A beginners guide to solving biological problems in R

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Course material:
http://logic.sysbiol.cam.ac.uk/teaching/Rcourse/

Original slides by Ian Roberts and Robert Stojnić

Day 1 schedule

1. Introduction to R and its environment
2. Data structures
3. Programming techniques
4. Data analysis
5. Statistics

Introduction to R and its environment

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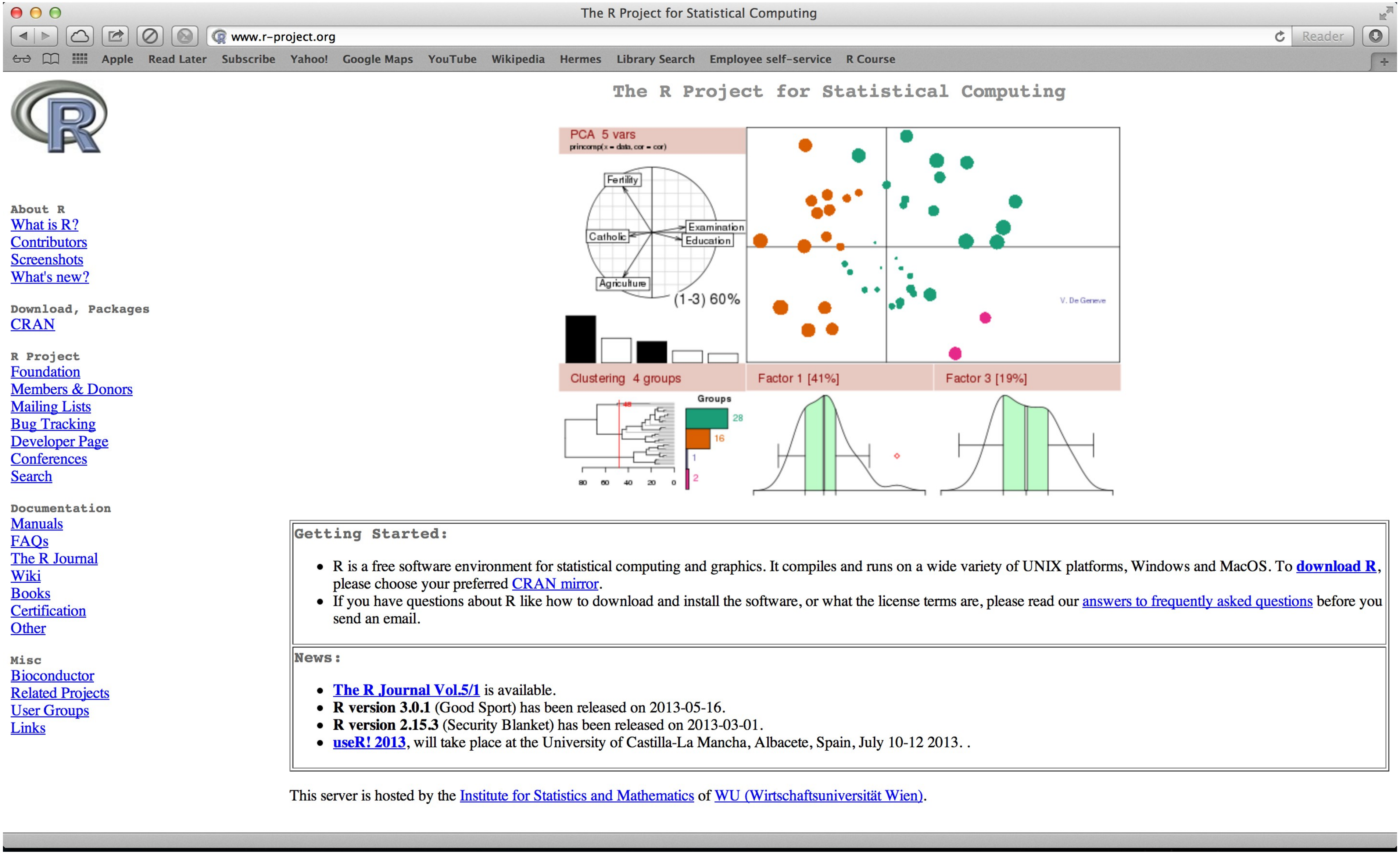
What’s R?

- A statistical programming environment
  - based on S
  - Suited to high level data analysis
- Open source & cross platform
- Extensive graphics capabilities
- Diverse range of add-on packages
- Active community of developers
- Thorough documentation



The R Project for Statistical Computing

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Getting Started:

- R is a free software environment for statistical computing and graphics. It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS. To **download R**, please choose your preferred CRAN mirror.
- If you have questions about R like how to download and install the software, or what the license terms are, please read our answers to frequently asked questions before you send an email.

News:

- **The R Journal Vol.5/1** is available.
- **R version 3.0.1** (Good Sport) has been released on 2013-05-16.
- **R version 2.15.3** (Security Blanket) has been released on 2013-03-01.
- **useR! 2013**, will take place at the University of Castilla-La Mancha, Albacete, Spain, July 10-12 2013. .

This server is hosted by the Institute for Statistics and Mathematics of WU (Wirtschaftsuniversität Wien).

www.r-project.org

Various platforms supported

- Release 3.0.1 (May 2013)
  - Base package
  - Contributed packages (general purposes extras)
  - ~4700 available packages
- Download from http://www.stats.bris.ac.uk/R/
- Windows, Mac and Linux versions available

- Executed using command line, or a graphical user interface (GUI)
- On this course, we use the RStudio GUI (www.rstudio.com)
- Everything you need is installed on the training machines
- If you are using your own machine, download both R and RStudio

Getting Started

- R is a program which, once installed on your system, can be launched and is immediately ready to take input directly from the user
- There are two ways to launch R:
    1) From the command line (particularly useful if you're quite familiar with Linux)
    2) As an application called RStudio (very good for beginners)

Prepare to launch R

From command line

- To start R in Linux we need to enter the Linux console (also called Linux terminal and Linux shell)
- To start R, at the prompt simply type:

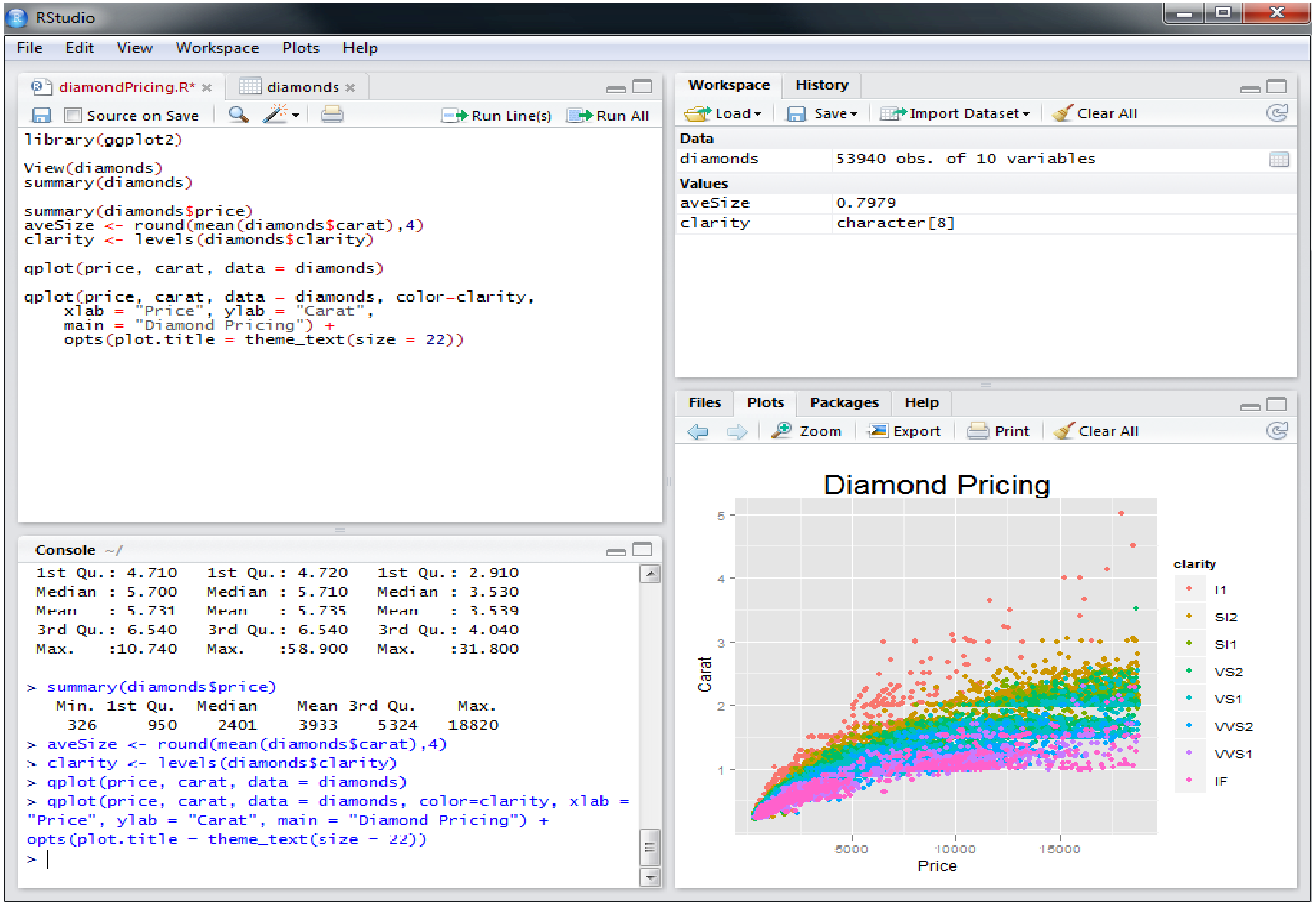
```
$ R
```

- If R doesn't print the welcome message, call us to help!

Prepare to launch R

Using RStudio

- To launch RStudio, find the RStudio icon in the menu bar on the left of the screen and double-click



```
library(ggplot2)

View(diamonds)
summary(diamonds)

summary(diamonds$price)
aveSize <- round(mean(diamonds$carat),4)
clarity <- levels(diamonds$clarity)

qplot(price, carat, data = diamonds)

qplot(price, carat, data = diamonds, color=clarity,
    xlab = "Price", ylab = "Carat",
    main = "Diamond Pricing") +
    opts(plot.title = theme_text(size = 22))
```

Data

diamonds 53940 obs. of 10 variables

Values

aveSize 0.7979

clarity character[8]

```
 1st Qu.: 4.710   1st Qu.: 4.720   1st Qu.: 2.910
 Median : 5.700   Median : 5.710   Median : 3.530
 Mean   : 5.731   Mean   : 5.735   Mean   : 3.539
 3rd Qu.: 6.540   3rd Qu.: 6.540   3rd Qu.: 4.040
 Max.   :10.740   Max.   :58.900   Max.   :31.800

> summary(diamonds$price)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    326     950    2401    3933    5324   18820
> aveSize <- round(mean(diamonds$carat),4)
> clarity <- levels(diamonds$clarity)
> qplot(price, carat, data = diamonds)
> qplot(price, carat, data = diamonds, color=clarity, xlab =
"Price", ylab = "Carat", main = "Diamond Pricing") +
opts(plot.title = theme_text(size = 22))
> |
```

The Working Directory (wd)

- Like many programs R has a concept of a working directory (wd)
- It is the place where R will look for files to execute and where it will save files, by default
- For this course we need to set the working directory to the location of the course scripts
- At the command prompt in the terminal or in RStudio console type:

```
> setwd(“R_course/Day_1_scripts”)
```

- Alternatively in RStudio use the mouse and browse to the directory location
- Tools → Set Working Directory → Choose Directory...

Basic concepts in R
command line calculation

- The command line can be used as a calculator. Type:

```
> 2 + 2
[1] 4


> 20/5 - sqrt(25) + 3^2
[1] 8


> sin(pi/2)
[1] 1
```

- Note: The number in the square brackets is an indicator of the position in the output. In this case the output is a 'vector' of length 1 (i.e. a single number). More on vectors coming up...

Basic concepts in R
variables

- A variable is a letter or word which takes (or contains) a value. We use the assignment 'operator', **<-**

```
> x <- 10
> x
[1] 10
> myNumber <- 25
> myNumber
[1] 25
```

- We can perform arithmetic on variables:

```
> sqrt(myNumber)
[1] 5
```

- We can add variables together:

```
> x + myNumber
[1] 35
```

Basic concepts in R
variables

- We can change the value of an existing variable:

```
> x <- 21
> x
[1] 21
```

- We can set one variable to equal the value of another variable:

```
> x <- myNumber
> x
[1] 25
```

- We can modify the contents of a variable:

```
> myNumber <- myNumber + sqrt(16)
[1] 29
```

Basic concepts in R
functions

- **Functions** in R perform operations on **arguments** (the input(s) to the function). We have already used **sin(x)** which returns the sine of **x.** In this case the function has one argument, **x.** Arguments are *always* contained in parentheses, i.e. curved brackets **()**, separated by commas.
- Try these:

```
> sum(3, 4, 5, 6)
[1] 18
> max(3, 4, 5, 6)
[1] 6
> min(3, 4, 5, 6)
[1] 3
```

- Arguments can be named or unnamed, but if they are unnamed they must be ordered (we will see later how to find the right order).

```
> seq(from=2, to=10, by=2)
[1] 2 4 6 8 10
> seq(2, 10, 2)
[1] 2 4 6 8 10
```

Basic concepts in R
vectors

- The basic data structure in R is a **vector** – an ordered collection of values. R even treats single values as 1-element vectors. The function **c()** *combines* its arguments into a vector:

```
> x <- c(3, 4, 5, 6)
> x
[1] 3 4 5 6
```

- As mentioned, the square brackets **[]** indicate position within the vector (the **index**). We can extract individual elements by using the **[]** notation:

```
> x[1]
[1] 3
> x[4]
[1] 6
```

- We can even put a vector inside the square brackets (vector indexing):

```
> y <- c(2, 3)
> x[y]
[1] 4 5
```

Basic concepts in R

vectors

- There are a number of shortcuts to create a vector. Instead of:

```
> x <- c(3, 4, 5, 6, 7, 8, 9, 10, 11, 12)
```

- we can write:

```
> x <- 3:12
```

- or we can use the **seq()** function, which returns a vector:

```
> x <- seq(2, 10, 2)
> x
 [1] 2 4 6 8 10
> x <- seq(2, 10, length.out = 7)
```

-
  ```
  > x
   [1] 2.00000 3.33333 4.66667 6.00000 7.33333 8.66667 10.00000
  ```

- or the **rep()** function:

```
> y <- rep(3, 5)
```

-
  ```
  > y
  [1] 3 3 3 3 3
  > y <- rep(1:3, 5)
  > y
  [1] 1 2 3 1 2 3 1 2 3 1 2 3 1 2 3
  ```

Basic concepts in R
vectors

- We have seen some ways of extracting elements of a vector. We can use these shortcuts to make things easier (or more complex!)

```
> x <- 3:12
> x[3:7]
[1] 5 6 7 8 9
> x[seq(2, 6, 2)]
[1] 4 6 8
> x[rep(3, 2)]
[1] 5 5
```

- We can add an element to a vector

```
> y <- c(x, 1)
> y
[1] 3 4 5 6 7 8 9 10 11 12 1
```

- We can glue vectors together

```
> z <- c(x, y)
> z
[1] 3 4 5 6 7 8 9 10 11 12 3 4 5 6 7 8 9 10 11 12 1
```

Basic concepts in R

vectors

- We can remove element(s) from a vector

```
> x <- 3:12
> x[-3]
  [1]  3  4  6  7  8  9 10 11 12
> x[-(5:7)]
 [1]  3  4  5  6 10 11 12
> x[-seq(2, 6, 2)]
 [1]  3  5  7  9 10 11 12
```

- Finally, we can modify the contents of a vector

```
> x[6] <- 4
> x
[1]  3  4  5  6  7  4  9 10 11 12
> x[3:5] <- 1
> x
[1]  3  4  1  1  1  4  9 10 11 12
```

- Remember! **Square** brackets for indexing **[]**, **parentheses** for function arguments **()**.

Basic concepts in R
vector arithmetic

- When applying all standard arithmetic operations to vectors, application is element-wise

```
> x <- 1:10
> y <- x*2
> y
[1] 2 4 6 8 10 12 14 16 18 20
> z <- x^2
> z
[1] 1 4 9 16 25 36 49 64 81 100
```

- Adding two vectors

```
> y + z
[1] 3 8 15 24 35 48 63 80 99 120
```

- Vectors don't have to be the same length (what's this?)...

```
> x + 1:2
[1] 2 4 4 6 6 8 8 10 10 12
```

- but that doesn't always work

```
> x + 1:3  (...?)
```

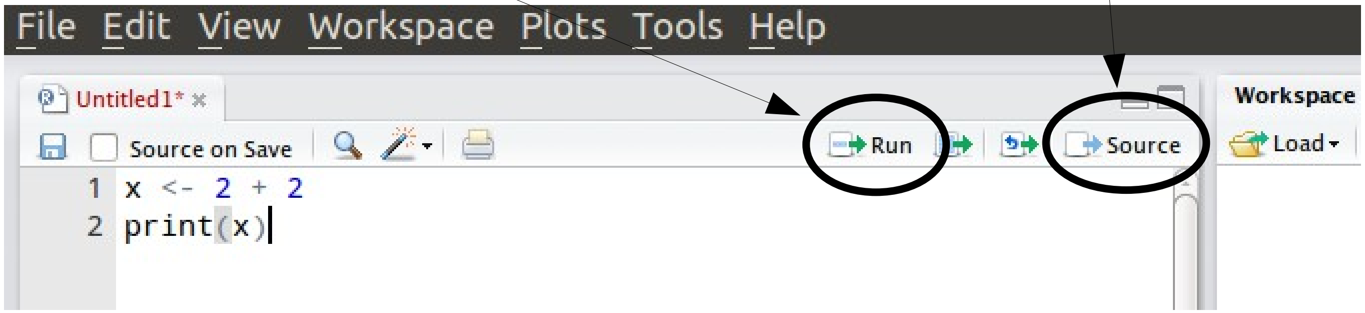
Writing scripts with Rstudio

Typing lots of commands directly to R can be tedious. A better way is to write the commands to a file and then load it into R.

- Click on **File -> New** in Rstudio
- Type in some R code, e.g.

```
x <- 2 + 2
print(x)
```

- Click on **Run** to execute the **current line**, and **Source** to execute the **whole script**



```
x <- 2 + 2
print(x)
```

Sourcing can also be performed manually with `source("myScript.R")`

Getting Help

- To get help on any R function, type **?** followed by the function name. For example:

  ```
  > ?seq
  ```

- This retrieves the syntax and arguments for the function. You can see the default order of arguments here. The help page also tells you which **package** it belongs to.
- There will typically be example usage, which you can test using the **example** function:

  ```
  > example(seq)
  ```

- If you can't remember the exact name type **??** followed by your guess. R will return a list of possibles

  ```
  > ??rint
  ```

Interacting with the R console

- R console symbols
  - ; end of line
    - Enables multiple commands to be placed on one line of text
  - # comment
    - indicates text is a comment and not executed
  - + command line wrap
    - R is waiting for you to complete an expression
- Ctrl-c or escape to clear input line and try again
- Ctrl-l to clear window
- Press q to leave help (using R from the terminal)
- Use the TAB key for command auto completion
- Use up and down arrows to scroll through the command history

R packages

- R comes ready loaded with various libraries of functions called **packages**. e.g. the function **sum()** is in the **base** package and **sd()**, which calculates the standard deviation of a vector, is in the **stats** package
- There are 1000s of additional packages provided by third parties, and the packages can be found in numerous server locations on the web called **repositories**
- The two repositories you will come across the most are
  - **The Comprehensive R Archive Network (CRAN)**
  - **Bioconductor**
- CRAN is mirrored in many locations. Set your local mirror in RStudio using Tools → Options, and choose a CRAN mirror
- Set the Bioconductor package download tool by typing:

```
> source("http://bioconductor.org/biocLite.R")
```

- Bioconductor packages are then loaded with the biocLite() function:

```
> biocLite(“PackageName”)
```

R packages

- 4700+ packages on CRAN:
  - Use CRAN search to find functionality you need:

    http://cran.r-project.org/search.html
  - Or, look for packages by theme:

    http://cran.r-project.org/web/views/
- 670+ packages in Bioconductor:
  - Specialised in genomics:

    http://www.bioconductor.org/packages/release/bioc/
- **Other repositiories:**
- 1600+ projects on R-forge:
  - http://r-forge.r-project.org/
- R graphical manual:
  - http://rgm3.lab.nig.ac.jp/RGM

Bottomline: **always** first look if there is already an R package that does what you want before trying to implement it yourself

Exercise: Install Packages Matrix and aCGH

- Matrix is a CRAN extras package
  - Use **install.packages()** function…

    ```
    install.packages("Matrix")
    ```

  - or in RStudio goto Tools → Install Packages… and type the package name
- aCGH is a BioConductor package (www.bioconductor.org)
  - Use **biocLite()** function

  ```
  biocLite("aCGH")
  ```

- R needs to be told to use the new functions from the installed packages
  - Use **library(…)** function to load the newly installed features

    ```
    library("Matrix") # loads matrix functions
    library("aCGH") # loads aCGH functions
    ```

  - **library()**
    - Lists all the packages you've got installed locally