



## Working in R environment

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R Foundations for Life Scientists

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# Working with R

There are several ways to work with/in R:

- from a command line,
- in batch mode,
- from a native GUI,
- using external editor, e.g. RStudio.

During this course, we will be focusing on working with **RStudio** and also in *batch mode*.

# Working from command line

1. Open Terminal.
  2. Type *R*.
  3. Type R commands...
  4. Type `q()` to quit R.
- Arrows let you browse throughout the history.
  - TAB attempts to autocomplete the command you have just started typing.

# The batch mode

If you are working on a computational cluster, such as the Uppmax, it is very likely you would like to run large jobs that one has to enqueue. This makes interactive work from the console virtually impossible. The solution is to run R code from a file, using the so-called **batch mode**:

1. Create a file with your code and give it extension **.R**.
2. In the console (or in the queue script) write:

```
R --vanilla < mycode.R
```

 [two minus signs in front of *vanilla*].

Should you like to log the output add either:

- `R --vanilla < mycode.R > output.log` or like this
- `R --vanilla < mycode.R | tee output.log`

# Getting help

```
help(t.test) # function level
?t.test # same as above
??t.test # extensive search
vignette("GenABEL") # package level demo(graphics)
example(barplot) # run help examples for barplot
demo() # see all currently available demos
demo('graphics') # run demo for 'graphics'
```

[Stackoverflow](#) is a great resource.

# Working with packages

Packages are organised in repositories. The three main repositories are:

- CRAN
- R-Forge
- Bioconductor

We also have [GitHub](#).

## Working with packages -- CRAN example.

### GenABEL: genome-wide SNP association analysis

a package for genome-wide association analysis between quantitative or binary traits and single-nucleotide polymorphisms (SNPs).

Version: 1.8-0  
Depends: R (≥ 2.15.0), methods, [MASS](#), [utils](#), [GenABEL.data](#)  
Suggests: [qvalue](#), [genetics](#), [haplo.stats](#), [DatABEL](#) (≥ 0.9-0), [hglm](#), [MetABEL](#), [PredictABEL](#), [VariABEL](#), [bigRR](#)  
Published: 2013-12-27  
Author: GenABEL project developers  
Maintainer: Yurii Aulchenko <yurii at bionet.nsc.ru>  
Contact: GenABEL project developers <genabel.project at gmail.com>  
BugReports: [http://r-forge.r-project.org/tracker/?group\\_id=505](http://r-forge.r-project.org/tracker/?group_id=505)  
License: [GPL-2](#) | [GPL-3](#) [expanded from: GPL (≥ 2)]  
URL: <http://www.genabel.org>, <http://forum.genabel.org>, <http://genabel.r-forge.r-project.org/>  
NeedsCompilation: yes  
Materials: [Changelog](#)  
In views: [Genetics](#)  
CRAN checks: [GenABEL results](#)

### Downloads:

Reference manual: [GenABEL.pdf](#)  
Package source: [GenABEL\\_1.8-0.tar.gz](#)  
Windows binaries: r-devel: [GenABEL\\_1.8-0.zip](#), r-release: [GenABEL\\_1.8-0.zip](#), r-oldrel: [GenABEL\\_1.8-0.zip](#)  
OS X Mavericks binaries: r-release: [GenABEL\\_1.8-0.tgz](#), r-oldrel: [GenABEL\\_1.8-0.tgz](#)  
Old sources: [GenABEL archive](#)

### Reverse dependencies:

Reverse depends: [Haplin](#), [ldlasso](#), [RepeatABEL](#)  
Reverse suggests: [DatABEL](#), [FREGAT](#), [MetABEL](#), [NAM](#), [PredictABEL](#), [ranger](#), [RVPedigree](#), [VariABEL](#)

# Working with packages -- installation

Only a few packages are pre-installed:

```
library("XLConnect")
```

```
## Error in library("XLConnect"): there is no package called 'XLConnect'
```

In order to install a package from command line, use:

```
install.packages('GenABEL',dependencies=TRUE)
```

# Working with packages -- details

It may happen that you want to also specify the repository, e.g. because it is geographically closer to you or because your default mirror is down:

```
install.packages('GenABEL',dependencies=TRUE,repos="http://cran.se.r-project.org")
```

But, sometimes, this does not work either because the package is not available for your platform. In such case, you need to *compile* it from its *source code*.



# Working with packages -- details cted.

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Author: GenABEL project developers  
Maintainer: Yurii Aulchenko <yurii at bionet.nsc.ru>  
Contact: GenABEL project developers <genabel.project at gmail.com>  
BugReports: [http://r-forge.r-project.org/tracker/?group\\_id=505](http://r-forge.r-project.org/tracker/?group_id=505)  
License: [GPL-2](#) | [GPL-3](#) [expanded from: GPL ( $\geq 2$ )]  
URL: <http://www.genabel.org>, <http://forum.genabel.org>, <http://genabel.r-forge.r-project.org/>  
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# Working with packages -- installing from source.

- Make sure you have appropriate tools installed, e.g. XCode or build-essentials.
- Download the source file, in our example *GenABEL\_1.8-0.tar.gz*.
- Install it:

```
install.packages("path/to/GenABEL_1.8-0.tar.gz",  
                 repos=NULL,  
                 type='source',  
                 dependencies=TRUE)
```

- Load it:

```
library('GenABEL') # always forces reloading  
require('GenABEL') # load only if not already loaded
```

- Enjoy!

# Packages -- GitHub

Nowadays, more and more developers contribute their packages via GitHub. The easiest way to install packages from the GitHub is via the *devtools* package:

- Install the *devtools* package.
- Load it.
- Install.
- Enjoy!

```
install.packages('devtools',dependencies=TRUE)  
library('devtools')  
install_github('talgalili/installr')
```

# Packages -- Bioconductor



First install Bioconductor Manager:

```
if (!requireNamespace("BiocManager",quietly = TRUE))  
  install.packages("BiocManager")
```

# Packages -- Bioconductor cted.

Now, you can install particular packages from Bioconductor:

```
BiocManager::install("GenomicRanges")
```

For more info, visit [Bioconductor website](#).

# One package to rule them all -- the magic of SciLifeLab

## renv

- first time do `renv::activate()` and `renv::init()`
- while working: `renv::hydrate()` and `renv::snapshot()`

Now, send `renv.lock` to your friend to share the environment and she can:

- restore the environment `renv::restore()`

Pure magic!

# RStudio -- a live demonstration

The screenshot displays the RStudio application window. The top menu bar includes 'File', 'Edit', 'Session', 'View', 'Help', and 'Addins'. The toolbar contains icons for file operations and running code. The main editor pane shows a script named 'analyse\_region.r' with R code for installing Bioconductor packages and setting up a development environment. The console pane at the bottom shows the output of the R script, including the command to run R Markdown and the resulting PDF file. The environment pane on the right shows the current environment with variables like 'i', 'my.gene', 'print', 'ptm', 'v', and 'vec'.

```
116 install.packages('devtools', dependencies=T)
117 library('devtools')
118 install_github('talgalili/installr')
119 
120 
121 ## Packages -- Bioconductor
122 
123 
124 First install Bioconductor:
125 ```{r inst.biocond, eval=F}
126 source("https://bioconductor.org/biocLite.R")
127 # If the above does not work, use http instead of https
128 biocLite()
129 
130 
131 ## Packages -- Bioconductor ctd.
132 Now, you can install particular packages from Bioconductor:
133 ```{r biocond.inst.pkg, eval=F}
134 biocLite(c("GenomicFeatures", "AnnotationDbi"))
135 
136 For more info, visit [Bioconductor website](http://www.bioconductor.org/install/)
136:81 Packages -- Bioconductor ctd. R Markdown
```

Console: R Markdown

```
.../Lecture 2 - R environment/REnvironment.Rmd

/Applications/RStudio.app/Contents/MacOS/pandoc/pandoc +RTS -K512m -RTS REnvironment.utf8
.md --to beamer --from markdown+autolink_bare_uris+ascii_identifiers+tex_math_single_back
slash --output REnvironment.pdf --highlight-style tango --latex-engine /Library/TeX/texbi
n/pdflatex
output file: REnvironment.knit.md

Output created: REnvironment.pdf
```

Environment: Global Environment

Values	
i	10L
my.gene	Formal class gene
print	function (x, ...)
ptm	Class 'proc_time' Named num [1:5] 33.9 25.6 21828.8 215...
v	int [1:10] 1 2 3 4 5 6 7 8 9 10
vec	int [1:10000] 1 2 3 4 5 6 7 8 9 10 ...

Functions: Files, Plots, Packages, Help, Viewer

R: Install Packages from Repositories or Local Files Find in Topic

dependencies logical indicating whether to also install uninstalled packages which these packages depend on/link to/import/suggest (and so on recursively). Not used if repos = NULL. Can also be a character vector, a subset of c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances").

Only supported if lib is of length one (or missing), so it is unambiguous where to install the dependent packages. If this is not the case it is ignored, with a warning.

The default, NA, means c("Depends", "Imports", "LinkingTo").

TRUE means to use c("Depends", "Imports", "LinkingTo", "Suggests") for pkgs and c("Depends", "Imports", "LinkingTo") for added dependencies: this installs all the packages needed to run pkgs, their examples, tests and vignettes (if the package author specified them correctly).

In all of these, "LinkingTo" is omitted for binary packages.

type character, indicating the type of package to download and install. Will be "source" except on Windows and some OS X builds: see the section on 'Binary packages' for those.

configure.args (Used only for source installs.) A character vector or a named list. If a character