Biometry. Lecture 6

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Outline

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Previous final question: the answer

What is a difference between
```
c(1, 2, 3)
```
and
```
a <- c(1, 2, 3)
```
?

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Previous final question: the answer

> What is a difference between
> ```
> c(1, 2, 3)
> ```
> and
> ```
> a <- c(1, 2, 3)
> ```
> ?

- The first outputs the vector and forgets it
- The second writes the vector into object "a"

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Processing data

Entering data into R

Put the data file into the folder

```
> download.file("http://ashipunov.info/data/mydata.txt",
+ "data/mydata.txt")
> dir("data")
```

`dir()` should show your file name (`mydata.txt`)

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Questions and answers
Processing data
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Saving data from R

Reading data from a text file

```
> file.show("data/mydata.txt") # this is a table!
> read.table("data/mydata.txt", sep=";", head=TRUE)
> f <- read.table("data/mydata.txt", sep=";", head=T)
> f
```

head=TRUE, head=T and h=T are the same

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Reading data from text file with row names

```
> download.file("http://ashipunov.info/data/mydata2.txt",
+ "data/mydata2.txt")
> file.show("data/mydata2.txt")
> read.table("data/mydata2.txt", sep=";", head=TRUE)
```

If the first row contains one less element, the first column will
be treated as row names.

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Questions and answers
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R data cycle

- Enter data to spreadsheet (e.g., MS Excel)
- Save it as a text file with separators (preferably semicolons or tabs)
- Load it into R
- Work with it
- If you need to change data, go to spreadsheet and repeat first steps

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R and Excel connection

There are two options: through text file or through clipboard. In Excel, make two columns with headings, copy them to clipboard, then:

```
> read.table("clipboard", h=T)
```

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R binary format

It is useful if you need to save and load big data objects faster

```
> x <- "apple"
> x
> save(x, file="data/x.rd")
> rm(x) # delete
> ls() # list all objects
> exists("x") # check if object exists
> load("data/x.rd")
> x
```

We saved R object, deleted it and loaded again from binary file.
If you want to remove all objects, run rm(list=ls()) (be careful!).

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Questions and answers
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Writing tables

```
> trees
> write.table(trees, file="trees.txt")
> file.show("trees.txt")
```

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Writing protocol

```
> sink("1.txt", split=TRUE)
> 2 + 2
> sink()
```

Questions and answers
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Saving history

```
> history()
> savehistory("20120127.r")
```

You should always save your R session. You may than convert it to the script to make your work automated.

Questions and answers
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Making a script

```
> file.edit("1.r")
> source("1.r")
```

When editor opens, enter `print("Hello, world!")`, close the editor and save the file.

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Final question (3 points)

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Final question (3 points)

File `eq.txt` has tabs instead of semicolons as delimiters. How to use `read.table()` command in this case?

Hints: you may consult the help `?read.table`, or do you own experiments with the file.

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Summary: most important commands

- `read.table()` to read text file into R
- `savehistory()` to save your R session

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For Further Reading

A. Shipunov.
Biometry [Electronic resource].
2012—onwards.
Mode of access: `http://ashipunov.info/shipunov/school/biol_299`

P. Dalgaard
Introductory Statistics with R. 2nd edition.
Springer, 2008.
Section 1.1.

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