Introduction to R environment

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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 comand line

- Open Terminal.
- **2** Type *R*.
- Type R commands...
- 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**:

- Create a file with your code and give it extension .R.
- In the console (or in the queue script) write:
 R --vanilla < mycode.R [two minus signs in front of vanilla].</p>

Should you like to log the output add either:

- R --vanilla < mycode.R > output.log or
- 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

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: ves

Materials: ChangeLog In views: Genetics CRAN checks: GenABEL results

Downloads:

License:

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, Idlasso, 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 call
```

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

```
install.packages('GenABEL', dependencies=T)
```

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:

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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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:

Load it:

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

Enjoy!

Packages – GitHub

Nowadays, mora 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=T)
library('devtools')
install_github('talgalili/installr')
```

Packages – Bioconductor



First install Bioconductor:

```
source("https://bioconductor.org/biocLite.R")
# If the above does not work,
# use http instead of https
biocLite()
```

Packages – Bioconductor cted.

Now, you can install particular packages from Bioconductor:

```
biocLite(c("GenomicFeatures", "AnnotationDbi"))
```

For more info, visit Bioconductor website.

RStudio – a live demonstration

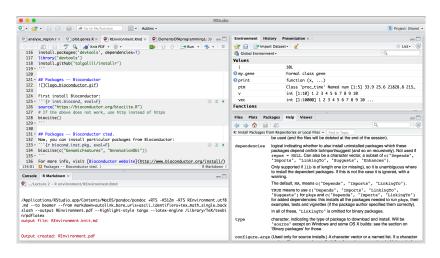


Figure 1: RStudio screenshot