, and specify named arguments after the positional arguments
   - If arguments to functions are given in the form *name=object* form, they may be given in any order
   - The argument sequence may be given in the unnamed, positional form
   - For example the following statements are equivalent

```
prob <- c(0.5, 0.9, 0.95, 0.975, 0.99)
args(qnorm)
qnorm(p = prob, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
qnorm(prob, 0, 1, log = FALSE, low = TRUE)
qnorm(prob, 0, 1, TRUE, FALSE)
```

3. Functions: A few points

   - Sometimes you may see the parameter "...", this is normally when functions call other functions and arguments are passed from one function to another.
   - If commands are stored in an external R script file, say `L2.R` they can be executed at any time in `R`

     ```
     source(paste(myPath, "L2.R",sep=''))
     ```

   - Once a function is defined, can call it from other functions
   - The built-in functions supplied with `R` are a valuable resource for learning about `R` programming

## 5.10 Writing functions: more technical discussion -Scoping

1. Scoping
   Symbols in the body of a function can be divided into three classes:

- Formal parameters (appear in the argument list of the function)
- Local variables (values are determined by the evaluation of expressions in the body of the functions)
- Free variables (neither of the above)

In this example: $x$ - formal parameter, $y$ - local variable, $z$ - free variable.

Example:

```
fn <- function(x) {
    y <- 2 * x
    print(x)
    print(y)
    print(z)
}

z <- 2
x <- 4
fn(x = 2)

## [1] 2
## [1] 4
## [1] 2
```

2. Lexical scope.

   Example: function called *cube*.

```
cube <- function(n) {
    sq <- function() n * n
    n * sq()
}
cube(2)

## [1] 8

n <- 4
cube(2)

## [1] 8
```

## 5.11 Options for Running memory or CPU intensive jobs in R

### 5.11.1 Distributed computing in R

There are two ways to split or distribute a big job. The simplest it to send jobs to different processors on the same machine (assuming it has multiple cores, which most new machines do). The second option is to split or parallelize a job across many machines or a cluster of machines. For both of these, see the Bioconductor package *parallel* which builds upon the older R packages snow and multicore

To install parallel use the Bioconductor package installer, BiocInstaller

```
library(BiocInstaller)
biocLite("parallel")
```

The package parallel has many functions which work like apply to distribute a computation. For example use mclapply just like lapply to split a job over 4 cores.

```
library(parallel)
system.time(mclapply(1:4, function(i) mc.cores <- 4))
```

mclapply is a parallelized version of lapply, and will not work on windows (as far as I know) but on Windows you can use functions parLapply, clusterApply and clusterApplyLB all in the parallel package.

The packages has several functions for different types of apply loops including parLapply, parSapply, and parApply which are parallel versions of lapply, sapply and apply respectively.

```
library(parallel)
cl <- makeCluster(3)
parLapply(cl, 1:3, sqrt)
stopCluster(cl)
```

For more help on this package, see the vignette

```
vignette("parallel", package = "parallel")
```

There are several other packages for distributed computing see the reviews of R packages on CRAN task views `http://cran.r-project.org/web/views/HighPerformanceComputing.html`. I have received recommendations on R packages biglm, ff and bigmemory.

### 5.11.2 Running R in the Cloud

One quick-start approaching to running R in the Cloud is to register for an Amazon cloud account and then simply direct your web browser at the Bioconductor RCloud instance

`http://www.bioconductor.org/help/bioconductor-cloud-ami/`.

It will open a RStudio interface and it has the same look and feel as the desktop version, making the transition pretty seamless.

If you wish to set up your own instance, Louis Alsett at Trinity College Dublin provides an RStudio Server Amazon Machine Image (AMI) which can install to your Cloud account see http://www.louisaslett.com/RStudio_AMI/.

For more information about distributed computing on the Cloud based including using Hadoop (which I think is used by Revolution Analytics) see the recent book "parallel R" by Q Ethan McCallum http://www.amazon.com/Parallel-R-Q-Ethan-McCallum/dp/1449309925

## 5.12 Efficient R coding

### 5.12.1 What is an R script

A R script is simply a text file, with R commands. There are two ways to call these R commands, start R and using the R function *source*, or at the command line using R CMD BATCH

### 5.12.2 What a script should look like ;-)

```
#####################
### Author: Mr Bob Parr
### Date: 2011-01-20
### Version: 1.0
### License: GPL (>= 3)
###
### Description: survival analysis function
#####################

## This function censors the survival data at a specific point in
## time. This is is useful if you used datasets having different
## follow-up periods.
##
## Arguments:
## -----------
## surv.time: vector of times to event occurrence [numeric]
## surv.event: vector of indicators for event occurrence [0/1]
## time.cens: point in time at which the survival data must
##             be censored [integer]. Defaults value is '0'
##
## Output: [list of two items]
## -------------------------
## surv.time.cens: vector of censored times to event occurrence [numeric]
## surv.event.cens: vector of censored indicators for event occurrence [0/1]

censor.time <- function(surv.time, surv.event, time.cens=0) {
   stc <- surv.time
   sec <- surv.event
   cc.ix <- complete.cases(stc, sec)
   if(time.cens != 0) {
      stc[cc.ix][surv.time[cc.ix] > time.cens] <- time.cens
      sec[cc.ix][surv.time[cc.ix] > time.cens] <- 0
   }
   return(list("surv.time.cens"=stc, "surv.event.cens"=sec))
}
```

You can save this script in a file named `censortime.R` in your working directory. If you want to define this function in your workspace, just type `source("censortime.R")`.

Of course, an R script may contain more than functions, it may also contain any analytical pipeline. Here is another example:

```
#####################
### Author: Mr Bob Parr
### Date: 2011-01-20
### Version: 1.0
### License: GPL (>= 3)
###
### Description: Script fitting a Cox model on the colon data
###  and writing the coefficients in a txt file
#####################

## load library
library(survival)

## load colon dataset
data(colon)

## Fit the cox model
coxm <- coxph(Surv(time, status) ~ rx, data=colon)

## save summary in a txt file in the working directory
write.table(t(coxm$coefficients), sep="\t", file="cox_coefficients_colon.txt",
  row.names=FALSE)
```

Save this script in a file named `coxColon.R` in your working directory. you can run it from your R session using the command **source("coxColon.R")** or you can run it in batch mode from a command line (e.g., shell console) using the command **R CMD BATCH coxColon.**

### 5.12.3 Coding Recommendations

These are the coding recommendations from the Bioconductor project, and whilst you do not have to do these, it is handy to adopt good working practice when you learn a new language.

1. Indentation
   - Use 4 spaces for indenting. No tabs.
   - No lines longer than 80 characters. No linking long lines of code using ";"
2. Variable Names
   - Use camelCaps: initial lowercase, then alternate case between words.
3. Function Names
   - Use camelCaps: initial lower case, then alternate case between words.
   - In general avoid '.', as in some.func
     Whilst beyond the scope of this class, R packages are written to either S3 or S4 standards. In the S3 class system, some(x) where x is class func will dispatch to this function. Use a '.' if the intention is to dispatch using S3 semantics.
4. Use of space
   - Always use space after a comma. This: a, b, c. Not: a,b,c.

- No space around "=" when using named arguments to functions. This: somefunc(a=1, b=2), not: somefunc(a = 1, b = 2).
- Space around all binary operators: a == b.

5. Comments
   - Use "##" to start comments.
   - Comments should be indented along with the code they comment.
6. Misc
   - Use "<-" not "=" for assignment.
7. For Efficient R Programming, see slides and exercises from Martin
   `http://www.bioconductor.org/help/course-materials/2010/BioC2010/`
8. R packages which tidy your code There is a package called formatR `https://github.com/yihui/formatR/wiki/` which will format all R script in a folder, indenting loops, convert the = to -> etc. See its wiki pages above if you are interesting in testing it.

### 5.12.4 Debugging R Code

Use the cat() and print() functions to print values in scripts as you go. I also use the *traceback* to find out what went wrong when a function doesn't work A full list of functions for debugging R code is beyond the scope of this lecture, but see the following useful tips from Duncan Murdoch `http://www.stats.uwo.ca/faculty/murdoch/software/debuggingR/`

### 5.12.5 End-User Messages

- message() communicates diagnostic messages (e.g., progress during lengthy computations) during code evaluation.
- warning() communicates unusual situations handled by your code.
- stop() indicates an error condition.
- cat() or print() are used only when displaying an object to the user, e.g., in a show method.

### 5.12.6 system.time

If you wish to check the efficient of your code to see how long it is taking to run, use the function *system.time* which gives the compute time for a function

```
df <- matrix(rnorm(5e+06), ncol = 20000)
system.time(apply(df, 1, mean))

##    user  system elapsed
##    0.24    0.00    0.23

system.time(rowMeans(df))
```

```
##    user  system elapsed
##    0.01    0.00    0.01
```

system.time()

### 5.12.7 Etiquette when emailing the R mailing list

When all else failed, ask an expert. The R mailing list is a wonderful resource with a very help bunch of experts who will be more than willing to help. But before you email, please do check if someone has asked the same question before or if there is a simple answer to your problem in the R manual or frequently asked questions (FAQ) documentation. The easiest way to do this is to search on `http://www.rseek.org`

If you still need to ask an expert on the mailing list

- Do Send in example code
- Include information about your operating system and version of R. The easiest way to do this is using sessionInfo() for example, see this recent post on the mailing list `https://stat.ethz.ch/pipermail/r-sig-mixed-models/2010q3/004467.html`

#### Writing R packages

Once you have written all your functions in one or several R files, you can use the function *package.skeleton* to generate the necessary directories and empty help pages for your package.

```
package.skeleton(name = "myFirstRPackage")
```

For coding recommendations see `http://google-styleguide.googlecode.com/svn/trunk/google-r-style.html` or `http://wiki.fhcrc.org/bioc/Coding_Standards`

**Hint:** all the packages on CRAN and BioConductor are open source, so you can easily download the source of any package to take a closer look at it. It may be extremely insightful to see how experienced R developers implemented their own packages.

**Using SVN**

RStudio v0.96 contains an easy interface to subversion (either GIT or SVN), but here is a detailed guide to using svn

`http://tortoisesvn.net/docs/release/TortoiseSVN_en/tsvn-repository.html#tsvn-repository-create-tortoisesvn`

Step 1. Create local SVN repository

1. Open the windows explorer
2. Create a new folder and name it e.g. SVNRepository
3. Right-click on the newly created folder and select TortoiseSVN Create Repository here....
4. A repository is then created inside the new folder. Don't edit those files yourself!!!. If you get any errors make sure that the folder is empty and not write protected.
5. For Local Access to the Repository you now just need the path to that folder. Just remember that Subversion expects all repository paths in the form file:///C:/SVNRepository/. Note the use of forward slashes throughout.
6. So far this is an empty repository, even though Subversion has created several directories and files! We need to fill it with our project files and connect it with our working project directory

Step 2: Initial import.

1. Somewhere in your hard drive create a directory (e.g. tmp) with the following three subdirectories:

```
C:\tmp\new\branches
C:\tmp\new\tags
C:\tmp\new\trunk
```

2. Backup and Tidy your existing scripts and project files (`C:\Projects\MyProject`). (ie delete unnecessary files)
3. Copy the contents of `\MyProject` into the trunk sub-directory (`C:\tmp\new\trunk`).
4. Import the 'new' directory into the repository (Right-click/TortoiseSVN/Import). Select URL as `file:///C:/SVNRepository/Myproject` (forward slashes!)
5. To see it works, right mouse click start `TortoiseSVN/Repo-browser...` see your Imported files.. Happy days. Now you have an SVN with all your files

Step 3. Using SVN

1. Now we have created the SVN, the trick is to use it!!! Start by checking out your data. Create a new scripts directory (or go back to your old one and delete its contents). And right mouse click and select "SVN Checkout"
2. To use the SVN Sending (checking in) your changes to the repository: Right-click on selected files then "SVN Commit"

3. To add new files to the repository. This is a two step process: , first Right-click on selected files then ”TortoiseSVN/Add” Then Right-click on selected files then ”SVN Commit”

4. If you wish to delete files (remember the SVN will always have a history of them) use ”TortoiseSVN/Delete”

5. Happy Subversioning!

# Chapter 6

# Introduction to graphics in R

To start let's look at the basic plots that can be produced in R using the `demo()` function

```
demo(graphics)
```

On start up, R initiates a graphics device driver which opens a special graphics window for the display of interactive graphics. If a new graphics window needs to be opened either *win.graph()* or *windows()* command can be issued.

Once the device driver is running, R plotting commands can be used to produce a variety of graphical displays and to create entirely new kinds of display.

## 6.1 The R function plot()

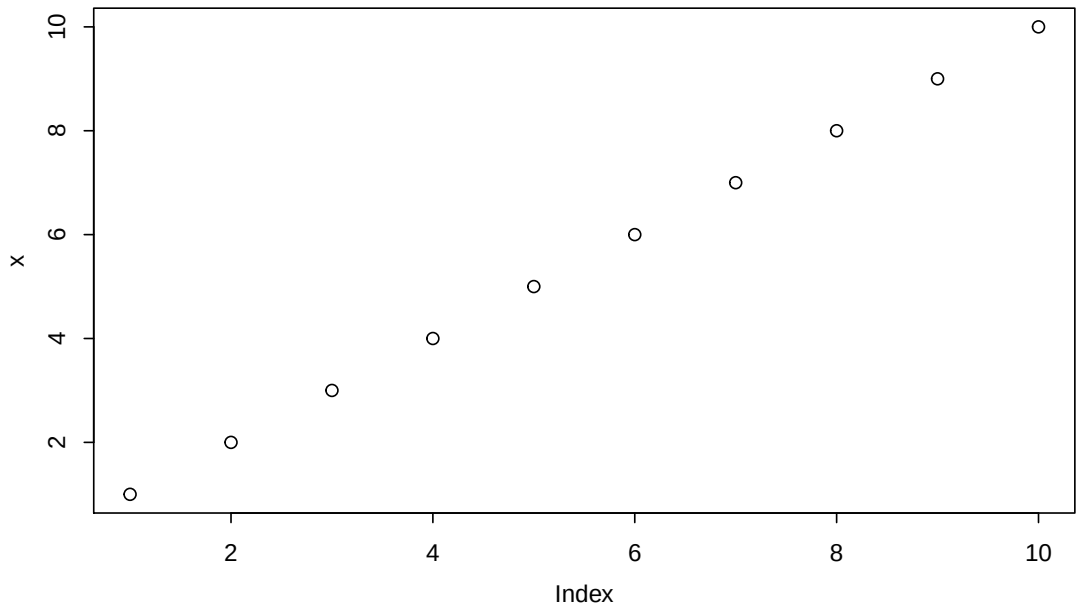
The *plot()* function is one of the most frequently used plotting functions in R.

IMPORTANT: This is a generic function, that is the type of *plot* produced is dependent on the *class* of the first argument.

- Plot of Vector(s)

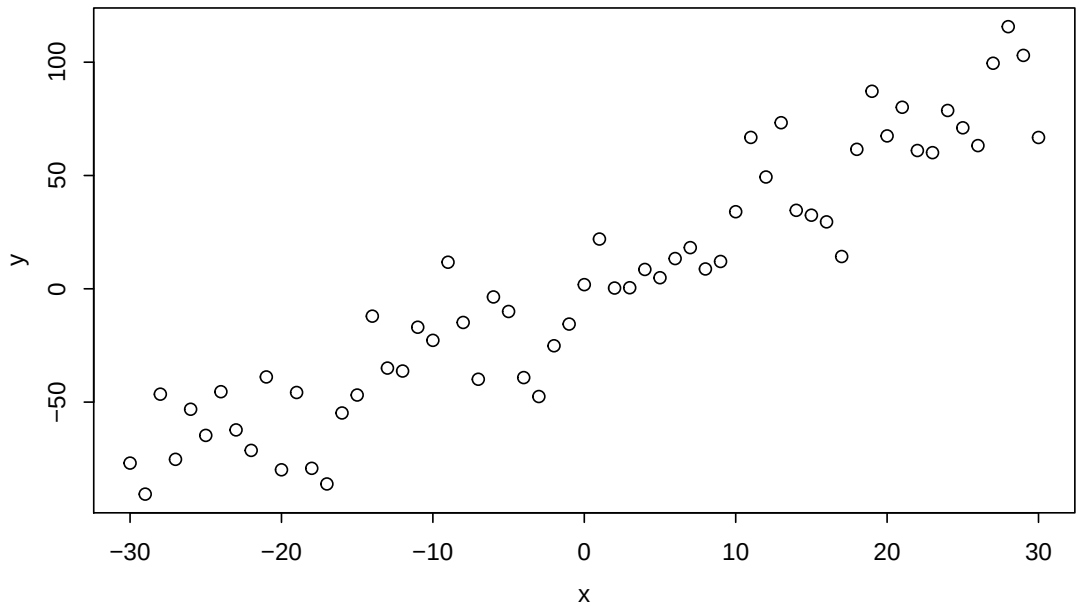
  1. One vector `x` (plots the vector against the index vector)

     ```
     x <- 1:10
     plot(x)
     ```




2. Scatter plot of two vectors `x` and `y`

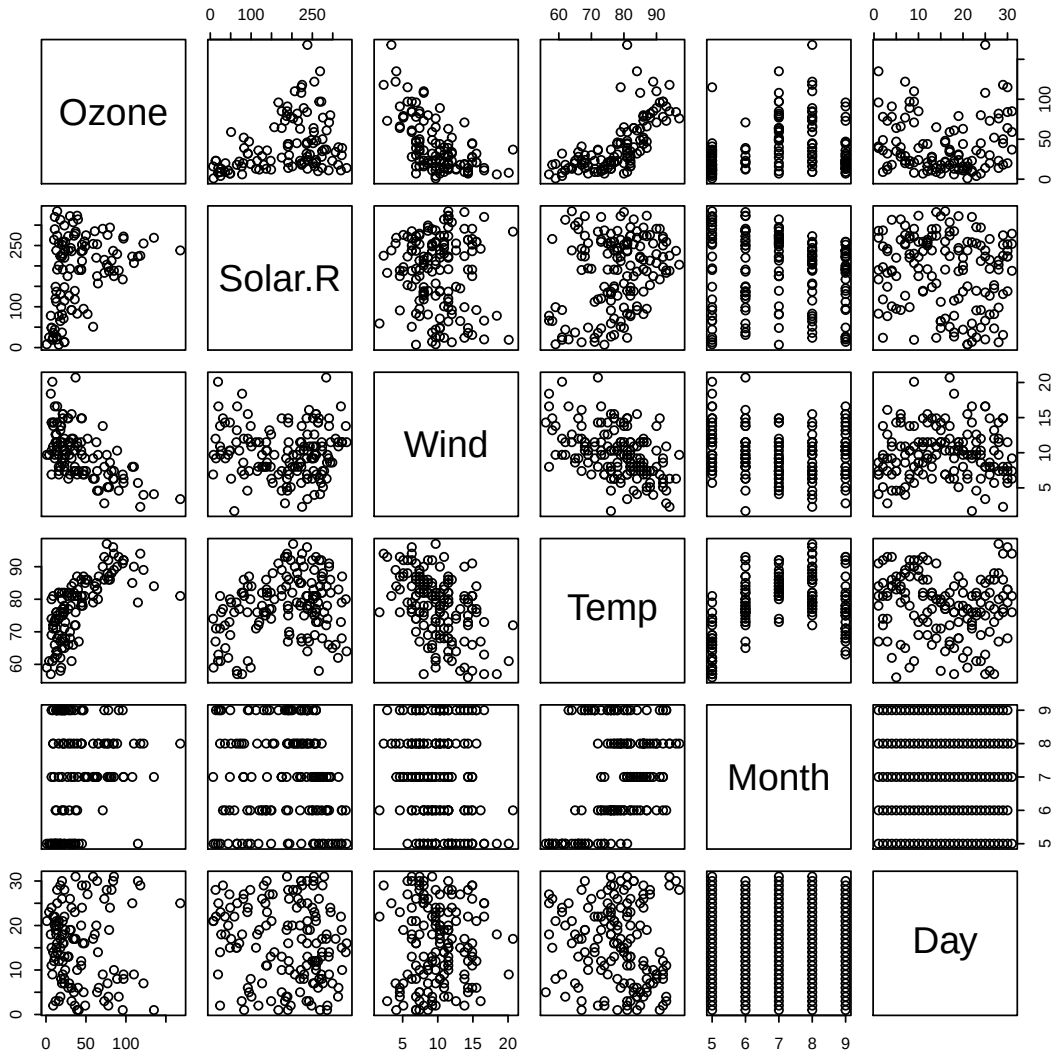
```
set.seed(13)
x <- -30:30
y <- 3 * x + 2 + rnorm(length(x), sd = 20)
plot(x, y)
```




- Plot of *data.frame* elements If the first argument to *plot()* is a *data.frame*, this can be as simply as *plot(x,y)* providing 2 columns (variables in the data.frame).

Lets look at the data in the *data.frame airquality* which measured the 6 air quality in New York, on a daily basis between May to September 1973. In total there are 154 observation (days).

```
airquality[1:2, ]

##   Ozone Solar.R Wind Temp Month Day
## 1    41     190  7.4   67     5   1
## 2    36     118  8.0   72     5   2

plot(airquality)  # all variables plotted against each other pairs()
```

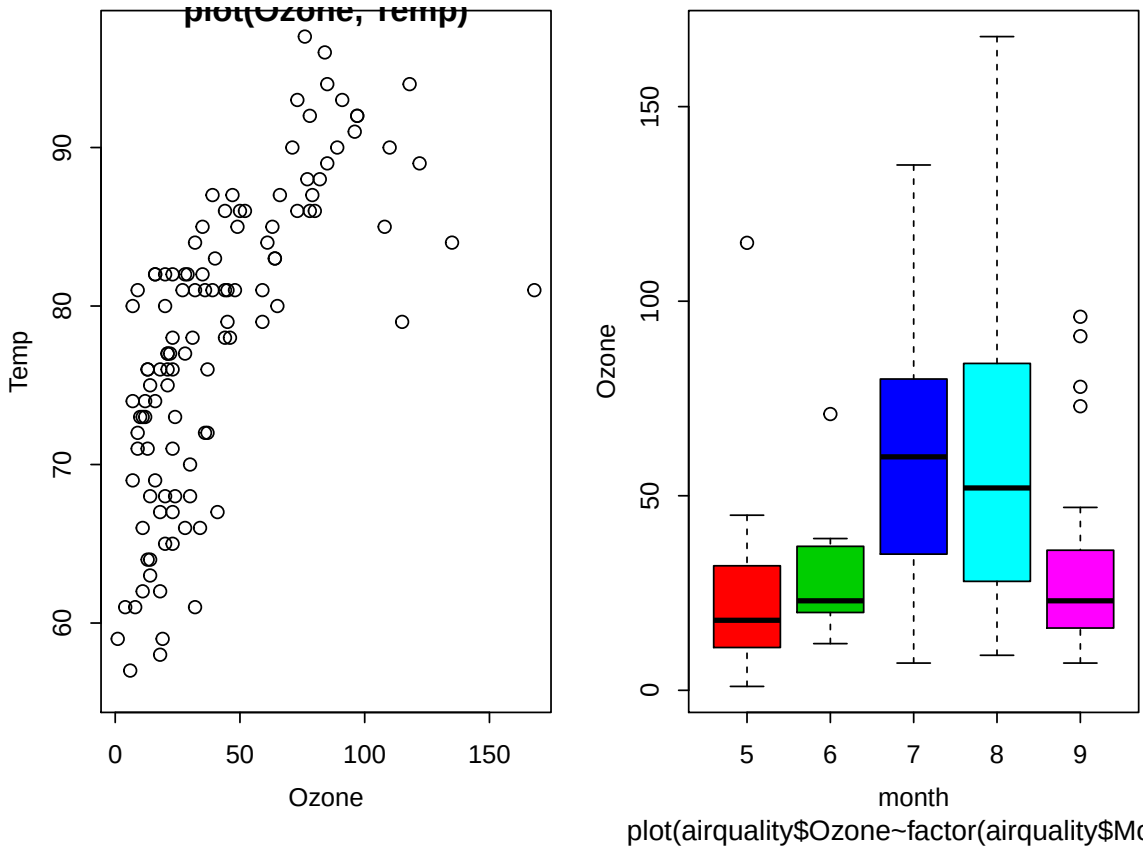



Note most plotting commands always start a new plot, erasing the current plot if necessary.

We'll discuss how to change the layout of plots so you can put multiple plots on the same page a bit later. But a simple way to put multiple plots in the same window is by splitting the display using *mfrow*

Note if you give plot a vector and factor plot(factor, vector) or plot(vector factor) it will produce a boxplot.

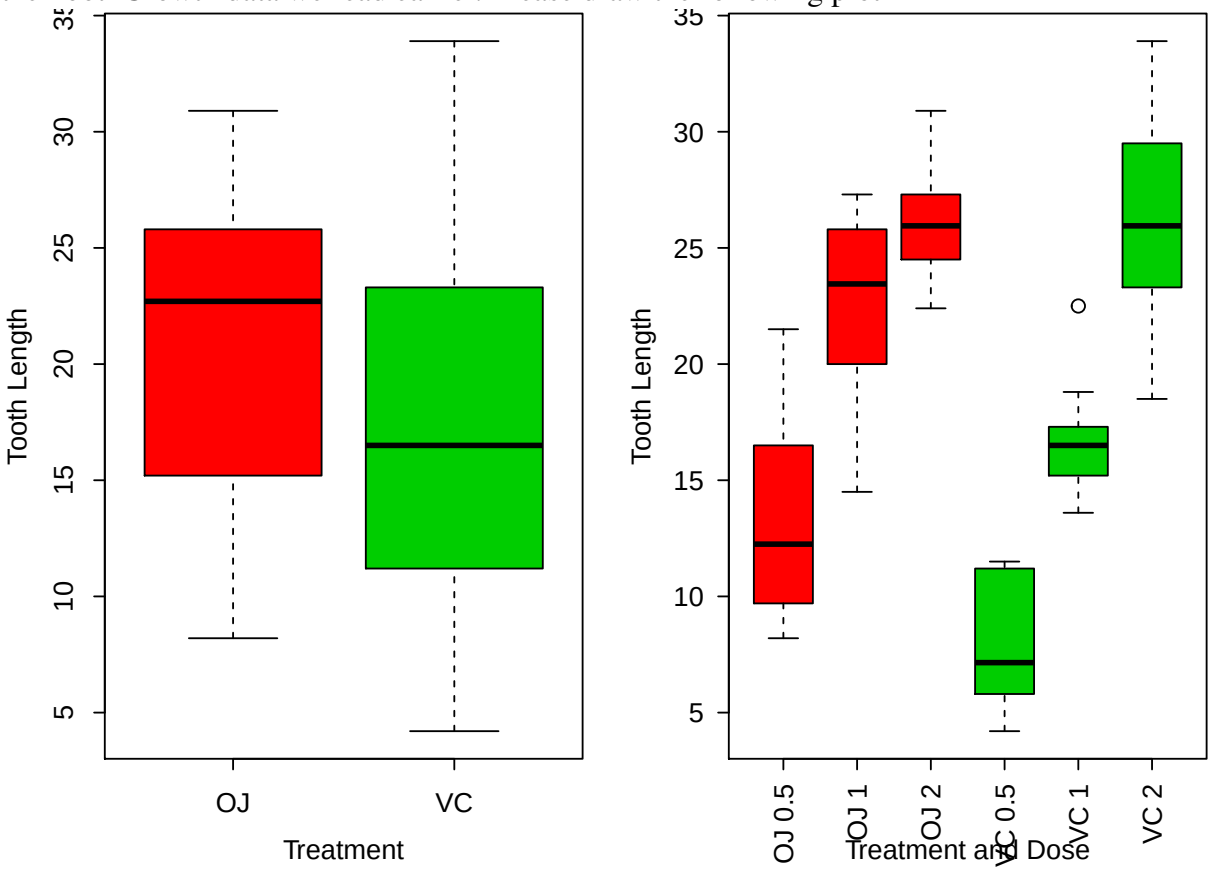
```
par(mfrow = c(1, 2))
attach(airquality)
plot(Ozone, Temp, main = "plot(Ozone, Temp)")
plot(airquality$Ozone ~ factor(airquality$Month), col = 2:6,
    sub = "plot(airquality$Ozone~factor(airquality$Month)", ylab = "Ozor
    xlab = "month")
```




```
detach(airquality)
```

## 6.2 Exercise 7

Using the ToothGrowth data we read earlier. Please draw the following plot



### 6.2.1 Arguments to plot

**axes=FALSE** Suppresses generation of axes-useful for adding your own custom axes with the `axis()` function. The default, axes=TRUE, means include axes.

**type=** The `type` argument controls the type of plot produced, as follows:

type="p" Plot individual points (the default)

type="l" Plot lines

type="b" Plot points connected by lines (both)

type="o" Plot points overlaid by lines

type="h" Plot vertical lines from points to the zero axis (high-density)

type="n" No plotting at all. However axes are still drawn (by default) and the coordinate system is set up according to the data. Ideal for creating plots with subsequent low-level graphics functions.

**xlab=string**

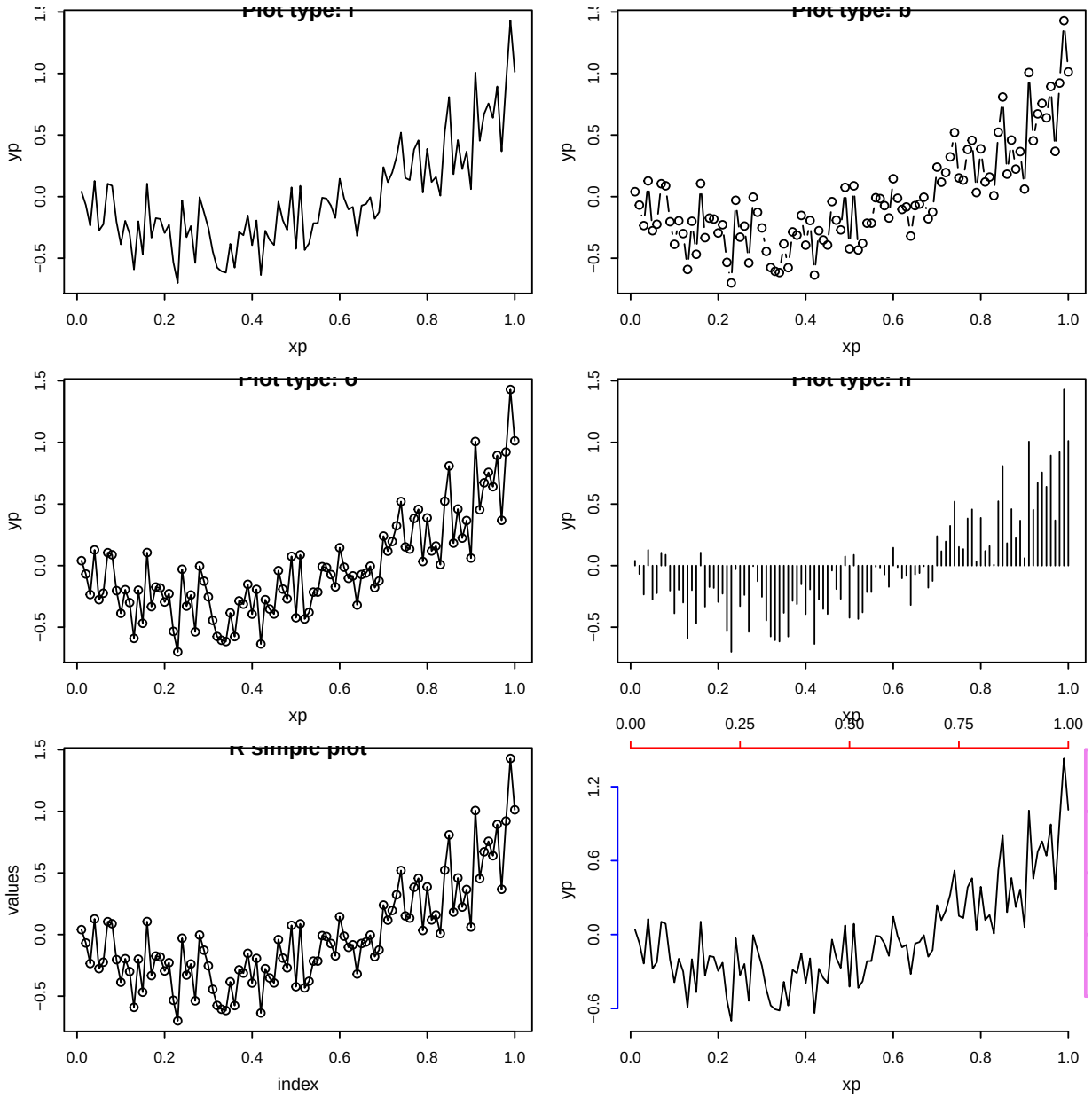
**ylab=string** Axis labels for the x and y axes. Use these arguments to change the default labels, usually the names of the objects used in the call to the high-level plotting function.

**main=string** Figure title, placed at the top of the plot in a large font.

**sub=string** Sub-title, placed just below the x-axis in a smaller font.

**Some Examples of Plotting using different plot types and axes**

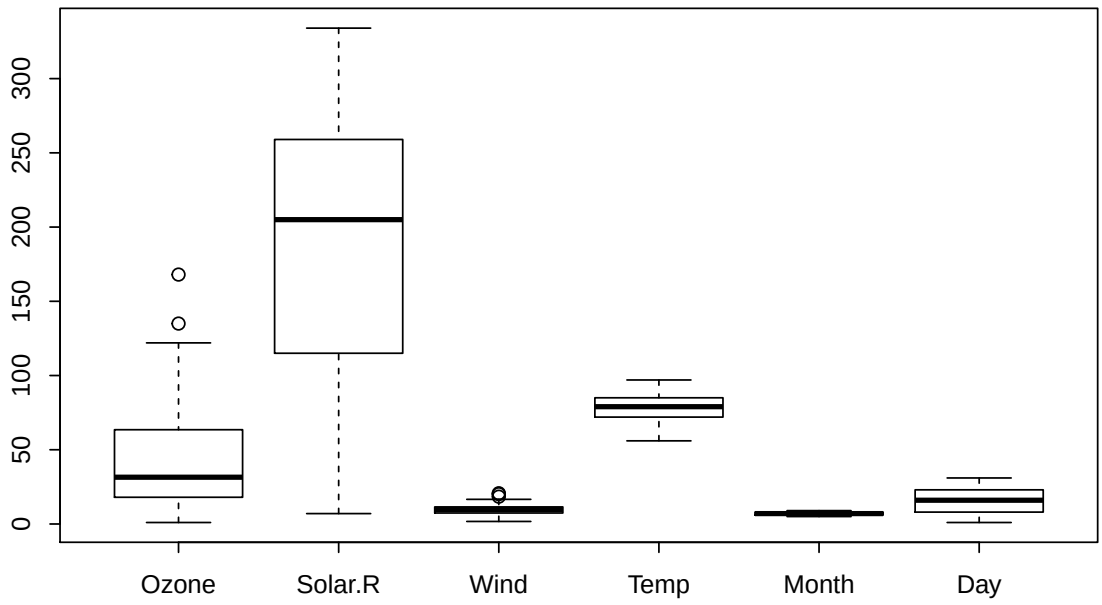
```
xp <- 1:100/100
yp <- 3 * xp^2 - 2 * xp + rnorm(100, sd = 0.2)

par(mfrow = c(3, 2))
for (i in c("l", "b", "o", "h")) plot(xp, yp, type = i, main = paste("Plot t
    i))

plot(xp, yp, type = "o", xlab = "index", ylab = "values",
    main = "R simple plot")
plot(xp, yp, type = "l", axes = FALSE)
axis(1)
axis(2, at = c(-0.6, 0, 0.6, 1.2), col = "blue")
axis(3, at = c(0, 0.25, 0.5, 0.75, 1), col = "red")
axis(4, col = "violet", col.axis = "dark violet", lwd = 2)
```




### 6.2.2 Other useful basic graphics functions

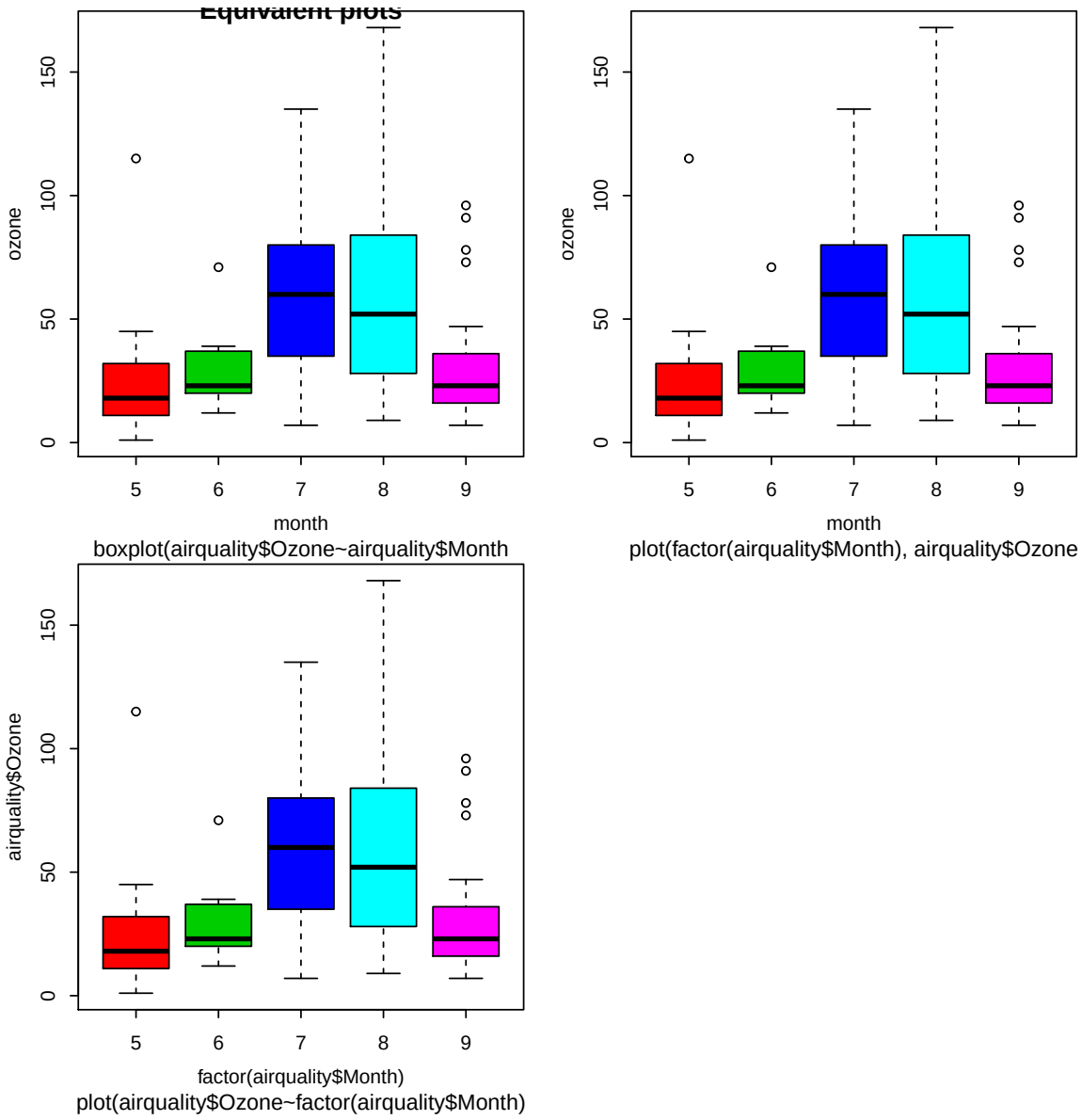
- *boxplot(x)* a boxplot show the distribution of a vector. It is very useful to example the distribution of different variables.

```
boxplot(airquality)
```



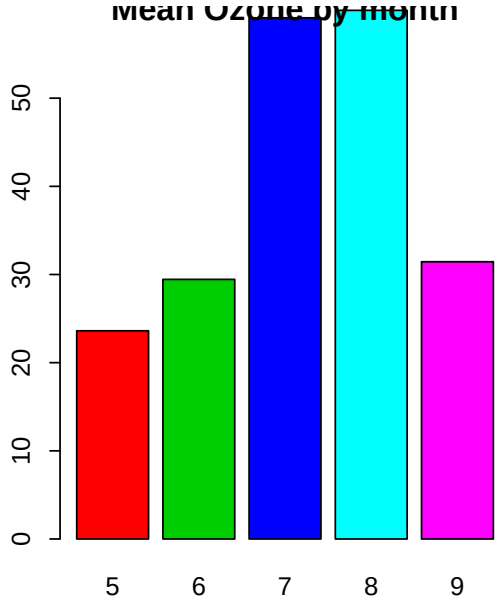

Note if you give plot a vector and factor plot(factor, vector) or plot(vector factor) it will produce a boxplot.

```
par(mfrow = c(2, 2))
boxplot(airquality$Ozone ~ airquality$Month, col = 2:6, xlab = "month",
    ylab = "ozone", sub = "boxplot(airquality$Ozone~airquality$Month")
title("Equivalent plots")
plot(factor(airquality$Month), airquality$Ozone, col = 2:6,
    xlab = "month", ylab = "ozone", sub = "plot(factor(airquality$Month)
plot(airquality$Ozone ~ factor(airquality$Month), col = 2:6,
    sub = "plot(airquality$Ozone~factor(airquality$Month)")
```




- barplot Plot a bar plot of the mean ozone quality by month. First use tapply to calculate the mean of ozone by month

```
OzMonthMean <- tapply(airquality$Ozone, factor(airquality$Month),
    mean, na.rm = TRUE)
par(mfrow = c(1, 2))
barplot(OzMonthMean, col = 2:6, main = "Mean Ozone by month")
```

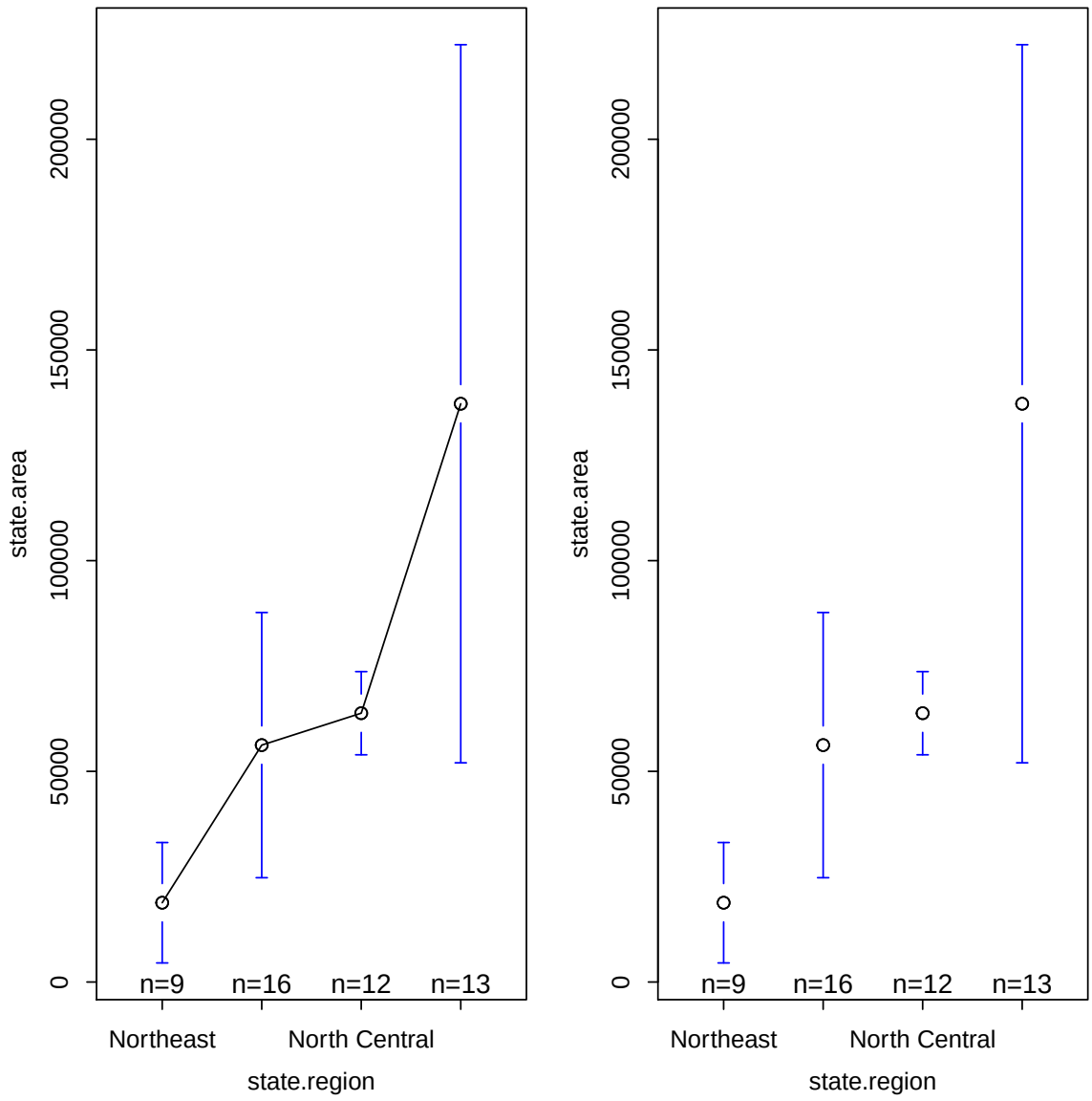



- barplot with confidence intervals

  To plot a barplot with CI, use the plotting functions in the gpplots package.

```
par(mfrow = c(1, 2))
require(gplots)

## Loading required package: gplots

## Loading required package: gtools

## Loading required package: gdata

## gdata: read.xls support for 'XLS' (Excel 97-2004) files gdata:
## ENABLED.

## NA

## gdata: read.xls support for 'XLSX' (Excel 2007+) files gdata:
## ENABLED.

## Attaching package: 'gdata'

## The following object(s) are masked from 'package:stats':
##
## nobs
```

```
## The following object(s) are masked from 'package:utils':
##
## object.size

## Loading required package: caTools

## Loading required package: bitops

## Loading required package: grid

## Loading required package: KernSmooth

## KernSmooth 2.23 loaded Copyright M. P. Wand 1997-2009

## Loading required package: MASS

## Attaching package: 'gplots'

## The following object(s) are masked from 'package:stats':
##
## lowess

plotmeans(state.area ~ state.region)
plotmeans(state.area ~ state.region, connect = FALSE)
```




```
# plotmeans( state.x77[,'Income'] ~ state.region, ylab='Income')
```

Note on Windows, the gplots package will warn if it can't find the programming language Perl. The above functions will still work, but this notice can be removed by installing Perl from `http://www.perl.org`. Linux and Mac OS X users won't see this error as both already have Perl installed. But it is not installed by default on windows.

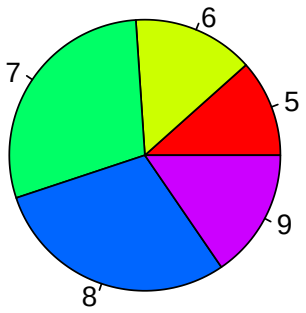
To fix this notice, install Perl. I tend to select the active state distribution of Perl. It will install into `C:\perl` Then run the following:

```
installXLSXsupport(perl = "C:/perl/bin/perl.exe")
```

To see more complex examples of plotting confidence intervals or standard error on plots, see `http://wiki.stdout.org/rcookbook/Graphs/Plotting%20means%20and%20error%20bars%20(ggplot2)/`

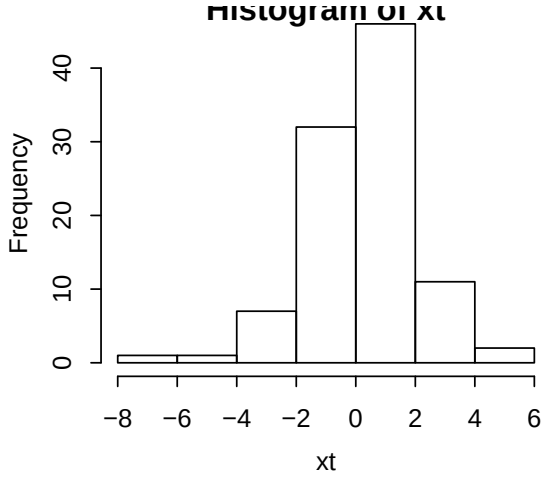
- pie chart

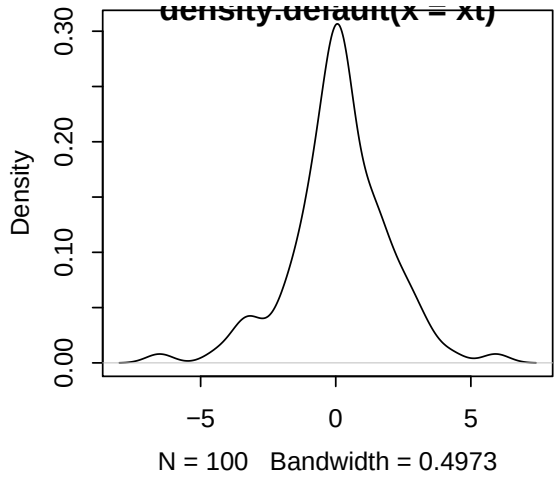
```
pie(OzMonthMean, col = rainbow(5))
```




- *hist(x)*- histogram of a numeric vector `x` with a few important optional arguments: `nclass=` for the number of classes, and *breaks*= for the breakpoints

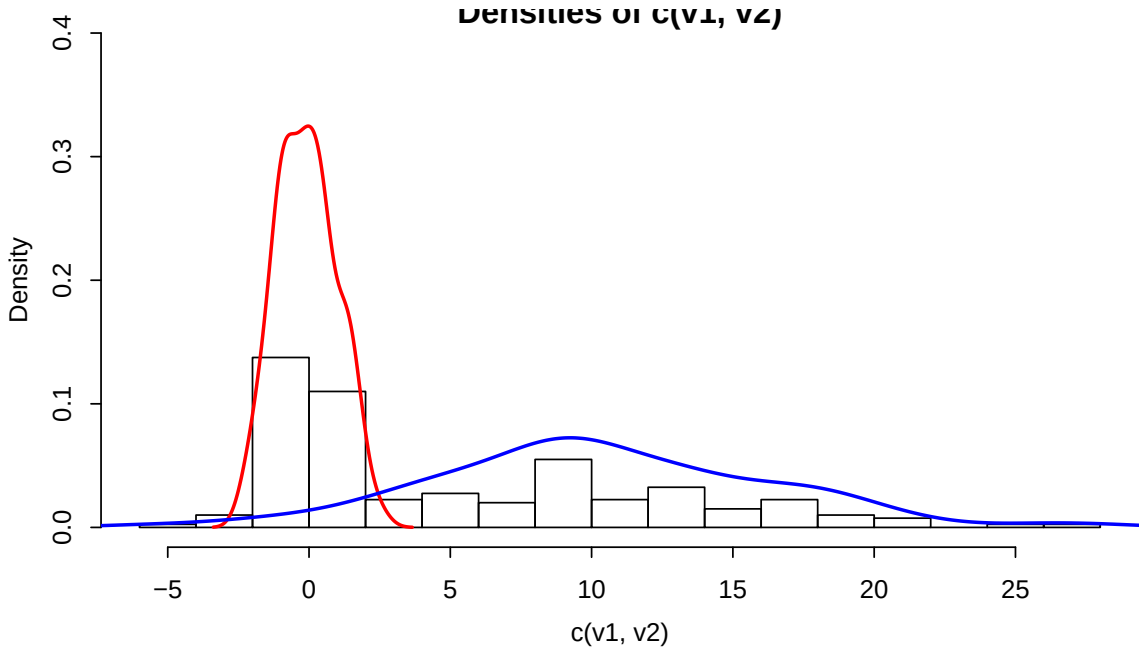
```
par(mfrow = c(1, 2))
xt <- rt(100, 3)
hist(xt)
plot(density(xt))
```




Sometimes we wish to view a bimodal distribution or the distributions of two groups

```r
# generate 2 populations of with different mean and sd
set.seed(54321)
v1 <- rnorm(100, 0, 1)
v2 <- rnorm(100, 10, 7)

# Draw a histogram of both populations
hist(c(v1, v2), freq = FALSE, ylim = c(0, 0.4), breaks = 20,
    main = "Densities of c(v1, v2)")


# Calculate a density function for each distribution plot as a line
# on the hist plot
dv1 <- density(v1)
lines(dv1, col = "red", lwd = 2)

dv2 <- density(v2)
lines(dv2, col = "blue", lwd = 2)
```




- 3D scatterplot

```r
require(scatterplot3d)

## Loading required package: scatterplot3d

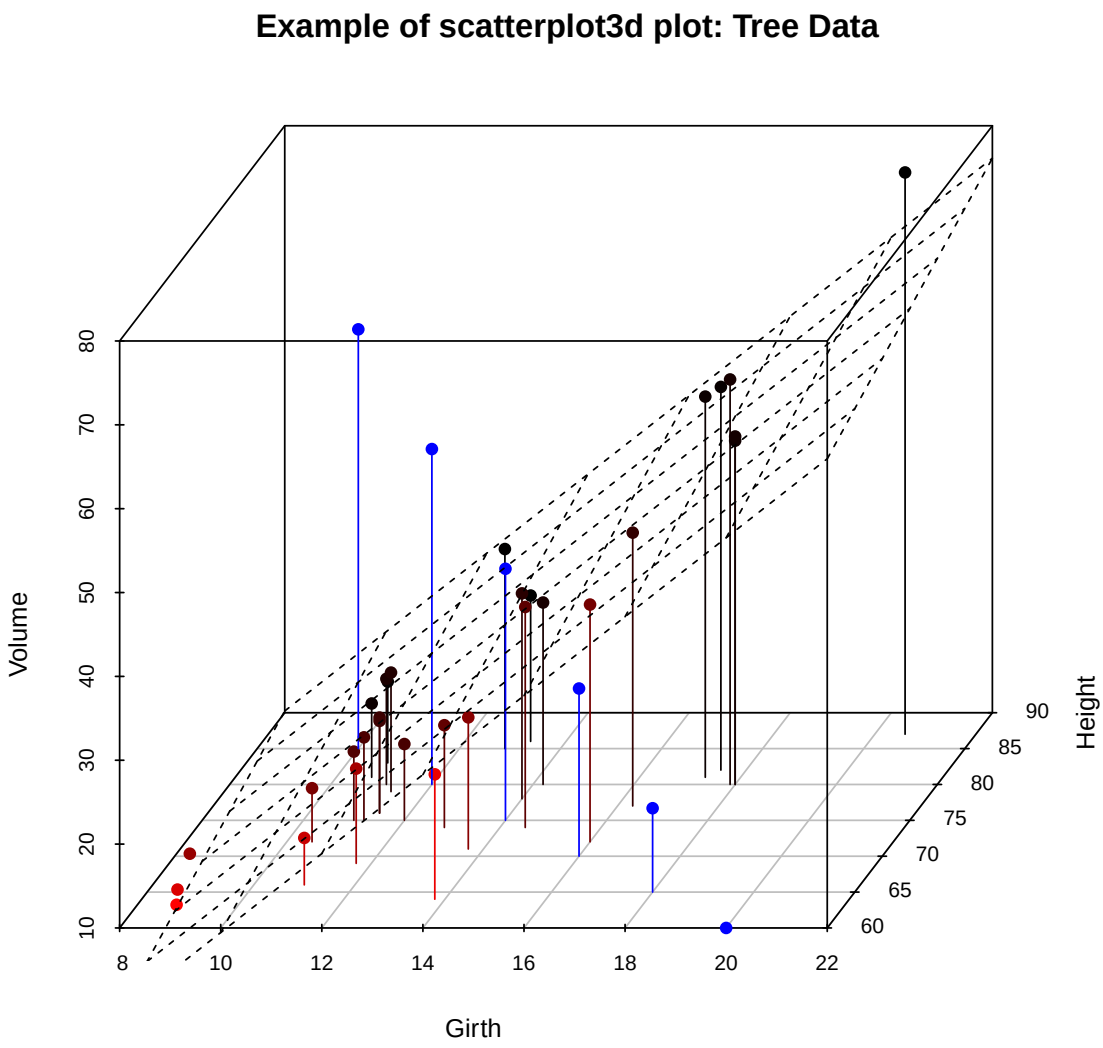
data(trees)
trees[1:2,]
```

```
##   Girth Height Volume
## 1   8.3     70   10.3
## 2   8.6     65   10.3

s3d <- scatterplot3d(trees, type="h", highlight.3d=TRUE,
                     angle=55, scale.y=0.7, pch=16,
                     main="Example of scatterplot3d plot: Tree Data")

# Now adding some points to the "scatterplot3d"
s3d$points3d(seq(10,20,2), seq(85,60,-5),
             seq(60,10,-10),  col="blue",
             type="h", pch=16)

# Now adding a regression plane to the "scatterplot3d"
attach(trees)
my.lm <- lm(Volume ~ Girth + Height)
s3d$plane3d(my.lm)
```




```
detach(trees)
```

- The R function *venn* - draws a venn diagram. Input is a list. It will draw a venn diagram showing the intersect between 2-6 vectors in a list.

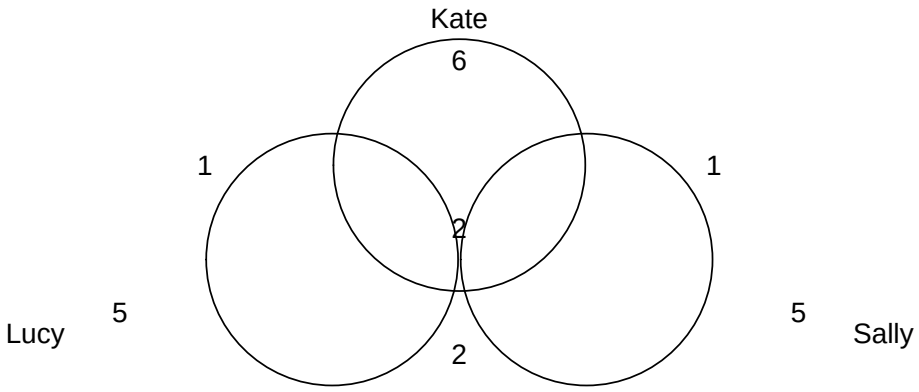
```
require(gplots)
sample(LETTERS, 10)

##  [1] "S" "F" "M" "U" "J" "D" "X" "G" "B" "Y"

tt <- lapply(1:3, function(x) sample(LETTERS, 10))
names(tt) <- c("Lucy", "Sally", "Kate")
tt
```

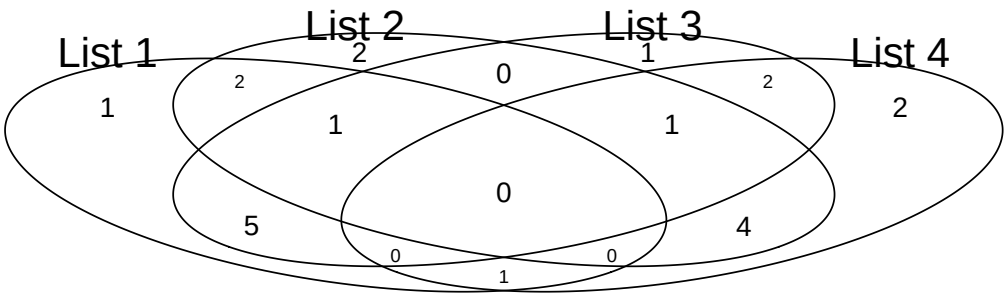
```
## $Lucy
##  [1] "C" "M" "I" "F" "W" "Z" "V" "R" "X" "U"
##
## $Sally
##  [1] "Z" "C" "A" "T" "S" "L" "W" "J" "Q" "M"
##
## $Kate
##  [1] "F" "D" "C" "M" "P" "N" "H" "E" "Q" "G"
##

venn(tt)
```




Plot 4 intersections

```
tt <- lapply(1:4, function(x) sample(LETTERS, 10))
names(tt) <- paste("List", 1:4)
venn(tt)
```



Color plots

```
require(venneuler)

## Loading required package: venneuler

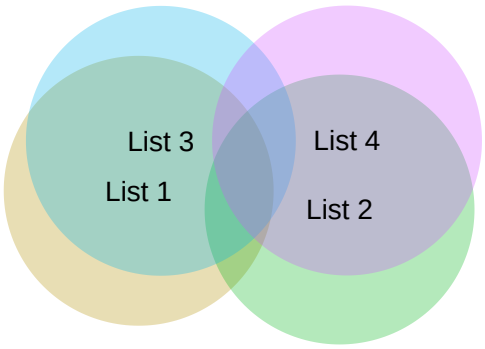
## Warning: package 'venneuler' was built under R version 2.15.2

## Loading required package: rJava


IntersectMatrix <- function(tt) {
    allElements <- unique(unlist(tt))
    outMat <- sapply(1:length(tt), function(i) allElements %in% tt[[i]])
    rownames(outMat) <- allElements
    colnames(outMat) <- names(tt)
    return(outMat)
}
xx <- IntersectMatrix(tt)
print(xx[1:4, ])

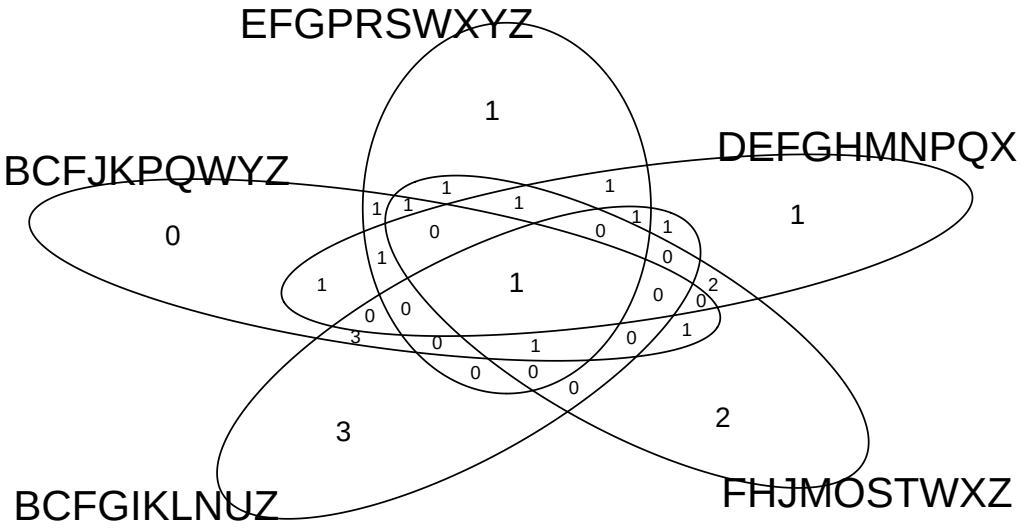
##   List 1 List 2 List 3 List 4
## Y   TRUE  FALSE   TRUE  FALSE
## A   TRUE   TRUE  FALSE  FALSE
## U   TRUE  FALSE   TRUE  FALSE
## K   TRUE  FALSE   TRUE  FALSE

plot(venneuler(xx))
```




It will even plot 5 intersections

```
tt <- lapply(1:5, function(x) sample(LETTERS, 10))
names(tt) <- sapply(tt, function(x) paste(sort(x), collapse = ""))
venn(tt)
```



## 6.3 Customize plot with low-level plotting commands

Sometimes the default plot doesn't produce the plot you desire. In this case, low-level plotting commands can be used to edit or add extra information (such as points, lines or text) to the current plot. Some of the more useful low-level plotting functions are:

**points(x, y)**

**lines(x, y)** Adds points or connected lines to the current plot.

**text(x, y, labels, ...)** Add text to a plot at points given by x, y. Normally labels is an integer or character vector in which case labels[i] is plotted at point (x[i], y[i]). The default is 1:length(x). Note: This function is often used in the sequence

The graphics parameter type="n" suppresses the points but sets up the axes, and the `text()` function supplies special characters, as specified by the character vector names for the points.

**abline(a, b)** Adds a line of slope b and intercept a to the current plot.

**abline(h=y)** Adds a horizontal line

**abline(v=x)** Adds a vertical line

**polygon(x, y, ...)** Draws a polygon defined by the ordered vertices in (x, y) and (optionally) shade it in with hatch lines, or fill it if the graphics device allows the filling of figures.

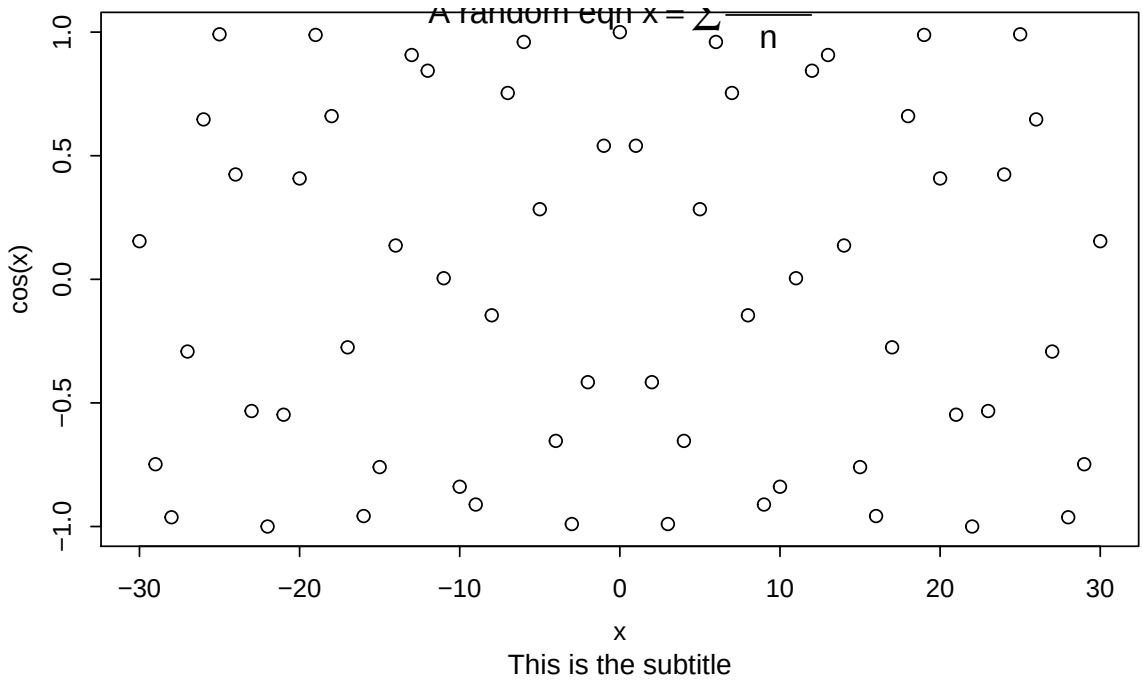
**legend(x, y, legend, ...)** Adds a legend to the current plot at the specified position. Plotting characters, line styles, colors etc., are identified with the labels in the character vector legend. At least one other argument v (a vector the same length as legend) with the corresponding values of the plotting unit must also be given, as follows:
legend( , fill=v) Colors for filled boxes
legend( , col=v) Colors in which points or lines will be drawn
legend( , lty=v) Line styles
legend( , lwd=v) Line widths
legend( , pch=v) Plotting characters

**title(main, sub)** Adds a title main to the top of the current plot in a large font and (optionally) a sub-title sub at the bottom in a smaller font.

**axis(side, ...)** Adds an axis to the current plot on the side given by the first argument (1 to 4, counting clockwise from the bottom.) Other arguments control the positioning of the axis within or beside the plot, and tick positions and labels. Useful for adding custom axes after calling plot() with the axes=FALSE argument.

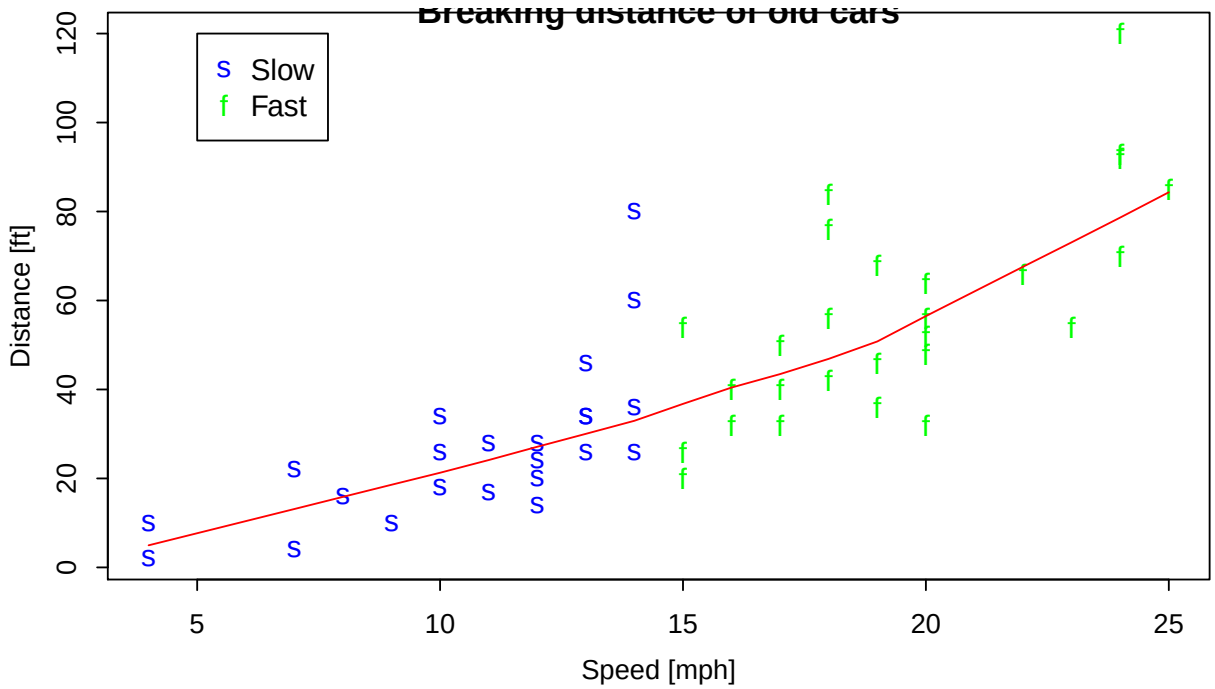
To add Greek characters, either specify font type 5 (see below) or use the function *expression*

```
plot(x, cos(x), main = expression(paste("A random eqn ", bar(x)) ==
    sum(frac(alpha[i] + beta[z], n))), sub = "This is the subtitle")
```




Example using points lines and legend

```
attach(cars)
plot(cars, type = "n", xlab = "Speed [mph]", ylab = "Distance [ft]")
points(speed[speed < 15], dist[speed < 15], pch = "s", col = "blue")
points(speed[speed >= 15], dist[speed >= 15], pch = "f", col = "green")
lines(lowess(cars), col = "red")
legend(5, 120, pch = c("s", "f"), col = c("blue", "green"),
    legend = c("Slow", "Fast"))
title("Breaking distance of old cars")
```

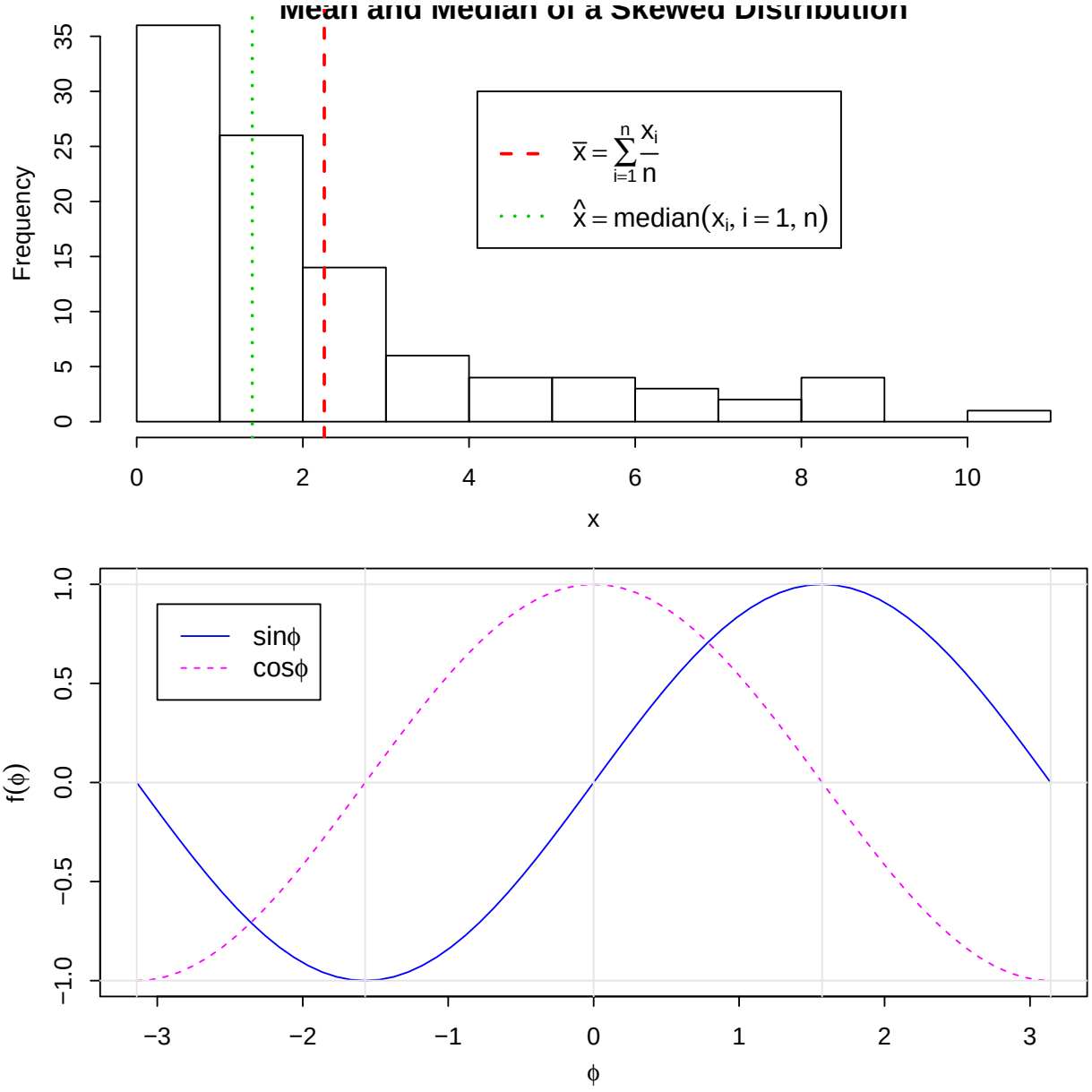



```
detach(2)
```

To add formulae or Greek characters to a plot

```
par(mfrow = c(2, 1))
# Mean and Median Plot
x <- rexp(100, rate = 0.5)
hist(x, main = "Mean and Median of a Skewed Distribution")
abline(v = mean(x), col = 2, lty = 2, lwd = 2)
abline(v = median(x), col = 3, lty = 3, lwd = 2)
ex1 <- expression(bar(x) == sum(over(x[i], n), i == 1, n),
    hat(x) == median(x[i], i == 1, n))
legend(4.1, 30, ex1, col = 2:3, lty = 2:3, lwd = 2)

x <- seq(-pi, pi, len = 65)
plot(x, sin(x), type = "l", col = "blue", xlab = expression(phi),
    ylab = expression(f(phi)))
lines(x, cos(x), col = "magenta", lty = 2)
abline(h = -1:1, v = pi/2 * (-6:6), col = "gray90")
ex2 <- expression(plain(sin) * phi, paste("cos", phi))
legend(-3, 0.9, ex2, lty = 1:2, col = c("blue", "magenta"),
    adj = c(0, 0.6))
```




## 6.4 Default parameters - par

When creating graphics, particularly for presentation or publication purposes, R's defaults do not always produce exactly that which is required. You can, however, customize almost every aspect of the display using graphics parameters. R maintains a list of a large number of graphics parameters which control things such as line style, colors, figure arrangement and text justification among many others. Every graphics parameter has a name (such as 'col', which controls colors,) and a value (a color number, for example.) Graphics parameters can be set in two ways: either permanently, affecting all graphics functions which access the current device; or temporarily, affecting only a single graphics function call.

The *par()* function is used to access and modify the list of graphics parameters for the current graphics device. See help on *par()* for more details.

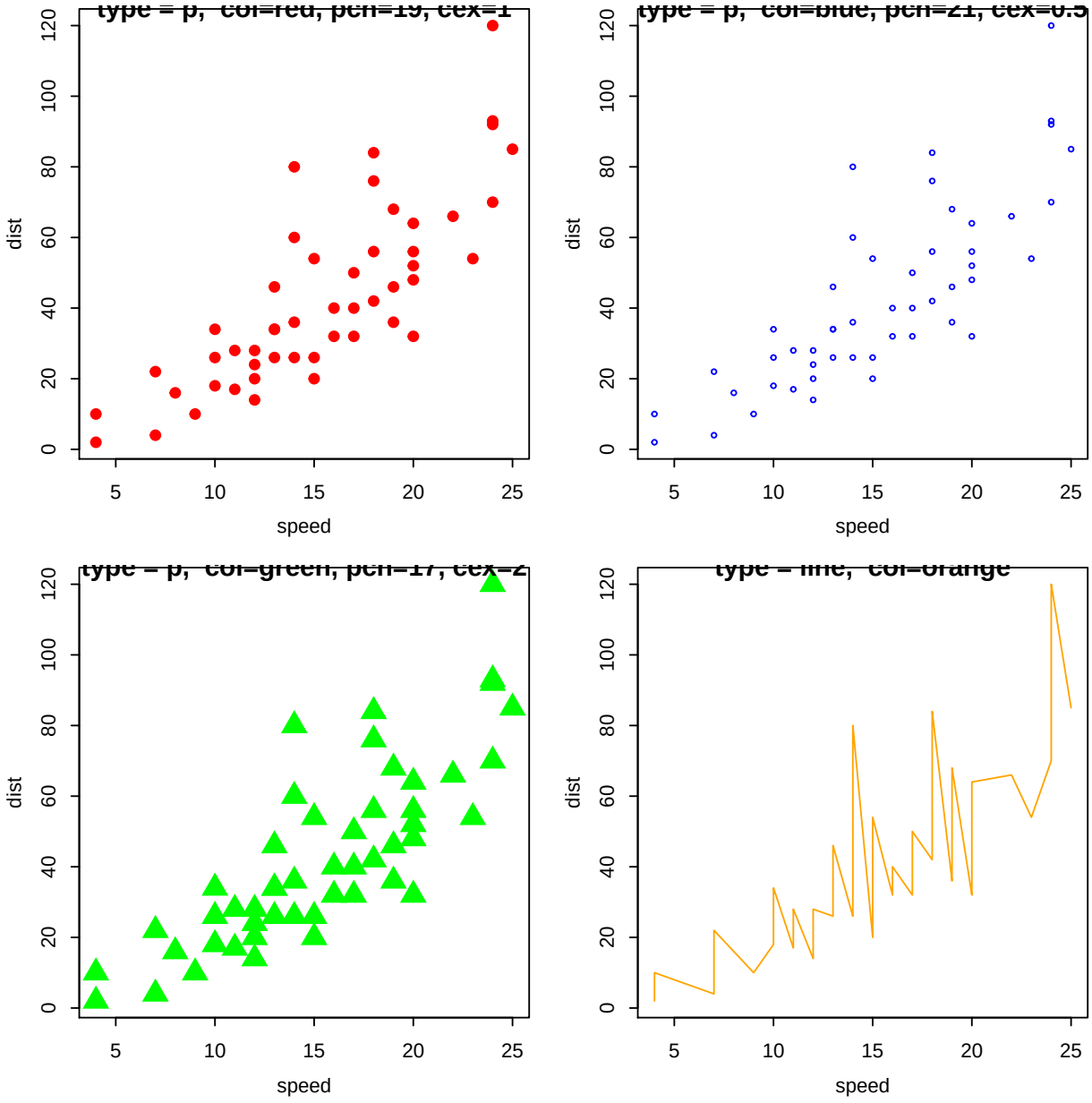
To see a sample of point type available in R, type

```
example(pch)
```

### 6.4.1 Interactive plots in R Studio - Effect of changing par

In RStudio the manipulate function accepts a plotting expression and a set of controls (e.g. slider, picker, or checkbox) which are used to dynamically change values within the expression. When a value is changed using its corresponding control the expression is automatically re-executed and the plot is redrawn.

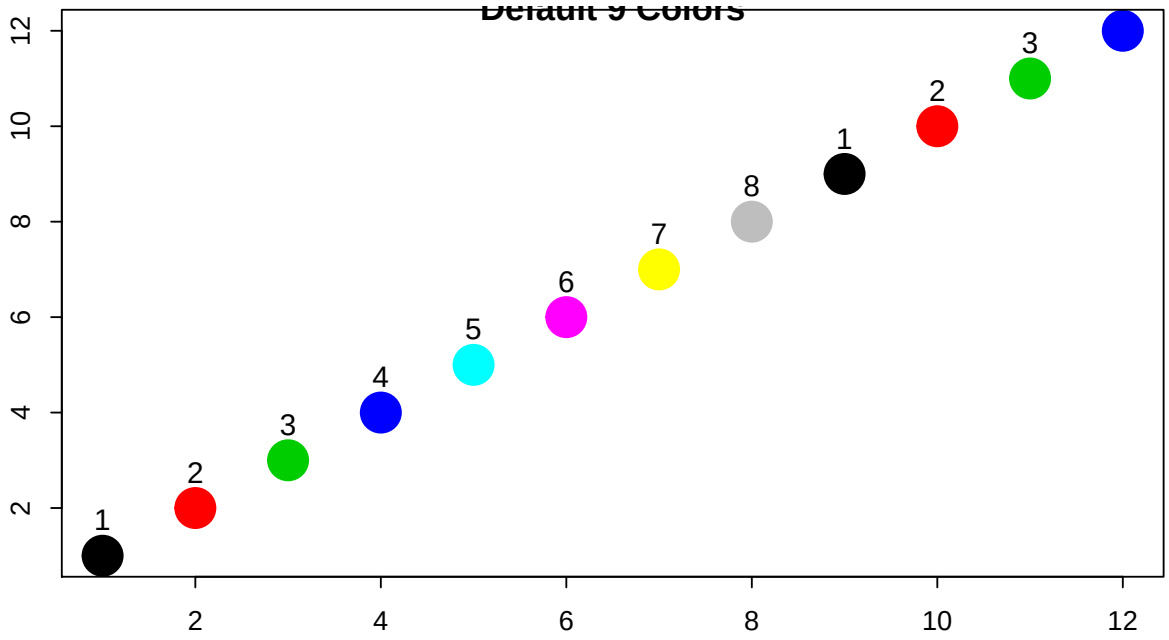
```
library(manipulate)
manipulate(plot(1:x), x = slider(1, 100))
manipulate(plot(cars, xlim = c(0, x.max), type = type, ann = label,
    col = col, pch = pch, cex = cex), x.max = slider(10, 25, step = 5,
    initial = 25), type = picker(Points = "p", Line = "l", Step = "s"),
    label = checkbox(TRUE, "Draw Labels"), col = picker(red = "red",
        green = "green", yellow = "yellow"), pch = picker(`1` = 1, `2` = 2,
        `3` = 3, `4` = 4, `5` = 5, `6` = 6, `7` = 7, `8` = 8, `9` = 9,
        `10` = 10, `11` = 11, `12` = 12, `13` = 13, `14` = 14, `15` = 15,
        `16` = 16, `17` = 17, `18` = 18, `19` = 19, `20` = 20, `21` = 21,
        `22` = 22, `23` = 23, `24` = 24), cex = picker(`1` = 1, `2` = 2,
        `3` = 3, `4` = 4, `5` = 5, `6` = 6, `7` = 7, `8` = 8, `9` = 9,
        `10` = 10))
```


type = p, col=red, pch=19, cex=1
type = p, col=blue, pch=21, cex=0.5
type = p, col=green, pch=17, cex=2
type = line, col=orange
dist
speed
0
20
40
60
80
100
120
5
10
15
20
25

### 6.4.2 R Colors

Thus far, we have frequently used numbers in plot to refer to a simple set of colors. There are 8 colors where 0:8 are white, black, red, green, blue, cyan, magenta, yellow and grey. If you provide a number greater than 8, the colors are recycled. Therefore for plots where other or greater numbers of colors are required, we need to access a larger palette of colors.

```
plot(1:12, col = 1:12, main = "Default 9 Colors", ylab = "",
    xlab = "", pch = 19, cex = 3)
text(1:12, c(1:12) + 0.75, c(1:8, 1:4))
```




R has a large list of over 650 colors that R knows about. This list is held in the vector *colors()*. Have a look at this list, and maybe search for a set you are interested in.

```
colors()[1:10]

##  [1] "white"          "aliceblue"      "antiquewhite"   "antiquewhite1"
##  [5] "antiquewhite2" "antiquewhite3" "antiquewhite4" "aquamarine"
##  [9] "aquamarine1"    "aquamarine2"

length(colors())

## [1] 657

grep("yellow", colors(), value = TRUE)

##  [1] "greenyellow"          "lightgoldenrodyellow"
```

```
##   [3] "lightyellow"           "lightyellow1"
##   [5] "lightyellow2"          "lightyellow3"
##   [7] "lightyellow4"          "yellow"
##   [9] "yellow1"               "yellow2"
##  [11] "yellow3"               "yellow4"
##  [13] "yellowgreen"
```

R are has defined palettes of colors, which provide complementing or contrasting color sets. For example look at the color palette rainbow.

```
example(rainbow)
```

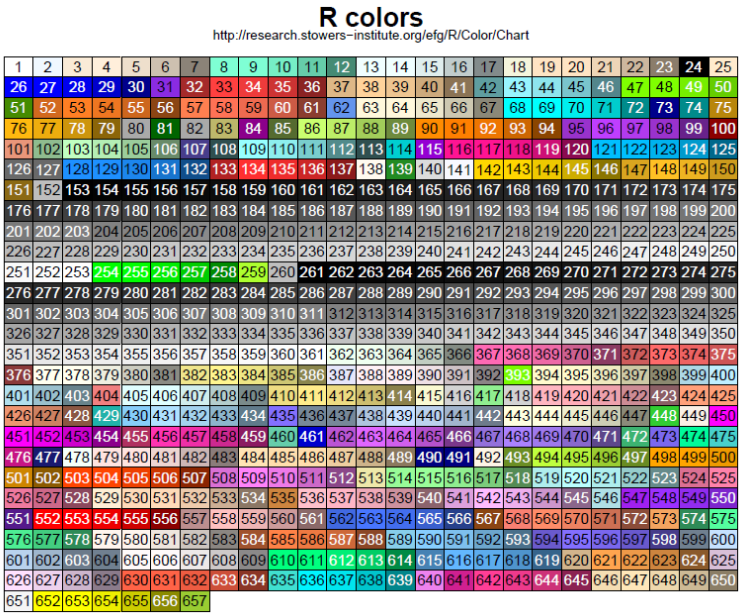



Figure 6.1: There are 657 colors available using the *colors()* function

| | | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 401 | lightblue2 | #B2DFEE | 178 | 223 | 238 | 451 | magenta1 | #FF00FF | 255 | 0 | 255 |
| 402 | lightblue3 | #9AC0CD | 154 | 192 | 205 | 452 | magenta2 | #EE00EE | 238 | 0 | 238 |
| 403 | lightblue4 | #68838B | 104 | 131 | 139 | 453 | magenta3 | #CD00CD | 205 | 0 | 205 |
| 404 | lightcoral | #F08080 | 240 | 128 | 128 | 454 | magenta4 | #8B008B | 139 | 0 | 139 |
| 405 | lightcyan | #E0FFFF | 224 | 255 | 255 | 455 | maroon | #B03060 | 176 | 48 | 96 |
| 406 | lightcyan1 | #E0FFFF | 224 | 255 | 255 | 456 | maroon1 | #FF34B3 | 255 | 52 | 179 |
| 407 | lightcyan2 | #D1EEEE | 209 | 238 | 238 | 457 | maroon2 | #EE30A7 | 238 | 48 | 167 |
| 408 | lightcyan3 | #B4CDCD | 180 | 205 | 205 | 458 | maroon3 | #CD2990 | 205 | 41 | 144 |
| 409 | lightcyan4 | #7A8B8B | 122 | 139 | 139 | 459 | maroon4 | #8B1C62 | 139 | 28 | 98 |
| 410 | lightgoldenrod | #EEDD82 | 238 | 221 | 130 | 460 | mediumaquamarine | #66CDAA | 102 | 205 | 170 |
| 411 | lightgoldenrod1 | #FFEC8B | 255 | 236 | 139 | 461 | mediumblue | #0000CD | 0 | 0 | 205 |

Figure 6.2: Colors can be defined by name, RGB, hex etc

The complete versions of the above plots, along with a complete listing of colors, RGB numbers

or hexadecimal for each colors, the following script will generate a multi-page pdf document called "ColorChart.pdf" which is a useful reference document on colors in R.

```
source("http://research.stowers-institute.org/efg/R/Color/Chart/ColorChart
```

### 6.4.3 More Colors Palettes; RColorBrewer

A very useful RColorBrewer `http://colorbrewer.org`. This package will generate a ramp color to provide a color palette that is sequential, diverging, or qualitative ramped, for example:

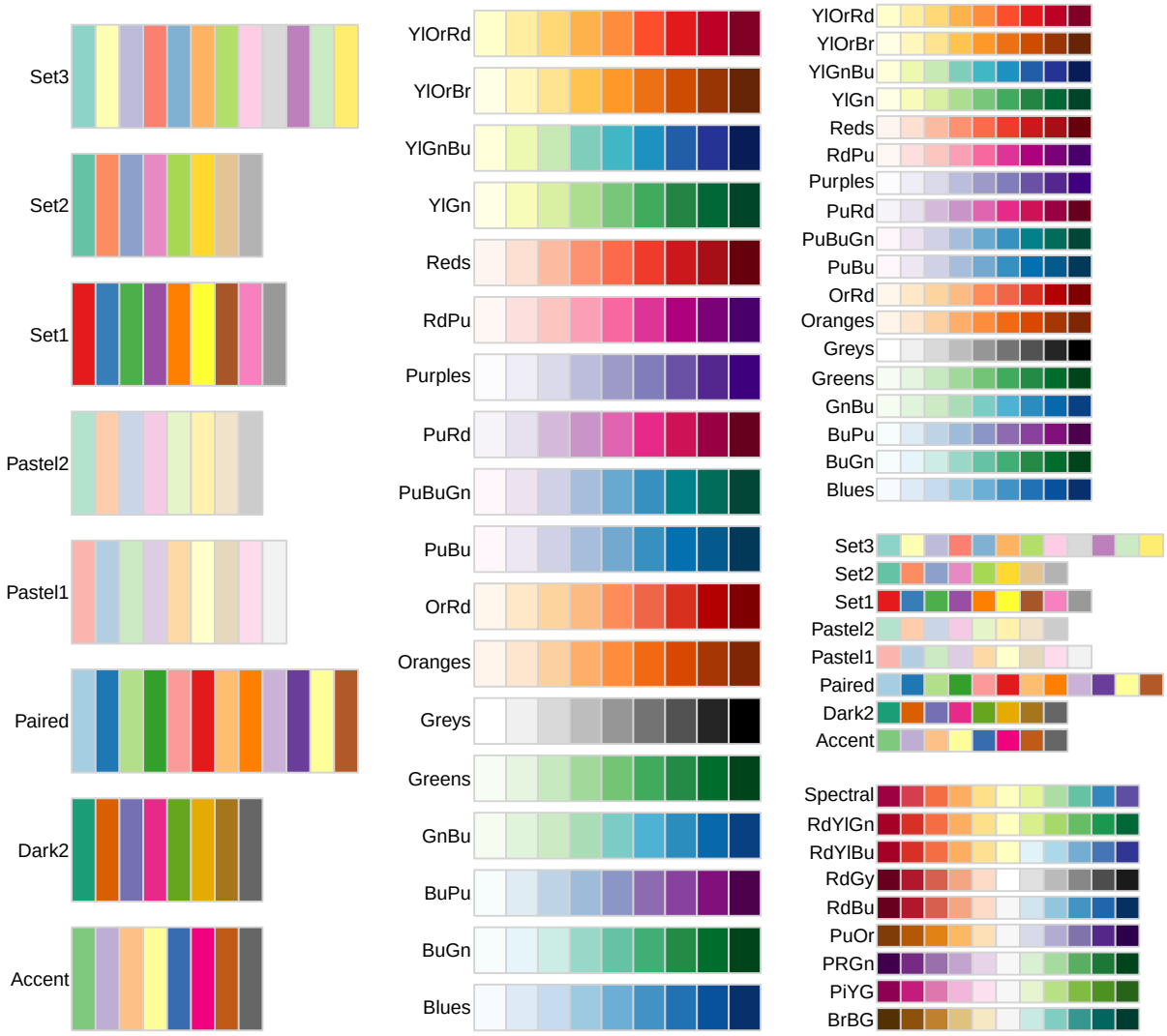
- Sequential palettes are suited to ordered data that progress from low to high. Lightness steps dominate the look of these schemes, with light colors for low data values to dark colors for high data values.
- Diverging palettes put equal emphasis on mid-range critical values and extremes at both ends of the data range. The critical class or break in the middle of the legend is emphasized with light colors and low and high extremes are emphasized with dark colors that have contrasting hues.
- Qualitative palettes do not imply magnitude differences between legend classes, and hues are used to create the primary visual differences between classes. Qualitative schemes are best suited to representing nominal or categorical data.

To see more about RColorBrewer run the example

```
require(RColorBrewer)

## Loading required package: RColorBrewer

par(mfrow = c(1, 3))
display.brewer.all(type = "qual")
display.brewer.all(type = "seq")
display.brewer.all(type = "all")
```




I use RColorBrewer to produce nicer colors in clustering heatmap. For example lets look at results of wine-tasting of French red wines.

load the library ade4

```
## Loading required package: ade4

## Warning: package 'ade4' was built under R version 2.15.2

## Attaching package: 'ade4'

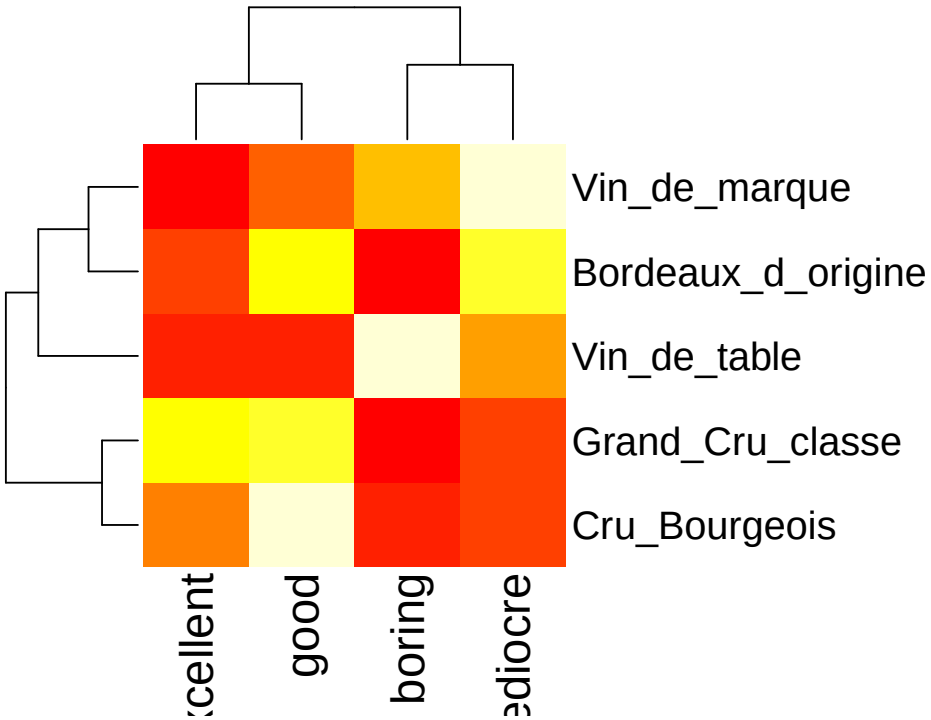
## The following object(s) are masked from 'package:base':
```

```
##
## within
```

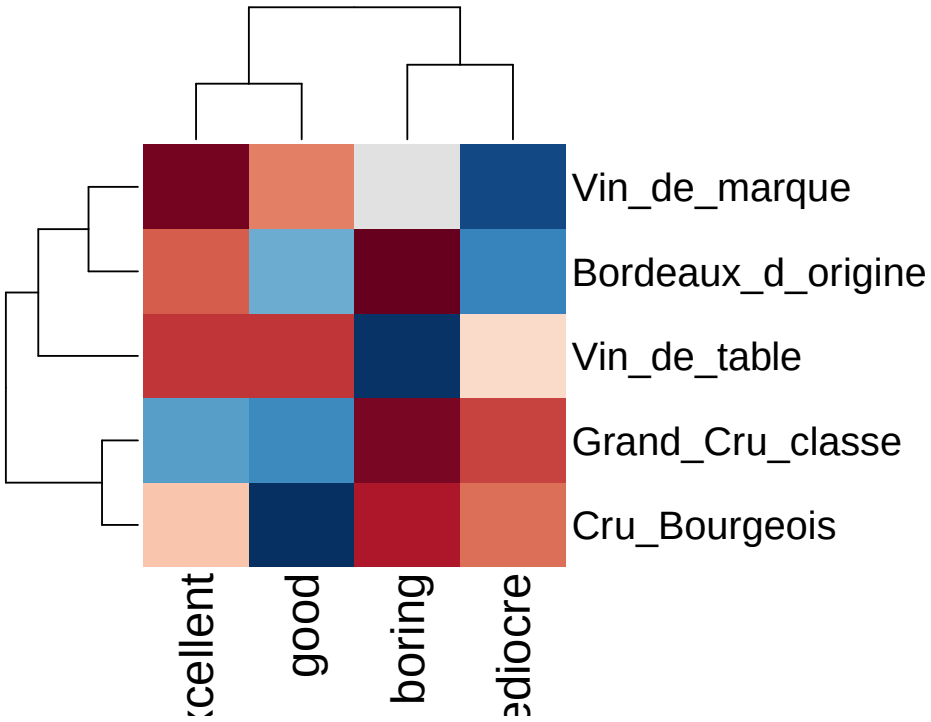
```
data(bordeaux)  ## this is a data.frame
bordeaux <- as.matrix(bordeaux)  ## Convert to a matrix
bordeaux
```

```
##                      excellent good mediocre boring
## Cru_Bourgeois               45  126       24      5
## Grand_Cru_classe            87   93       19      1
## Vin_de_table                 0    0       52    148
## Bordeaux_d_origine          36   68       74     22
## Vin_de_marque                0   30      111     59
```

```
heatmap(bordeaux)  # Using default colors
```




```
# with a color palette from RColorBrewer
require(RColorBrewer)
hmcol <- colorRampPalette(brewer.pal(10, "RdBu"))(500)
heatmap(bordeaux, col = hmcol)
```


Vin_de_marque
Bordeaux_d_origine
Vin_de_table
Grand_Cru_classe
Cru_Bourgeois
xcellent
good
boring
ediocre

## 6.5 Interacting with graphics

R also provides functions which allow users to extract or add information to a plot using a mouse via *locator()* and *verb+identify()* functions respectively.

```
plot(1:20, rt(20, 1))
text(locator(1), "outlier", adj = 0)
```

Waits for the user to select locations on the current plot using the left mouse button.

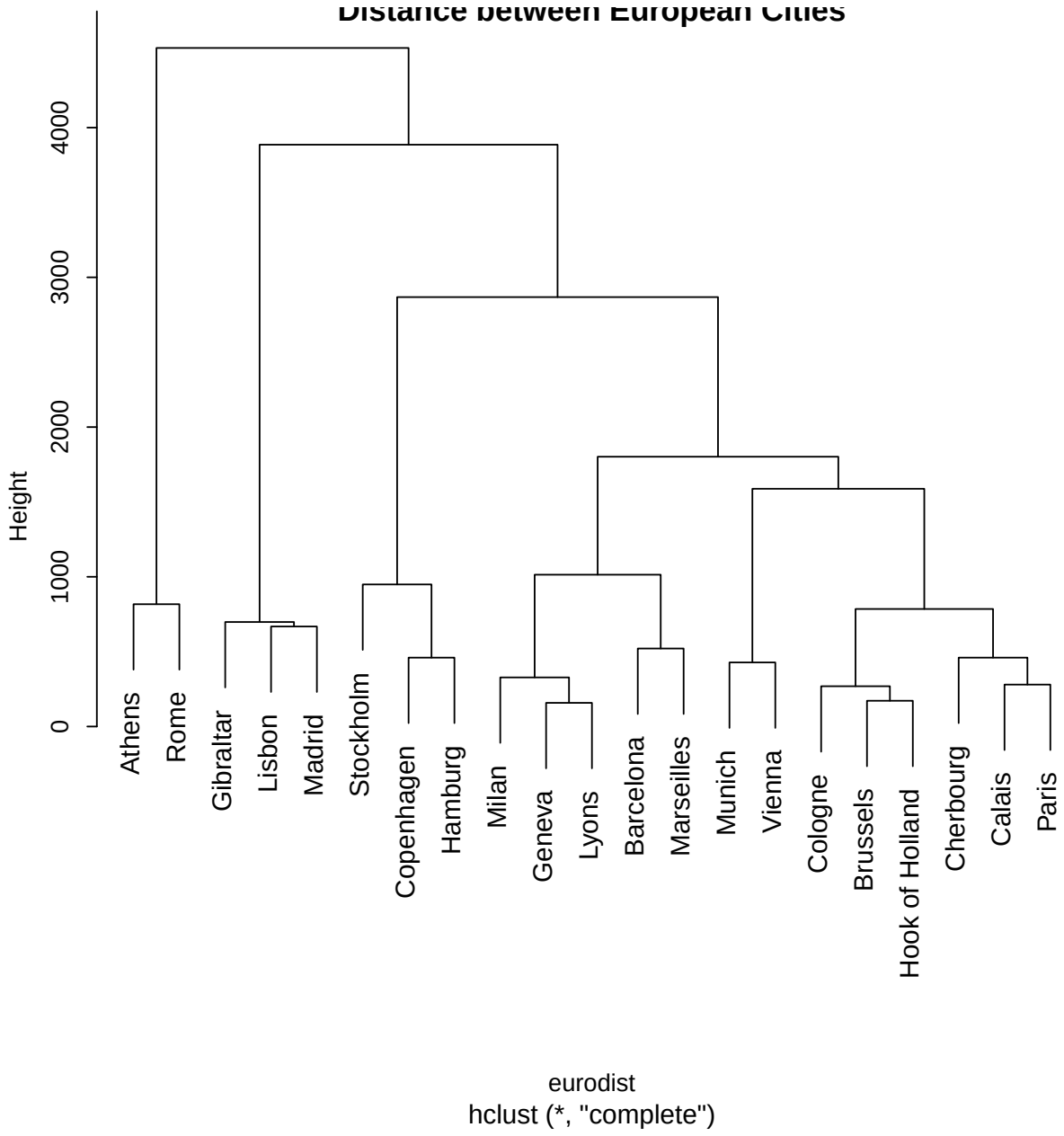
```
attach(women)
plot(height, weight)
identify(height, weight, women)
detach(2)
```

Allow the user to highlight any of the points (`identify(x,y,label)`) defined by x and y (using the left mouse button) by plotting the corresponding component of labels nearby (or the index number of the point if labels is absent).

Right mouse click, to ”stop”.

Identify members in a hierarchical cluster analysis of distances between European cities

```
hca <- hclust(eurodist)
plot(hca, main = "Distance between European Cities")
```




```
(x <- identify(hca))
x
```

### 6.5.1 Exercise 8 - Plotting

Using the women dataset

1. Set the plot layout to be a 2 x 2 grid (ie 2 rows, 2 columns)
2. Draw weight on the Y axis and height on the X axis.
3. Switch the orientation, Draw weight on the X axis and height on the Y axis.
4. Drawing a new plot, set the pch (point type) to be a solid circle, and color them red. Add a title ”study of Women” to the plot
5. Drawing another plot, set the pch (point type) to be a solid square, Change the X axis label to be ”Weight of Women” and make the point size (using the parameter cex) larger to 1.5

## 6.6 Saving plots

### 6.6.1 Rstudio

In RStudio, there is a simple interface to export plots. Click on the "Export" button in the plot window.

### 6.6.2 Devices

R can generate graphics (of varying levels of quality) on almost any type of display or printing device. Before this can begin, however, R needs to be informed what type of device it is dealing with. This is done by starting a device driver. The purpose of a device driver is to convert graphical instructions from R ("draw a line," for example) into a form that the particular device can understand. Device drivers are started by calling a device driver function. There is one such function for every device driver: type *help(Devices)* for a list of them all.

The most useful formats for saving `R` graphics:

**postscript()** For printing on PostScript printers, or creating PostScript graphics files.

**pdf()** Produces a PDF file, which can also be included into PDF files.

**jpeg()** Produces a bitmap JPEG file, best used for image plots.

### 6.6.3 Difference between vector and pixel images

Note there is a big difference between saving files in jpeg or postscript files. Image files save in jpg, bmp, gif etc are pixel image files, these are like photographs, where you can just select a line and change its color. By contact vector graphic, such as postscript, or windows meta files can be imported into drawing packages such as Adobe illustrator (or some even into PowerPoint), you can double click on an axes, and since its a vector graphic you can change the color of the line easily.

| Format * | Type | Description (name) | Designed for |
|---|---|---|---|
| TIFF, TIF | image | Tagged Image File Format | High resolution printing of images, even to postscript printers |
| PNG | image | Portable network graphic | High resolution bitmap image,Screen display, printing |
| BMP | image | bitmap image | Screen display under Windows |
| GIF | image | Graphic Interchange Format | Screen display especially online images/Web |
| JPEG, JPG | image | Joint Photographic Experts Group | Screen display especially online images/Web * |
| EPS, PS | vector | (Encapsulated) postscript | High resolution printing of illustrations, Printing to PostScript printers/Imagesetters |
| PDF | vector | Portable Document File | High resolution printing of illustrations, Printing to PostScript/PDF printers/Imagesetters |
| EMF, WMF ** | vector | (Enhanced) Windows Metafile | Screen display under Windows printing to non-PostScript printer |

For more information on image file format see `http://en.wikipedia.org/wiki/Image_file_formats`

** EMF files are a vector like files that can be inserted into PowerPoint. To insert an EMF image in a PowerPoint slide, click on Insert-Picture-From File and locate the file. Click OK. This will add the EMF file to your page. Right mouse click on the image to "ungroup", now you can select lines/points to change colors/widths etc.

When in doubt, I save files an postscript format (eps), as several journals request this format. EPS files can be open directly in adobe illustrator or other vector editing graphics packages.

In R, to save the current image to file. Either use the file menu File -> Save as. Or use the functions *dev2bitmap*, *dev.copy2eps* or *dev.copy(device, file)*, where device can be one of *png*, *jpeg* or *pdf* and file is your filename. For example:

```
plot(1:10, col = "red", pch = 19)
dev.copy(png, file = "test.png")
dev.off()
```

```
plot(1:10, col = "red", pch = 19)
dev.copy(pdf, file = "test.pdf")
dev.off()
```

To find out more about the image formats that can be saved in R, see the help on *?Devices*.

If you wish to write an image directly to a file, without "seeing" the plot screen (called X11 or Quartz depending on the operating system). Use the functions *pdf()*, *postscript()*, *jpeg()* with the syntax:

```
pdf(file = "myplot.pdf")
plot(1:10, col = "blue", xlab = "X axis", ylab = "Y axis")
dev.off()
```

Remember it is very important to type *dev.off* in order to properly save the file

To list the current graphics devices that are open use *dev.cur*. When you have finished with a device, be sure to terminate the device driver by issuing the command *dev.off()*.

If you have open a device to write to for example *pdf* or *png*, *dev.off* will ensures that the device finishes cleanly; for example in the case of hard-copy devices this ensures that every page is completed and has been sent to the printer or file.

**Example:**

```
myPath <- file.path("P:/Bio503/Plots")
pdf(file = paste(myPath, "nicePlot.pdf", sep = ""))
x <- seq(0, 2 * pi, length = 100)
y <- sin(3 * x) + cos(x) + rnorm(100, sd = 0.2)
plot(x, y)
dev.off()
```

## 6.7 Useful Graphics Resources

If you have plots saved in a non-vector format, we have found the web-site VectorMagic from Stanford `http://vectormagic.stanford.edu/` to be very useful. It will convert bmp or jpeg files to vector format.

The free software ImageMagick `http://www.imagemagick.org` can be downloaded and is also useful for converting between image format.

# Chapter 7

# Advanced Graphics

## 7.1 Advanced plotting using Trellis; ggplots2, Lattice

One of the strengths of R is the variety and quality of its graphics capabilities. Both Lattice and ggplots2 offer trellis (layered graphics) which are both prettier and much more flexible than basic R plotting. Between these two packages, there is no clear winner, but like Lattice other say ggplots2 is more flexible. But it is worth investigating these packages if you wish to generate nice R graphics.

### 7.1.1 ggplots2

qplot is the basic plotting function in the ggplot2 package and is a convenient wrapper for creating a number of different types of plots using a consistent calling scheme. See `http://had.co.nz/ggplot2/book/qplot.pdf` for the chapter in the ggplot2 book which describes the usage of qplot in detail.

A nice introductions to ggplots is written by its author Hadley Wickham and is available from `http://www.ceb-institute.org/bbs/wp-content/uploads/2011/09/handout_ggplot2.pdf`. The following examples are taking from that tutorial

Basic "Quick Plot" aka qplot in ggplots2

```
require("ggplot2")

## Loading required package: ggplot2

data(mtcars)
head(mtcars)

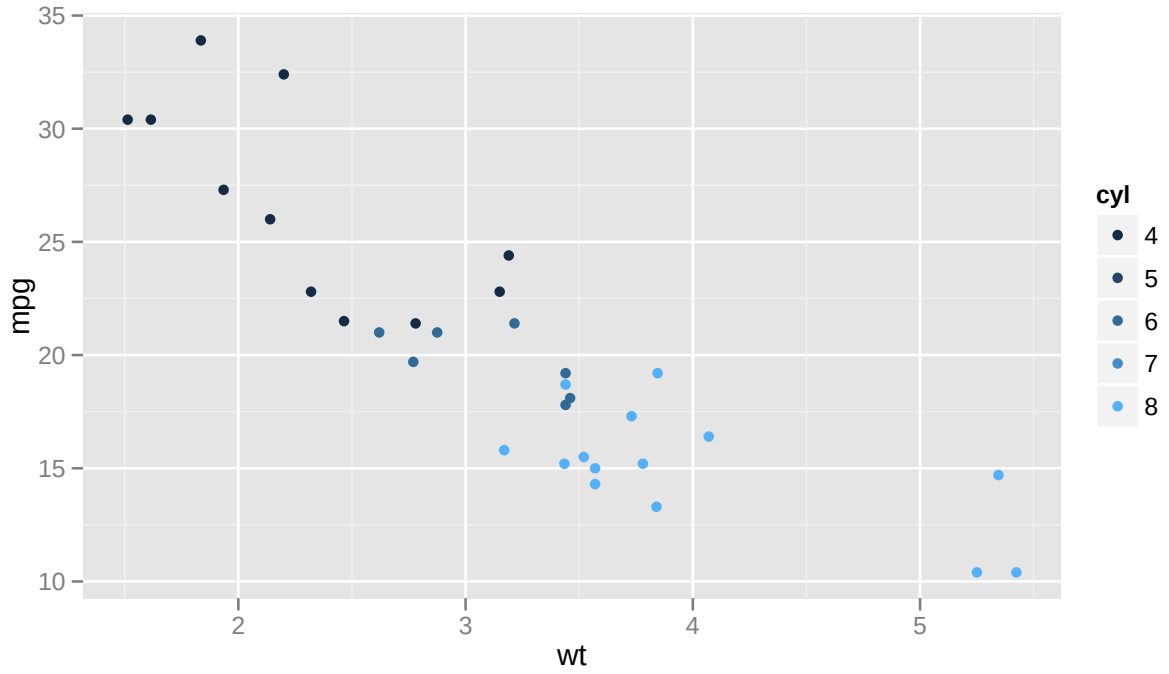
##                   mpg cyl disp  hp drat    wt  qsec vs am gear
## Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4
## Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4
## Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4
## Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3
## Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3
## Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3
##                   carb
```

```
## Mazda RX4             4
## Mazda RX4 Wag         4
## Datsun 710            1
## Hornet 4 Drive        1
## Hornet Sportabout     2
## Valiant               1
```

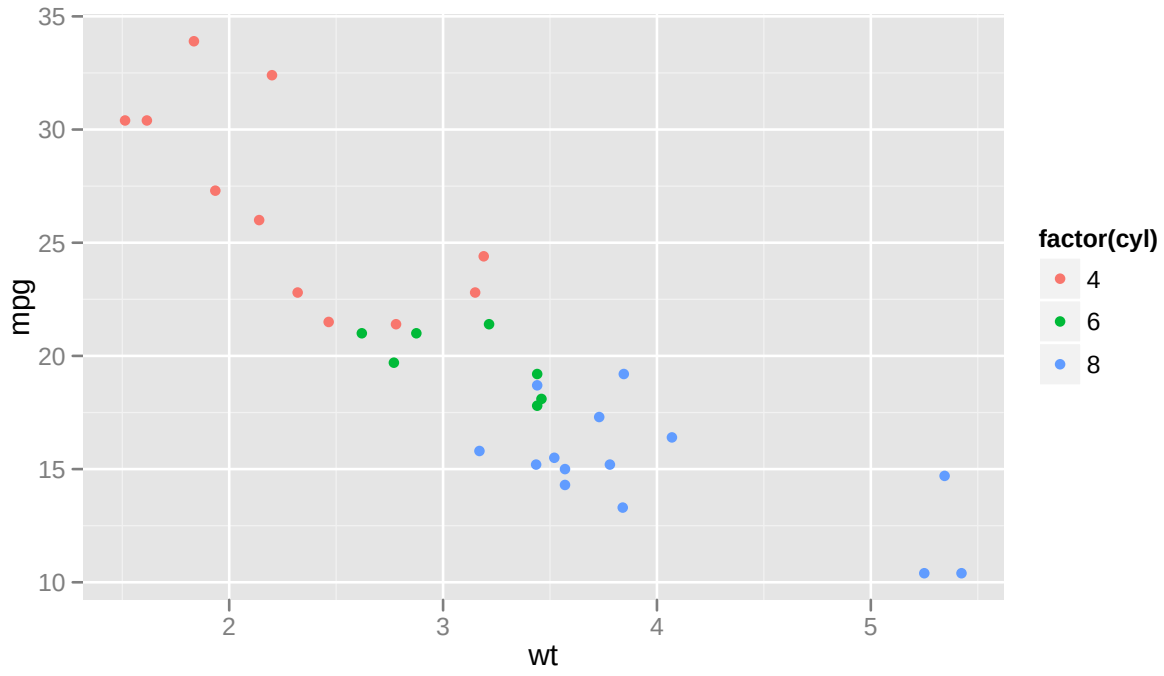
```
levels(mtcars$cyl)
```

```
## NULL
```

```
qplot(wt, mpg, data = mtcars, colour = cyl)
```



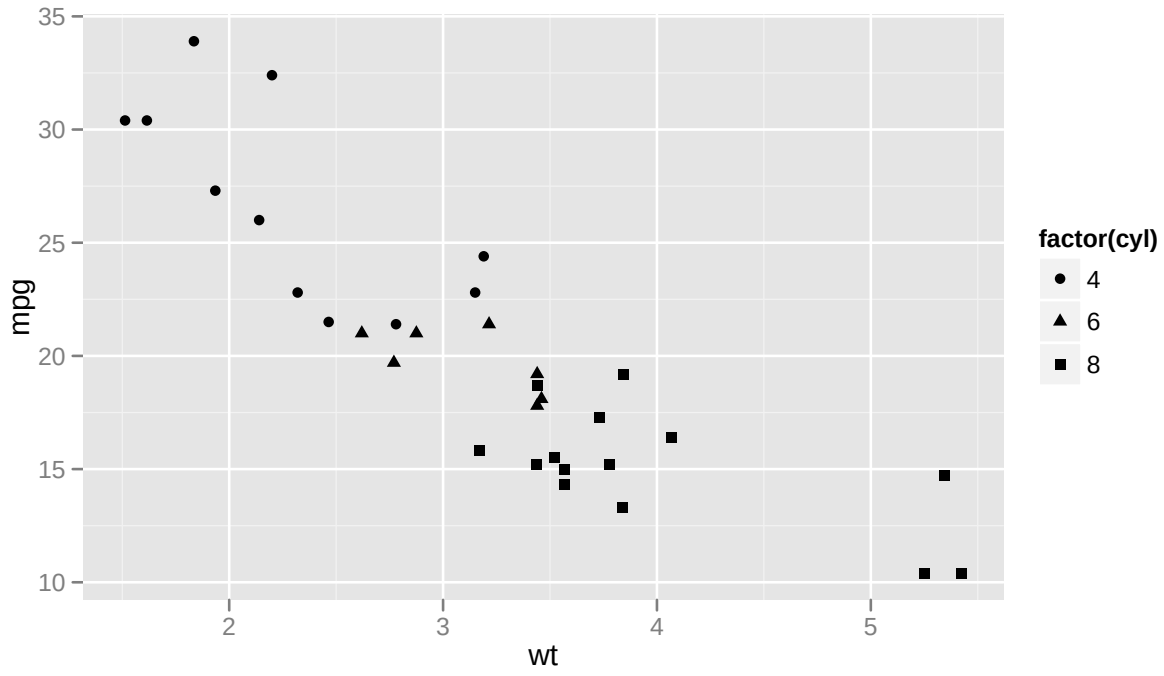

```
qplot(wt, mpg, data = mtcars, colour = factor(cyl))
```



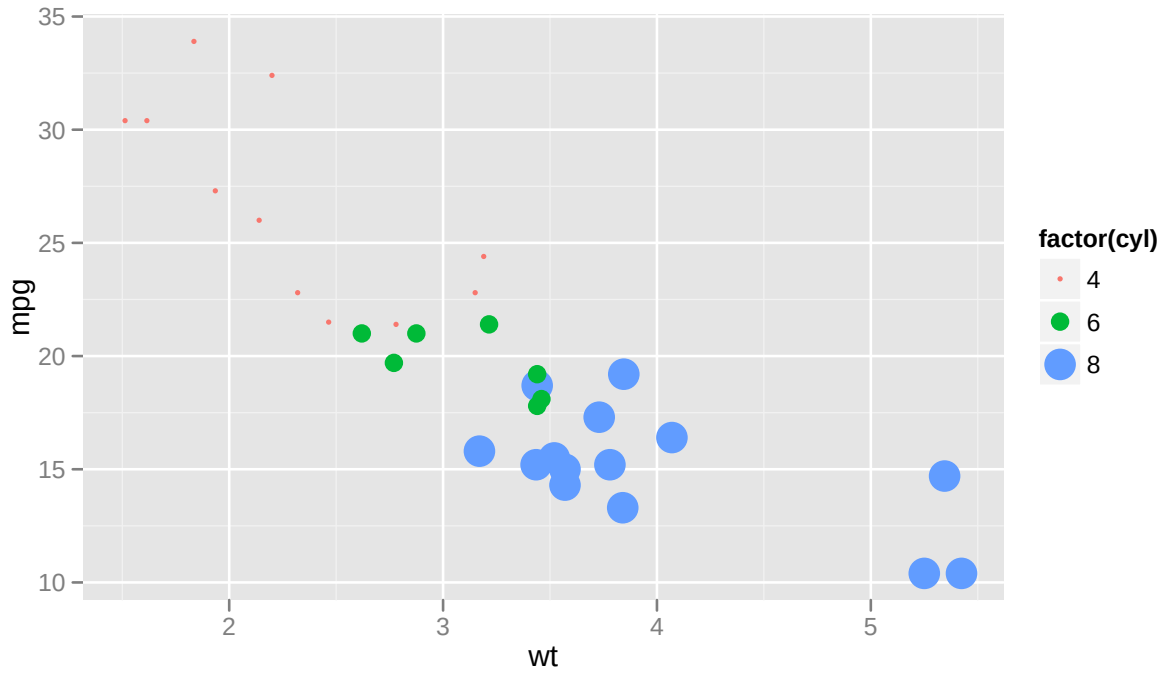

mtcars is a dataset from 1974 Motor Trend US magazine, and comprises fuel consumption and 10 aspects of automobile design and performance (eg miles/gallon, number of cylinders, displacement, gross horsepower, weight, seconds to complete a quarter mile, etc) for 32 automobiles. In the above plot we see a plot of weight x miles per gallon given the number of cylinders in the car.

In the above plot, we view cylinder by color, but it could also be by shape or size

```
qplot(wt, mpg, data = mtcars, shape = factor(cyl))
```




```
qplot(wt, mpg, data = mtcars, size = factor(cyl), colour = factor(cyl))
```

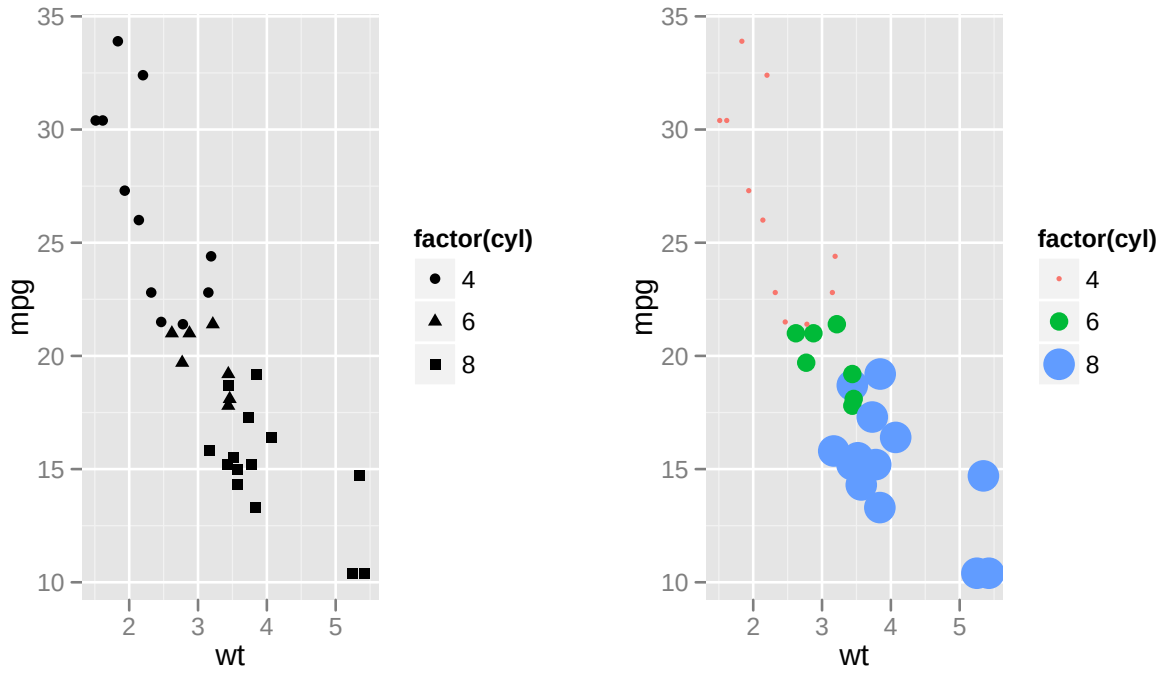



The function mfrow and layout don't work with ggplots2, so here is a little script to make layout of multiple plots using ggplots2 (acknowledgement to Stephen Turner). First assign each ggplot2 plots to an object, and then use the arrange function to display two or more.

```
arrange <- function(..., nrow = NULL, ncol = NULL, as.table = FALSE) {
    vp.layout <- function(x, y) viewport(layout.pos.row = x, layout.pos.col
    dots <- list(...)
    n <- length(dots)
    if (is.null(nrow) & is.null(ncol)) {
        nrow <- floor(n/2)
        ncol <- ceiling(n/nrow)
    }
    if (is.null(nrow)) {
        nrow <- ceiling(n/ncol)
    }
    if (is.null(ncol)) {
        ncol <- ceiling(n/nrow)
    }
    ## NOTE see n2mfrow in grDevices for possible alternative

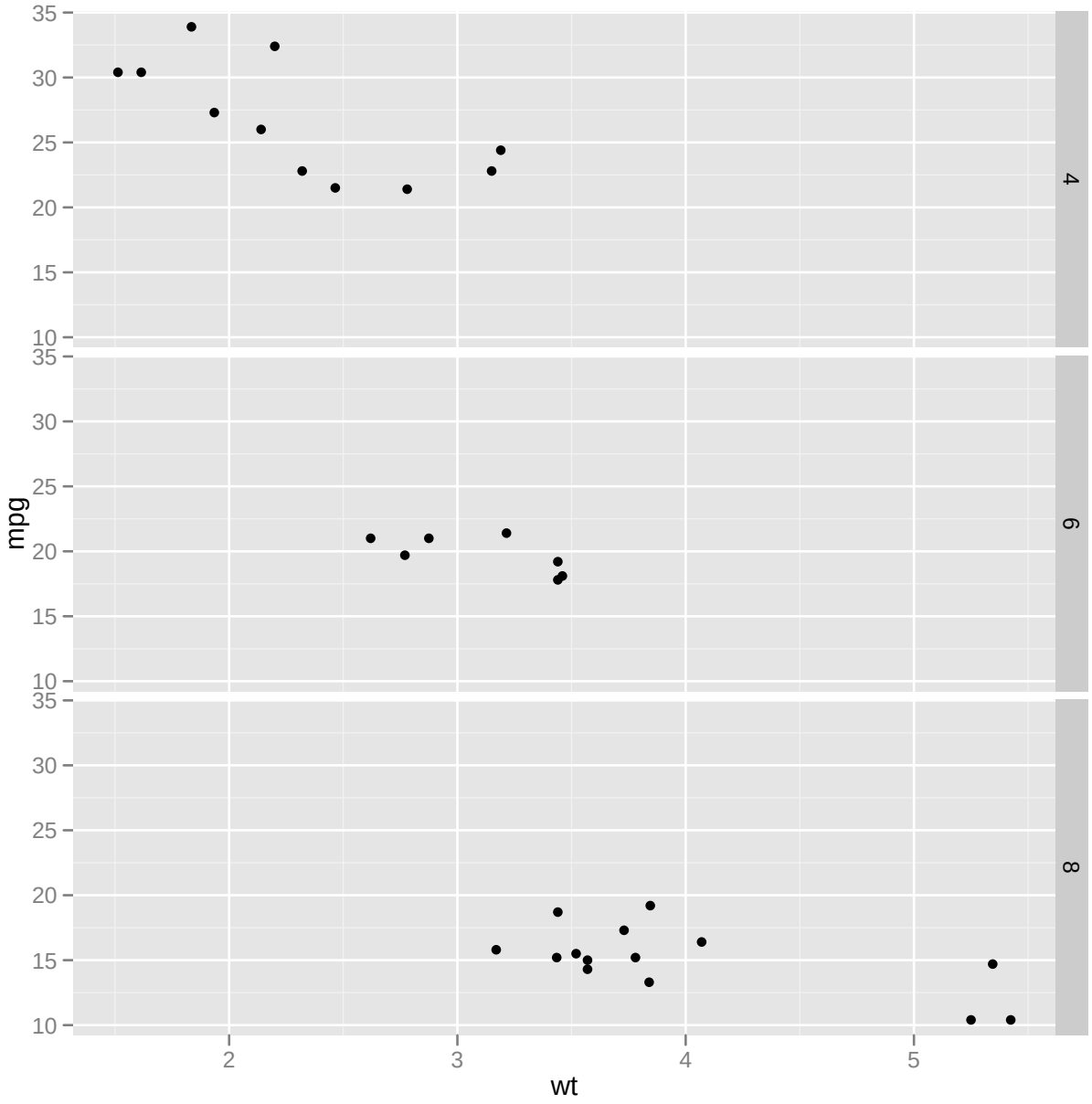
    grid.newpage()
    pushViewport(viewport(layout = grid.layout(nrow, ncol)))
    ii.p <- 1
    for (ii.row in seq(1, nrow)) {
        ii.table.row <- ii.row
        if (as.table) {
            ii.table.row <- nrow - ii.table.row + 1
        }
        for (ii.col in seq(1, ncol)) {
            ii.table <- ii.p
            if (ii.p > n)
                break
            print(dots[[ii.table]], vp = vp.layout(ii.table.row, ii.col))
            ii.p <- ii.p + 1
        }
    }
}
```

```
p1 <- qplot(wt, mpg, data = mtcars, shape = factor(cyl))
p2 <- qplot(wt, mpg, data = mtcars, size = factor(cyl), colour = factor(cyl
# Arrange and display the plots into a 2x1 grid
arrange(p1, p2, nrow = 1)
```




Using Facets to plot several plots

```
qplot(wt, mpg, data = mtcars, facets = cyl ~ .)
```



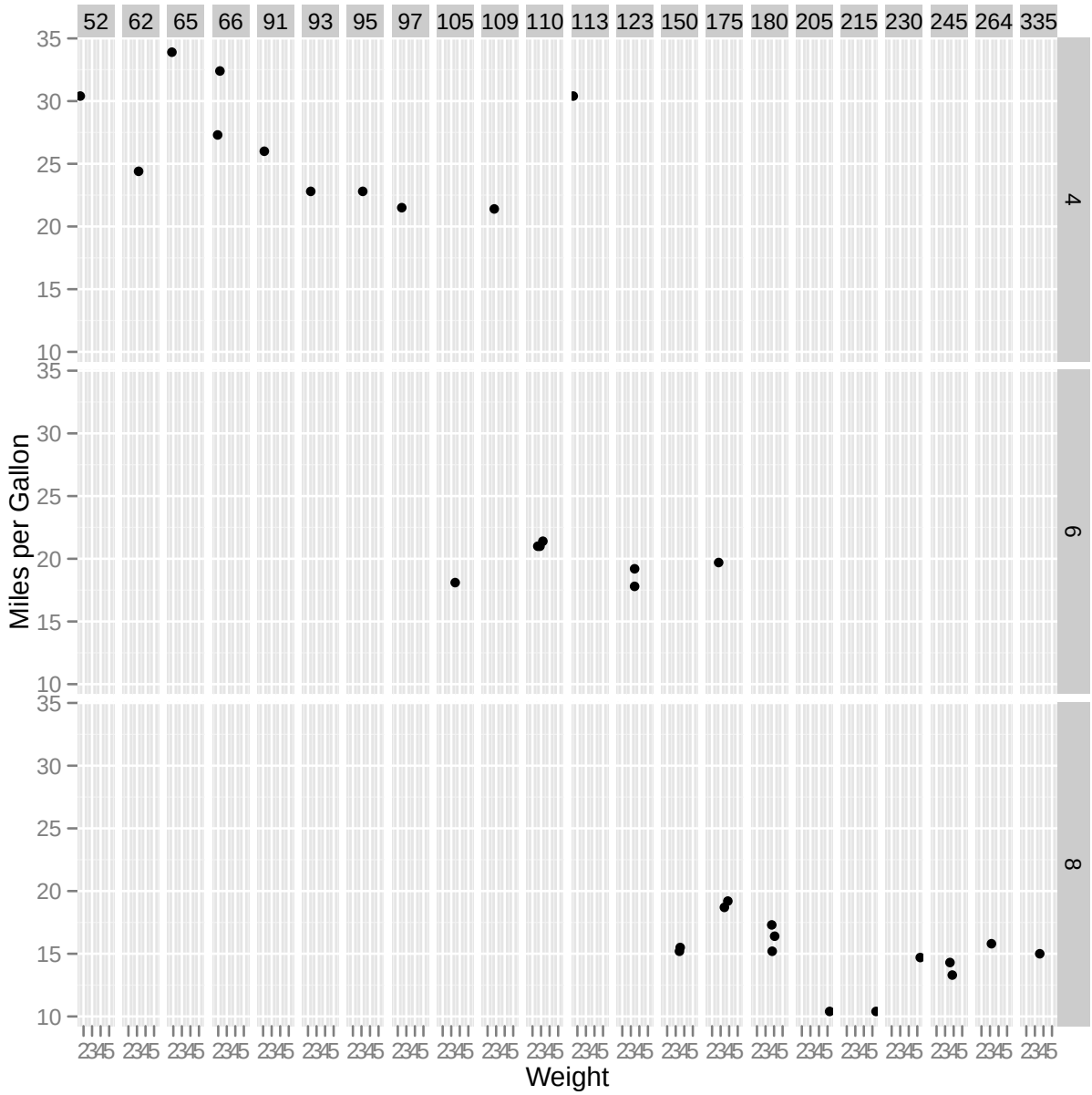

More complex Facets to view cross-tabulated categories. For example you would expect a strong interaction between cylinder and horsepower.

```
table(mtcars$cyl, mtcars$hp)
```

```
##
##      52 62 65 66 91 93 95 97 105 109 110 113 123 150 175 180 205 215
##   4   1  1  1  2  1  1  1  1   0   1   0   1   0   0   0   0   0   0
##   6   0  0  0  0  0  0  0  0   1   0   3   0   2   0   1   0   0   0
##   8   0  0  0  0  0  0  0  0   0   0   0   0   0   2   2   3   1   1
##
##      230 245 264 335
```

```
##    4    0    0    0    0
##    6    0    0    0    0
##    8    1    2    1    1

qplot(wt, mpg, data = mtcars, facets = cyl ~ hp, xlab = "Weight",
    ylab = "Miles per Gallon")
```




In the scatterplot examples above, we implicitly used a *point geom*, the default when you supply two arguments to qplot(). qplots can produce several other plots, if a different geom is defined

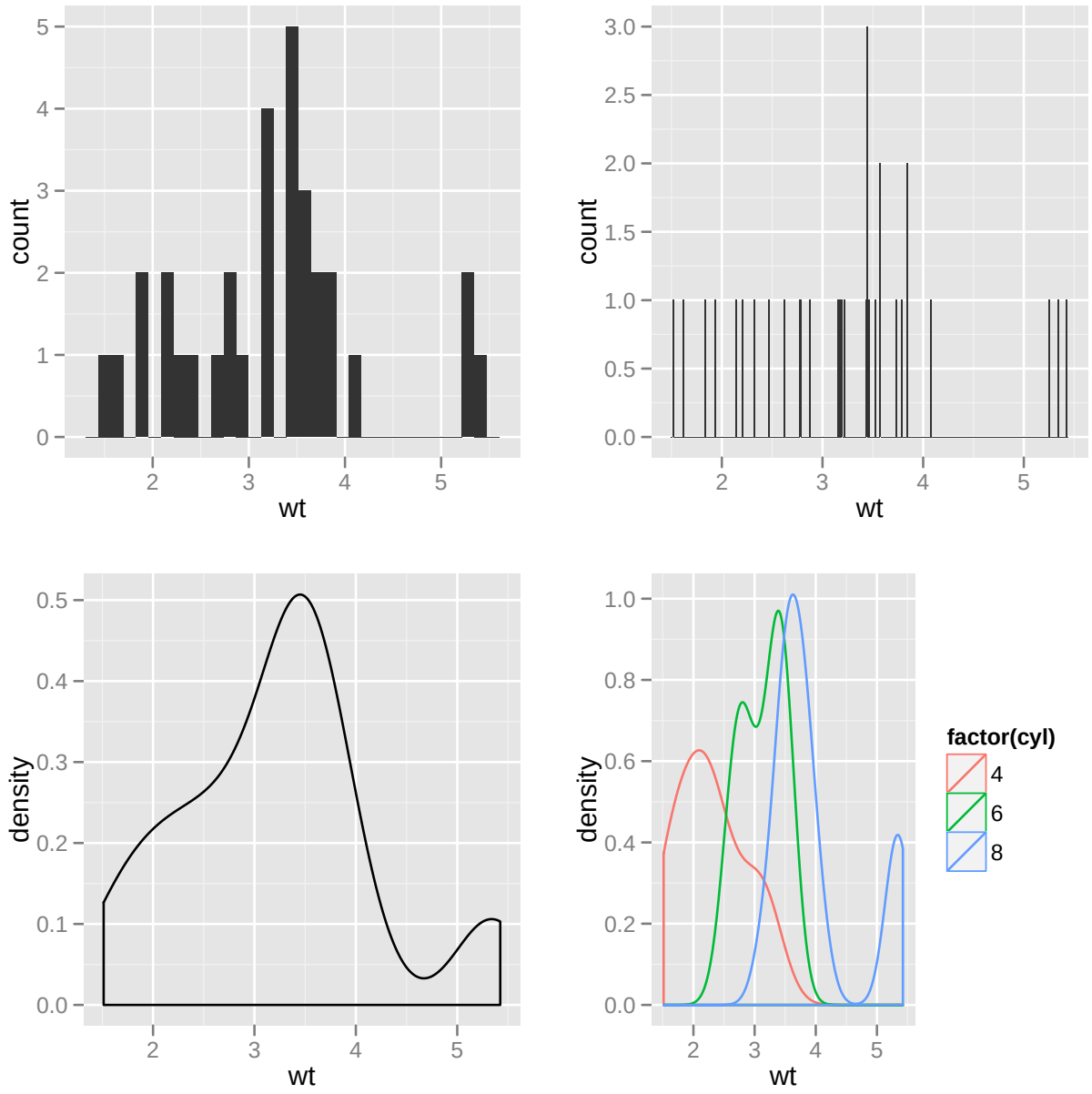
(modified from ggplots2: Elegant Graphics for Data Analysis, Chapter 3)

When given a single vector, the default geom is Histogram. Defining geom as density will instead draw a density (smoothed histogram)

| | Plot | Geom | Other features |
|---|---|---|---|
| scatterplot | point | | |
| bubblechart | point | size defined by variable | |
| barchart | bar | | |
| box-whisper | boxplot | | |
| line | line | | |

```
p1 <- qplot(wt, data = mtcars)
p2 <- qplot(wt, data = mtcars, binwidth = 0.01)
p3 <- qplot(wt, data = mtcars, geom = "density")
p4 <- qplot(wt, data = mtcars, geom = "density", colour = factor(cyl))
# Arrange and display the plots into a 2x1 grid
arrange(p1, p2, p3, p4, nrow = 2, ncol = 2)

## stat_bin: binwidth defaulted to range/30. Use 'binwidth = x' to
## adjust this.
```

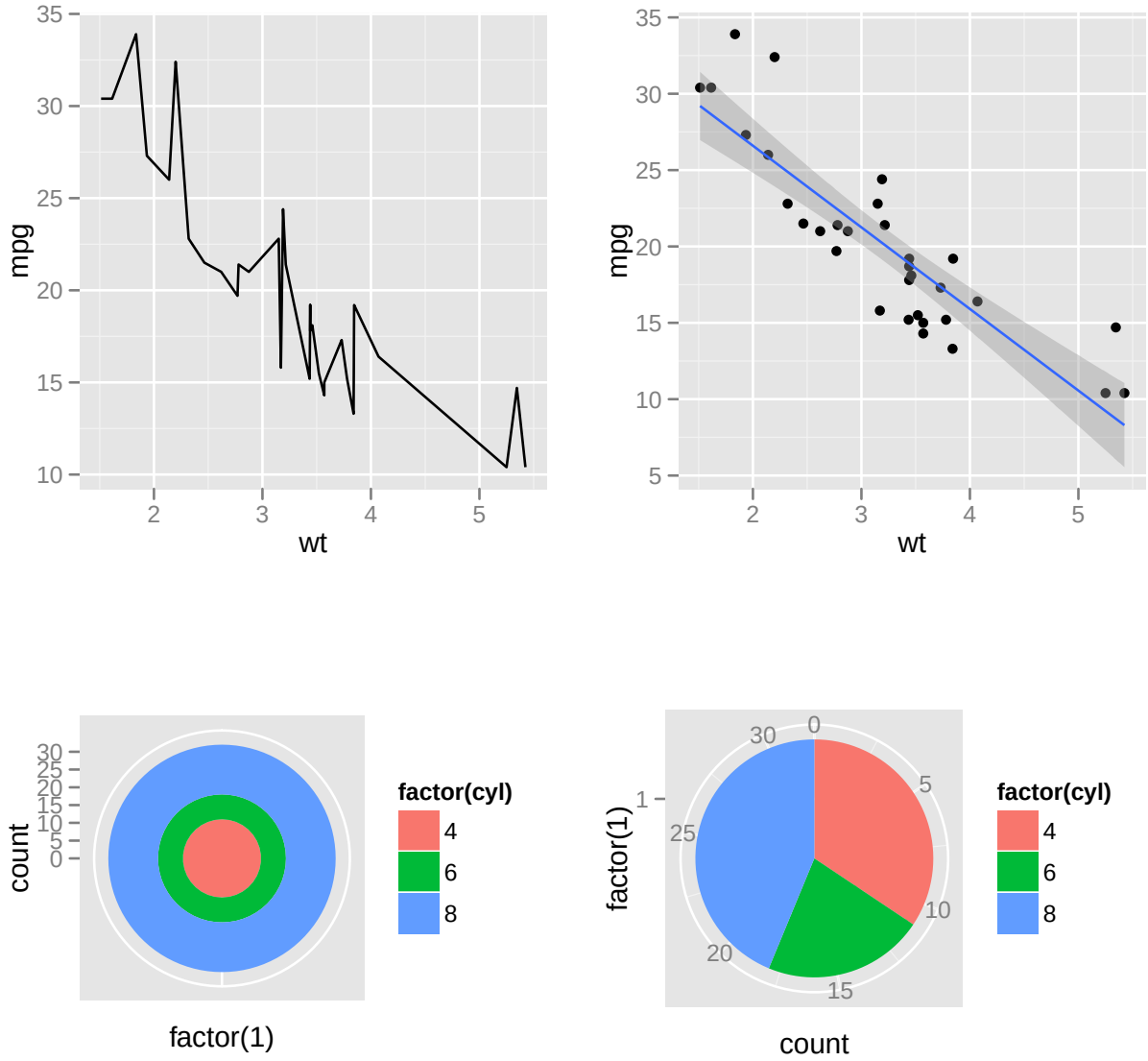



Geoms - point and smooth and $\texttt{coord}_{p}olar(PieCharts)$

```
p1 <- qplot(wt, mpg, data = mtcars, geom = "line")
p2 <- qplot(wt, mpg, data = mtcars, geom = c("point", "smooth"),
    method = "lm")

px <- ggplot(mtcars, aes(x = factor(1), fill = factor(cyl))) +
    geom_bar(width = 1)
# map a barchart to a polar coordinate system
p3 <- px + coord_polar()
p4 <- px + coord_polar(theta = "y")
```

```
arrange(p1, p2, p3, p4, nrow = 2, ncol = 2)
```




### 7.1.2 lattice

Lattice plots allow the use of the layout on the page to reflect meaningful aspects of data structure. They offer abilities similar to those in the S-PLUS trellis library.

The lattice package sits on top of the grid package. To use lattice graphics, both these packages must be installed. Providing it is installed, the grid package will be loaded automatically when lattice is loaded.

Resources for lattice

- Book on Lattice `http://lmdvr.r-forge.r-project.org/figures/figures.html`
- See examples at `http://cm.bell-labs.com/cm/ms/departments/sia/project/trellis/display.examples.html`
- To get on help on lattice functions, use help just like you would do for any package *help(package = lattice)*

### 7.1.3 Examples that Present Panels of Scatterplots using xyplot()

The basic function for drawing panels of scatterplots is `xyplot()`. We will use the data frame 'ChickWeight' to demonstrate the use of `xyplot()`. The 'ChickWeight' data frame has 578 rows and 4 columns from an experiment on the effect of diet on early growth of chicks. This data frame contains the following columns:

**weight** a numeric vector giving the body weight of the chick (gm).

**Time** a numeric vector giving the number of days since birth when the measurement was made.

**Chick** an ordered factor with levels '18' ¡ ... ¡ '48' giving a unique identifier for the chick. The ordering of the levels groups chicks on the same diet together and orders them according to their final weight (lightest to heaviest) within diet.

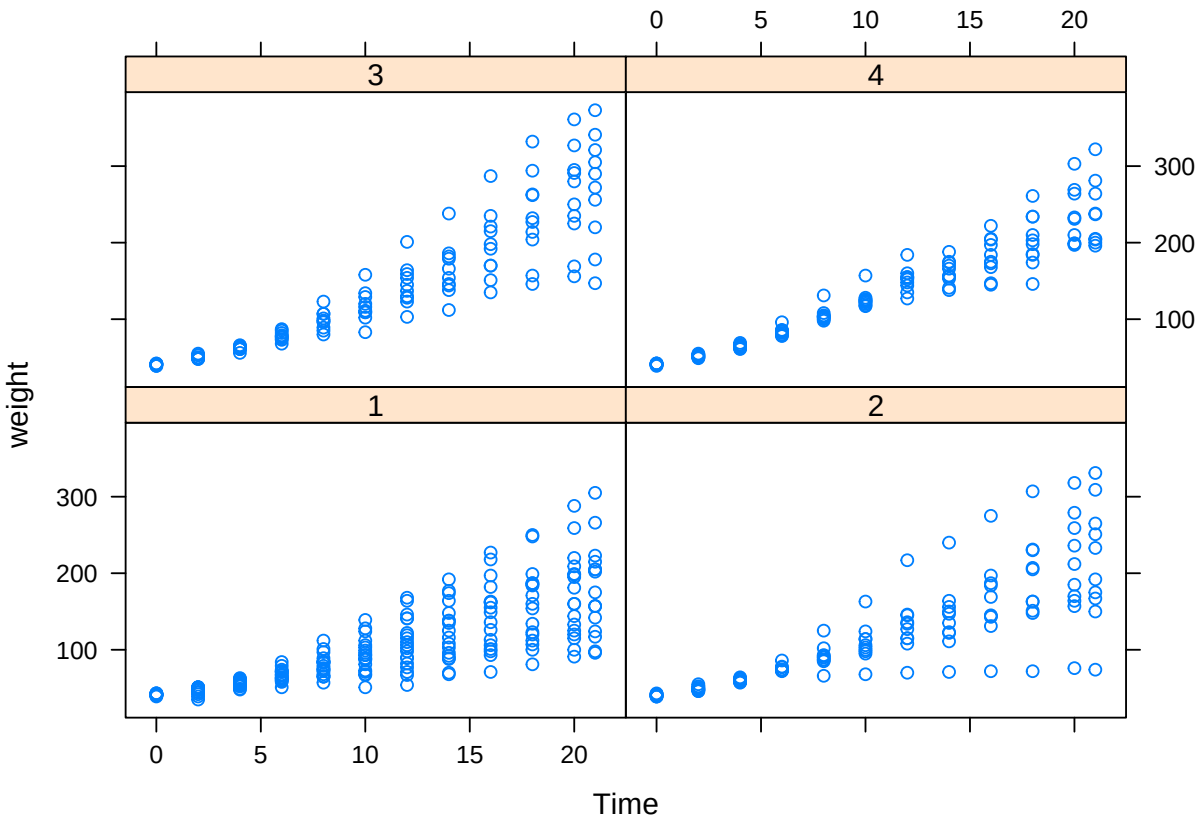
**Diet** a factor with levels 1,...,4 indicating which experimental diet the chick received.

Figure below shows the style of graph that one can get from *xyplot()*.

### 7.1.4 Simple use of xyplot

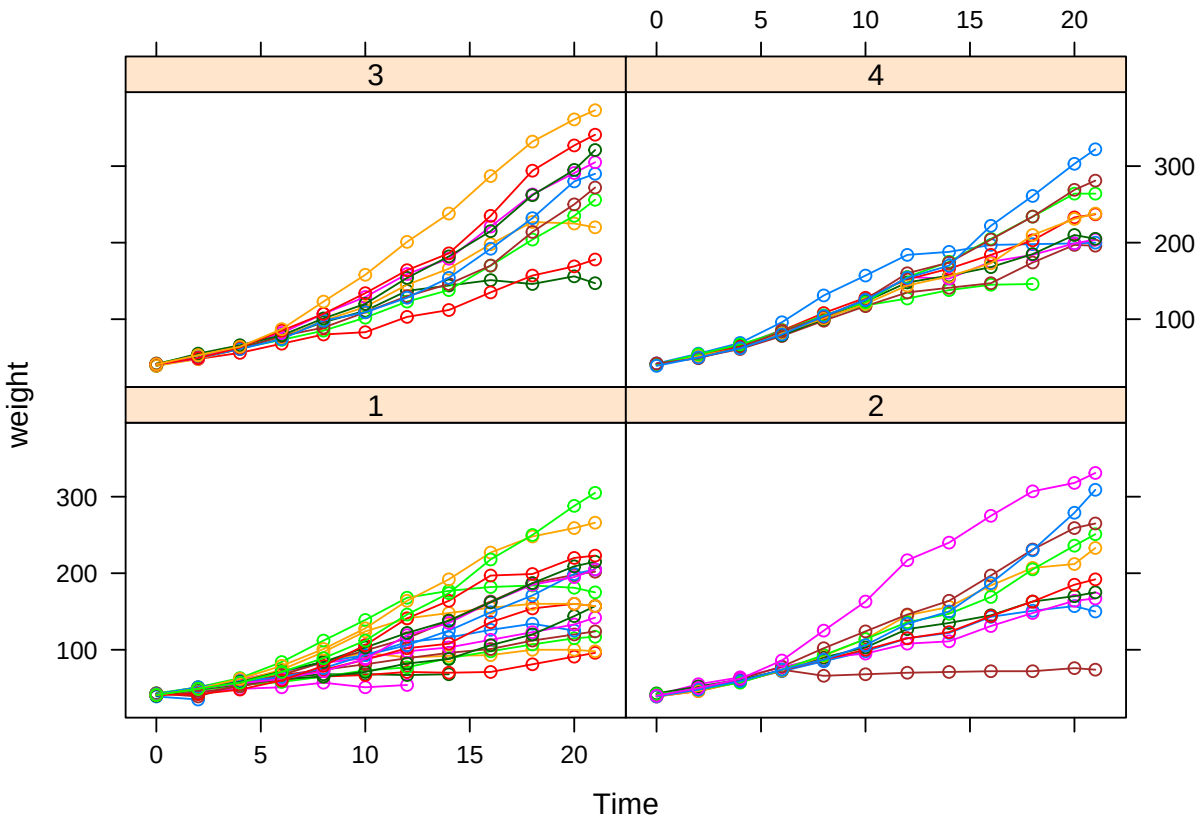
The lattice function *xyplot()* is the most commonly used lattice function, and plots pairs of variables. Whilst designed mainly for two continuous variates, factors can be supplied as well, in which case they will simply be coerced to numeric.

```
library(lattice)
xyplot(weight ~ Time | Diet, data = ChickWeight)  # Simple use of xyplot
```




Here is the statement used to get a figure with the observations for the same Chick connected via lines.

```
xyplot(weight ~ Time | Diet, data = ChickWeight, panel = panel.superpose,
    groups = Chick, type = "b")
```




This function shows the defaults for the graphical display of Trellis displays

```
show.settings()
```

An incomplete list of lattice Functions

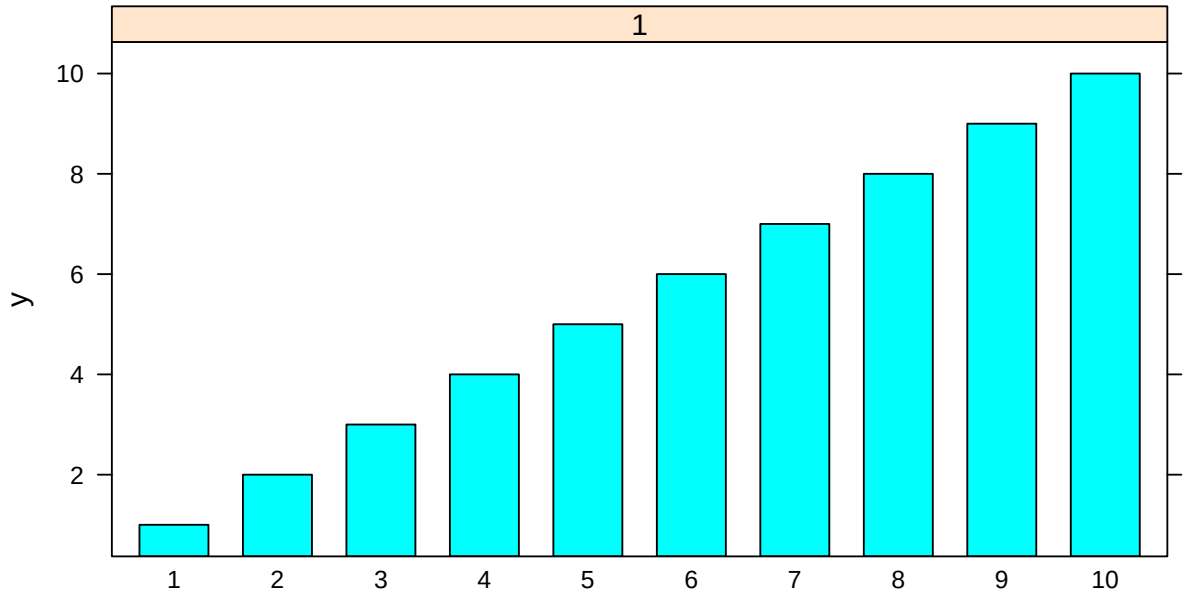
```
splom( ~ data.frame)       # Scatterplot matrix
bwplot(factor ~ numeric , . .) # Box and whisker plot
dotplot(factor ~ numeric , . .) # 1-dim. Display
stripplot(factor ~ numeric , . .) # 1-dim. Display
barchart(character ~ numeric,...)
histogram( ~ numeric, ...)      # Histogram
densityplot( ~ numeric, ...)    # Smoothed version of histogram
qqmath(numeric ~ numeric, ...) # QQ plot
splom( ~ dataframe, ...)        # Scatterplot matrix
parallelplot( ~ dataframe, ...)    # Parallel coordinate plots
```

In each instance, conditioning variables can be added.

**Examples:**

```
x <- 1:10
y <- 1:10
g <- factor(1:10)
```

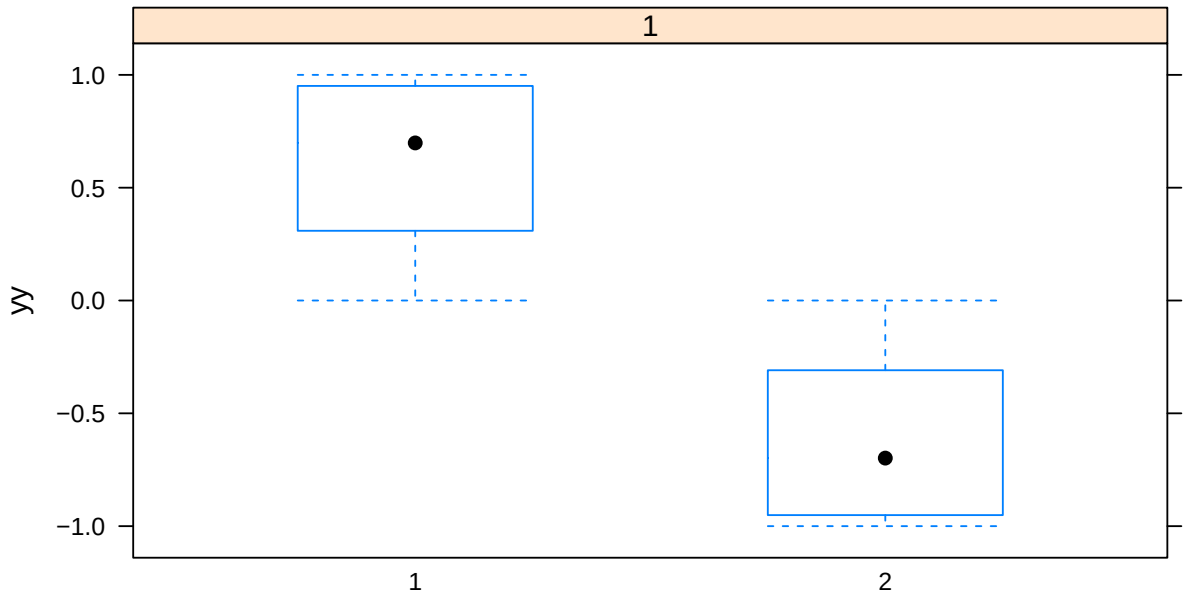
```
barchart(y ~ g | 1)
```



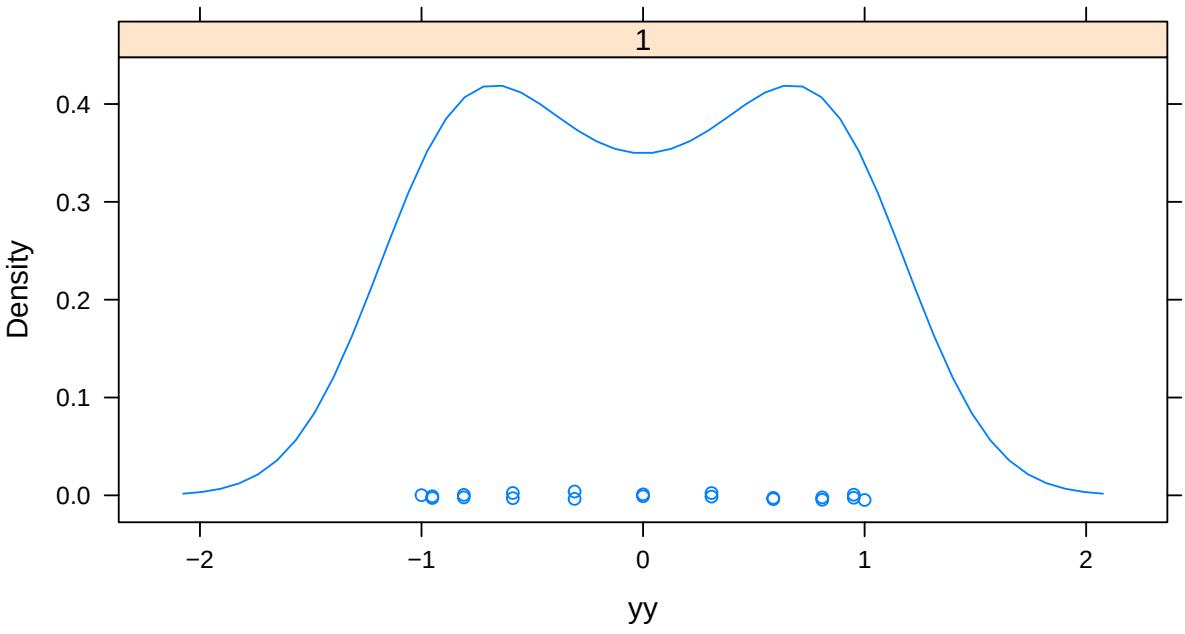

More examples:Lattice density histogram splom and more

```
angle <- seq(0, 2 * pi, length = 21)[-21]
xx <- cos(angle)
yy <- sin(angle)
gg <- factor(rep(1:2, each = 10))

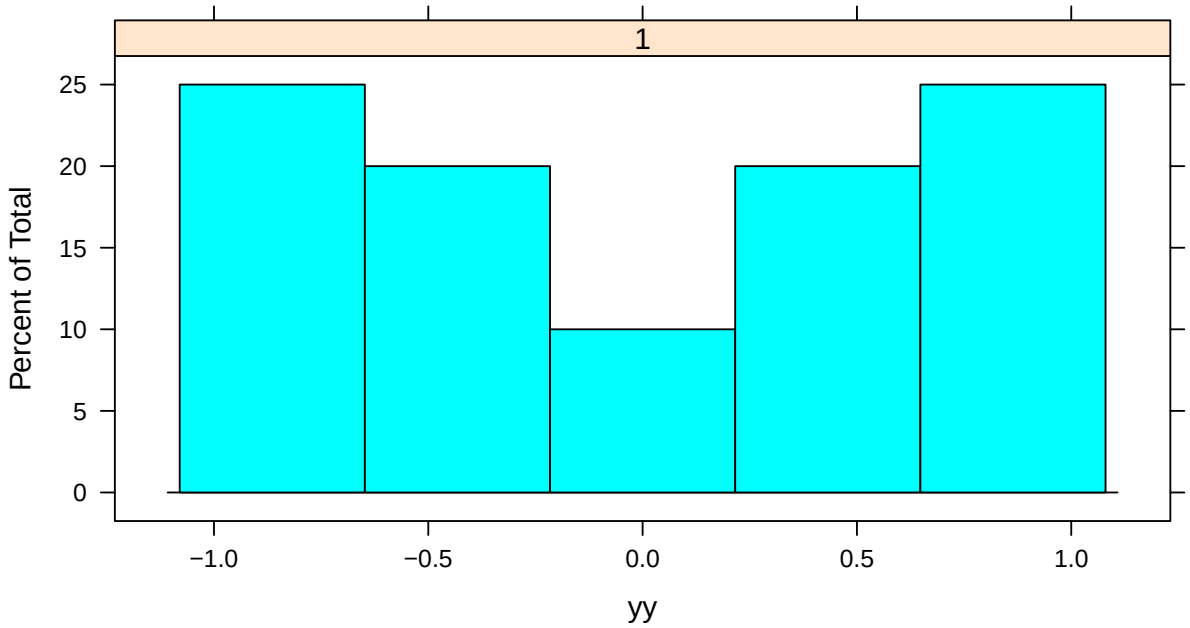
bwplot(yy ~ gg | 1)
```



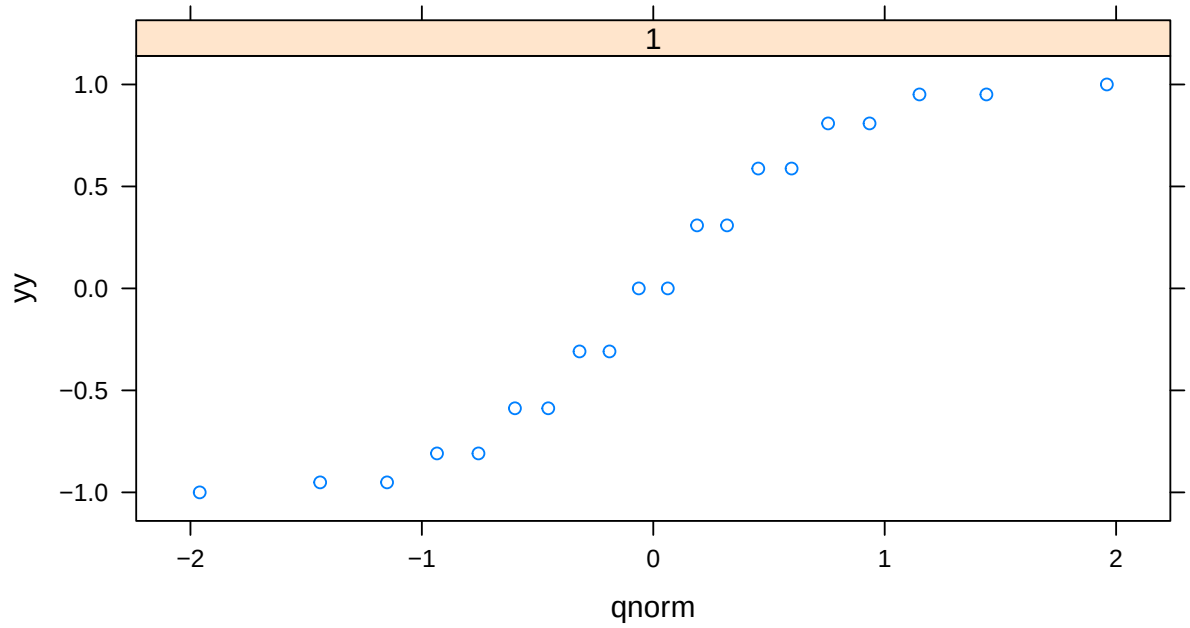

```
densityplot(~yy | 1)
```



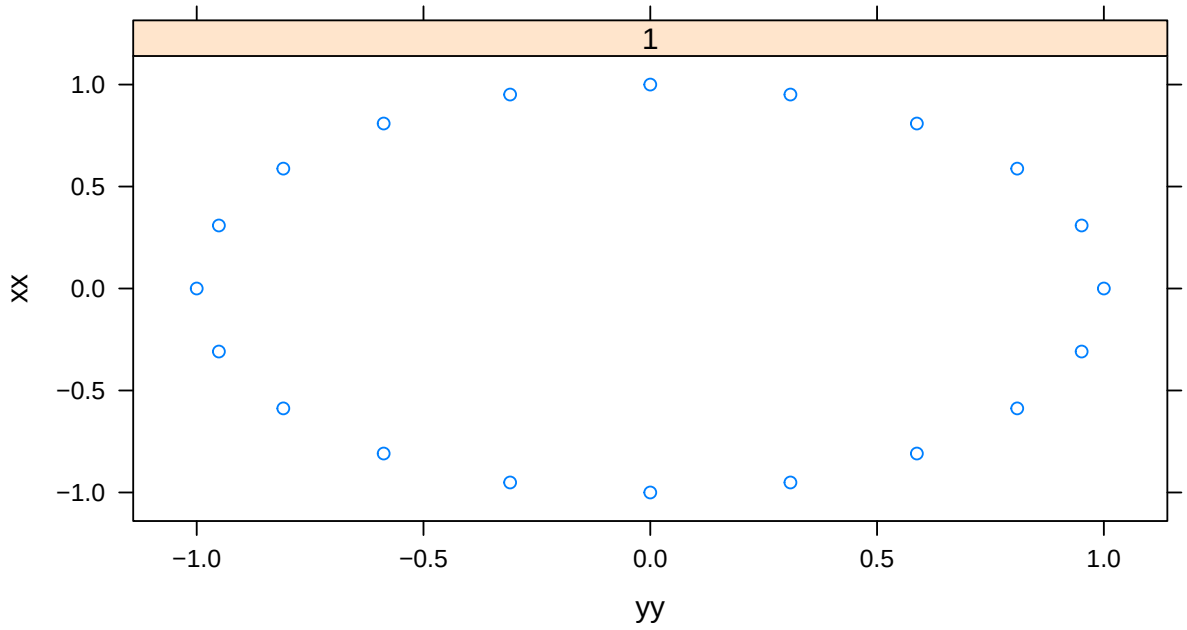
```
histogram(~yy | 1)
```



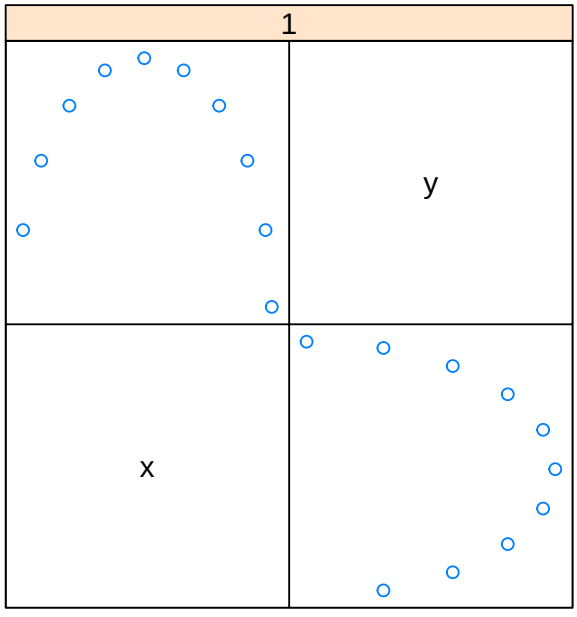

```
qqmath(~yy | 1)
```



```
xyplot(xx ~ yy | 1)
```

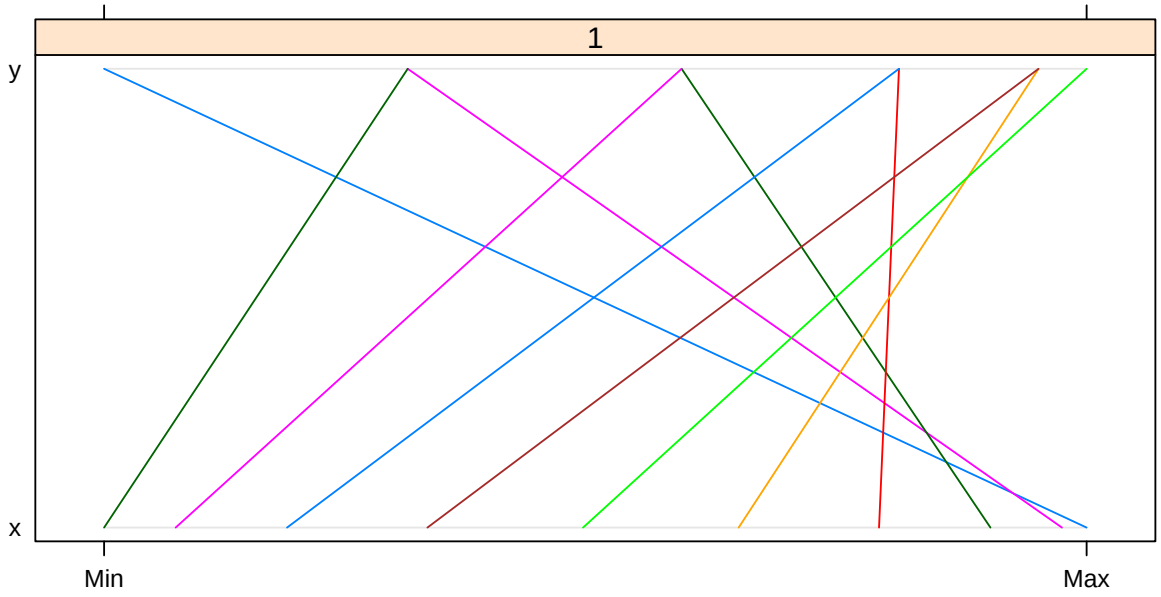



```
splom(~data.frame(x = xx[1:10], y = yy[1:10]) | 1, pscales = 0)
```




Scatter Plot Matrix

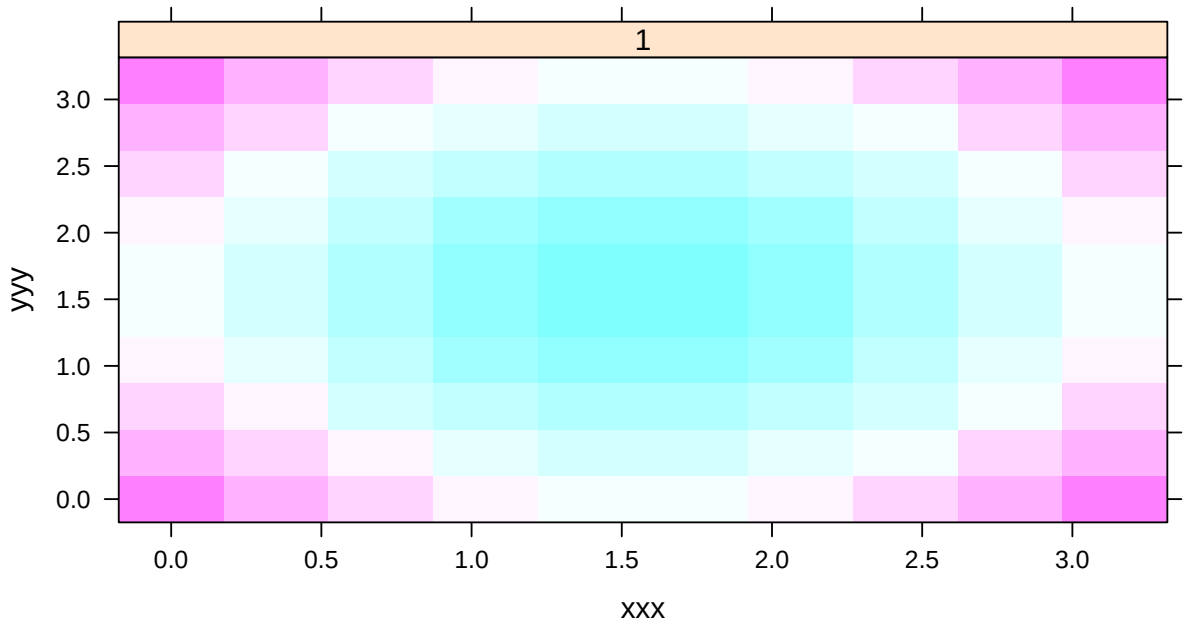
```
parallelplot(~data.frame(x = xx[1:10], y = yy[1:10]) | 1)
```



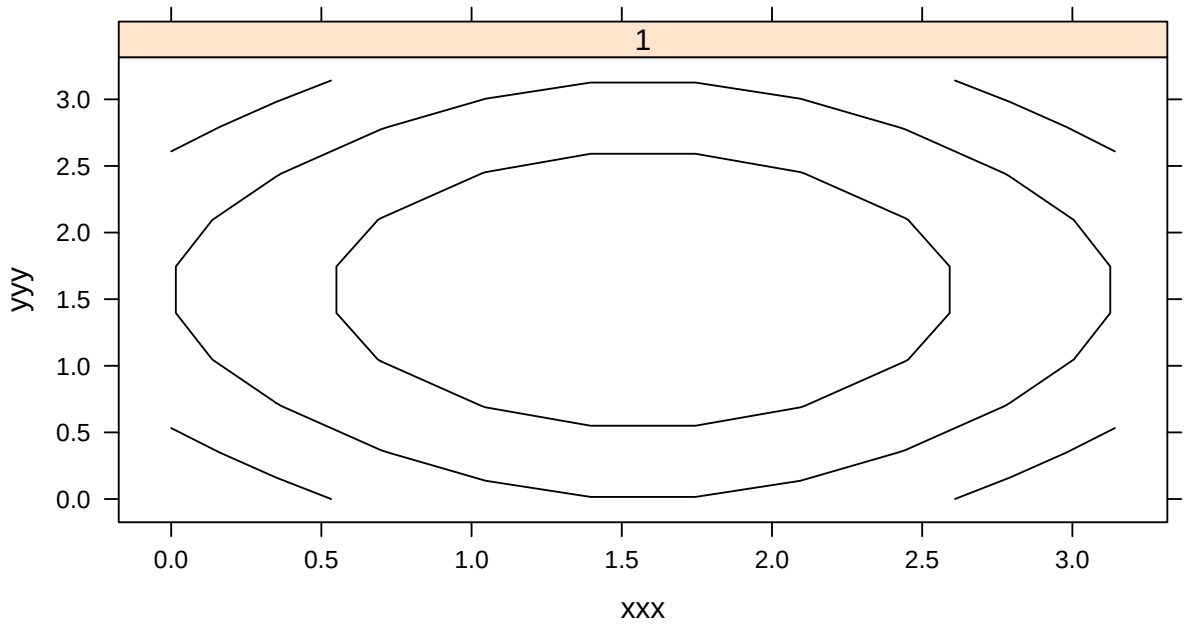

More than two variables

```
aaa <- seq(0, pi, length = 10)
xxx <- rep(aaa, 10)
yyy <- rep(aaa, each = 10)
zzz <- sin(xxx) + sin(yyy)

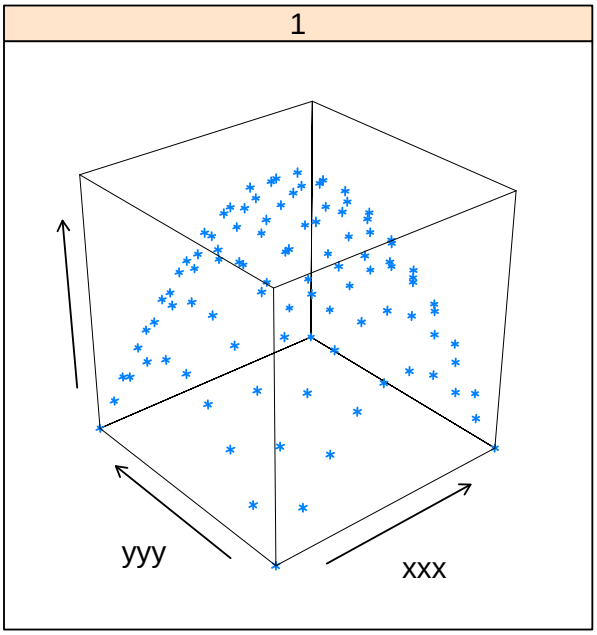
levelplot(zzz ~ xxx + yyy | 1, colorkey = FALSE)
```



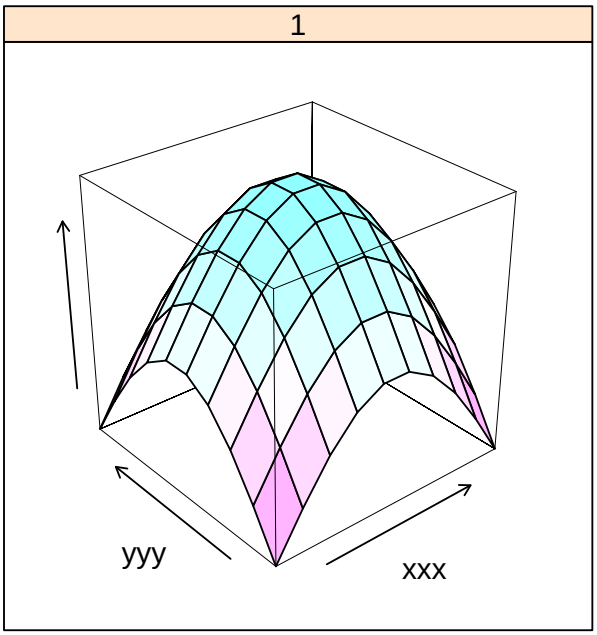

```
contourplot(zzz ~ xxx + yyy | 1, labels = FALSE, cuts = 8)
```



```
cloud(zzz ~ xxx + yyy | 1, zlab = NULL, zoom = 0.9, par.settings = list(box
```




```
wireframe(zzz ~ xxx + yyy | 1, zlab = NULL, zoom = 0.9, drape = TRUE,
    par.settings = list(box.3d = list(lwd = 0.01)), colorkey = FALSE)
```



Note whilst, lattice plots are highly customizable. **Note:** the base graphics settings; in particular, *par()* settings usually have no effect on lattice plots. Use *trellis.par.get()* and *trellis.par.set()* to change default plot parameters.

## 7.2 GoogleVis and GoogleMaps visualization

There are multiple visualization tools available within the googleVis library. These include the Hans Rosling type bubble plots. See `http://code.google.com/apis/visualization/documentation/gallery/motionchart.html`

See `http://blog.revolutionanalytics.com/graphics/` for some examples of R code

```
# install.packages('googleVis')
library(googleVis)

## Loading required package: RJSONIO

## Welcome to googleVis version 0.2.16
##
## Please read the Google API Terms of Use before you use the package:
## http://code.google.com/apis/terms/index.html
##
## Type ?googleVis to access the overall documentation and
## vignette('googleVis') for the package vignette. You can execute a
## demo of the package via: demo(googleVis)
##
## More information is available on the googleVis project web-site:
## http://code.google.com/p/google-motion-charts-with-r/
##
## Contact: <rvisualisation@gmail.com>
##
## To suppress the this message use:
## suppressPackageStartupMessages(library(googleVis))

M <- gvisMotionChart(Fruits, "Fruit", "Year")
plot(M)
cat(M$html$chart, file = "tmp.html")
```

GoogleVis also provide support for Maps and spatial visualization of trends.

```
# Pretty plots competition
library(googleVis)
help(package = "googleVis")

# looking at all loaded datasets
data(state)
states <- as.data.frame(state.x77)
states$location <- rownames(states)
attach(states)

## The following object(s) are masked from 'package:googleVis':
```

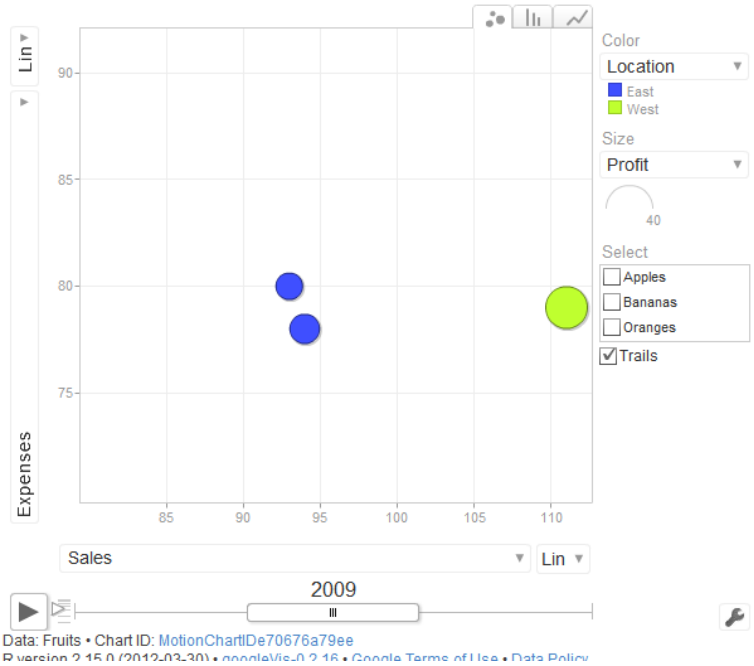



Figure 7.1: Results of Fruits data using GoogleViz gvisMotionChart
This is actually an interactive animated html file

```
##
##     Population

states.Inc <- gvisGeoMap(states, locationvar = "location",
    numvar = "Income", options = list(region = "US", dataMode = "regions",
        colors = "[0xBEBEBE, 0x00008B]"))
# note this is per capita income by state from 1974

plot(states.Inc)

states.Illit <- gvisGeoMap(states, locationvar = "location",
    numvar = "Illiteracy", options = list(region = "US", dataMode = "regions
        colors = "[0xBEBEBE, 0x8B0000]"))
plot(states.Illit)

merge <- gvisMerge(states.Inc, states.Illit, horizontal = FALSE)
merge.plot <- plot(merge)
detach(states)
```

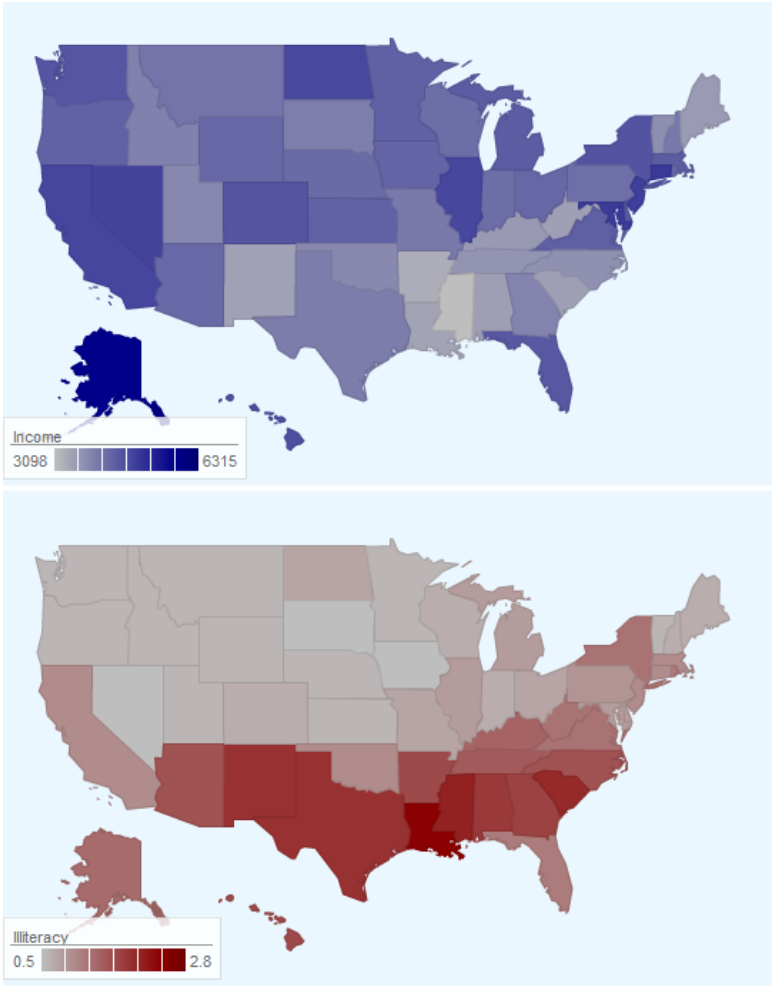



Figure 7.2: This is actually an interactive html file, if you hover over a state you see its information

### 7.2.1 Geocodes and maps

The package RgoogleMaps which provide a comfortable R interface to query the Google server for static maps, and to also use the map as a background image to overlay plots within R. Another packages is osmar (OpenStreetMap and R) which package provides infrastructure to access OpenStreetMap data.

The package ggmap is written by Hadley Wickham, who also authors the ggplots packages. Therefore it has particularly nice graph capabilities. It has functions to extracts maps and provides an interface to query geocode (location data) from Google Maps, OpenStreetMap, or Stamen Maps server.

```
require(ggmap)
# longtitude, latitude from google maps api
HSPH <- geocode("Harvard School of Public Health")
mapdist("Harvard School of Public Health", "New York", mode = "walking")
```

The *qmap* has a layered appear to maps similar to qplot in ggplot2. It allows you to extract a map from google Maps or the other map distribution, and layer on data. A in-depth review of the functions in ggmap is beyond the scope of this course, but I am happy to demo these should there be sufficient interest.

There are online demonstrations on my website

`http://bcb.dfci.harvard.edu/~aedin/courses/R/CDC/maps.html`

and of worldwide species diversity `http://vijaybarve.wordpress.com/tag/rgbif/`

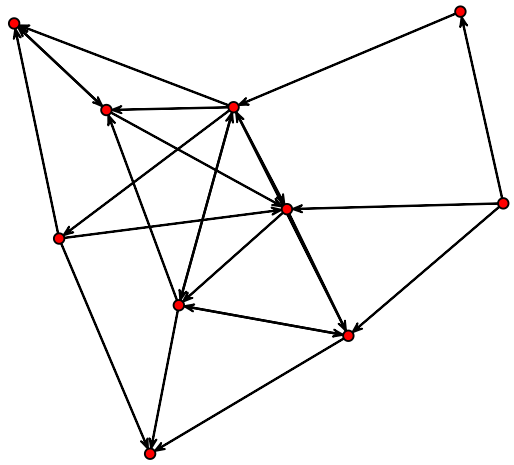
and Napa valley vineyard `http://blog.revolutionanalytics.com/2012/07/making-beaut`
`html`

## 7.3 Graph theory and Network visualization using R packages network and igraph

```
# install.packages(network)
library(network)

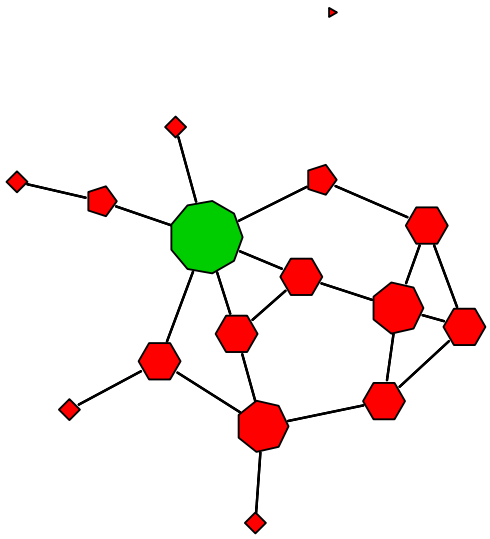
## network: Classes for Relational Data Version 1.7-1 created on March
## 1, 2012. copyright (c) 2005, Carter T. Butts, University of
## California-Irvine Mark S. Handcock, University of Washington David
## R. Hunter, Penn State University Martina Morris, University of
## Washington For citation information, type citation("network").
## Type help("network-package") to get started.

m <- matrix(rbinom(100, 1, 1.5/9), 10)
diag(m) <- 0
g <- network(m)
# Plot the graph
plot(g)
```



```
# Load Padgett's marriage data
data(flo)
nflo <- network(flo)
# Display the network, indicating degree and flagging the Medicis
plot(nflo, vertex.cex = apply(flo, 2, sum) + 1, usearrows = FALSE,
```

```
    vertex.sides = 3 + apply(flo, 2, sum), vertex.col = 2 + (network.vertex
        "Medici"))
```



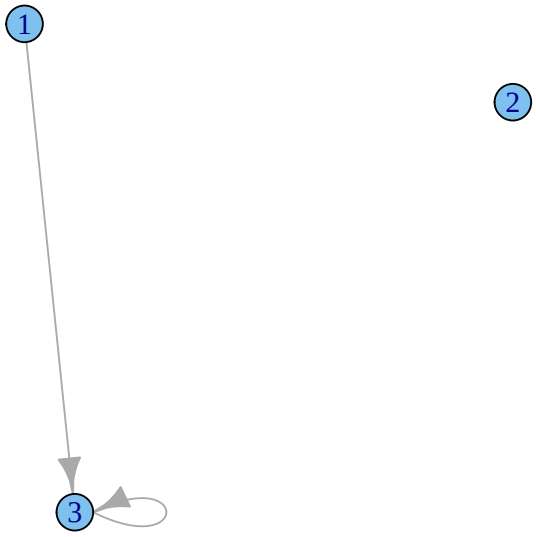
using the package igraph

```
# install.packages('igraph')
library(igraph)

## Attaching package: 'igraph'

## The following object(s) are masked from 'package:network':
##
## %c%, %s%, add.edges, add.vertices, delete.edges, delete.vertices,
## get.edge.attribute, get.edges, get.vertex.attribute, is.bipartite,
## is.directed, list.edge.attributes, list.vertex.attributes,
## set.edge.attribute, set.vertex.attribute

adj.mat <- matrix(sample(c(0, 1), 9, replace = TRUE), nr = 3)
g <- graph.adjacency(adj.mat)
plot(g)
```




## 7.4 Tag Clouds, Literature Mining

The following script will create tag cloud given a list of PubMed abstract identifiers.

```
## ------------------------------------------------------ Given a
## list of PMIDs get their annotation Aedin, Dec 2011 To Run given
## pmids2tagcloud a list of pmids eg pmids=c(10521349, 10582678,
## 11004666, 11108479, 11108479, 11114790, 11156382, 11156382,
## 11156382, 11165872) pmids2tagcloud(pmids)
## ------------------------------------------------------
getPMIDAnnot <- function(pmidlist) {
    require(annotate)
    require(XML)
    print("Using annotate and XML to get info on each PMID")
    pubmedRes <- xmlRoot(pubmed(pmidlist))
    numAbst <- length(xmlChildren(pubmedRes))
    absts <- list()
    for (i in 1:numAbst) {
        absts[[i]] <- buildPubMedAbst(pubmedRes[[i]])
    }

    # unlist(lapply(absts, function(x) authors(x)[1]))

    ## Write Output to PMIDInfo
```

```
    PMIDInfo <- data.frame(matrix(NA, nrow = length(pmidlist)))
    PMIDInfo$FirstAuthor <- unlist(lapply(absts, function(x) authors(x)[1]))
    PMIDInfo$Journal <- unlist(lapply(absts, function(x) journal(x)[1]))
    PMIDInfo$pubDate <- unlist(lapply(absts, function(x) pubDate(x)[1]))
    PMIDInfo$articleTitle <- unlist(lapply(absts, function(x) articleTitle(x
    PMIDInfo$abstText <- unlist(lapply(absts, function(x) abstText(x)[1]))
    PMIDInfo$PubMedID <- unlist(lapply(absts, function(x) pmid(x)[1]))
    rownames(PMIDInfo) <- PMIDInfo$PubMedID
    PMIDInfo <- PMIDInfo[, -1]

    # Res<-cbind(outMat, Total= apply(outMat, 1, sum), PMIDInfo[,c(5,
    # 1,3,4,2)]) Res$pubDate<-unlist(strsplit(Res$pubDate, ' '))[seq(2,
    # length(Res$pubDate)*2, 2)] names(Res)[10] ='Year' print(Res)

    # print(PMIDInfo[1:2,])
    return(PMIDInfo)
}



pmids2tagcloud <- function(pmids, addTitle = TRUE, colorPalette = c("orange"
    "cyan", "green4", "maroon", "slateblue")) {
    require(tm)
    require(wordcloud)
    require(RColorBrewer)
    print(paste("Using tm and wordcloud to create tag cloud from", length(pm
        "abstracts"))
    pubmedAbsts <- getPMIDAnnot(as.character(unique(pmids)))
    words <- tolower(unlist(strsplit(as.character(pubmedAbsts$abstText),
        " ")))
    # remove parentheses, comma, [semi-]colon, period, quotation marks
    words <- words[-grep("[\\)\\(,;:\\.\\'\\\"]", words)]
    words <- words[-grep("^\\d+$", words)]
    words <- words[!words %in% stopwords()]
    wt <- table(words)

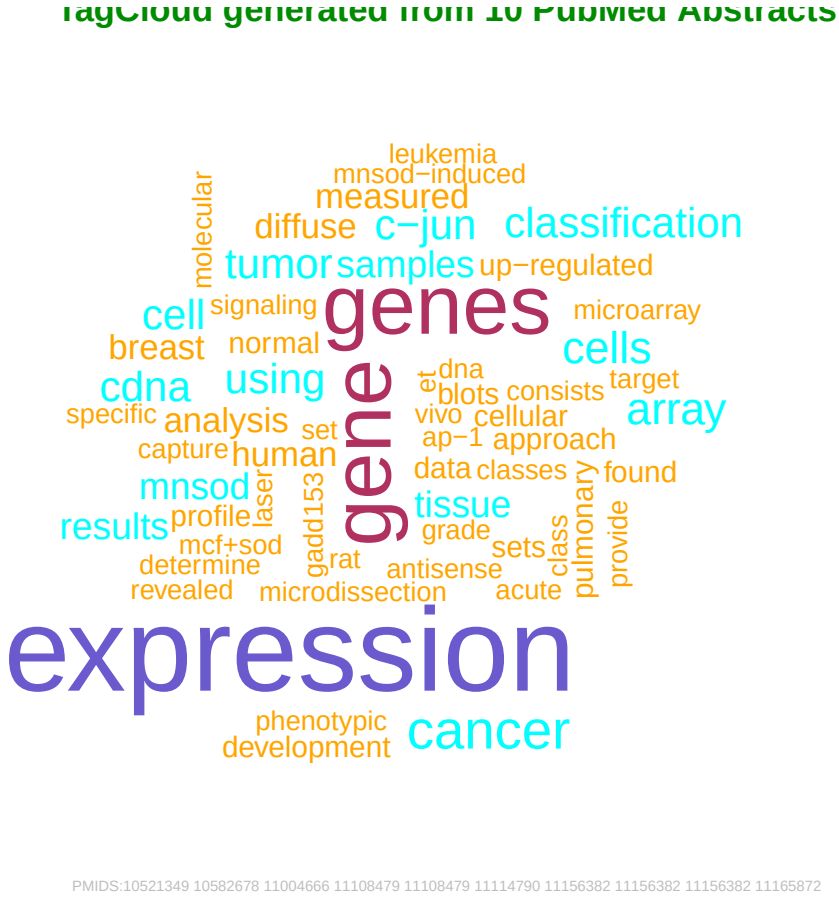
    ## Use R Color Brewer Colors
    pal <- brewer.pal(9, "BuGn")
    pal <- pal[-(1:4)]

    wordcloud(names(wt), as.vector(wt), colors = colorPalette)
    if (addTitle)
        title(main = paste("TagCloud generated from", length(pmids),
            "PubMed Abstracts"), sub = paste("PMIDS:", paste(pmids, collapse
            sep = ""), cex.sub = 0.5, col.main = "green4", col.sub = "gray"
}
```

```
pmids <- c(10521349, 10582678, 11004666, 11108479, 11108479,
    11114790, 11156382, 11156382, 11156382, 11165872)
pmids2tagcloud(pmids)

## [1] "Using tm and wordcloud to create tag cloud from 10 abstracts"

## [1] "Using annotate and XML to get info on each PMID"
```




## 7.5 Other visualization resources

Note whilst we have only looked at "static" plotting, R can generate dynamic plots using R packages JavaGD or ggobi and `http://www.ggobi.org/`. Dynamic plots can be interactively manipulated, rotated or animated. see `http://cran.r-project.org/src/contrib/Views/Graphics.html`.

Other visualization resources that you may like to explore

1. Rggobi `http://www.ggobi.org/rggobi/` 3D visualization of multidimensional data `http://www.ggobi.org/rggobi/introduction.pdf`

2. For a discussion on different graph packages see

   using Rgraphviz `http://www2.warwick.ac.uk/fac/sci/moac/students/peter_cock/r/rgraphviz/` or see the many examples on the Bioconductor website

   a recent discussion online about the topic: `http://stats.stackexchange.com/questions/6155/graph-theory-analysis-and-visualization`

   R cytoscape `http://db.systemsbiology.net:8080/cytoscape/RCytoscape/vignette/RCytoscape.html`

3. Additional demos available in the graphics package: *demo(image)*, *demo(persp)* and *example(symbol)*.

The following web pages have many examples (and code) to produce different R plots. Browse through the plots, see what you like and try some.

- Basic plotting examples from Paul Murrell book, R Graphics `http://www.stat.auckland.ac.nz/~paul/RGraphics/rgraphics.html`
- The homepage of the R package ggplot2 `http://had.co.nz/ggplot2/`. This package produces nice plots and can easily add color scale legend bars to plots
- rggobi and ggplot2 run workshops in R graphics. Their course website provides examples of basic and advanced plots, animated movies, lectures and R code to reproduce the plots at `http://lookingatdata.com/`
- The R Gallery wiki provides examples of R plots and code to reproduce these `http://addictedtor.free.fr/graphiques/`. Here is one random sample from this website:

## 7.6 Summary on plotting

- Basic plotting:
  - *plot()*, *pairs(), histogram, pie etc*
  - Low-level plotting: *points()*, *lines()*, *abline()*
    low-level other: *text()*, *legend()*, *title()*
- Manipulating the plotting window
  - Temporary changes to just one command: "..." argument to *plot()* function
  - To view or change default plot settings: *par()*. This will change the settings for all subsequent plot commands.
- Advanced plotting using ggplots2 library.

# Chapter 8

# Statistical Analysis, linear models and survival analysis in R

## 8.1 This section

1. Basic statistics such as t-test, $\chi^2$,...
2. Intro to linear models in R
3. Model formulae and model options
4. Output and extraction from fitted models
5. model.matrix, contrasts
6. Models considered:
   - Linear regression: *lm()*
   - Logistic regression: *glm()*, Poisson regression: *glm()*
   - Survival analysis: *Surv()*, *coxph()* in the survival and functions in the package survcomp
7. Advanced model options are covered in detail in the recommended text of Venables and Ripley.
   - Generalized Linear Mixed-Effects Models *lmer*, *lme*
   - Generalized additive models *gam()*
   - Non-Linear models *nls*, *nlme*
   - Other useful packages lme4, gmodels
   - The *arm* package contains R functions for Bayesian inference using *lm*, *glm*, *mer* and *polr* objects. The bayesm is aims at marketing and micro economics fields but includes functions for Bayes Regression and Hierarchical Linear Models.
   - The R package doBy is useful for groupwise computations of summary statistics. Facilities for groupwise computations of summary statistics and other facilities for working with grouped data (similar to what can be achieved by proc means or proc summary of the sas system).

- See `http://cran.r-project.org/src/contrib/Views/` for lists of more R packages.

## 8.2 Basic Statistics

### 8.2.1 Continuous Data: t test

The *t.test* performs a one or two sample t test. To see the arguments of *t.test*, look at the help documentation *?t.test*

Arguments include *alternative* which is one of "two.sided", "less" or "greater", and *var.equal* which is a logical (FALSE or TRUE) to indicate unequal or equal variance (default is unequal). The input to *t.test* is one vector (one sample t test), two vectors or a formula (two sample t test). A formula is given by $y \sim x$, where the tilde '$\sim$' operator specifies "described by"

One sample t test:

```
data(ChickWeight)
ChickWeight[1:2, ]

##   weight Time Chick Diet
## 1     42    0     1    1
## 2     51    2     1    1

t.test(ChickWeight[, 1], mu = 100)

##
##  One Sample t-test
##
## data:  ChickWeight[, 1]
## t = 7.38, df = 577, p-value = 5.529e-13
## alternative hypothesis: true mean is not equal to 100
## 95 percent confidence interval:
##  116.0 127.6
## sample estimates:
## mean of x
##     121.8
##
```

Two sample t test. Note these are equivalent

```
t.test(ChickWeight$weight[ChickWeight$Diet == "1"], ChickWeight$weight[Chic
    "2"])

##
##  Welch Two Sample t-test
##
## data:  ChickWeight$weight[ChickWeight$Diet == "1"] and ChickWeight$weight
## t = -2.638, df = 201.4, p-value = 0.008995
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -34.900  -5.042
## sample estimates:
```

```
## mean of x mean of y
##     102.6     122.6
##

t.test(weight ~ Diet, data = ChickWeight, subset = Diet %in%
    c("1", "2"))

##
##  Welch Two Sample t-test
##
## data:  weight by Diet
## t = -2.638, df = 201.4, p-value = 0.008995
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -34.900  -5.042
## sample estimates:
## mean in group 1 mean in group 2
##           102.6           122.6
##
```

For a pairwise comparisons or multiple testing use:

```
pairwise.t.test(ChickWeight$weight, ChickWeight$Diet,
                p.adjust.method="bonferroni")

##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  ChickWeight$weight and ChickWeight$Diet
##
##   1       2       3
## 2 0.06838 -       -
## 3 2.5e-06 0.14077 -
## 4 0.00026 0.95977 1.00000
##
## P value adjustment method: bonferroni
```

### 8.2.2 adjusting for multiple testing

The *p.adjust* can be used to correct p-values for multiple testing. Adjustment methods include the Bonferroni correction in which the p-values are multiplied by the number of comparisons. Less conservative corrections are also included by Holm (1979) ("holm"), Hochberg (1988) ("hochberg"), Hommel (1988) ("hommel"), Benjamini and Hochberg (1995) ("BH" or its alias "fdr"), and Benjamini and Yekutieli (2001) ("BY")

```
x <- rnorm(50, mean = c(rep(0, 25), rep(3, 25)))
p <- 2 * pnorm(sort(-abs(x)))

pVal <- round(p, 3)
Bonferroni <- round(p.adjust(p, "bonferroni"), 3)

## FDR and BH are equivalent

FDR <- round(p.adjust(p, "fdr"), 3)
BH <- round(p.adjust(p, "BH"), 3)

res <- cbind(none = pVal, Bonferroni = Bonferroni, FDR = FDR,
    BH = BH)
res <- res[order(res[, "Bonferroni"]), ]
print(res[1:20, ])

##        none Bonferroni   FDR    BH
##  [1,] 0.000      0.000 0.000 0.000
##  [2,] 0.000      0.000 0.000 0.000
##  [3,] 0.000      0.000 0.000 0.000
##  [4,] 0.000      0.001 0.000 0.000
##  [5,] 0.000      0.001 0.000 0.000
##  [6,] 0.000      0.002 0.000 0.000
##  [7,] 0.000      0.004 0.001 0.001
##  [8,] 0.000      0.004 0.001 0.001
##  [9,] 0.000      0.015 0.002 0.002
## [10,] 0.000      0.019 0.002 0.002
## [11,] 0.001      0.034 0.003 0.003
## [12,] 0.001      0.036 0.003 0.003
## [13,] 0.001      0.053 0.004 0.004
## [14,] 0.001      0.054 0.004 0.004
## [15,] 0.005      0.241 0.015 0.015
## [16,] 0.005      0.257 0.015 0.015
## [17,] 0.005      0.261 0.015 0.015
## [18,] 0.006      0.300 0.017 0.017
## [19,] 0.010      0.481 0.025 0.025
## [20,] 0.014      0.710 0.036 0.036
```

@

### 8.2.3 Continuous Data: One- and two-way analysis of variance

To run a one-way analysis of variance, use *lm*. To use *lm*, the input is a *vector* and a *factor*. Note here that Diet is a factor. The function *lm* provides limited information. Use *summary* to provide a short summary of the distribution of each of the variables. Extract the analysis of variance with *anova*.

```
lmDiet <- lm(weight ~ Diet, data = ChickWeight)
lmDiet

##
## Call:
## lm(formula = weight ~ Diet, data = ChickWeight)
##
## Coefficients:
## (Intercept)        Diet2        Diet3        Diet4
##       102.6         20.0         40.3         32.6
##

summary(lmDiet)

##
## Call:
## lm(formula = weight ~ Diet, data = ChickWeight)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -104.0  -53.6  -13.6   40.4  230.1
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   102.65       4.67   21.96  < 2e-16 ***
## Diet2          19.97       7.87    2.54    0.011 *
## Diet3          40.30       7.87    5.12  4.1e-07 ***
## Diet4          32.62       7.91    4.12  4.3e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 69.3 on 574 degrees of freedom
## Multiple R-squared: 0.0535,Adjusted R-squared: 0.0485
## F-statistic: 10.8 on 3 and 574 DF,  p-value: 6.43e-07
##

anova(lmDiet)

## Analysis of Variance Table
##
## Response: weight
##            Df  Sum Sq Mean Sq F value  Pr(>F)
## Diet        3  155863   51954    10.8 6.4e-07 ***
## Residuals 574 2758693    4806
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In some statistical packages, the sum of the squares are labeled "between groups" and "within groups". Since lm and anova tables are used for a wide range of statistical models, the output from R is different. The Between groups sum of the squares is labeled by the name of the factor groupings (Diet). The within sum of the squares is labeled Residuals. The *aov* function is a wrapper which calls *lm*, but express the results these in the traditional language of the analysis of variance rather than that of linear models.

For examples of different analysis of variance (using *aov*) at `http://personality-project.org/r/r.anova.html`

```
aov(weight ~ Diet, data = ChickWeight)

## Call:
##    aov(formula = weight ~ Diet, data = ChickWeight)
##
## Terms:
##                     Diet Residuals
## Sum of Squares   155863   2758693
## Deg. of Freedom       3       574
##
## Residual standard error: 69.33
## Estimated effects may be unbalanced
```

For a two-way analysis of variance, provide a second factor to *lm*

```
lmDiet <- lm(weight ~ Diet + Time, data = ChickWeight)
summary(lmDiet)

##
## Call:
## lm(formula = weight ~ Diet + Time, data = ChickWeight)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -136.8  -17.1   -2.6   15.0  141.8
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   10.924      3.361    3.25   0.0012 **
## Diet2         16.166      4.086    3.96  8.6e-05 ***
## Diet3         36.499      4.086    8.93  < 2e-16 ***
## Diet4         30.233      4.107    7.36  6.4e-13 ***
## Time           8.750      0.222   39.45  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 36 on 573 degrees of freedom
```

```
## Multiple R-squared: 0.745,Adjusted R-squared: 0.744
## F-statistic:  419 on 4 and 573 DF,  p-value: <2e-16
##

anova(lmDiet)

## Analysis of Variance Table
##
## Response: weight
##            Df  Sum Sq Mean Sq F value Pr(>F)
## Diet        3  155863   51954    40.1 <2e-16 ***
## Time        1 2016357 2016357  1556.4 <2e-16 ***
## Residuals 573  742336    1296
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### 8.2.4 Discrete Data: Contingency Table

A contingency table (also referred to as cross tabulation or cross tab) is often used to record and analyze the relation between two or more discrete/categorical variables. It displays the (multivariate) frequency distribution of the variables in a matrix format. Test for association between such categorical variables are very common in research. Given two *factors* of at least 2 (usually unordered) levels, you can use the package vcd to compute several association statistics for a contingency table.

The simplest measure of association between two categorical variables is the $\phi$ coefficient defined by

$\phi = \sqrt{\frac{\chi^2}{N}}$

with $N$ is the total number of observation and $\chi^2 = \sum_{i=1}^{n} \frac{(O_i - E_i)^2}{E_i}$

where

$\chi^2$ = Pearson's cumulative test statistic

$O_i$ = an observed frequency;

$E_i$ = an expected (theoretical) frequency, asserted by the null hypothesis;

$n$ = the number of cells in the table.

Another measure of association is the Cramer's V statistic that is generalizable to rectangular contingency table

$V = \sqrt{\frac{\chi^2}{N(k-1)}}$,

$k$ being the number of rows or the number of columns, whichever is less.

See `http://en.wikipedia.org/wiki/Contingency_table` for more details about

measure of association in a contingency table.
In R, first create a contingency table and then use the function *assocstats* to computes the Pearson chi-Squared test, the Likelihood Ratio, chi-Squared test, the phi coefficient, the contingency coefficient, and Cramer's V statistics.

```
## load library
library(vcd)

## Loading required package: colorspace


## load data
attach(Arthritis)

## check the variables of interest
is.factor(Arthritis$Treatment)

## [1] TRUE

print(levels(Arthritis$Treatment))

## [1] "Placebo" "Treated"

is.factor(Arthritis$Improved)

## [1] TRUE

print(levels(Arthritis$Improved))

## [1] "None"   "Some"   "Marked"


## build the contingency table
tab <- table(Arthritis$Treatment, Arthritis$Improved)
print(tab)

##
##           None Some Marked
##   Placebo   29    7      7
##   Treated   13    7     21


## compute statistics
res <- assocstats(tab)
print(res)
```

```
##                      X^2 df  P(> X^2)
## Likelihood Ratio 13.530  2 0.0011536
## Pearson          13.055  2 0.0014626
##
## Phi-Coefficient   : 0.394
## Contingency Coeff.: 0.367
## Cramer's V        : 0.394

detach(Arthritis)
```

The structure of the *res* object can be printed using the *str* function

```
str(res)

## List of 5
##  $ table      : 'table' int [1:2, 1:3] 29 13 7 7 7 21
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:2] "Placebo" "Treated"
##   .. ..$ : chr [1:3] "None" "Some" "Marked"
##  $ chisq_tests: num [1:2, 1:3] 13.52981 13.05502 2 2 0.00115 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:2] "Likelihood Ratio" "Pearson"
##   .. ..$ : chr [1:3] "X^2" "df" "P(> X^2)"
##  $ phi        : num 0.394
##  $ contingency: num 0.367
##  $ cramer     : num 0.394
##  - attr(*, "class")= chr "assocstats"
```

You can easily access the various statistics from the *res* object

```
## Pearson chi squared test
print(res$chisq_tests[2, ])

##       X^2        df  P(> X^2)
## 13.055020  2.000000  0.001463


## Cramer's V statistic
print(res$cramer)

## [1] 0.3942
```

If you want to compute the agreement between two classifications or raters, you can estimate the $\kappa$ coefficient which can have the following typical values

| Kappa value | magnitude of agreement |
|---|---|
| $< 0$ | no |
| 0 - 0.2 | small |
| 0.2 - 0.4 | fair |
| 0.4 - 0.6 | moderate |
| 0.6 - 0.8 | substantial |
| 0.8 - 1 | almost perfect |

```
## two random classification
set.seed(12345)
c1 <- sample(0:1, 100, replace = TRUE)
c2 <- sample(0:1, 100, replace = TRUE)
tab <- table(C1 = c1, C2 = c2)
Kappa(x = tab, weights = matrix(rep(1, 4), ncol = 2))

##                value     ASE
## Unweighted -0.04839 0.10073
## Weighted         NaN 0.08598
```

In a practical situation, your Kappa coefficient needs to be over 0.6 to claim that your categorization is valid. You may also want to report both the agreement (%)

```
agr <- sum(diag(tab))/sum(tab)
cat(sprintf("Agreement: %.2g%%\n", agr))

## Agreement: 0.48%
```

### 8.2.5 Common statistical Tests in R

Here is a quick (incomplete) list of useful R functions for basic statistical comparisons:

- Continuous Data
  - *t.test*
  - *pairwise.t.test*: pairwise comparisons
  - *var.test*: comparison of two variances.
  - *lm(y∼x)*: linear regression analysis
  - *lm(y∼f1)*: one-way analysis of variance
  - *lm(y∼f1+f2)*: two-way analysis of variance (ANOVA), f1 and f2 are factors.
  - *lm(y∼f1+x)*: analysis of co-variance
  - *lm(y∼x1+x2+x3)*: multiple regression analysis
  - *bartlett.test*: Bartlett's test of the null that the variances in each of the groups (samples) are the same
- Non-Parametric

- *wilcox.test*: one- and two-sample Wilcoxon tests on vectors of data; the latter is also known as Mann-Whitney test.
- *kruskal.test*: non-parametric one-way analysis of variance.
- *friedman.test*: non-parametric two-way analysis of variance.

- Correlation

  *cor*, *cor.test*: correlation and Correlation tests. Cor.test methods include ”kendall” ”spearman” or ”pearson”.

- Discrete response data

  - *chisq.test*: chi-squared contingency table tests, *fisher.test* exact test for small tables.
  - *binom.test*: binomial test
  - *prop.test*: *prop.trend.test* comparison of proportions.
  - *glm(y x1+x2+x3, binomial)*: logistic regression

* As a complete aside and to continue stories of Ireland's mathematicians and statisticians, which I started with the story of George Boole, the first professor of mathematics of University College Cork. The t statistic was introduced by William Sealy Gosset to monitoring the quality of brewing in the Guinness brewery in Dublin, Ireland. Guinness's has an innovative policy of recruiting the best graduates from Oxford and Cambridge to apply biochemistry and statistics to Guinness' industrial processes. Gosset published the t test in Biometrika in 1908, but published using the pen name Student.

## 8.3 Model formulae and model options

- Most modeling done in a standard way
- Data set is usually a single *data frame* object
- Model is fitted using *model fitting function*
- Form of the model specified by a *formula*
- Resulting *fitted model* object can be interrogated, analyzed and modified

Basic output of the model fitting process is minimal. Details obtained via extractor functions.

### 8.3.1 Model formulae

We have already seen in several functions (boxplot, t.test, lm) that a simply function is defined by y $\sim$ x. We will now discuss formulae in much more detail.

Define a template for statistical models

$$y_i = \sum_{j=0}^{p} \beta_j x_{ij} + \epsilon_i, \qquad \epsilon_i \sim \text{NID}(0, \sigma^2), \qquad i = 1, \ldots, n$$

In the matrix form this model is

$$\boldsymbol{y} = X\boldsymbol{\beta} + \boldsymbol{\epsilon}$$

where $\boldsymbol{y}$ is the response vector, $X$ is the *model matrix* or *design matrix* with columns $\boldsymbol{x_0}, \boldsymbol{x_1}, \ldots, \boldsymbol{x_p}$.
NOTATION:
`y, x, x0, x1, x2, ...` - numeric variables
`A, B, C, ...` - factors

Examples of model *formula* with numeric variables:

```
y ~ x
y ~ 1 + x            - simple regression (first - implicit intercept,
                       second - explicit intercept)
-------------------------------------------------------------------
y ~ 0 + x
y ~ x - 1
y ~ -1 + x           - regression through the origin
-------------------------------------------------------------------
y ~ x1 + x2 + x3     - multiple regression
-------------------------------------------------------------------
y ~ x + I(x^2)       - quadratic regression
-------------------------------------------------------------------
log(y) ~ x1 + x2     - multiple regression of transformed variable
```

Examples of model *formula* with factors and numeric variables:

```
y ~ A                - single analysis of variance model
y ~ A + x            - single analysis of covariance model with
                       covariate x
-------------------------------------------------------------------
y ~ A*B
y ~ A + B + A:B      - two-factor model with interaction
-------------------------------------------------------------------
y ~ (A + B + C)^2    - all two-factor interactions
```

```
-------------------------------------------------------------------------
y ~ A*B + Error(C)    - two factor model with interaction and error
                        strata determined by C
```

**General form:**

```
response ~ op_1 term_1 + op_2 term_2 + ...
```

where

```
response    - a vector or expression evaluating to a vector defining the
              response variable
op_i        - an operator, either '+' (inclusion of a term)
              or '-' (exclusion of a term) in the model
term_i      - either a vector or matrix expression,
              or 1, a factor,
              or a formula expression consisting of factors, vectors or
              matrices connected by formula operators.
```

### 8.3.2 Example of linear regression

Will use data 'cats' from the MASS library.

```
library(MASS)
help("cats")
str(cats)

## 'data.frame': 144 obs. of  3 variables:
##  $ Sex: Factor w/ 2 levels "F","M": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Bwt: num  2 2 2 2.1 2.1 2.1 2.1 2.1 2.1 2.1 ...
##  $ Hwt: num  7 7.4 9.5 7.2 7.3 7.6 8.1 8.2 8.3 8.5 ...

cats.lmB <- lm(Hwt ~ Bwt, data = cats)
cats.lmS <- lm(Hwt ~ Sex, data = cats)
cats.lmBS <- lm(Hwt ~ Bwt + Sex, data = cats)
cats.lmBxS <- lm(Hwt ~ Bwt * Sex, data = cats)
cats.lmB2 <- lm(Hwt ~ Bwt + I(Bwt^2), data = cats)
```

### 8.3.3 Contrasts, model.matrix

We need to understand how model formulae specify the columns of the model matrix.

1. Continuous variables (simplest): each variable provides a column of the model matrix (and the intercept will provide a column of ones if included in the model).

2. k-level factor `A`
   The answer differs for unordered and ordered factors.

   - Unordered factors
     $k-1$ columns are generated for the indicators of the second, third, . . . , up to k$^{th}$ levels of the factor. (Implicit parameterization is to contrast the response at each level with that at the first.)
   - Ordered factors
     $k-1$ columns are the orthogonal polynomials on $1, \ldots, k$, omitting the constant term.

   If the intercept is omitted in a model that contains a factor term, the first such term is encoded into k columns giving the indicators for all the levels.

   `R` default setting is:

   ```
   options(contrasts = c("contr.treatment", "contr.poly"))
   ```

Contrasts can be defined using the *contrasts* or *C* function **Example**

```
contr.treatment(n = 3, base = 2)
```

```
##   1 3
## 1 1 0
## 2 0 0
## 3 0 1
```

```
contr.sum(n = 3)
```

```
##   [,1] [,2]
## 1    1    0
## 2    0    1
## 3   -1   -1
```

## 8.4 Exercise 9

```
# What is the difference in output?
lm(Hwt ~ Sex, data = cats)

##
## Call:
## lm(formula = Hwt ~ Sex, data = cats)
##
## Coefficients:
## (Intercept)         SexM
##        9.20         2.12
##

lm(Hwt ~ Sex - 1, data = cats)

##
## Call:
## lm(formula = Hwt ~ Sex - 1, data = cats)
##
## Coefficients:
## SexF  SexM
##  9.2  11.3
##
```

*model.matrix* is useful to view the terms in the fitted model.

## 8.5 Output and extraction from fitted models

As mentioned earlier, the printed output of the model fit is minimal. However, the value of a fitted model object is stored in an object. Information about the fitted model can be displayed, extracted and plotted.

Extractor functions:

```
coef(obj)             - regression coefficients
resid(obj)            - residuals
fitted(obj)           - fitted values
summary(obj)          - analysis summary
predict(obj,newdata = ndat)  -   predict for new data
deviance(obj)         - residual sum of squares
print(obj)            - Print concise summary
plot(obj)             - produce diagnostic plots
formula(obj)          - extract the model formula
anova(obj1, obj2)     - compare 2 models (one is a submodel with the outer mo
step(obj)             - add, drop terms
update(obj, formula) - update a model with a new formula
```

Let's go back to the *cats* example. Now, we can extract more information about the fits.

```
attach(cats)
cats.lmBS <- lm(Hwt ~ Bwt + Sex, data = cats)
coef(cats.lmBS)

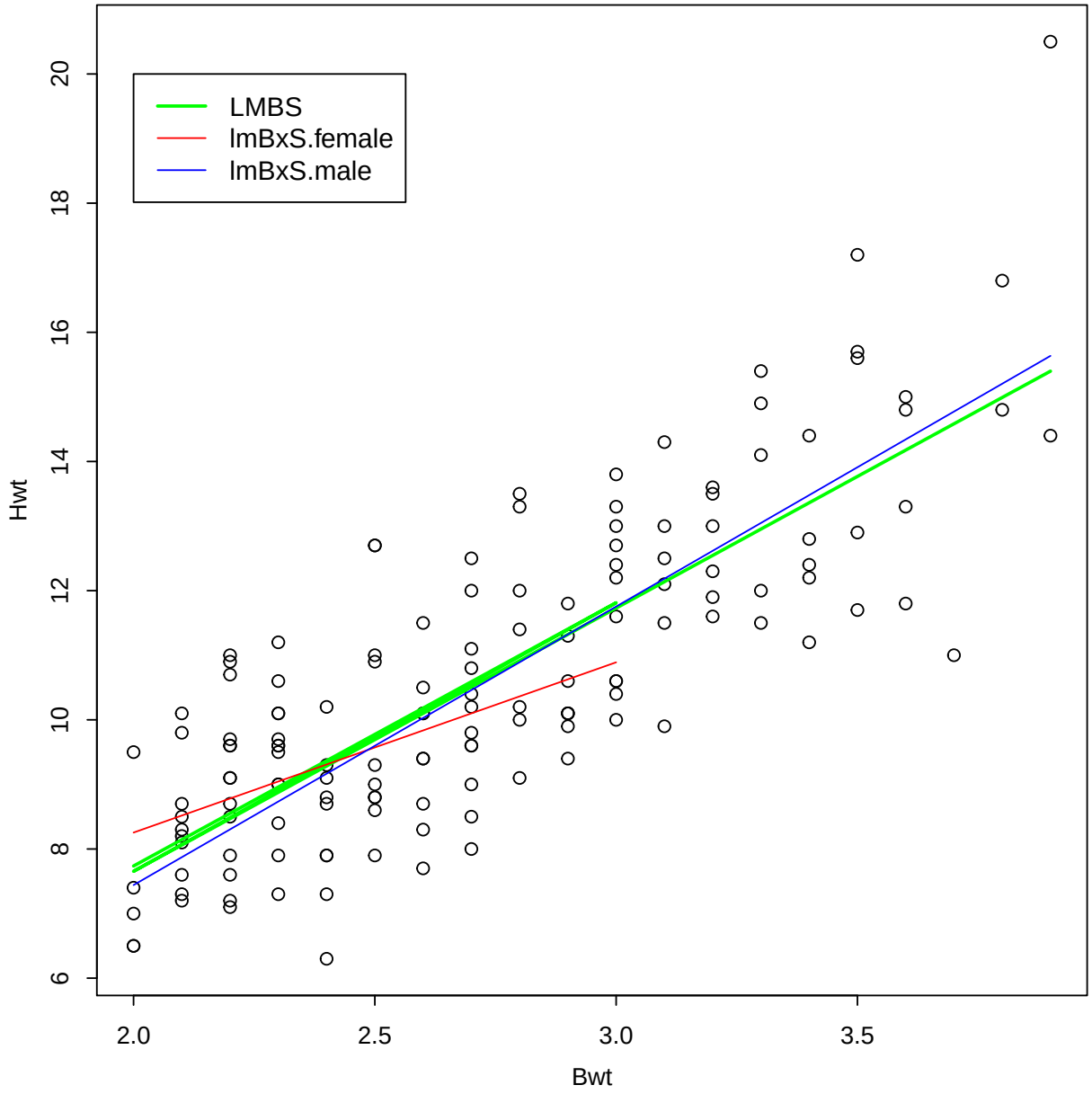
## (Intercept)         Bwt        SexM
##     -0.4150      4.0758     -0.0821

fit.catsBS <- fitted(cats.lmBS)
```

```
cats.lmBxS <- lm(Hwt ~ Bwt * Sex, data = cats)
fit.catsBxS <- fitted(cats.lmBxS)
```

Plot these 2 models.

```
plot(Bwt, Hwt)
lines(Bwt, fit.catsBS, col = "green", lwd = 2)  # OR
# abline(cats.lmBS, col='green', lwd=2)
lines(Bwt[Sex == "F"], fit.catsBxS[Sex == "F"], col = "red")
lines(Bwt[Sex == "M"], fit.catsBxS[Sex == "M"], col = "blue")
legend(x = 2, y = 20, legend = c("LMBS", "lmBxS.female", "lmBxS.male"),
    col = c("green", "red", "blue"), lwd = c(2, 1, 1))
```




Prediction of *Hwt* values

```
predict(cats.lmBxS, data.frame(Bwt = seq(2, 5, 1), Sex = "M"))

##      1      2      3      4
##  7.441 11.754 16.067 20.379

detach(cats)
```

Some more useful, but non-standard, ways of extracting information from a model.

```
df.residual(obj)     - residual degrees of freedom
names(obj)           - gives names of the components in obj
```

`names(summary(obj)) - gives names of the components in summary(obj)`

How to get the residual variance of the fit? There are at least 2 ways. The first is the direct calculation

```
# direct calculation
var.catsB <- deviance(cats.lmB)/df.residual(cats.lmB)

var.catsB <- summary(cats.lmB)$sigma^2
```

## 8.6 Exercise 10 :Multivariate linear regression

- Read the data contained in the file `lungs.csv` from the course website into R. Fit a multivariate regression model (function *lm*) of *pemax* using all variables. Call the result *lungFit*.
- Which terms appear to be significant (summary)?
- What is the residual error of this model?
- Which are the most and least significant variables in this model?

### 8.6.1 Residual plots, diagnostics

Important part of modeling - checking the model assumptions. Some easy to check and interpret model diagnostics

1. Fit to the data (predictions) vs. raw data (observations)
2. Histogram of the residuals
3. Scatterplot of the residuals vs. fitted values
4. QQ-plot of the residuals

```
attach(cats)
plot(Bwt, Hwt, main = "Model fit")
abline(cats.lmB, col = "green", lwd = 2)
```

**Fit the model**

```
hist(resid(cats.lmB), main = "Residual histogram")
```

**Residual histogram**

```
plot(fitted(cats.lmB), resid(cats.lmB), main = "Residuals vs. fitted values"
lines(lowess(fitted(cats.lmB), resid(cats.lmB)), col = "red")
abline(h = 0)
```

**Residuals vs. fitted values**

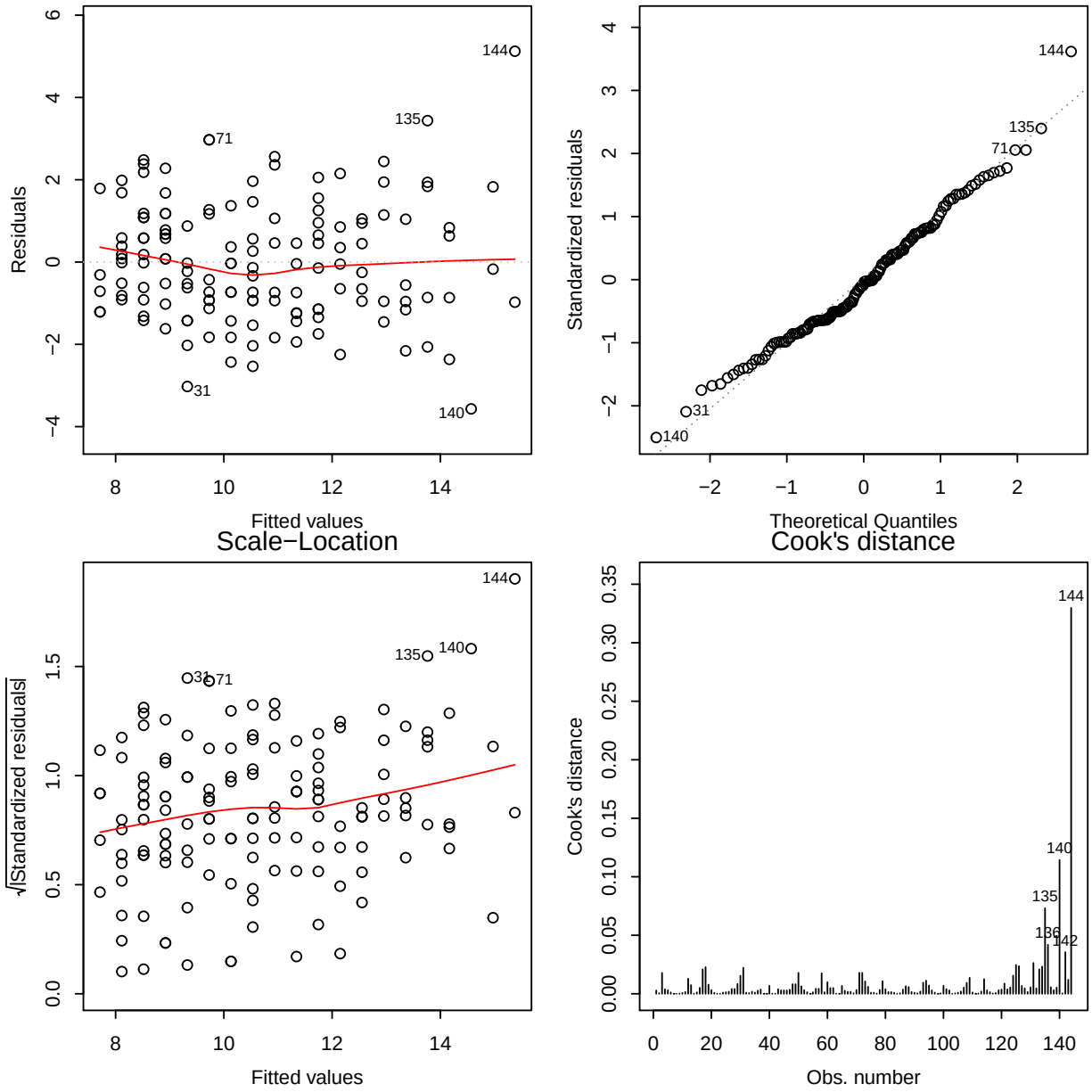
```
qqnorm(resid(cats.lmB))
qqline(resid(cats.lmB))
detach()
```

Figure 8.1: Plots of the fitted Model,Residuals vs. fitted values and QQ-PLots of the residuals

**QQ-plot of residuals**

Default plots available in *plot* of class *lm*

```
par(mfrow = c(2, 2))
plot(cats.lmB, which = 1:4, id.n = 5)
```




### 8.6.2 ANOVA and updating models

Anova tables for a sequence of fitted models

```
anova(obj_1, obj_2)  - compare two models where obj_1 and obj_2 are two regi
```

The sums of squares shown are the decrease in the residual sums of squares resulting from an inclusion of that term in the model at that place in the sequence. Only for orthogonal experiments will the order of inclusion be inconsequential.

```
anova(cats.lmB, cats.lmBS)

## Analysis of Variance Table
##
## Model 1: Hwt ~ Bwt
## Model 2: Hwt ~ Bwt + Sex
##   Res.Df RSS Df Sum of Sq    F Pr(>F)
## 1    142 300
## 2    141 299  1     0.155 0.07   0.79

anova(cats.lmB, cats.lmBxS)

## Analysis of Variance Table
##
## Model 1: Hwt ~ Bwt
## Model 2: Hwt ~ Bwt * Sex
##   Res.Df RSS Df Sum of Sq    F Pr(>F)
## 1    142 300
## 2    140 291  2      8.49 2.04   0.13

anova(cats.lmB, cats.lmBS, cats.lmBxS)

## Analysis of Variance Table
##
## Model 1: Hwt ~ Bwt
## Model 2: Hwt ~ Bwt + Sex
## Model 3: Hwt ~ Bwt * Sex
##   Res.Df RSS Df Sum of Sq    F Pr(>F)
## 1    142 300
## 2    141 299  1      0.15 0.07  0.785
## 3    140 291  1      8.33 4.01  0.047 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The *update()* function allows a model to be fitted that differs from one previously fitted usually by just a few additional or removed terms.
Syntax:

```
new.model <- update(old.model, new.formula)
```

Special name in the *new formula* - a period '.' - can be used to stand for "corresponding part of the old model formula".

**Example**:

Data set *mtcars*, fuel consumption and 10 aspects of automobile design and performance for 32 automobiles.

```
help("mtcars")
cars.lm <- lm(mpg ~ hp + wt, data = mtcars)
cars.lm2 <- update(cars.lm, . ~ . + disp)
# cars.lms <- update(cars.lm2, sqrt(.) ~ .)
```

what does the following do?

```
# anova(cars.lm, cars.lm2, cars.lms)
anova(cars.lm, cars.lm2)

## Analysis of Variance Table
##
## Model 1: mpg ~ hp + wt
## Model 2: mpg ~ hp + wt + disp
##   Res.Df RSS Df Sum of Sq    F Pr(>F)
## 1     29 195
## 2     28 195  1    0.0571 0.01   0.93
```

### 8.6.3 Model selection

There are functions in R automating the choice of terms in the statistical models. Adding, dropping and performing stepwise selection in a sequence of models.

- Dropping terms: `drop1()` or `dropterm()` from the MASS library
- Adding terms: `add1()` or `addterm()` from the MASS library
- Stepwise selection: `step()` or `stepAIC()` from the MASS library

More details:

**dropterm** Fits all models that differ from the current model by dropping a single term, maintaining marginality.

```
dropterm(model.big, test='F')        # for linear models
dropterm(model.big, test='Chisq')    # for generalized linear models
```

**addterm** Fits all models that differ from the current model by adding a single term from those supplied, maintaining marginality

```
addterm(model.small, scope=model.big, test='F') # for linear models
```

**stepAIC** Performs stepwise model selection by exact AIC

```
stepAIC(model.small,
       scope=list(upper=model.big, lower= ~1),
       test='F')                    # for linear models
```

**Example**

Data set *mtcars*

```
# Fit regression model with all other covariates as predictors
cars.all <- lm(mpg ~ ., data=mtcars)
# Drop terms
dropterm(cars.all, test = "F")

# Probably not appropriate analysis. Try
cars.some <- lm(mpg ~ factor(cyl) + hp + wt + disp + qsec + factor(gear),
                data=mtcars)
dropterm(cars.some, test = "F")

# Start with one variable
cars.sm <- update(cars.some, .~ wt)
addterm(cars.sm, cars.some, test='F')

# Stepwise selection
cars.step <- stepAIC(cars.some, scope=list(lower = ~ wt))
```

## 8.7 Cross-validation

Another approach, developed by the machine Learning community, is *cross-validation*. The idea is to sequentially divide the dataset in training and test sets to fit and assess the performance of the model, respectively. This approach enables to use all the observations both for training and testing the prediction model.

Here is an example of a 10-fold cross-validation on the *mtcars* dataset where we compare the model with one variable (*wt*) and all the variables to predict *mpg*. Once the root mean squared error (RMSE) is computed for each fold, a paired Wilcoxon Rank Sum test is used to compare the performance of the small and big models.

```
nfold <- 10
## nr is the number of observations
nr <- nrow(mtcars)
## nfold is the number of folds in the cross-validation
if(nfold > 1) k <- floor(nr/nfold) else {
k <- 1
nfold <- nr
}
smpl <- sample(nr)
mse.big <- mse.small <- NULL

for (i in 1:nfold) {
        if (i == nfold) s.ix <- smpl[c(((i - 1) * k + 1):nr)] else s.ix <- s
## fit the model
```

```
mm.big <- lm(mpg ~ ., data=mtcars[-s.ix, , drop=FALSE])
mm.small <- lm(mpg ~ wt, data=mtcars[-s.ix, , drop=FALSE])
## assess the performance of the model
pp.big <- predict(object=mm.big, newdata=mtcars[s.ix, !is.element(colnames(m
pp.small <- predict(object=mm.small, newdata=mtcars[s.ix, !is.element(colnam
## compute mean squared error (MSE)
mse.big <- c(mse.big, sqrt(mean((mtcars[s.ix, "mpg"] - pp.big)^2)))
mse.small <- c(mse.small, sqrt(mean((mtcars[s.ix, "mpg"] - pp.small)^2)))
}
names(mse.big) <- names(mse.small) <- paste("fold", 1:nfold, sep=".")

## compare the performance of the big and small models using a Wilcoxon Rank
wilcox.test(mse.big, mse.small, paired=TRUE, alternative="less")

##
##  Wilcoxon signed rank test
##
## data:  mse.big and mse.small
## V = 35, p-value = 0.7842
## alternative hypothesis: true location shift is less than 0
##
```

As can be seen, there is not enough evidence in the dataset to claim that the big prediction model outperforms the small one (p-value $> 0.05$). You can easily change the number of folds in the cross-validation by setting the variable *nfold* to another value, $nfold = 1$ for leave-one-out cross-validation.

## 8.8 Statistical models

Will talk today about 3 classes of statistical models: linear regression, generalized linear models (e.g. logistic and Poisson regression), and survival models.

### 8.8.1 Linear Regression: Weighted Models, Missing Values

We have talked and went through examples of linear regression using the function *lm()*. Will expand here on the options for the function *lm()*

```
lm(formula, data, subset, weights, na.action, ...)
```

**subset** - (optional) a subset of observations to be used in the fitting process

**weights** - (optional) weights to fit the model using weighted list squares method

**na.action** - what happens to data containing missing values 'NA's;
*na.omit* - is the default; another option *na.fail*

```
attach(ChickWeight)
time.wgt <- tapply(weight, Time, var)
time.wgt.rep <- as.numeric(time.wgt[match(Time, as.numeric(names(time.wgt))
detach(2)
Chick.anl <- data.frame(ChickWeight, time.wgt.rep = time.wgt.rep)
chick.lm.wgt <- lm(weight ~ Time, data = Chick.anl, weight = 1/time.wgt.rep
chick.lm.T0 <- lm(weight ~ Time, data = Chick.anl, subset = (Time ==
    0))
```

### 8.8.2 Generalized linear modeling

- One generalization of multiple linear regression.
- Response, $y$, predictor variables $x_1, x_2, \ldots, x_p$
- The distribution of $Y$ depends on the $x$'s through a single linear function, the 'linear predictor'
$$\nu = \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_p x_p \tag{8.1}$$
with $x_i$ having no influence on $y$ if and only if $\beta_i = 0$
- There may be an unknown 'scale' (or 'variance') parameter $\phi$ to estimate as well
- The mean, $\mu$, is a smooth invertible function of the linear predictor
$$\mu = m(\nu), \qquad \nu = m^{-1}(\mu) = l(\mu) \tag{8.2}$$
and this inverse function, $l()$, is called the *link function*
- The deviance is a generalization of the residual sum of squares.
- The protocols are very similar to linear regression and the inferential logic is virtually identical.

The class of generalized linear models handled by facilities supplied in R includes Gaussian, binomial, Poisson, inverse Gaussian and gamma response distributions.

**Families of distributions and links**

```
Distribution       Link
-------------      ------------------------------
binomial           logit, probit, log, cloglog
gaussian           identity, log, inverse
Gamma              identity, inverse, log
inverse.gaussian   1/mu^2, identity, inverse, log
poisson            identity, log, sqrt
```

The `R` function to fit a generalized linear model is *glm()* which uses the form

```
fitted.model <- glm(formula, family=family.generator, data=data.frame)
```

The only difference from *lm()* is the `family.generator`, which is the instrument by which the family is described. It is the name of a function that generates a list of functions and expressions that together define and control the model and estimation process.

We will concentrate on the *binomial* family with the *logit* link or as you probably know it 'logistic regression',.

**Logistic regression**

To fit a binomial model using `glm()` there are three possibilities for the response:

1. If the response is a vector it is assumed to hold binary data, and so must be a 0/1 vector.
2. If the response is a two-column matrix it is assumed that the first column holds the number of successes for the trial and the second holds the number of failures.
3. If the response is a factor, its first level is taken as failure (0) and all other levels as 'success' (1).

Syntax:

```
glm(y ~ x, family=binomial(link=logit), data = data.frame)
```

Link is optional, since the default link is *logit*. Necessary, if another link is desired, e.g. *probit*.

**Example** of logistic regression using data set *esophagus*

Data from a case-control study of (o)esophageal cancer in Ile-et-Vilaine, France containing records for 88 age/alcohol/tobacco combinations with the 3 covariates grouped into 6, 4 and 4 groups respectively.

```
summary(esoph)
```

```
##    agegp          alcgp         tobgp        ncases
##  25-34:15   0-39g/day:23   0-9g/day:24   Min.   : 0.00
##  35-44:15   40-79    :23   10-19   :24   1st Qu.: 0.00
##  45-54:16   80-119   :21   20-29   :20   Median : 1.00
##  55-64:16   120+     :21   30+     :20   Mean   : 2.27
##  65-74:15                                3rd Qu.: 4.00
##  75+  :11                                Max.   :17.00
##    ncontrols
##  Min.   : 1.0
##  1st Qu.: 3.0
##  Median : 6.0
##  Mean   :11.1
##  3rd Qu.:14.0
##  Max.   :60.0
```

effects of alcohol and tobacco, age-adjusted

```
eso.age <- glm(cbind(ncases, ncontrols) ~ agegp, data = esoph,
    family = binomial())
```

```
eso.base <- glm(cbind(ncases, ncontrols) ~ agegp + tobgp +
    alcgp, data = esoph, family = binomial())
```

```
eso.base <- update(eso.age, . ~ . + tobgp + alcgp)

eso.TA <- glm(cbind(ncases, ncontrols) ~ agegp + tobgp * alcgp,
    data = esoph, family = binomial())
eso.2way <- glm(cbind(ncases, ncontrols) ~ (agegp + tobgp +
    alcgp)^2, data = esoph, family = binomial())
```

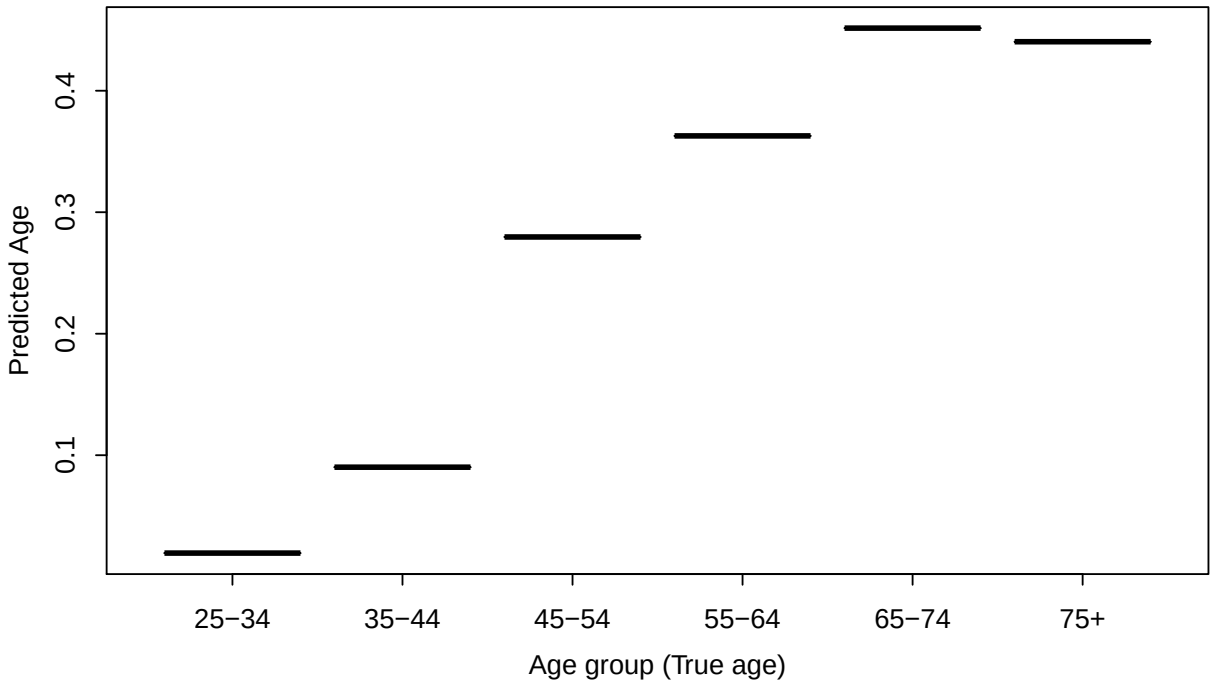
Stepwise model selection

```
eso.base <- glm(cbind(ncases, ncontrols) ~ agegp + tobgp +
    alcgp, data = esoph, family = binomial())
eso.stp <- stepAIC(eso.age, scope = list(upper = ~agegp +
    tobgp + alcgp, lower = ~1), test = "Chisq")

## Start:  AIC=298.6
## cbind(ncases, ncontrols) ~ agegp
##
##         Df Deviance AIC  LRT Pr(Chi)
## + alcgp  3     64.6 230 74.5 4.5e-16 ***
## + tobgp  3    120.0 286 19.1 0.00026 ***
## <none>       139.1 299
## - agegp  5    227.2 377 88.1 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step:  AIC=230.1
## cbind(ncases, ncontrols) ~ agegp + alcgp
##
##         Df Deviance AIC  LRT Pr(Chi)
## + tobgp  3     54.0 226 10.6   0.014 *
## <none>         64.6 230
## - agegp  5    138.8 294 74.2 1.4e-14 ***
## - alcgp  3    139.1 299 74.5 4.5e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step:  AIC=225.4
## cbind(ncases, ncontrols) ~ agegp + alcgp + tobgp
##
##         Df Deviance AIC  LRT Pr(Chi)
## <none>         54.0 226
## - tobgp  3     64.6 230 10.6   0.014 *
## - alcgp  3    120.0 286 66.1 3.0e-14 ***
## - agegp  5    131.5 293 77.5 2.8e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

**Prediction and residuals** Plot the fitted values for 'age' effect

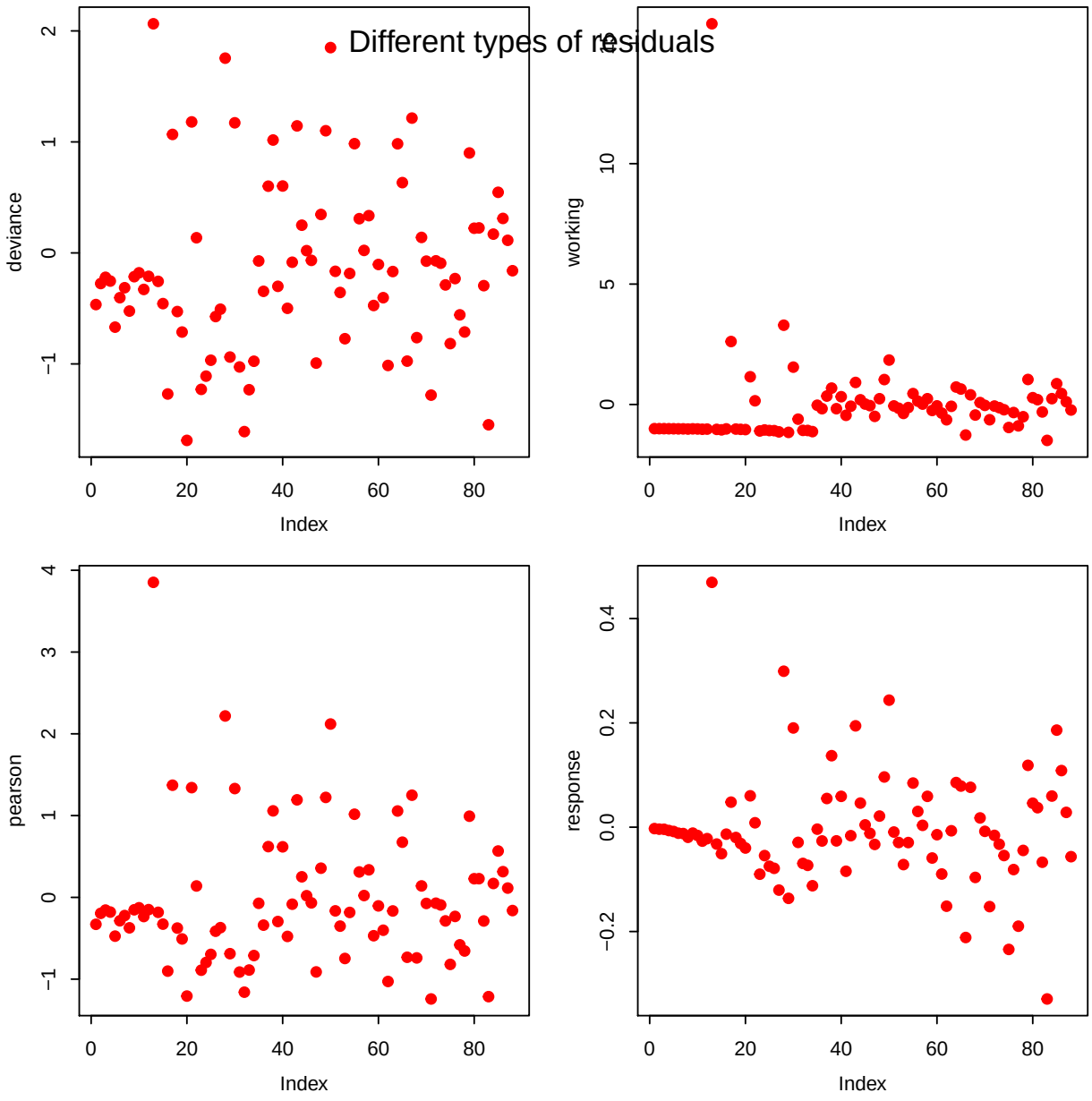
```
attach(esoph)
eso.pred.age <- predict.glm(eso.base, data.frame(agegp = agegp,
    tobgp = rep("30+", 88), alcgp = rep("40-79", 88)), type = "response")
plot(eso.pred.age ~ agegp, ylab = "Predicted Age", xlab = "Age group (True a
```




```
detach(esoph)
```

4 types of residuals can be requested for the *glm()* models: *deviance, working, Pearson, response*

```
opar <- par(mfrow=c(2,2))
for (i in c('deviance', 'working', 'pearson', 'response'))
 plot(resid(eso.base, type=i), ylab=i, pch=19, col="red")
mtext('Different types of residuals',line=-2, outer=T, cex=1.2)
```




```
par(opar)
```

### 8.8.3 Other packages

- Tibshirani and Hastie's provide elastic net, lasso, ridge regression, adaptive lasso and the adaptive elastic net regularized generalized linear models available in the package glmnet
- Other packages for machine learning are listed on `http://cran.r-project.org/web/views/MachineLearning.html`

## 8.9 Survival modeling

*Survival Analysis* is a class of statistical methods for studying the occurrence and timing of events. These methods are most often applied to the study of deaths but can also handle different kinds of events, including the onset of disease and equipment failure for instance. For instance a disease consists of a transition from an healthy state to a diseased state. Moreover, the timing of the event is also considered for analysis.

Survival data have a common feature, namely *censoring*, that is difficult to handle with conventional statistical methods. Consider the following example, which illustrates the problem of censoring. A sample of breast cancer patients were followed during 10 years after diagnosis. The event of interest was the appearance of a distant metastasis (a tumor initiated from the primary breast tumor cells and that is located in another organ). The aim was to determine how the occurrence and timing of distant metastasis appearance depended on several variables.

### 8.9.1 Censored Data

An observation on a random variable $\mathbf{t}$ is right-censored if all you know about $\mathbf{t}$ is that it is greater than some value $c$. In survival analysis, $\mathbf{t}$ is typically the time of occurrence for some event, and cases are right-censored because observation is terminated before the event occurs.

*Random censoring* occurs when observations are terminated for reasons that are not under the control of the investigator. This situation can be illustrated in our example. Patients who are still free of distant metastasis after 10 years are censored by a mechanism identical to that applied to the singly right-censored data. But some patients may move away, and it may be impossible to contact them. Some patients may die from another cause. Still other patients may refuse to participate after, say, 5 years. These kinds of censoring are depicted in Figure 8.2, where the symbol "+" for the patients A and C indicates that observation is censored at that point in time.

Figure 8.2: Randomly censored data.

The vast majority of the he functions we need to do survival analysis are in the package survival. Check if the package survival is already loaded into your work space, if it isn't load the library survival

```
search()
library(survival)

## Loading required package: splines
```

We will work with the data set 'leukemia' containing times of death or censoring in patients with Acute Myelogenous Leukemia. The survival data are usually stored in a *Surv* object that is a one-column matrix containing the survival times and events/censoring.

```
data(leukemia)
head(leukemia)
```

```
##   time status          x
## 1    9      1 Maintained
## 2   13      1 Maintained
## 3   13      0 Maintained
## 4   18      1 Maintained
## 5   23      1 Maintained
## 6   28      0 Maintained

`?`(Surv)
mysurv <- Surv(leukemia$time, leukemia$status)
head(mysurv)

## [1]  9  13  13+ 18  23  28+
```

Several methods for survival analysis are implemented in R, mainly in the survival package:

**Surv** - creates a survival object used as a response variable in a model formula, e.g. *Surv(time, status)*

**survfit** - computes an estimate of a survival curve for censored data using the Kaplan-Meier method, e.g. *survfit(Surv(time, status) group)*

**survdiff** - Tests if there is a difference between two or more survival curves, e.g. *survdiff(Surv(time, status) group)*

**survreg** - regression for a parametric survival model with special case, the accelerated failure models that use a log transformation of the response.

**coxph** - fits a Cox proportional hazards regression model

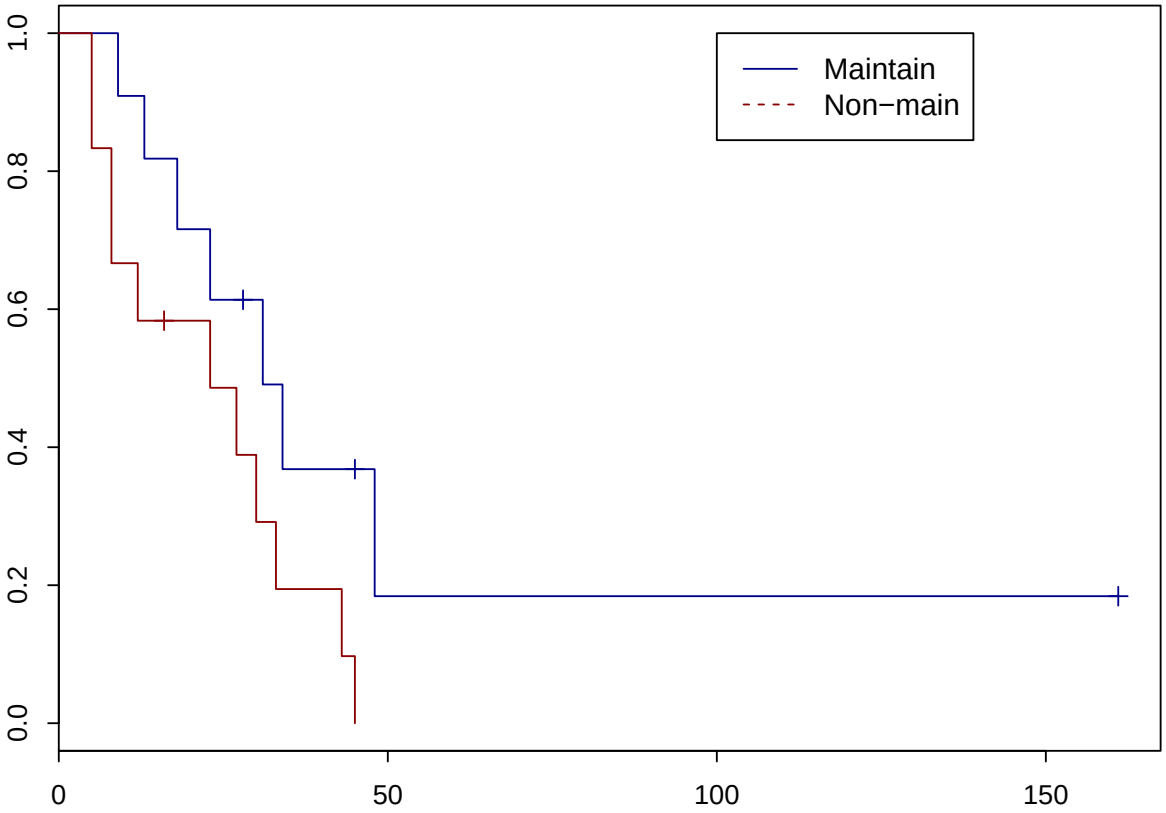
### 8.9.2 Kaplan-Meier curve estimation

We can easily draw the survival curve of patients representing the proportion of patients who survived over time. We provide the function *survfit* with the following set of arguments

```
survfit(formula, data, weights, subset, na.action,
       newdata, individual=F, conf.int=.95, se.fit=T,
       type=c("kaplan-meier","fleming-harrington", "fh2"),
       error=c("greenwood","tsiatis"),
       conf.type=c("log","log-log","plain","none"),
       conf.lower=c("usual", "peto", "modified"))

# To see help on this function or a description of these arguments
?survfit
```

```
leuk.km <- survfit(Surv(time, status) ~ x, data = leukemia)
plot(leuk.km, lty = 1, col = c("darkblue", "darkred"))
legend(100, 1, legend = c("Maintain", "Non-main"), lty = 1:2,
    col = c("darkblue", "darkred"))
```



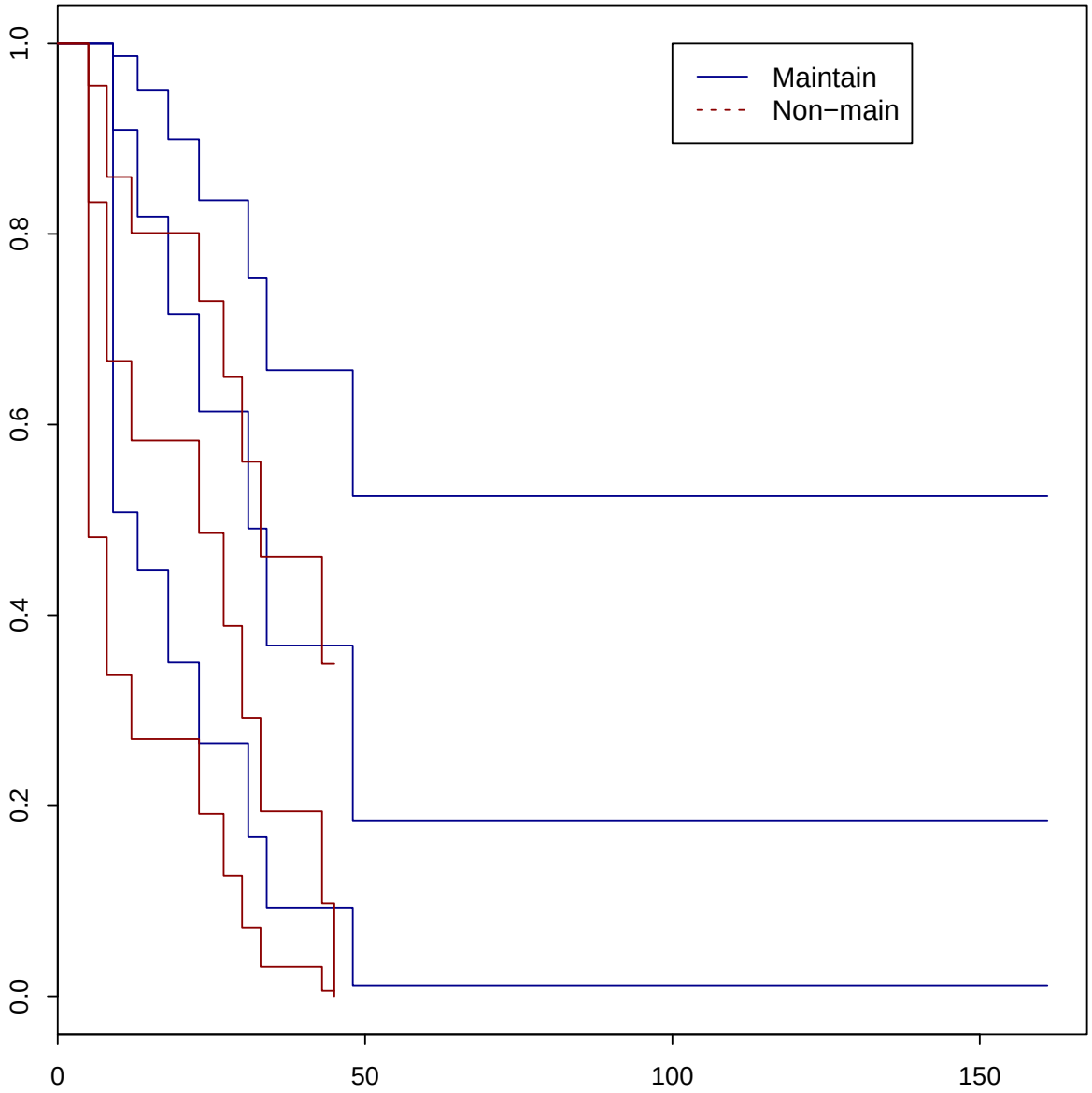

Compute confidence intervals and plot them

```
leuk.km2 <- survfit(Surv(time, status) ~ x, data = leukemia,
    conf.type = "log-log")
summary(leuk.km2)

## Call: survfit(formula = Surv(time, status) ~ x, data = leukemia, conf.typ
##
##                 x=Maintained
##  time n.risk n.event survival std.err lower 95% CI upper 95% CI
##     9     11       1    0.909  0.0867       0.5081        0.987
##    13     10       1    0.818  0.1163       0.4474        0.951
##    18      8       1    0.716  0.1397       0.3502        0.899
##    23      7       1    0.614  0.1526       0.2658        0.835
##    31      5       1    0.491  0.1642       0.1673        0.753
##    34      4       1    0.368  0.1627       0.0928        0.657
```

```
##     48       2        1    0.184  0.1535       0.0117        0.525
##
##                  x=Nonmaintained
##   time n.risk n.event survival std.err lower 95% CI upper 95% CI
##      5     12       2   0.8333  0.1076      0.48171        0.956
##      8     10       2   0.6667  0.1361      0.33702        0.860
##     12      8       1   0.5833  0.1423      0.27014        0.801
##     23      6       1   0.4861  0.1481      0.19188        0.730
##     27      5       1   0.3889  0.1470      0.12627        0.650
##     30      4       1   0.2917  0.1387      0.07240        0.561
##     33      3       1   0.1944  0.1219      0.03120        0.461
##     43      2       1   0.0972  0.0919      0.00575        0.349
##     45      1       1   0.0000     NaN           NA           NA
##

plot(leuk.km2, mark.time = FALSE, conf.int = TRUE, lty = 1,
    col = c("darkblue", "darkred"))
legend(100, 1, legend = c("Maintain", "Non-main"), lty = 1:2,
    col = c("darkblue", "darkred"))
```




Test for difference (log-rank test)

```
survdiff(Surv(time, status) ~ x, data = leukemia)

## Call:
## survdiff(formula = Surv(time, status) ~ x, data = leukemia)
##
##                  N Observed Expected (O-E)^2/E (O-E)^2/V
## x=Maintained    11        7    10.69      1.27       3.4
## x=Nonmaintained 12       11     7.31      1.86       3.4
##
##  Chisq= 3.4  on 1 degrees of freedom, p= 0.0653
```

### 8.9.3 Cox proportional hazards model

The (semi-parametric) Cox regression model refers to the method first proposed in 1972 by the British statistician Cox in his seminal paper "Regression Models and Life Tables". It is difficult to exaggerate the impact of this paper. In the 1992 *Science Citation Index*, it was cited over 800 times, making it the most highly cited journal article in the entire literature of statistics. In fact, Garfield reported that its cumulative citation count placed it among the top 100 papers in all branches of science.

This enormous popularity can be explained by the fact that, unlike the parametric methods, Cox's method does not require the selection of some particular probability distribution to represent survival times. For this reason, the method is called *semi-parametric*. Cox made two significant innovations. First, he proposed a model that is often referred to as the *proportional hazards model*. Second, he proposed a new estimation method that was later named *maximum partial likelihood*. The term *Cox regression* refers to the combination of the model and the estimation method

Here is an example of Cox regression estimating the benefit of maintaining chemotherapy of with respect to the survival of the patients.

```
leuk.ph <- coxph(Surv(time, status) ~ x, data = leukemia)
summary(leuk.ph)

## Call:
## coxph(formula = Surv(time, status) ~ x, data = leukemia)
##
##   n= 23, number of events= 18
##
##                 coef exp(coef) se(coef)    z Pr(>|z|)
## xNonmaintained 0.916     2.498    0.512 1.79    0.074 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##                exp(coef) exp(-coef) lower .95 upper .95
## xNonmaintained       2.5        0.4     0.916      6.81
##
## Concordance= 0.619  (se = 0.073 )
## Rsquare= 0.137   (max possible= 0.976 )
## Likelihood ratio test= 3.38  on 1 df,   p=0.0658
## Wald test            = 3.2  on 1 df,   p=0.0737
## Score (logrank) test = 3.42  on 1 df,   p=0.0645
##

# plot(leuk.km2, mark.time=F, lty=1:2) lines(survfit(leuk.ph),
# lty=1:2, lwd=2)
```

It is not trivial to estimate the relevance of a variable with survival. If this variable is categorical, you can draw the survival curves and statistically compare them. If the variable under interest is continuous you can arbitrarily discretize it (not advisable) or use many existing performance criteria published so far for survival analysis: hazard ration (see *coxph*), D.index, concordance.index,

time-dependent ROC curve, Brier score,... The survcomp package contains functions to estimate these criteria.

## 8.10 Exercise 11: Survival Analysis

- Use the *colon* dataset from the library survival
- draw the Kaplan-Meier survival curves for the three group of patients encode by 'rx'.
- Use different colors for the curves and plot the lines twice as thick as the default size (parameter *lwd*).
- Which color encodes which group? Add a legend to the plot to make this clear.
- Generate a PDF output of the plot and put it in the website dropbox along with your code.
- Test if the different patient group have significantly different outcome?

# Chapter 9

# Data summaries (including SAS style)

We will look at some of the summary methods in R.

Define datasets

```
data(mtcars)
df <- mtcars
dim(df)

## [1] 32 11
```

View data

```
View(df)
head(df)

##                    mpg cyl disp  hp drat    wt  qsec vs am gear
## Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4
## Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4
## Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4
## Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3
## Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3
## Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3
##                   carb
## Mazda RX4            4
## Mazda RX4 Wag        4
## Datsun 710           1
## Hornet 4 Drive       1
## Hornet Sportabout    2
## Valiant              1

tail(df)

##                 mpg cyl  disp  hp drat    wt qsec vs am gear carb
## Porsche 914-2  26.0   4 120.3  91 4.43 2.140 16.7  0  1    5    2
## Lotus Europa   30.4   4  95.1 113 3.77 1.513 16.9  1  1    5    2
```

```
## Ford Pantera L 15.8   8 351.0 264 4.22 3.170 14.5  0  1    5    4
## Ferrari Dino   19.7   6 145.0 175 3.62 2.770 15.5  0  1    5    6
## Maserati Bora  15.0   8 301.0 335 3.54 3.570 14.6  0  1    5    8
## Volvo 142E     21.4   4 121.0 109 4.11 2.780 18.6  1  1    4    2
```

```
str(df)
```

```
## 'data.frame': 32 obs. of  11 variables:
##  $ mpg : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ...
##  $ cyl : num  6 6 4 6 8 6 8 4 4 6 ...
##  $ disp: num  160 160 108 258 360 ...
##  $ hp  : num  110 110 93 110 175 105 245 62 95 123 ...
##  $ drat: num  3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69 3.92 3.92 ...
##  $ wt  : num  2.62 2.88 2.32 3.21 3.44 ...
##  $ qsec: num  16.5 17 18.6 19.4 17 ...
##  $ vs  : num  0 0 1 1 0 1 0 1 1 1 ...
##  $ am  : num  1 1 1 0 0 0 0 0 0 0 ...
##  $ gear: num  4 4 4 3 3 3 3 4 4 4 ...
##  $ carb: num  4 4 1 1 2 1 4 2 2 4 ...
```

Basic Summary

```
summary(df)
```

```
##       mpg             cyl             disp             hp       
##  Min.   :10.4   Min.   :4.00   Min.   : 71.1   Min.   : 52.0  
##  1st Qu.:15.4   1st Qu.:4.00   1st Qu.:120.8   1st Qu.: 96.5  
##  Median :19.2   Median :6.00   Median :196.3   Median :123.0  
##  Mean   :20.1   Mean   :6.19   Mean   :230.7   Mean   :146.7  
##  3rd Qu.:22.8   3rd Qu.:8.00   3rd Qu.:326.0   3rd Qu.:180.0  
##  Max.   :33.9   Max.   :8.00   Max.   :472.0   Max.   :335.0  
##       drat             wt             qsec             vs        
##  Min.   :2.76   Min.   :1.51   Min.   :14.5   Min.   :0.000  
##  1st Qu.:3.08   1st Qu.:2.58   1st Qu.:16.9   1st Qu.:0.000  
##  Median :3.69   Median :3.33   Median :17.7   Median :0.000  
##  Mean   :3.60   Mean   :3.22   Mean   :17.8   Mean   :0.438  
##  3rd Qu.:3.92   3rd Qu.:3.61   3rd Qu.:18.9   3rd Qu.:1.000  
##  Max.   :4.93   Max.   :5.42   Max.   :22.9   Max.   :1.000  
##        am              gear            carb      
##  Min.   :0.000   Min.   :3.00   Min.   :1.00  
##  1st Qu.:0.000   1st Qu.:3.00   1st Qu.:2.00  
##  Median :0.000   Median :4.00   Median :2.00  
##  Mean   :0.406   Mean   :3.69   Mean   :2.81  
##  3rd Qu.:1.000   3rd Qu.:4.00   3rd Qu.:4.00  
##  Max.   :1.000   Max.   :5.00   Max.   :8.00
```

Using the describe function

```
library(Hmisc)
describe(df)

## df
##
##  11  Variables      32  Observations
## ---------------------------------------------------------------
## mpg
##       n missing  unique    Mean     .05     .10     .25     .50
##      32       0      25   20.09   12.00   14.34   15.43   19.20
##     .75     .90     .95
##   22.80   30.09   31.30
##
## lowest : 10.4 13.3 14.3 14.7 15.0, highest: 26.0 27.3 30.4 32.4 33.9
## ---------------------------------------------------------------
## cyl
##       n missing  unique    Mean
##      32       0       3   6.188
##
## 4 (11, 34%), 6 (7, 22%), 8 (14, 44%)
## ---------------------------------------------------------------
## disp
##       n missing  unique    Mean     .05     .10     .25     .50
##      32       0      27   230.7   77.35   80.61  120.83  196.30
##     .75     .90     .95
##  326.00  396.00  449.00
##
## lowest :  71.1  75.7  78.7  79.0  95.1
## highest: 360.0 400.0 440.0 460.0 472.0
## ---------------------------------------------------------------
## hp
##       n missing  unique    Mean     .05     .10     .25     .50
##      32       0      22   146.7   63.65   66.00   96.50  123.00
##     .75     .90     .95
##  180.00  243.50  253.55
##
## lowest :  52  62  65  66  91, highest: 215 230 245 264 335
## ---------------------------------------------------------------
## drat
##       n missing  unique    Mean     .05     .10     .25     .50
##      32       0      22   3.597   2.853   3.007   3.080   3.695
##     .75     .90     .95
##   3.920   4.209   4.314
##
## lowest : 2.76 2.93 3.00 3.07 3.08, highest: 4.08 4.11 4.22 4.43 4.93
## ---------------------------------------------------------------
```

```
## wt
##       n missing  unique    Mean     .05     .10     .25     .50
##      32       0      29   3.217   1.736   1.956   2.581   3.325
##     .75     .90     .95
##   3.610   4.048   5.293
##
## lowest : 1.513 1.615 1.835 1.935 2.140
## highest: 3.845 4.070 5.250 5.345 5.424
## ---------------------------------------------------------------
## qsec
##       n missing  unique    Mean     .05     .10     .25     .50
##      32       0      30   17.85   15.05   15.53   16.89   17.71
##     .75     .90     .95
##   18.90   19.99   20.10
##
## lowest : 14.50 14.60 15.41 15.50 15.84
## highest: 19.90 20.00 20.01 20.22 22.90
## ---------------------------------------------------------------
## vs
##       n missing  unique     Sum    Mean
##      32       0       2      14  0.4375
## ---------------------------------------------------------------
## am
##       n missing  unique     Sum    Mean
##      32       0       2      13  0.4062
## ---------------------------------------------------------------
## gear
##       n missing  unique    Mean
##      32       0       3   3.688
##
## 3 (15, 47%), 4 (12, 38%), 5 (5, 16%)
## ---------------------------------------------------------------
## carb
##       n missing  unique    Mean
##      32       0       6   2.812
##
##            1  2 3  4 6 8
## Frequency  7 10 3 10 1 1
## %         22 31 9 31 3 3
## ---------------------------------------------------------------
```

## 9.1 1,2 and 3-way Cross Tabulations

Basic Tables

```
table(df$cyl)

##
##  4  6  8
## 11  7 14

table(df$cyl, df$gear)

##
##      3  4  5
##   4  1  8  2
##   6  2  4  1
##   8 12  0  2

# Number of cyclinders, numbers of gear, transmission type
table(df$cyl, df$gear, df$am)

## , ,  = 0
##
##
##      3  4  5
##   4  1  2  0
##   6  2  2  0
##   8 12  0  0
##
## , ,  = 1
##
##
##      3  4  5
##   4  0  6  2
##   6  0  2  1
##   8  0  0  2
##
```

Crosstabulation using formula format

```
xtabs(cyl ~ gear, df)

## gear
##   3   4   5
## 112  56  30

xtabs(cyl ~ gear + am + vs, df)

## , , vs = 0
##
##     am
```

```
## gear  0  1
##    3 96  0
##    4  0 12
##    5  0 26
##
## , , vs = 1
##
##     am
## gear  0  1
##    3 16  0
##    4 20 24
##    5  0  4
##
```

### 9.1.1 Contingency Tables

Standard R tables

```
`?`(ftable)
ftable(df$cyl, df$vs, df$am, df$gear, row.vars = c(2, 4),
    dnn = c("Cylinders", "V/S", "Transmission", "Gears"))

##            Cylinders     4     6     8
##            Transmission  0  1  0  1  0  1
## V/S Gears
## 0   3                    0  0  0  0 12  0
##     4                    0  0  0  2  0  0
##     5                    0  1  0  1  0  2
## 1   3                    1  0  2  0  0  0
##     4                    2  6  2  0  0  0
##     5                    0  1  0  0  0  0


ftable(df$cyl, df$vs, df$am, df$gear, row.vars = c(2, 3),
    dnn = c("Cylinders", "V/S", "Transmission", "Gears"))

##                  Cylinders  4        6        8
##                  Gears      3  4  5  3  4  5  3  4  5
## V/S Transmission
## 0   0                       0  0  0  0  0  0 12  0  0
##     1                       0  0  1  0  2  1  0  0  2
## 1   0                       1  2  0  2  2  0  0  0  0
##     1                       0  6  1  0  0  0  0  0  0
```

Two way cross tabulation in SAS format

```
library(gmodels)
CrossTable(df$cyl, df$gear, format = "SAS")

##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  32
##
##
##              | df$gear
##       df$cyl |         3 |         4 |         5 | Row Total |
## -------------|-----------|-----------|-----------|-----------|
##            4 |         1 |         8 |         2 |        11 |
##              |     3.350 |     3.640 |     0.046 |           |
##              |     0.091 |     0.727 |     0.182 |     0.344 |
##              |     0.067 |     0.667 |     0.400 |           |
##              |     0.031 |     0.250 |     0.062 |           |
## -------------|-----------|-----------|-----------|-----------|
##            6 |         2 |         4 |         1 |         7 |
##              |     0.500 |     0.720 |     0.008 |           |
##              |     0.286 |     0.571 |     0.143 |     0.219 |
##              |     0.133 |     0.333 |     0.200 |           |
##              |     0.062 |     0.125 |     0.031 |           |
## -------------|-----------|-----------|-----------|-----------|
##            8 |        12 |         0 |         2 |        14 |
##              |     4.505 |     5.250 |     0.016 |           |
##              |     0.857 |     0.000 |     0.143 |     0.438 |
##              |     0.800 |     0.000 |     0.400 |           |
##              |     0.375 |     0.000 |     0.062 |           |
## -------------|-----------|-----------|-----------|-----------|
## Column Total |        15 |        12 |         5 |        32 |
##              |     0.469 |     0.375 |     0.156 |           |
## -------------|-----------|-----------|-----------|-----------|
##
##

CrossTable(df$cyl, df$gear, expected = TRUE, format = "SAS")
```

```
## Warning: Chi-squared approximation may be incorrect

##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |              Expected N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  32
##
##
##              | df$gear
##       df$cyl |         3 |         4 |         5 | Row Total |
## -------------|-----------|-----------|-----------|-----------|
##            4 |         1 |         8 |         2 |        11 |
##              |     5.156 |     4.125 |     1.719 |           |
##              |     3.350 |     3.640 |     0.046 |           |
##              |     0.091 |     0.727 |     0.182 |     0.344 |
##              |     0.067 |     0.667 |     0.400 |           |
##              |     0.031 |     0.250 |     0.062 |           |
## -------------|-----------|-----------|-----------|-----------|
##            6 |         2 |         4 |         1 |         7 |
##              |     3.281 |     2.625 |     1.094 |           |
##              |     0.500 |     0.720 |     0.008 |           |
##              |     0.286 |     0.571 |     0.143 |     0.219 |
##              |     0.133 |     0.333 |     0.200 |           |
##              |     0.062 |     0.125 |     0.031 |           |
## -------------|-----------|-----------|-----------|-----------|
##            8 |        12 |         0 |         2 |        14 |
##              |     6.562 |     5.250 |     2.188 |           |
##              |     4.505 |     5.250 |     0.016 |           |
##              |     0.857 |     0.000 |     0.143 |     0.438 |
##              |     0.800 |     0.000 |     0.400 |           |
##              |     0.375 |     0.000 |     0.062 |           |
## -------------|-----------|-----------|-----------|-----------|
## Column Total |        15 |        12 |         5 |        32 |
##              |     0.469 |     0.375 |     0.156 |           |
## -------------|-----------|-----------|-----------|-----------|
##
```

```
##
## Statistics for All Table Factors
##
##
## Pearson's Chi-squared test
## ------------------------------------------------------------
## Chi^2 =  18.04     d.f. =  4     p =  0.001214
##
##
##
```

Two way cross tabulation in SPSS format

```
library(gmodels)
CrossTable(df$cyl, df$gear, format = "SPSS")
```

```
##
##    Cell Contents
## |-------------------------|
## |                   Count |
## | Chi-square contribution |
## |             Row Percent |
## |          Column Percent |
## |           Total Percent |
## |-------------------------|
##
## Total Observations in Table:  32
##
##              | df$gear
##       df$cyl |         3  |         4  |         5  | Row Total |
## -------------|------------|------------|------------|-----------|
##            4 |         1  |         8  |         2  |        11 |
##              |     3.350  |     3.640  |     0.046  |           |
##              |     9.091% |    72.727% |    18.182% |    34.375% |
##              |     6.667% |    66.667% |    40.000% |           |
##              |     3.125% |    25.000% |     6.250% |           |
## -------------|------------|------------|------------|-----------|
##            6 |         2  |         4  |         1  |         7 |
##              |     0.500  |     0.720  |     0.008  |           |
##              |    28.571% |    57.143% |    14.286% |    21.875% |
##              |    13.333% |    33.333% |    20.000% |           |
##              |     6.250% |    12.500% |     3.125% |           |
## -------------|------------|------------|------------|-----------|
##            8 |        12  |         0  |         2  |        14 |
##              |     4.505  |     5.250  |     0.016  |           |
##              |    85.714% |     0.000% |    14.286% |    43.750% |
```

```
##              |   80.000% |    0.000% |   40.000% |           |
##              |   37.500% |    0.000% |    6.250% |           |
## -------------|-----------|-----------|-----------|-----------|
## Column Total |       15  |       12  |        5  |       32  |
##              |   46.875% |   37.500% |   15.625% |           |
## -------------|-----------|-----------|-----------|-----------|
##
##
```

```
CrossTable(df$cyl, df$gear, expected = TRUE, format = "SPSS")
```

```
## Warning: Chi-squared approximation may be incorrect
```

```
##
##    Cell Contents
## |-------------------------|
## |                   Count |
## |         Expected Values |
## | Chi-square contribution |
## |             Row Percent |
## |          Column Percent |
## |           Total Percent |
## |-------------------------|
##
## Total Observations in Table:  32
##
##              | df$gear
##       df$cyl |         3 |         4 |         5 | Row Total |
## -------------|-----------|-----------|-----------|-----------|
##            4 |         1 |         8 |         2 |        11 |
##              |     5.156 |     4.125 |     1.719 |           |
##              |     3.350 |     3.640 |     0.046 |           |
##              |     9.091% |    72.727% |    18.182% |    34.375% |
##              |     6.667% |    66.667% |    40.000% |           |
##              |     3.125% |    25.000% |     6.250% |           |
## -------------|-----------|-----------|-----------|-----------|
##            6 |         2 |         4 |         1 |         7 |
##              |     3.281 |     2.625 |     1.094 |           |
##              |     0.500 |     0.720 |     0.008 |           |
##              |    28.571% |    57.143% |    14.286% |    21.875% |
##              |    13.333% |    33.333% |    20.000% |           |
##              |     6.250% |    12.500% |     3.125% |           |
## -------------|-----------|-----------|-----------|-----------|
##            8 |        12 |         0 |         2 |        14 |
##              |     6.562 |     5.250 |     2.188 |           |
##              |     4.505 |     5.250 |     0.016 |           |
```

```
##              |   85.714% |    0.000% |   14.286% |   43.750% |
##              |   80.000% |    0.000% |   40.000% |           |
##              |   37.500% |    0.000% |    6.250% |           |
## -------------|-----------|-----------|-----------|-----------|
## Column Total |       15  |       12  |        5  |       32  |
##              |   46.875% |   37.500% |   15.625% |           |
## -------------|-----------|-----------|-----------|-----------|
##
##
## Statistics for All Table Factors
##
##
## Pearson's Chi-squared test
## ------------------------------------------------------------
## Chi^2 =  18.04     d.f. =  4     p =  0.001214
##
##
##
##        Minimum expected frequency: 1.094
## Cells with Expected Frequency < 5: 6 of 9 (66.67%)
##
```

# Chapter 10

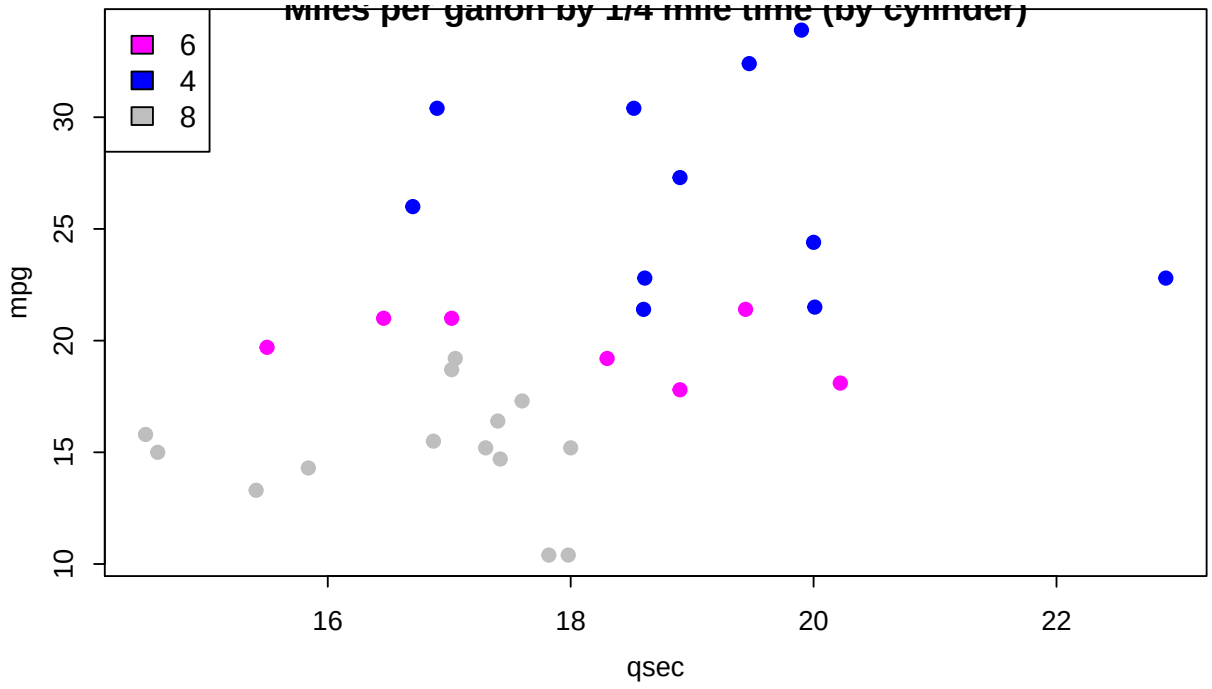
# Exploratory Data Analysis

Basic scatterplot

```
attach(df)

## The following object(s) are masked from 'package:ggplot2':
##
##     mpg

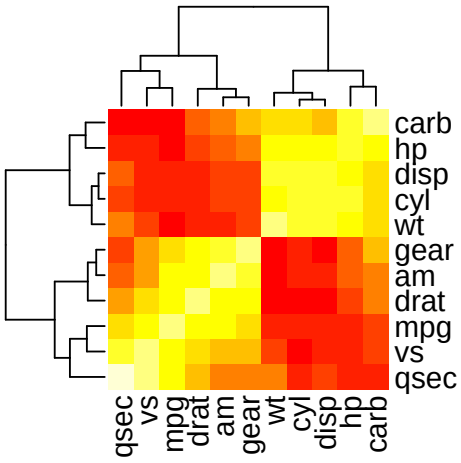
plot(qsec, mpg, col=cyl, pch=19,
     main="Miles per gallon by 1/4 mile time (by cylinder)")
legend("topleft", legend=unique(cyl), fill=unique(cyl))
```



## 10.1 Hierarchical Cluster Analysis

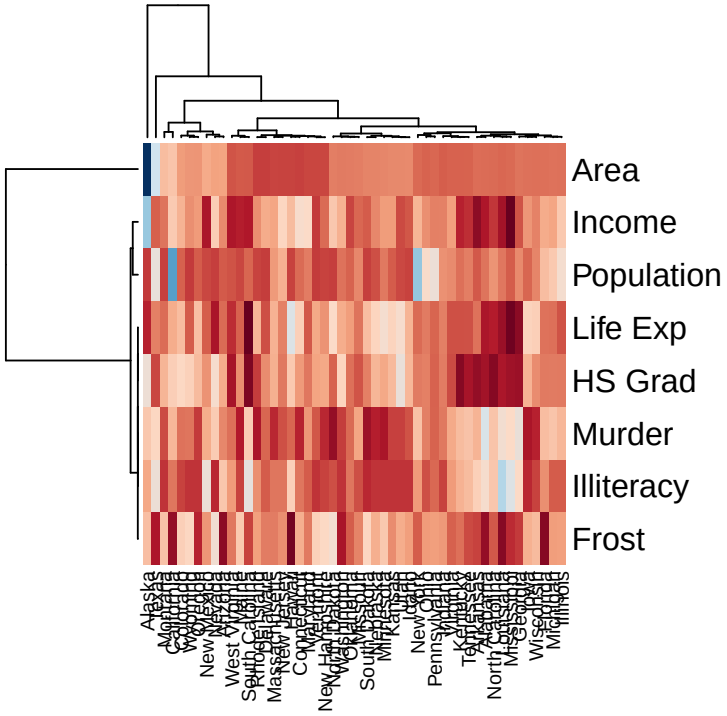
Or calculate correlation and view on heatmap

```
heatmap(cor(df))
```

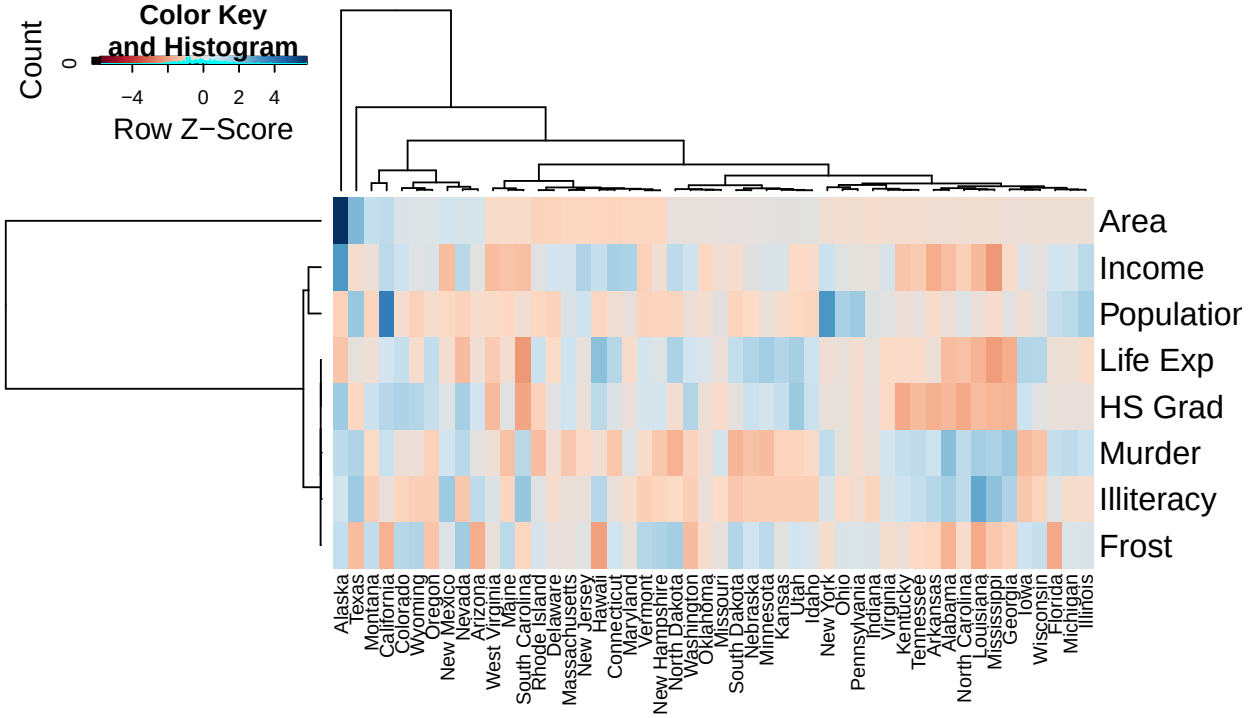



We can look at the US state fact and figure information in the package state, which contains a matrix called state.x77 containing information on 50 US states (50 rows) on population, income, Illiteracy, life expectancy, murder, high school graduation, number of days with frost, and area (8 columns). The default clustering of this uses a rather ugly red-yellow color scheme which I changed to a red/brown-blue.

```
require(RColorBrewer)
hmcol <- colorRampPalette(brewer.pal(10, "RdBu"))(500)
heatmap(t(state.x77), col = hmcol, scale = "row")
```

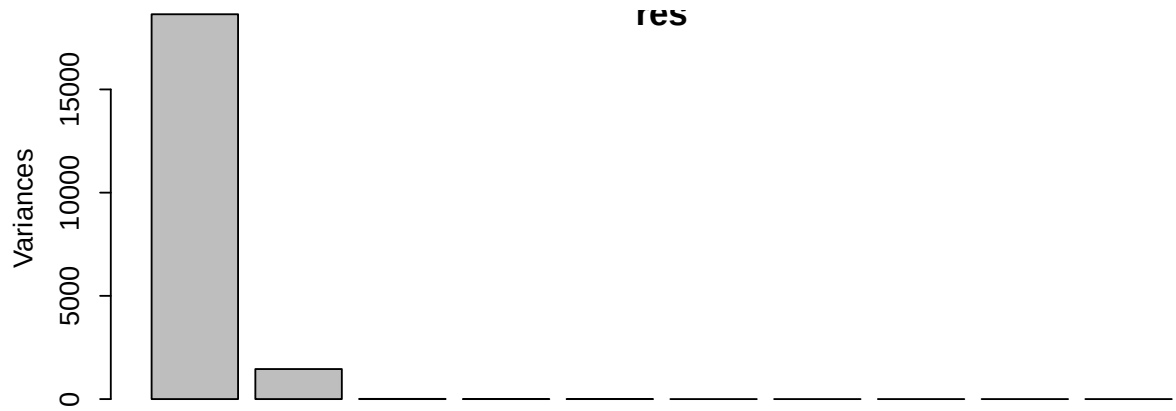



```
heatmap.2(t(state.x77), col = hmcol, scale = "row", trace = "none")
```

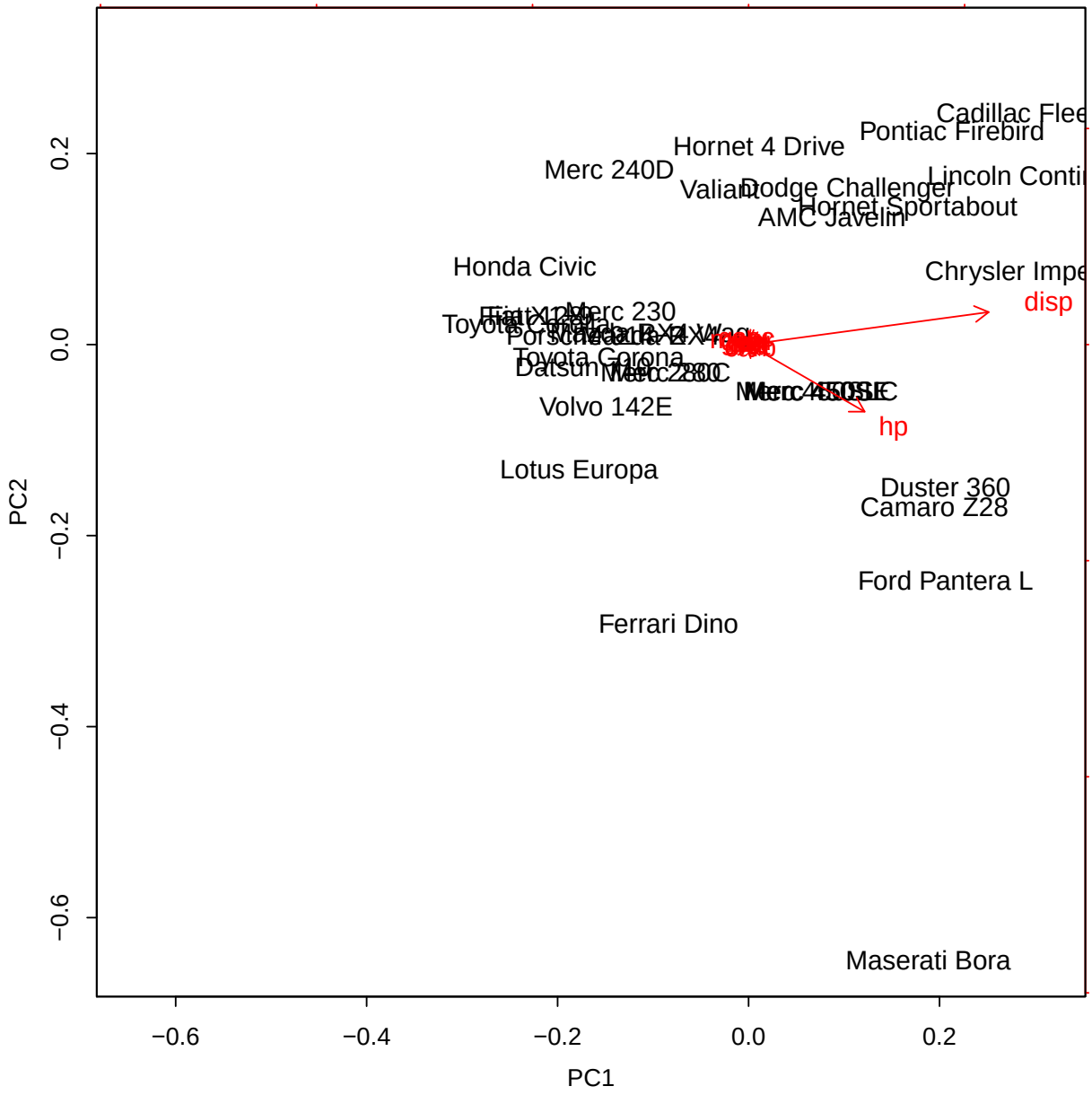



## 10.2 Principcal component analysis

```
res <- prcomp(df)
screeplot(res)
```




```
biplot(res)
```



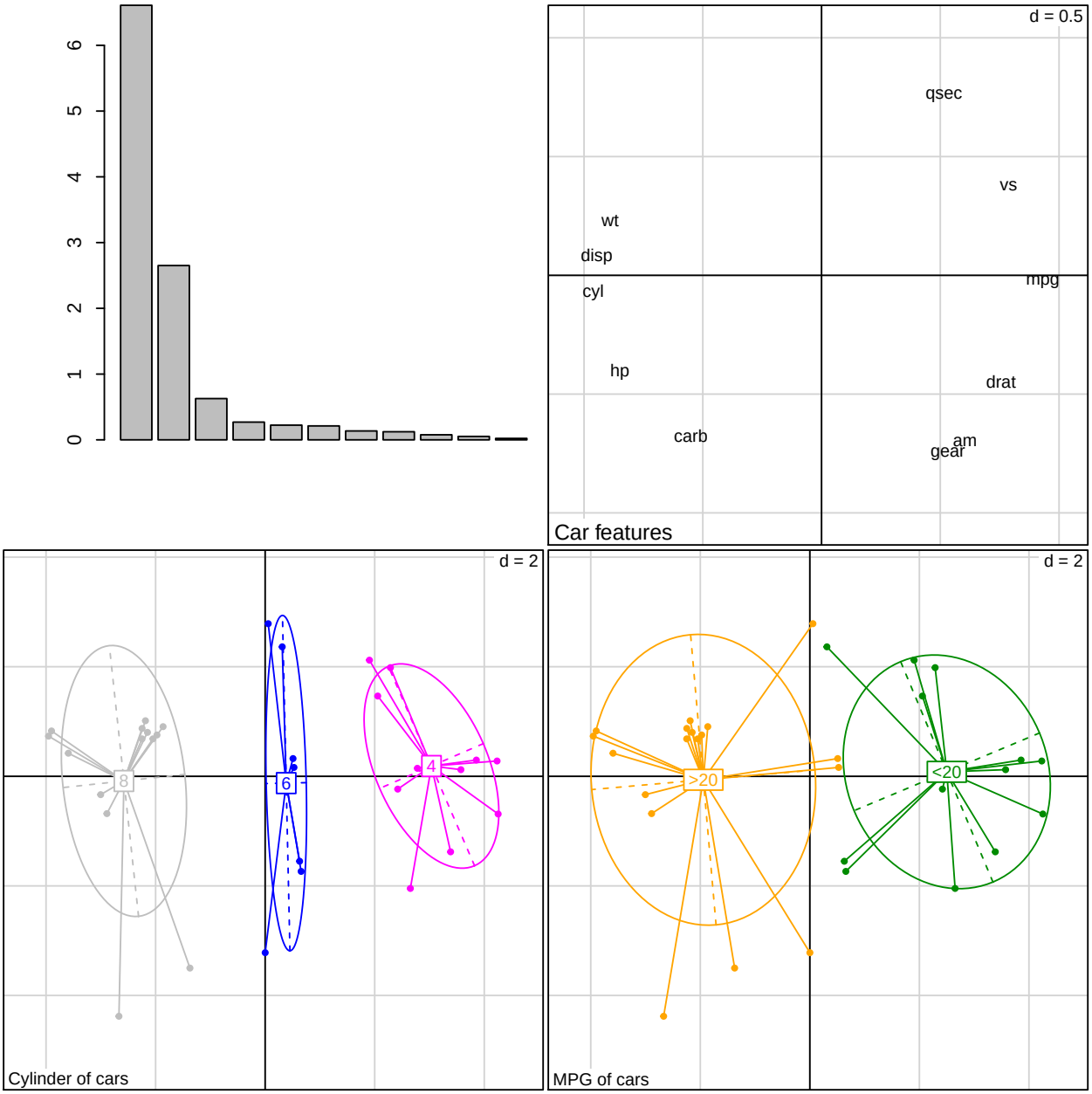

Or using fast.prcomp (optimized for big wide datasets)

```
res <- fast.prcomp(df)
```

Or using dudi.pca in ade4. The R package has some very nicely graphicing tools for visualizing the results of PCA

```
res <- dudi.pca(df, scan = FALSE)
par(mfrow = c(2, 2))
barplot(res$eig)
s.label(res$co, sub = "Car features", boxes = FALSE)
s.class(res$li, factor(cyl), col = unique(cyl), sub = "Cylinder of cars")
```

```
s.class(res$li, factor(mpg < 20, labels = c("<20", ">20")),
    sub = "MPG of cars", col = c("green4", "orange"))
```




## 10.3 Multivariate methods for exploring covariance across multiple data sets

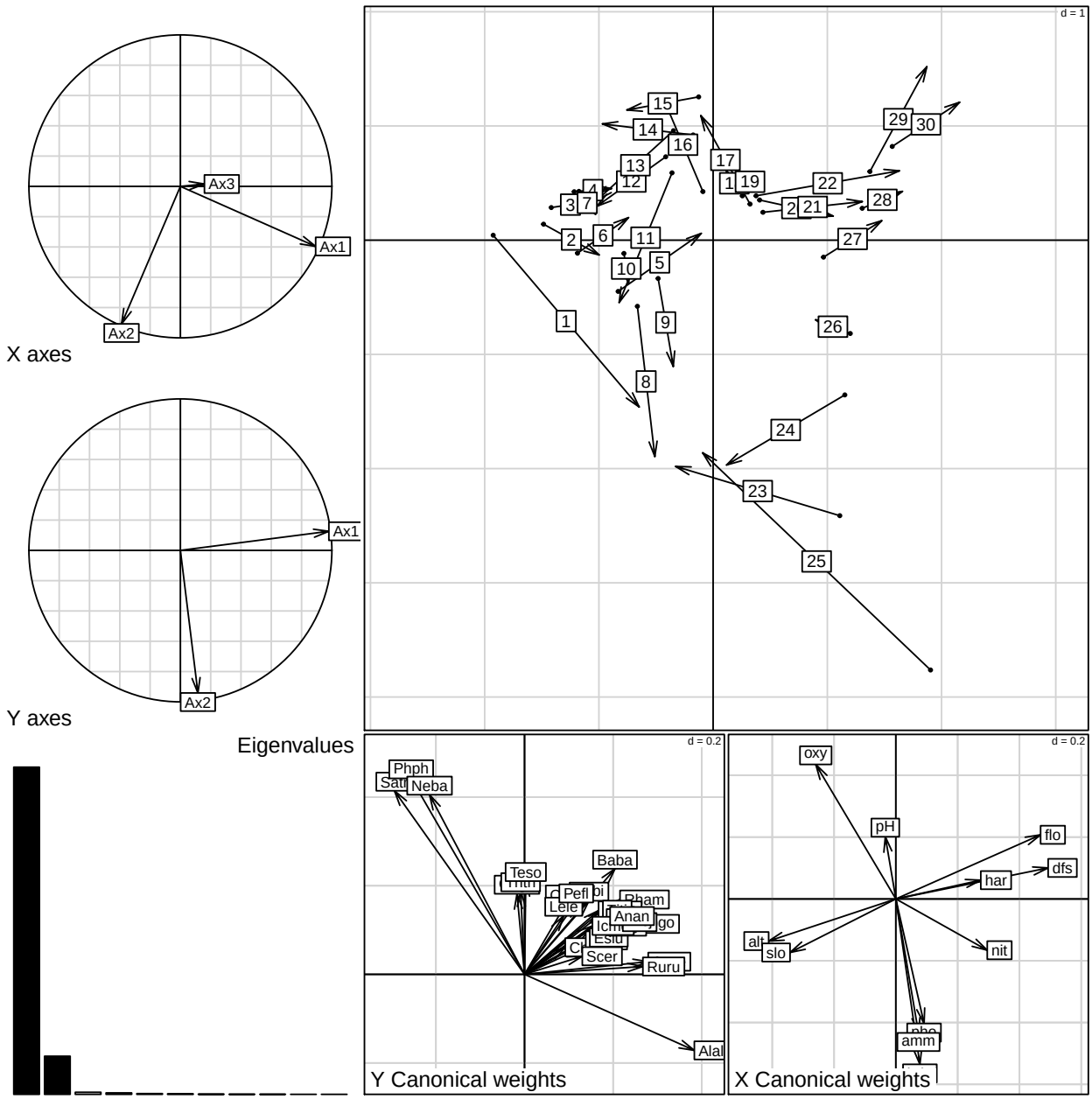
Often we have 2 or more matrices either reflecting different time points of the same sample population or different measurements on the same population and we wish to explore the correlation or covariance between these datasets.

Lets look at the doubs data in the ade4 package. This data set gives environmental variables, fish species and spatial coordinates for 30 sites

```
require(ade4)
data(doubs)
lapply(doubs, head, 2)

## $env
##   dfs alt   slo flo pH har pho nit amm oxy bdo
## 1   3 934 6.176  84 79  45   1  20   0 122  27
## 2  22 932 3.434 100 80  40   2  20  10 103  19
##
## $fish
##   Cogo Satr Phph Neba Thth Teso Chna Chto Lele Lece Baba Spbi Gogo
## 1    0    3    0    0    0    0    0    0    0    0    0    0    0
## 2    0    5    4    3    0    0    0    0    0    0    0    0    0
##   Eslu Pefl Rham Legi Scer Cyca Titi Abbr Icme Acce Ruru Blbj Alal
## 1    0    0    0    0    0    0    0    0    0    0    0    0    0
## 2    0    0    0    0    0    0    0    0    0    0    0    0    0
##   Anan
## 1    0
## 2    0
##
## $xy
##    x  y
## 1 88  7
## 2 94 14
##
## $species
##           Scientific       French           English code
## 1       Cottus gobio       chabot european bullhead Cogo
## 2 Salmo trutta fario truite fario       brown trout Satr
##
```

```
dudi1 <- dudi.pca(doubs$env, scale = TRUE, scannf = FALSE,
    nf = 3)
dudi2 <- dudi.pca(doubs$fish, scale = FALSE, scannf = FALSE,
    nf = 2)
coin1 <- coinertia(dudi1, dudi2, scan = FALSE, nf = 2)
plot(coin1)
```




```
# s.arrow(coin1$l1, clab = 0.7)
```

# Chapter 11

# Writing Reports and Reproducible Research

The aim of reproducible research is to provide code such that an experiement/analysis can be easily repeated. The best approach is to create a document of results, in which the code to generate those results are embedded.

## 11.1 Stitch and Spin

There are simplest way to generate reproducible documents in R is to generate a report from a simple R script.

The knitr calls Roxgyen to do this. Anything written after a comment ## is converted to text, all other text is assumed to be R code and will be executed using the function *spin*.

```
spin("myScript.R")  ## Create a markdown file (default
spin("myScript.R", format = "Rhtml")  # create webpage
spin("myScript.R", format = "Rtex")  # latex file
```

For more options see help on spin (?spin). The markdown file can be easily convert to MSOffice using pandoc. There is an example below.

Another function from Knitr called *stitch()* will insert an R script into a template to create a simple report. Knitr supplies a template web page (html), markdown and latex file.

## 11.2 Sweave

Therefore there is broad support for Sweave. Most of the documentation in R is written in Sweave files

Seaves "weaves" R (or S) code into latex. This document is written in Sweave, but had recently been converted to knitr (more about how to do that later).

You can also write R code embedded in a html template file and process this using Sweave

In each case the native document format is written tex or html, but R code is put in chunks. These chunks are marked by <<>> and @.

You can also put shorter snippets of R code in text using the function eg \Sexprs{a3+ will evaluate a3 +

### 11.2.1 Converting an Rnw file in Sweave to Knitr

Whilst Sweave is still used widely, increasingly its being replaced by knitr which has more functionality.

Its easy to convert a Sweave rnw file to a knitr rnw

- knitr does not allow spaces in code chunks, so either remove or subsitute spaces for any other character eg

```
<<My Code Example 1>>= ## Allowed by Sweave not knitr
@
<<MyCodeExample1>>=    ## Ok for either Sweave or knitr
 @
```

- knitr has many more option for formating code withint the document. Most of these are not available in Sweave so these do not affect conversion. For example, Sweave has the results options verbatim/hide/tex, knitr has options 'markup', 'hide', 'asis'. Note knitr requires the option be enclosed in single quotes.

```
<<M1, results=hide>>=  ## Allowed by Sweave not knitr
 @
<<M1, results='hide'>>= ## Ok for knitr
 @
```

## 11.3 knitr, knit, purl

knitr is a relatively new R package that extends Sweave, pdfSweave or cacheSweave and can created R code embedded in many different formats. It has several features, including its ability to cache results and nice colors of code for easier reading.

## 11.4 Creating Markdown Documents

Markdown is a very simple formatting syntax for authoring web pages which can be converted to numerous format. R markdown files conventionaly have the file ending "rmd".

Within a markdown document you embed R code in triple single back quotes. Within the curly braces, you specificy you are running r code and can give the code chunk a label. eg

```
```{r MyRCode}

```{r}
summary(cars)
```
```

You can also embed plots, for example:
```

```
```{r fig.width=7, fig.height=6}
plot(cars)
```
```

Then to create the markdown file with embedded R code and results, run the command knit.

### 11.4.1 Converting markdown to other file formats including MSOffice

Markdown is versatible and its simplicity means it can be converted to numerous formats, including pdf and html files, but also MSOffice files or HTML5 slides using a FREE softare called pandoc `http://johnmacfarlane.net/pandoc/index.html`

I have much more details and examples on the webpage `http://bcb.dfci.harvard.edu/~aedin/courses/ReproducibleResearch/`

# Chapter 12

# Solutions to Exercises

## 12.1 Solution to Exercise 1

Women Data

```
myURL <- "http://bcb.dfci.harvard.edu/~aedin/courses/R/Women.txt"
women <- read.table(myURL, sep = "\t", header = TRUE)
`?`(colnames)
women
```

```
##    height weight age
## 1      58    115  33
## 2      59    117  34
## 3      60    120  37
## 4      61    123  31
## 5      62    126  31
## 6      63    129  34
## 7      64    132  31
## 8      65    135  39
## 9      66    139  35
## 10     67    142  34
## 11     68    146  34
## 12     69    150  36
## 13     70    154  33
## 14     71    159  30
## 15     72    164  37
```

```
class(women)
```

```
## [1] "data.frame"
```

```
str(women)
```

```
## 'data.frame': 15 obs. of  3 variables:
##  $ height: int  58 59 60 61 62 63 64 65 66 67 ...
##  $ weight: int  115 117 120 123 126 129 132 135 139 142 ...
##  $ age   : int  33 34 37 31 31 34 31 39 35 34 ...
```

```
nrow(women)

## [1] 15

ncol(women)

## [1] 3

dim(women)

## [1] 15  3

summary(women)

##      height          weight          age
##  Min.   :58.0   Min.   :115   Min.   :30.0
##  1st Qu.:61.5   1st Qu.:124   1st Qu.:32.0
##  Median :65.0   Median :135   Median :34.0
##  Mean   :65.0   Mean   :137   Mean   :33.9
##  3rd Qu.:68.5   3rd Qu.:148   3rd Qu.:35.5
##  Max.   :72.0   Max.   :164   Max.   :39.0

colMeans(women)

## height weight    age
##  65.00 136.73  33.93

colnames(women)

## [1] "height" "weight" "age"

`?`(colnames)
sum(women$weight < 120)

## [1] 2

women[order(women$weight), ]

##    height weight age
## 1      58    115  33
## 2      59    117  34
## 3      60    120  37
## 4      61    123  31
## 5      62    126  31
## 6      63    129  34
## 7      64    132  31
## 8      65    135  39
## 9      66    139  35
## 10     67    142  34
```

```
## 11      68    146   34
## 12      69    150   36
## 13      70    154   33
## 14      71    159   30
## 15      72    164   37
```

```
mean(women$height[women$weight > 124 & women$weight < 150])
```

```
## [1] 65
```

```
rownames(women)[5] <- "Lucy"
```

## 12.2 Solution to Exercise 2

ToothGrowth data

```
TG <- read.table("ToothGrowth.txt", sep = "\t", header = TRUE)
TG2 <- read.csv("ToothGrowth.csv")
nrow(TG)
```

```
## [1] 60
```

```
nrow(TG2)
```

```
## [1] 60
```

```
mean(TG$len)
```

```
## [1] 18.81
```

```
sd(TG$len)
```

```
## [1] 7.649
```

```
mean(TG2$len)
```

```
## [1] 18.81
```

```
sd(TG2$len)
```

```
## [1] 7.649
```

```
anova(lm(len ~ supp + dose, data = TG))
```

```
## Analysis of Variance Table
##
## Response: len
##           Df Sum Sq Mean Sq F value  Pr(>F)
## supp       1    205     205    11.4  0.0013 **
## dose       1   2224    2224   124.0 6.3e-16 ***
## Residuals 57   1023      18
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## 12.3 Solution to Exercise 3

```
women <- read.table("http://bcb.dfci.harvard.edu/~aedin/courses/R/WomenStats
    sep = "\t", header = TRUE)
nrow(women)

## [1] 16

ncol(women)

## [1] 1

colnames(women)

## [1] "X.html."

summary(women)

##                                   X.html.
##  </div>                               :2
##  </body>                              :1
##  </head>                              :1
##  </html>                              :1
##  </td></tr></table>                   :1
##  <body style=background-color:#fff>:1
##  (Other)                              :9

rownames(women) <- LETTERS[1:nrow(women)]
write.table(women, "modifedWomen.txt", sep = "\t")
women2 <- read.table("modifedWomen.txt", sep = "\t", as.is = TRUE,
    header = TRUE)
```

## 12.4 Solution to Exercise 4

```
myVec <- c(LETTERS[1:20], seq(0, 200, 10))
myVec

##  [1] "A"   "B"   "C"   "D"   "E"   "F"   "G"   "H"   "I"   "J"
## [11] "K"   "L"   "M"   "N"   "O"   "P"   "Q"   "R"   "S"   "T"
## [21] "0"   "10"  "20"  "30"  "40"  "50"  "60"  "70"  "80"  "90"
## [31] "100" "110" "120" "130" "140" "150" "160" "170" "180" "190"
## [41] "200"

myVec <- sample(myVec)
myVec

##  [1] "T"   "70"  "80"  "200" "160" "130" "Q"   "M"   "100" "120"
## [11] "180" "30"  "S"   "110" "50"  "N"   "I"   "190" "C"   "10"
## [21] "A"   "F"   "140" "P"   "0"   "20"  "B"   "G"   "150" "J"
## [31] "40"  "L"   "60"  "90"  "H"   "E"   "170" "R"   "K"   "D"
## [41] "O"

cat(myVec, file = "myVec.txt")
scan("myVec.txt", n = 10, what = "text")

##  [1] "T"   "70"  "80"  "200" "160" "130" "Q"   "M"   "100" "120"

scan("myVec.txt", n = 10, what = 123)

## Error: scan() expected 'a real', got 'T'

scan("myVec.txt", n = 10, what = TRUE)

## Error: scan() expected 'a logical', got '70'
```

## 12.5 Solution to Exercise 5

```
for (i in 1:10) print(2^i)

## [1] 2
## [1] 4
## [1] 8
## [1] 16
## [1] 32
## [1] 64
## [1] 128
## [1] 256
## [1] 512
## [1] 1024
```

```
x <- 1
while (2^x < 1000) {
    print(2^x)
    x <- x + 1
}
```

```
## [1] 2
## [1] 4
## [1] 8
## [1] 16
## [1] 32
## [1] 64
## [1] 128
## [1] 256
## [1] 512
```

## 12.6 Solution to Exercise 6

```
require(XML)
## Reads all the tables in the webpage into a list
worldPop <- readHTMLTable("http://en.wikipedia.org/wiki/World_population")

# There are 19 tables
class(worldPop)
```

```
## [1] "list"
```

```
length(worldPop)
```

```
## [1] 19
```

```
# With the following names, so of the names are very long so we
# have trucated them using substr
substr(names(worldPop), 1, 60)
```

```
##  [1] "NULL"
##  [2] "toc"
##  [3] "NULL"
##  [4] "World population milestones (USCB estimates)"
##  [5] "The 10 countries with the largest total population:"
##  [6] "10 most densely populated countries (with population above 1"
##  [7] "Countries ranking highly in terms of both total population ("
##  [8] "NULL"
```

```
##  [9] "UN (medium variant  2010 revision) and US Census Burea"
## [10] "UN 2008 estimates and medium variant projections (in million"
## [11] "World historical and predicted populations (in millions)[101"
## [12] "World historical and predicted populations by percentage dis"
## [13] "Estimated world and regional populations at various dates (i"
## [14] "Starting at 500 million"
## [15] "Starting at 375 million"
## [16] "NULL"
## [17] "NULL"
## [18] "NULL"
## [19] "NULL"

worldPop <- worldPop[[13]]  # Just look at Table 13
```

To **tidy up this tables**, lets look at dates after 1750AD, so lets remove rows 1 to 14 as these have only world population information. Also we will remove row 32 which is just column names

```
## Now lets check the structure of the table The data are factors,
## lets convert to characters as these are easier to edit
str(worldPop)

## 'data.frame': 31 obs. of  9 variables:
##  $ Year                 : Factor w/ 31 levels "10,000 BC","1000",..: 27 1
##  $ World                : Factor w/ 31 levels "< 0.015","1",..: 1 2 14 22
##  $ Africa               : Factor w/ 18 levels "","1,022","106",..: 1 1 1
##  $ Asia                 : Factor w/ 18 levels "","1,398","1,542",..: 1 1
##  $ Europe               : Factor w/ 18 levels "","163","203",..: 1 1 1 1
##  $ Latin America[Note 1]: Factor w/ 18 levels "","16","167",..: 1 1 1 1 1
##  $ Northern America     : Factor w/ 18 levels "","172","187",..: 1 1 1 1
##  $ Oceania              : Factor w/ 16 levels "","12.8","14.3",..: 1 1 1
##  $ Notes                : Factor w/ 5 levels "","[103]","[104]",..: 2 1 1



## We need to convert them to numeric. But first lets get rid of
## the BC and $<$ characters

worldPop <- apply(worldPop, 2, as.character)
str(worldPop)

##  chr [1:31, 1:9] "70,000 BC" "10,000 BC" "9000 BC" ...
##  - attr(*, "dimnames")=List of 2
##   ..$ : NULL
##   ..$ : chr [1:9] "Year" "World" "Africa" "Asia" ...
```

```
## Remove rows 1-14, 32
worldPop <- worldPop[-c(1:14, 32), ]

## Remove 'Notes' Column
worldPop <- worldPop[, -9]

## Lets convert to numeric and remove the period
worldPop <- apply(worldPop, 2, function(x) as.numeric(sub(",",
    "", x)))
worldPop <- as.data.frame(worldPop)

## Lets get rid of 'Note 1' To get rid of the square brakets we
## have to put \\ before them
colnames(worldPop) <- sub("\\[Note 1\\]", "", colnames(worldPop))
str(worldPop)

## 'data.frame': 17 obs. of  8 variables:
##  $ Year            : num  1750 1800 1850 1900 1950 ...
##  $ World           : num  791 978 1262 1650 2519 ...
##  $ Africa          : num  106 107 111 133 221 247 277 314 357 408 ...
##  $ Asia            : num  502 635 809 947 1398 ...
##  $ Europe          : num  163 203 276 408 547 575 601 634 656 675 ...
##  $ Latin America   : num  16 24 38 74 167 191 209 250 285 322 ...
##  $ Northern America: num  2 7 26 82 172 187 204 219 232 243 ...
##  $ Oceania         : num  2 2 2 6 12.8 14.3 15.9 17.6 19.4 21.5 ...


# In what year did the population of Europe, Africa and Asia exceed
# 500 million?
for (i in c("Europe", "Asia", "Africa")) {
    print(paste(i, min(worldPop$Year[worldPop[, i] > 500]), sep = "  "))
}

## [1] "Europe  1950"
## [1] "Asia  1750"
## [1] "Africa  1985"
```

Now that the data are tidy, lets create the bonus plot

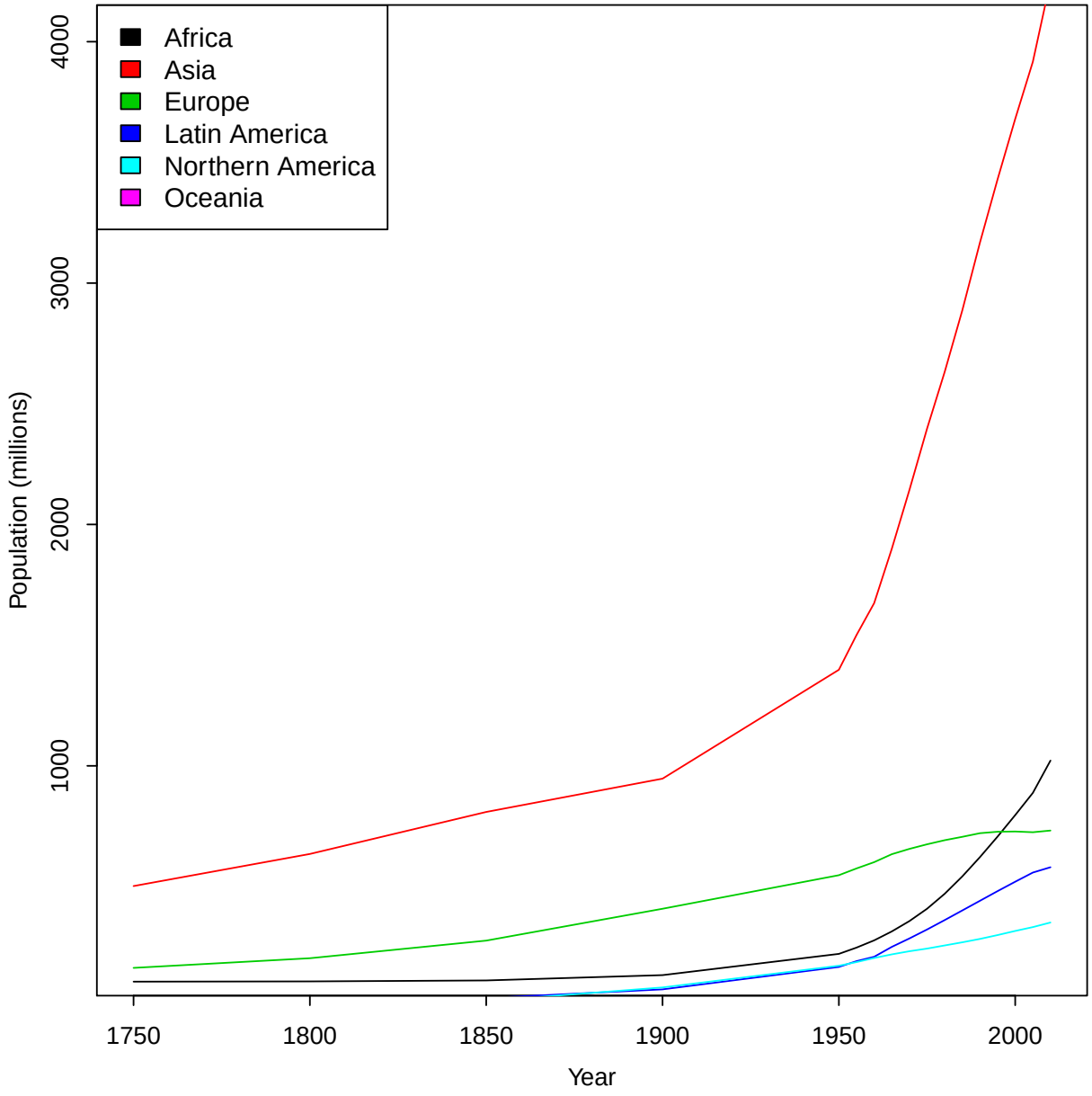
```
## Make a vector regions (exclude World and Year)
regions <- colnames(worldPop)[-c(1:2)]
regions

## [1] "Africa"           "Asia"             "Europe"
## [4] "Latin America"    "Northern America" "Oceania"
```

```r
## Create a empty Plot
plot(worldPop$Year, worldPop$Asia, xlab = "Year", ylab = "Population (millio
    col = "red", type = "n", ylim = c(200, 4000))

for (i in 1:length(regions)) {
    region <- regions[i]
    print(region)
    lines(worldPop$Year, worldPop[, region], col = i, type = "l")
}
```

```
## [1] "Africa"
## [1] "Asia"
## [1] "Europe"
## [1] "Latin America"
## [1] "Northern America"
## [1] "Oceania"
```

```r

legend("topleft", regions, fil = 1:length(regions))
```



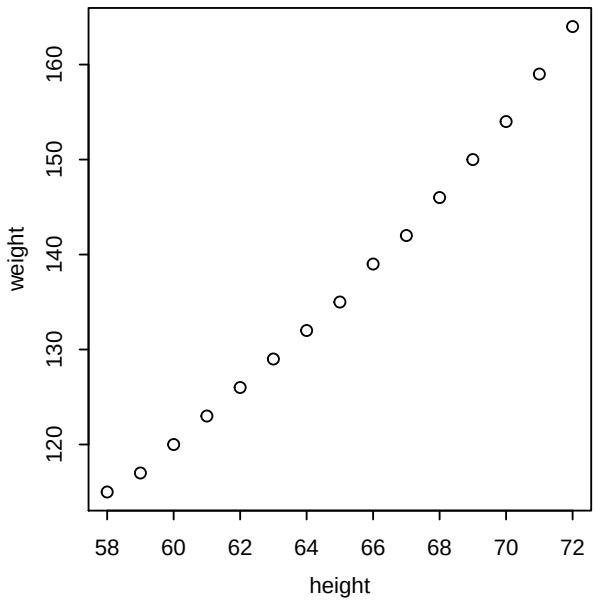

## 12.7 Solution to Exercise 7

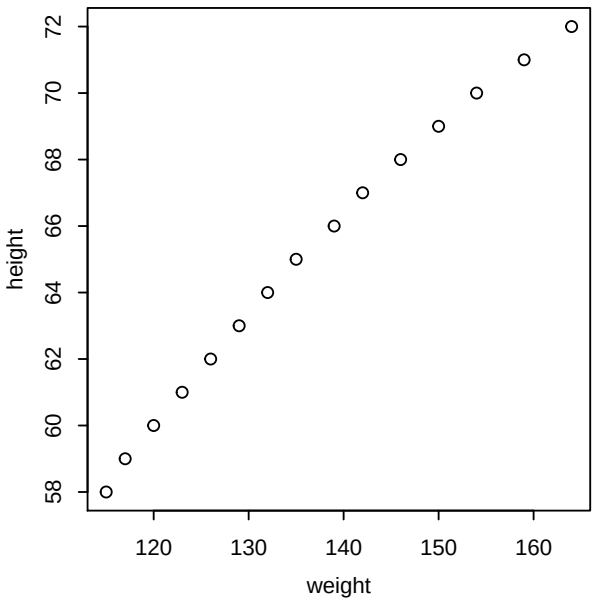
```
TG <- read.table("ToothGrowth.txt", sep = "\t", header = TRUE)
summary(TG)

##       len        supp         dose
##  Min.   : 4.2   OJ:30   Min.   :0.50
##  1st Qu.:13.1   VC:30   1st Qu.:0.50
##  Median :19.2           Median :1.00
```

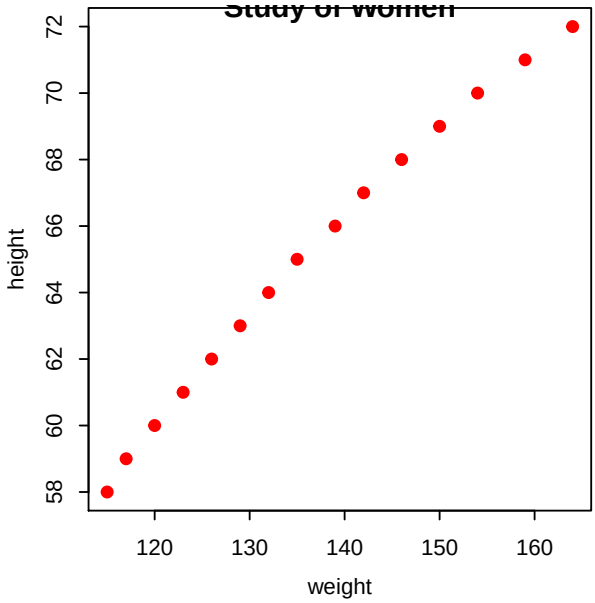
```
##  Mean   :18.8           Mean   :1.17
##  3rd Qu.:25.3           3rd Qu.:2.00
##  Max.   :33.9           Max.   :2.00

par(mfrow = c(1, 2))
boxplot(TG$len ~ TG$supp, col = 2:4, las = 2, xlab = "Treatment",
    ylab = "Tooth Length")
boxplot(TG$len ~ paste(TG$supp, TG$dose), col = rep(2:3, each = 3),
    las = 2, xlab = "Treatment and Dose", ylab = "Tooth Length")
```

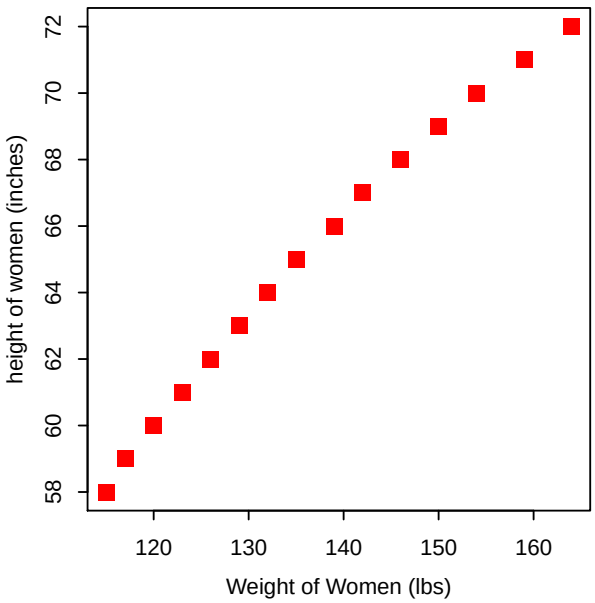
## 12.8 Solution to Exercise 8

```
par(mfrow = c(2, 2))
data(women)
attach(women)
plot(height, weight)
plot(weight, height)
plot(weight, height, pch = 19, col = "red", main = "Study of Women")
plot(weight, height, xlab = "Weight of Women (lbs)", ylab = "height of women
    pch = 15, col = "red", cex = 1.5)
```


weight
120
130
140
150
160
58
60
62
64
66
68
70
72
height


height
58
60
62
64
66
68
70
72
120
130
140
150
160
weight


Study of Women
height
58
60
62
64
66
68
70
72
120
130
140
150
160
weight


height of women (inches)
58
60
62
64
66
68
70
72
120
130
140
150
160
Weight of Women (lbs)

## 12.9 Solution to Exercise 9

```
mod1 <- lm(Hwt ~ Sex, data = cats)
model.matrix(mod1)[1:10, ]

##    (Intercept) SexM
## 1            1    0
## 2            1    0
## 3            1    0
## 4            1    0
## 5            1    0
## 6            1    0
## 7            1    0
## 8            1    0
## 9            1    0
## 10           1    0

mod1 <- lm(Hwt ~ Sex - 1, data = cats)
model.matrix(mod1)[1:10, ]

##    SexF SexM
## 1     1    0
## 2     1    0
## 3     1    0
## 4     1    0
## 5     1    0
## 6     1    0
## 7     1    0
## 8     1    0
## 9     1    0
## 10    1    0
```

## 12.10 Solution to Exercise 10

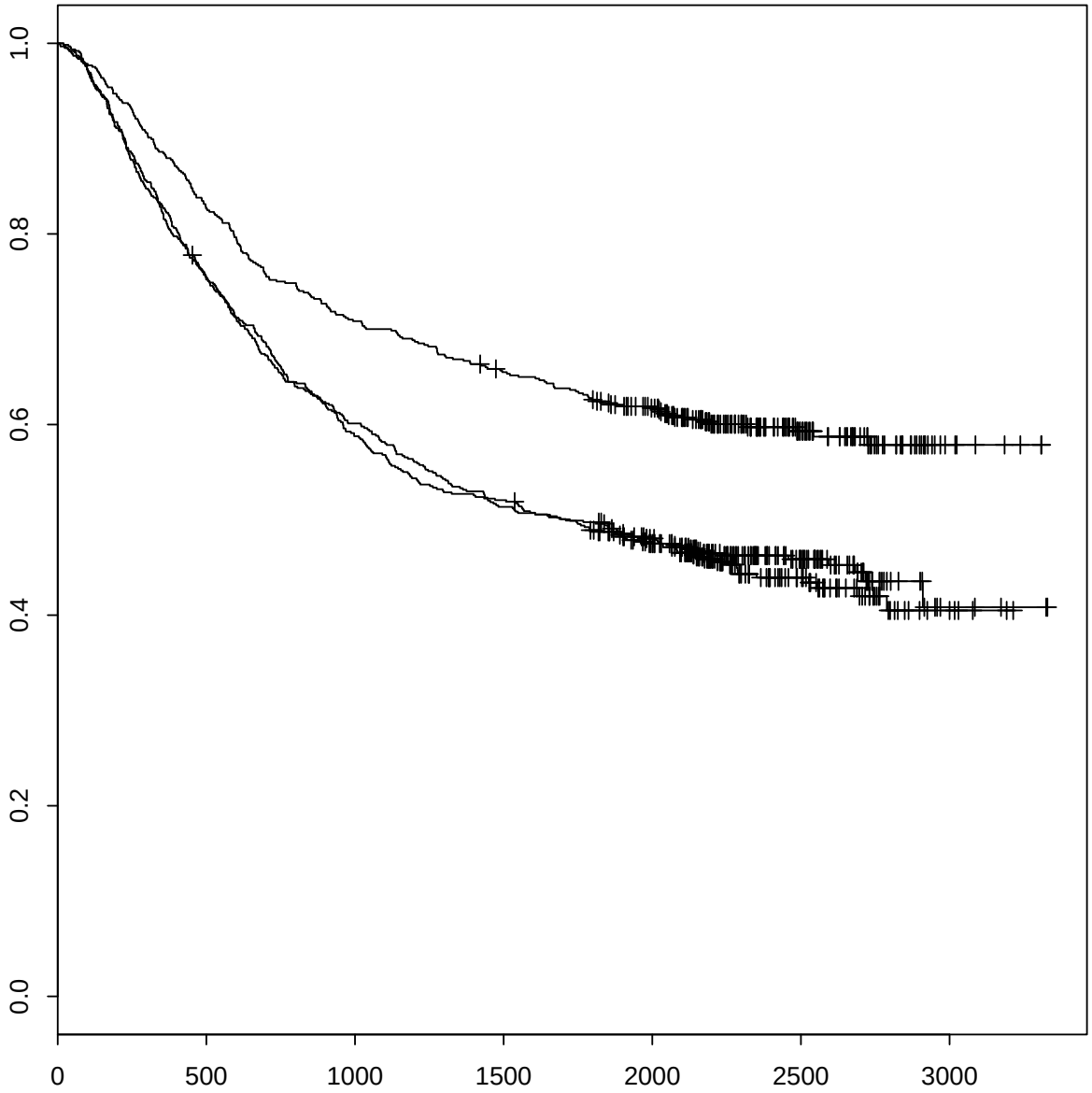
```
data.lungs <- read.csv("lungs.csv", stringsAsFactors = FALSE)
head(data.lungs)

##   age sex height weight bmp fev1  rv frc tlc pemax
## 1   7   0    109   13.1  68   32 258 183 137    95
## 2   7   1    112   12.9  65   19 449 245 134    85
## 3   8   0    124   14.1  64   22 441 268 147   100
## 4   8   1    125   16.2  67   41 234 146 124    85
## 5   8   0    127   21.5  93   52 202 131 104    95
## 6   9   0    130   17.5  68   44 308 155 118    80
```

```
lungFit <- lm(pemax ~ ., data = data.lungs)
summary(lungFit)

##
## Call:
## lm(formula = pemax ~ ., data = data.lungs)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -37.34 -11.53   1.08  13.39  33.41
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  176.058    225.891    0.78     0.45
## age           -2.542      4.802   -0.53     0.60
## sex           -3.737     15.460   -0.24     0.81
## height        -0.446      0.903   -0.49     0.63
## weight         2.993      2.008    1.49     0.16
## bmp           -1.745      1.155   -1.51     0.15
## fev1           1.081      1.081    1.00     0.33
## rv             0.197      0.196    1.00     0.33
## frc           -0.308      0.492   -0.63     0.54
## tlc            0.189      0.500    0.38     0.71
##
## Residual standard error: 25.5 on 15 degrees of freedom
## Multiple R-squared: 0.637,Adjusted R-squared: 0.42
## F-statistic: 2.93 on 9 and 15 DF,  p-value: 0.032
##


resid(lungFit)

##       1       2       3       4       5       6       7       8
##  10.031  -3.414  13.386 -11.532  18.691 -31.552 -11.480  20.034
##       9      10      11      12      13      14      15      16
## -20.307 -13.182  15.646  10.748  -3.664 -33.118  10.460  33.405
##      17      18      19      20      21      22      23      24
##  21.034  -3.002  12.096   1.081 -37.338  11.864  -4.332 -34.233
##      25
##  28.677

## most significant
sort(summary(lungFit)$coefficients[, 4], decreasing = FALSE)[1]

##    bmp
## 0.1517
```

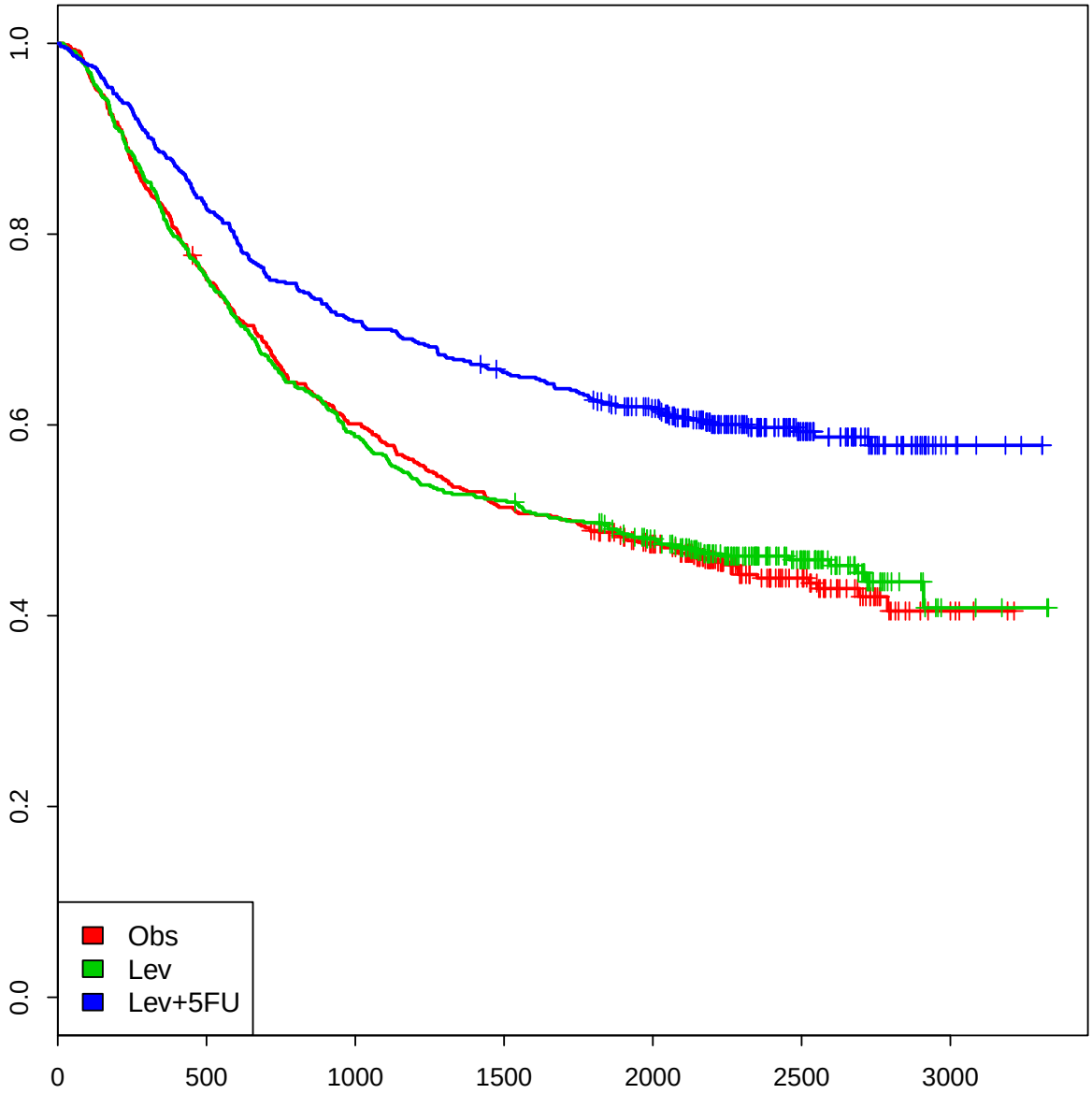
```
## least significant
sort(summary(lungFit)$coefficients[, 4], decreasing = TRUE)[1]

##    sex
## 0.8123
```

## 12.11 Solution to Exercise 11

```
library(survival)
head(colon)

##   id study      rx sex age obstruct perfor adhere nodes status
## 1  1     1 Lev+5FU   1  43        0      0      0     5      1
## 2  1     1 Lev+5FU   1  43        0      0      0     5      1
## 3  2     1 Lev+5FU   1  63        0      0      0     1      0
## 4  2     1 Lev+5FU   1  63        0      0      0     1      0
## 5  3     1     Obs   0  71        0      0      1     7      1
## 6  3     1     Obs   0  71        0      0      1     7      1
##   differ extent surg node4 time etype
## 1      2      3    0     1 1521     2
## 2      2      3    0     1  968     1
## 3      2      3    0     0 3087     2
## 4      2      3    0     0 3087     1
## 5      2      2    0     1  963     2
## 6      2      2    0     1  542     1

colonFit <- survfit(Surv(time, status) ~ rx, data = colon)
plot(colonFit)
```




```
plot(colonFit, col = 2:4, lwd = 2)
plot(colonFit, col = 2:4, lwd = 2)
legend("bottomleft", legend = levels(colon$rx), fill = 2:4)
```




```
pdf(file = "Surv.pdf")
plot(colonFit, col = 2:4, lwd = 2)
legend("bottomleft", legend = levels(colon$rx), fill = 2:4)
dev.off()

## pdf
##   2


survdiff(Surv(time, status) ~ rx, data = colon)
```

```
## Call:
## survdiff(formula = Surv(time, status) ~ rx, data = colon)
##
##              N Observed Expected (O-E)^2/E (O-E)^2/V
## rx=Obs     630      345      299      7.01     10.40
## rx=Lev     620      333      295      4.93      7.26
## rx=Lev+5FU 608      242      326     21.61     33.54
##
##  Chisq= 33.6  on 2 degrees of freedom, p= 4.99e-08
```

```
cp <- coxph(Surv(time, status) ~ rx, data = colon)
summary(cp)
```

```
## Call:
## coxph(formula = Surv(time, status) ~ rx, data = colon)
##
##   n= 1858, number of events= 920
##
##               coef exp(coef) se(coef)     z Pr(>|z|)
## rxLev     -0.0209    0.9793   0.0768 -0.27     0.79
## rxLev+5FU -0.4410    0.6434   0.0839 -5.26  1.5e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##           exp(coef) exp(-coef) lower .95 upper .95
## rxLev         0.979       1.02     0.842     1.138
## rxLev+5FU     0.643       1.55     0.546     0.758
##
## Concordance= 0.545  (se = 0.009 )
## Rsquare= 0.019   (max possible= 0.999 )
## Likelihood ratio test= 35.2  on 2 df,   p=2.23e-08
## Wald test            = 33.1  on 2 df,   p=6.45e-08
## Score (logrank) test = 33.6  on 2 df,   p=4.99e-08
##
```

## 12.12 SessionInfo

```
sessionInfo()

## R version 2.15.1 (2012-06-22)
## Platform: i386-pc-mingw32/i386 (32-bit)
##
## locale:
## [1] LC_COLLATE=English_United States.1252
## [2] LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## attached base packages:
## [1] splines   grid      stats     graphics  grDevices utils
## [7] datasets  methods   base
##
## other attached packages:
##  [1] Hmisc_3.9-3           gmodels_2.15.2
##  [3] survival_2.36-14      vcd_1.2-13
##  [5] colorspace_1.1-1      annotate_1.33.2
##  [7] AnnotationDbi_1.17.22 Biobase_2.15.3
##  [9] BiocGenerics_0.1.7    wordcloud_2.2
## [11] Rcpp_0.9.11           tm_0.5-8
## [13] igraph_0.6-2          network_1.7-1
## [15] googleVis_0.2.16      RJSONIO_0.98-1
## [17] lattice_0.20-6        ggplot2_0.9.1
## [19] ade4_1.5-1            RColorBrewer_1.0-5
## [21] venneuler_1.1-0       rJava_0.9-3
## [23] scatterplot3d_0.3-33  gplots_2.11.0
## [25] MASS_7.3-18           KernSmooth_2.23-7
## [27] caTools_1.13          bitops_1.0-4.1
## [29] gdata_2.11.0          gtools_2.7.0
## [31] XML_3.9-4.1           SAScii_0.2
## [33] stringr_0.6           R2HTML_2.2
## [35] knitr_0.6.3
##
## loaded via a namespace (and not attached):
##  [1] cluster_1.14.2  DBI_0.2-5       dichromat_1.2-4 digest_0.5.2
##  [5] evaluate_0.4.2  formatR_0.5     IRanges_1.13.26 labeling_0.1
##  [9] memoise_0.1     munsell_0.3     parser_0.0-15   plyr_1.7.1
## [13] proto_0.3-9.2   reshape2_1.2.1  RSQLite_0.11.1  scales_0.2.1
## [17] slam_0.1-26     tools_2.15.1    xtable_1.7-0
```