# Introduction to R and BioConductor

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## 1 Starting with R/BioC

### Why use R?

See http://monkeysuncle.stanford.edu/?p=367

### Introductory material

R reference card: a useful and brief 4-page intro: `http://www.rpad.org/Rpad/R-refcard.pdf`

Recommended book with example source codes online: `http://www.bioconductor.org/pub/docs/mogr/`

The project pages www.r-project.org and www.bioconductor.org provide extensive resources.

### R-Matlab dictionary

If you already know Matlab this may help: http://www.math.umaine.edu/~hiebeler/comp/matlabR.pdf

### Search engine for R

Seeking R-related information from www is challenging. This solves the problem: http://www.rseek.org/

### IRC

For online support, go to #r-project@IRCnet (Finnish community) or #R@FreeNode (International channel).

### Graphics

R has excellent graphics capabilities with publication quality. See graphics galleries for *examples with source code* (!):
http://addictedtor.free.fr/graphiques/
http://bm2.genes.nig.ac.jp/RGM2/

### R and LaTeX

Automated LaTeXdocument generation with parameters and plots:
http://www.stat.uni-muenchen.de/~leisch/Sweave/

This document was produced with Sweave. The source (.Rnw) is provided at course home page, and can be converted into LaTeXcode in R with the command 'Sweave('handout.Rnw')'.

'brew' is an alternative package which allows the use of for loops in document generation.

**Graphical User Interfaces (GUIs) for R?**

Miscellaneous GUIs for R, in case you need one:

- Tinn-R
- R Commander (basic-statistics GUI)
- Rattle (data mining)
- RKWard (KDE libraries)
- JGR (universal Java GUI)
- PMG

### 1.1 Installing packages in Aalto/TKK computer system

It is recommended that you install R (r-project.org) and BioConductor (bioconductor.org) on your personal computer.

It is often necessary to install new packages with specific functionality. In Aalto/TKK computer system, the quickest option is to install to your home directory (if you have enough disk space). For example the following commands can be used to install packages within R:

```
> install.packages("vabayelMix")
```

or from source tarball

```
> install.packages("mypackage.tar.gz", repos = NULL)
```

This works for BioConductor packages (installs 'qvalue'):

```
> source("http://www.bioconductor.org/getBioC.R")
> getBioC("qvalue")
```

If the package would be useful for other people (or if you want to save your personal disk space), check if it the package has debian source available using command line 'apt-cache search î-'. If a debian package is available, request installation from servicedesk@tkk.fi. Otherwise, send mail to leo.lahti@tkk.fi.

## 2 Hands-on exercises

Download R reference card: `http://www.rpad.org/Rpad/R-refcard.pdf`. Start R by typing 'R'. Let's start with

```
> print("Hello, world!")
```

```
[1] "Hello, world!"
```

Random samples from normal distribution and a histogram:

```
> set.seed(123)
> random.data <- rnorm(1000, mean = 0, sd = 1)
> hist(random.data)
```

(Note: *rnorm* generates random samples from normal distribution. If you don't set random seed (*set.seed*), the code will draw different random data at each run. By setting random seed, you can retrieve the same random data later on, if necessary. This is standard procedure which allows exact reproducibility of the results.)

Define title and axes:

```
> hist(random.data, main = "Random histogram", xlab = "X values",
+      ylab = "Count")
```

See histogram function in more detail: type '?hist' or 'help(hist)'.

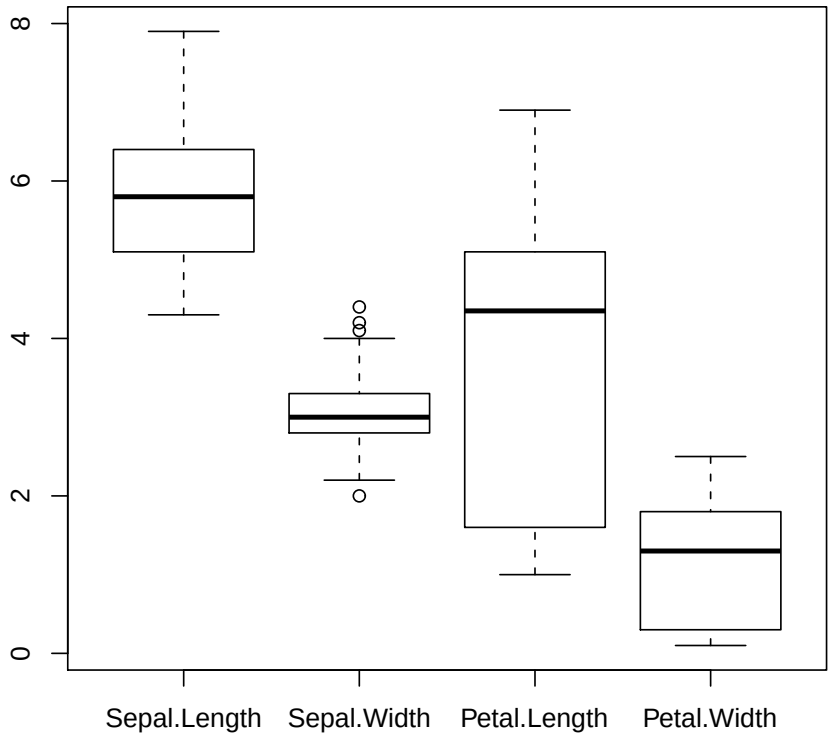
**Example data set**

Investigate example data:

```
> iris
> dim(iris)
> dimnames(iris)
> summary(iris)
```

Boxplot of the first four columns.

```
> boxplot(iris[, 1:4])
```




Compare sepal length between two flower species with t-test:

```
> setosaRows = (iris[, "Species"] == "setosa")
> virginicaRows = (iris[, "Species"] == "virginica")
> x = iris[setosaRows, "Sepal.Length"]
> y = iris[virginicaRows, "Sepal.Length"]
> t.test(x, y)

        Welch Two Sample t-test
```

```
data:  x and y
t = -15.3862, df = 76.516, p-value < 2.2e-16
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -1.786760 -1.377240
sample estimates:
mean of x mean of y
    5.006     6.588
```

### Principal component analysis (PCA)

Investigate variable contents with 'names', call subvariables with '$' or '@':

```
> iris.pca <- prcomp(iris[, 1:4])
> names(iris.pca)
```

```
[1] "sdev"     "rotation" "center"   "scale"    "x"
```

Plot variance along each principal component

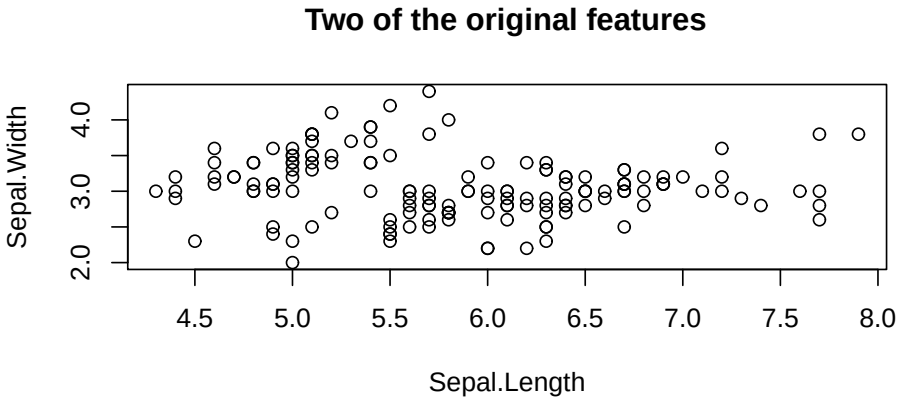
```
> barplot(iris.pca$sdev)
```

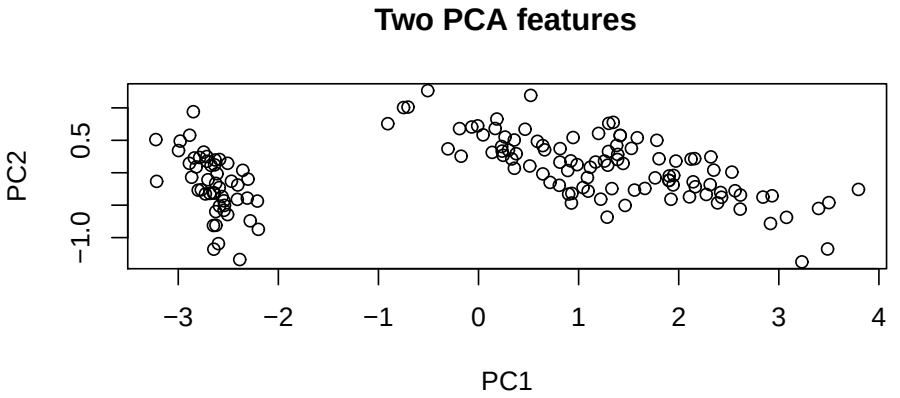
Plot first principal component

```
> barplot(iris.pca$rotation[, "PC1"], main = "PCA")
```

Plot data for two random features, and then along the most important principal components:

```
> par(mfrow = c(2, 1))
> plot(iris[, 1:2], main = "Two of the original features")
> plot(iris.pca$x[, 1:2], main = "Two PCA features")
```




**Plots with different colors**

```
> plot(iris[iris[, "Species"] == "setosa", 1:2], col = "red", xlim = range(iris[,
+     1:2]), ylim = range(iris[, 1:2]))
> points(iris[iris[, "Species"] == "virginica", 1:2], col = "blue")
```

Order and plot correlations between 20 random samples using first 4 features:

```
> random.samples <- sample(nrow(iris), 20)
> flower.correlations <- cor(t(iris[random.samples, 1:4]))
> heatmap(flower.correlations, scale = "none")
```

**Produce PDF**

This will save 'myFigure.pdf' in your working directory (check with 'getwd()')

```
> pdf("myFigure.pdf")
> heatmap(flower.correlations, scale = "none", col = grey(seq(0,
+     1, length = 100)))
> dev.off()
```

Remember to close the output stream with 'dev.off()'!

**K-means**

Based on the plot it seems that there are two groups of flowers. Use K-means to detect these clusters. It turns out that the clusters are explainable by flower species:

```
> km <- kmeans(iris[random.samples, 1:4], centers = 2)
> names(km)
> iris[names(which(km$cluster == 1)), "Species"]
> iris[names(which(km$cluster == 2)), "Species"]
```

**Hierarchical clustering**

```
> d <- dist(iris[, 1:4])
> hc <- hclust(d, method = "ave")
> plot(hc, hang = -1)
```

Check source code of the function with 'hclust'.

# 3 FAQ

**How to create multidimensional matrices?**

```
> a <- array(0, dim = c(10, 4, 2))
```

**How to run R scripts from source file?**

```
> source("myscript.R")
```

**How to run R scripts on command line (batch mode)?**

Something along these lines:
#!/bin/sh
/your.R.path/R CMD BATCH –no-save myscript.R myscript.Rlog

**Why my figure does not pop up?**

Typically the previous output stream has been *opened* but *not closed*. Close output stream(s) using dev.off(), this may need to be applied several times.

# 4 Advanced tips, tricks & hacks

If you already know R, check the following packages:

- Matrix (improved matrix operations capabilities)
- plyr (efficient data manipulation)
- ggplot2 (high-quality graphics tools)
- tikzdevice (R and LaTeXgraphics combined)
- http://cran.r-project.org/web/views/HighPerformanceComputing.html (parallel computing etc.)