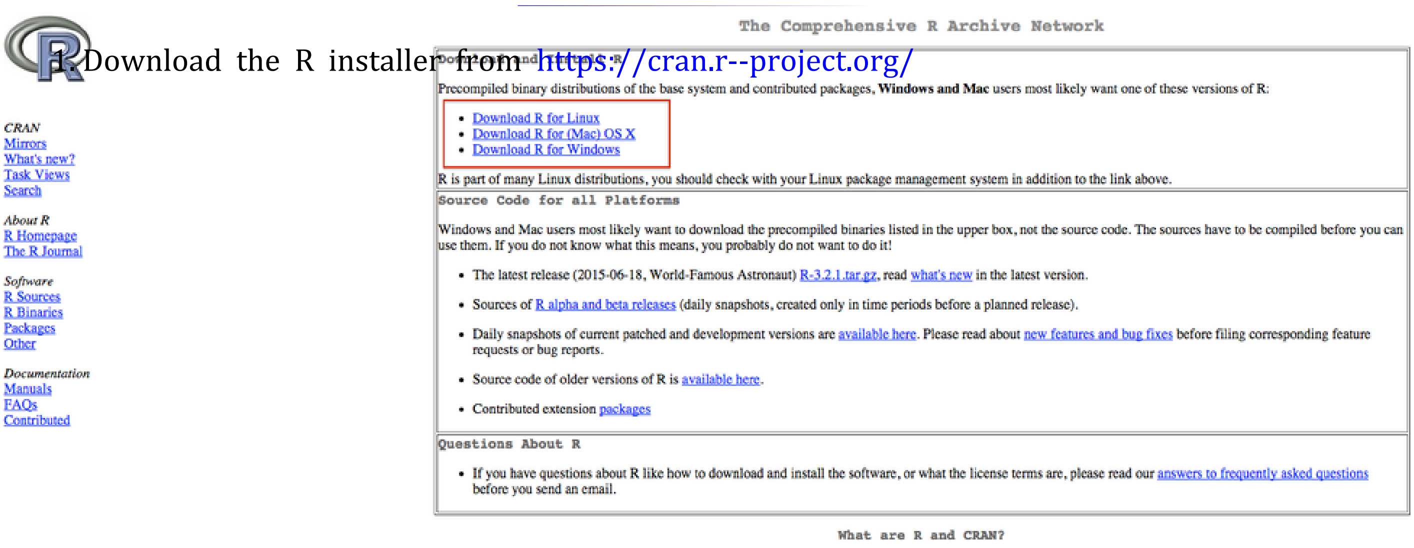
Installation guide for R and RStudio

Step 1 – Install R

1. Download the R installer from https://cran.r--project.org/



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Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- Download R for Linux
- Download R for (Mac) OS X
- Download R for Windows

R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

Source Code for all Platforms

Windows and Mac users most likely want to download the precompiled binaries listed in the upper box, not the source code. The sources have to be compiled before you can use them. If you do not know what this means, you probably do not want to do it!

- The latest release (2015-06-18, World-Famous Astronaut) R-3.2.1.tar.gz, read what's new in the latest version.
- Sources of R alpha and beta releases (daily snapshots, created only in time periods before a planned release).
- Daily snapshots of current patched and development versions are available here. Please read about new features and bug fixes before filing corresponding feature requests or bug reports.
- Source code of older versions of R is available here.
- Contributed extension packages

Questions About R

- 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.

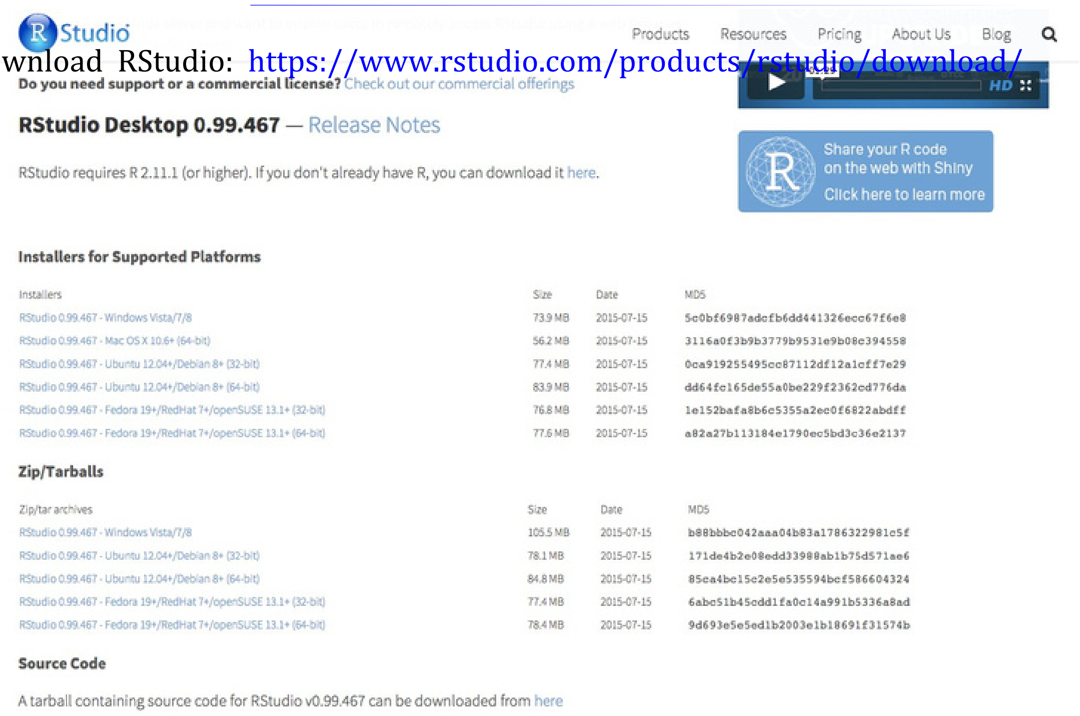
What are R and CRAN?

Figure 1. Screenshot of http://cran.csiro.au/

2. Run the installer. Default settings are fine. If you do not have admin rights on your laptop, then . In that case, it is important that you also ask them to give you full permissions to the R directories. Without this, you will not be able to install additional packages later

Step 2 – Install RStudio

1. Download RStudio: https://www.rstudio.com/products/rstudio/download/



Do you need support or a commercial license? Check out our commercial offerings

RStudio Desktop 0.99.467 — Release Notes

RStudio requires R 2.11.1 (or higher). If you don't already have R, you can download it here.

Share your R code
on the web with Shiny
Click here to learn more

Installers for Supported Platforms

Installers	Size	Date	MD5
RStudio 0.99.467 - Windows Vista/7/8	73.9 MB	2015-07-15	5c0bf6987adcfb6dd441326ecc67f6e8
RStudio 0.99.467 - Mac OS X 10.6+ (64-bit)	56.2 MB	2015-07-15	3116a0f3b9b3779b9531e9b08c394558
RStudio 0.99.467 - Ubuntu 12.04+/Debian 8+ (32-bit)	77.4 MB	2015-07-15	0ca919255495cc87112df12a1cff7e29
RStudio 0.99.467 - Ubuntu 12.04+/Debian 8+ (64-bit)	83.9 MB	2015-07-15	dd64fc165de55a0be229f2362cd776da
RStudio 0.99.467 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (32-bit)	76.8 MB	2015-07-15	1e152bafa8b6c5355a2ec0f6822abdff
RStudio 0.99.467 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (64-bit)	77.6 MB	2015-07-15	a82a27b113184e1790ec5bd3c36e2137

Zip/Tarballs

Zip/tar archives	Size	Date	MD5
RStudio 0.99.467 - Windows Vista/7/8	105.5 MB	2015-07-15	b88bbbc042aaa04b83a1786322981c5f
RStudio 0.99.467 - Ubuntu 12.04+/Debian 8+ (32-bit)	78.1 MB	2015-07-15	171de4b2e08edd33988ab1b75d571ae6
RStudio 0.99.467 - Ubuntu 12.04+/Debian 8+ (64-bit)	84.8 MB	2015-07-15	85ca4bc15c2e5e535594bcf586604324
RStudio 0.99.467 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (32-bit)	77.4 MB	2015-07-15	6abc51b45cdd1fa0c14a991b5336a8ad
RStudio 0.99.467 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (64-bit)	78.4 MB	2015-07-15	9d693e5e5ed1b2003e1b18691f31574b

Source Code

A tarball containing source code for RStudio v0.99.467 can be downloaded from here

Figure 2. Download RStudio on https://www.rstudio.com/products/rstudio/download/

2. Once the installation of R has completed successfully (and not before), run the RStudio installer.

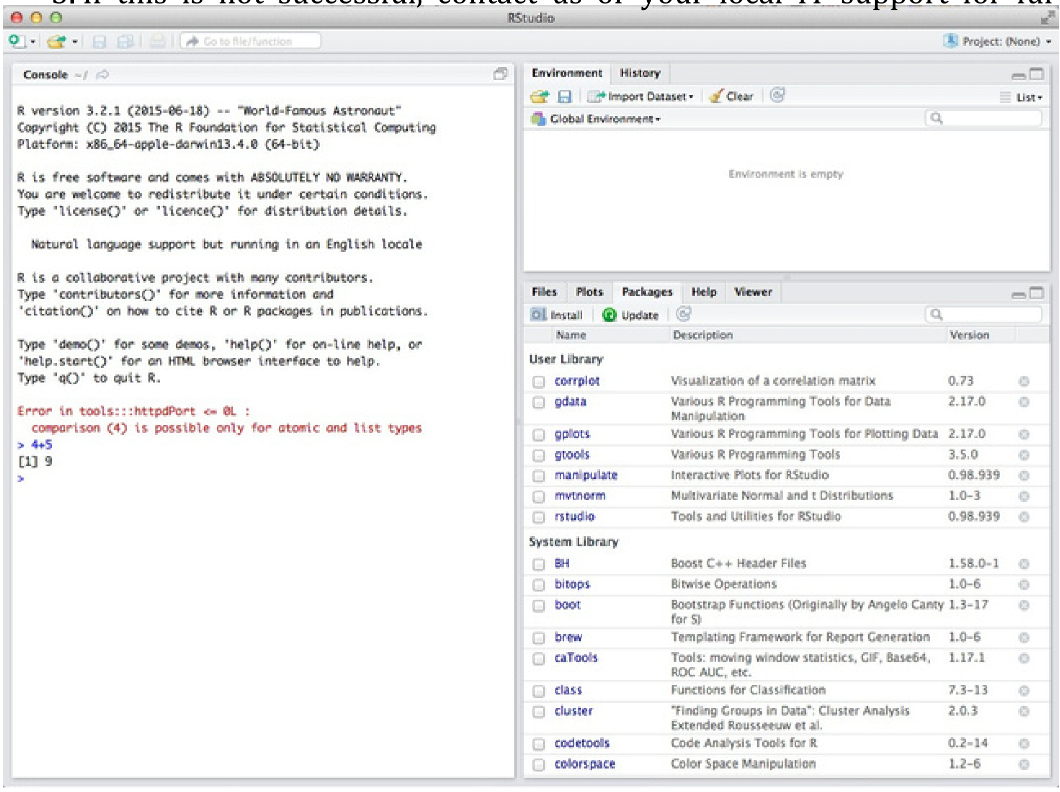
3. If you do not have administrative rights on your laptop, step 2 may fail. Ask your IT Support or download a pre--built zip archive of RStudio which doesn't need installing. The link for this is towards the bottom of the download page, highlighted in Image 2.
   a. Download the appropriate archive for your system (Windows/Linux only – the Mac version can be installed into your personal "Applications" folder without admin rights).
   b. Double clicking on the zip archive should automatically unpack it on most Windows machines.

Step 3 – Check that R and RStudio are working

1. Open RStudio. It should open a window that looks similar to image 3 below.

2. In the left hand window, by the '>'sign, type '4+5'(without the quotes) and hit enter. An output line reading '[1] 9' should appear. This means that R and RStudio are working.

3. If this is not successful, contact us or your local IT support for further advice



```
R version 3.2.1 (2015-06-18) -- "World-Famous Astronaut"
Copyright (C) 2015 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin13.4.0 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

Error in tools:::httpdPort <= 0L :
  comparison (4) is possible only for atomic and list types
> 4+5
[1] 9
>
```

	Name	Description	Version
	User Library		
☐	corrplot	Visualization of a correlation matrix	0.73
☐	gdata	Various R Programming Tools for Data Manipulation	2.17.0
☐	gplots	Various R Programming Tools for Plotting Data	2.17.0
☐	gtools	Various R Programming Tools	3.5.0
☐	manipulate	Interactive Plots for RStudio	0.98.939
☐	mvtnorm	Multivariate Normal and t Distributions	1.0-3
☐	rstudio	Tools and Utilities for RStudio	0.98.939
	System Library		
☐	BH	Boost C++ Header Files	1.58.0-1
☐	bitops	Bitwise Operations	1.0-6
☐	boot	Bootstrap Functions (Originally by Angelo Canty for S)	1.3-17
☐	brew	Templating Framework for Report Generation	1.0-6
☐	caTools	Tools: moving window statistics, GIF, Base64, ROC AUC, etc.	1.17.1
☐	class	Functions for Classification	7.3-13
☐	cluster	"Finding Groups in Data": Cluster Analysis Extended Rousseeuw et al.	2.0.3
☐	codetools	Code Analysis Tools for R	0.2-14
☐	colorspace	Color Space Manipulation	1.2-6

Figure 3. Running R with RStudio

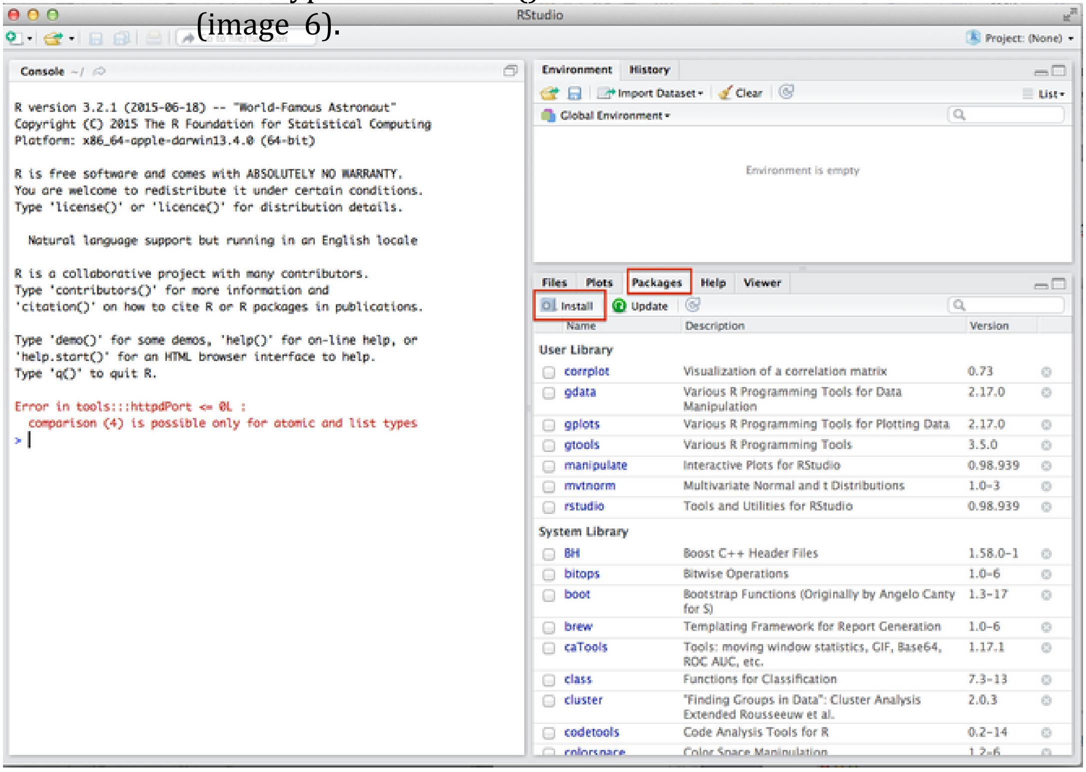
Step 4 – Install R packages required for the workshop

1. Click on the tab ' Packages' then 'Install' as shown in Image 4. Or Tools --> Install

2. packages. **Install the following packages**
   : `mixOmics` **version 6.1.0**`, mvtnorm, RColorBrewer, corrplot, igraph`
   (see Image 4). **For apple mac users,** if you are unable to install the mixOmics imported library rgl, you will need to install the XQuartz software first https://www.xquartz.org/

```
library(mixOmics)
```

3. Check that the packages are installed by typing ‘ ’ (without the quotes) in the prompt and press enter (see Image 5).
4. Then type ‘sessionInfo()’ and check that mixOmics version 6.1.0 has been installed (image 6).



```
R version 3.2.1 (2015-06-18) -- "World-Famous Astronaut"
Copyright (C) 2015 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin13.4.0 (64-bit)

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Type 'q()' to quit R.

Error in tools:::httpdPort <= 0L :
  comparison (4) is possible only for atomic and list types
> |
```

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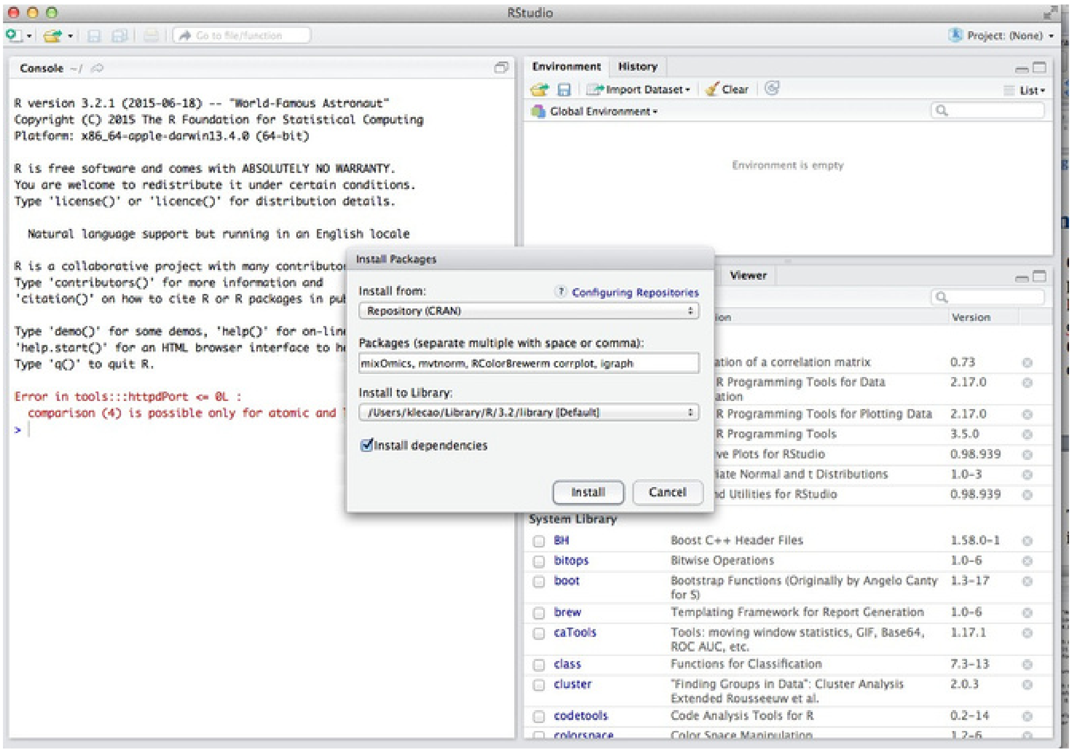
☐ cluster	"Finding Groups in Data": Cluster Analysis Extended Rousseeuw et al.	2.0.3
☐ codetools	Code Analysis Tools for R	0.2-14
☐ colorspace	Color Space Manipulation	1.2-6

Figure 4. Click on Install to install R packages.



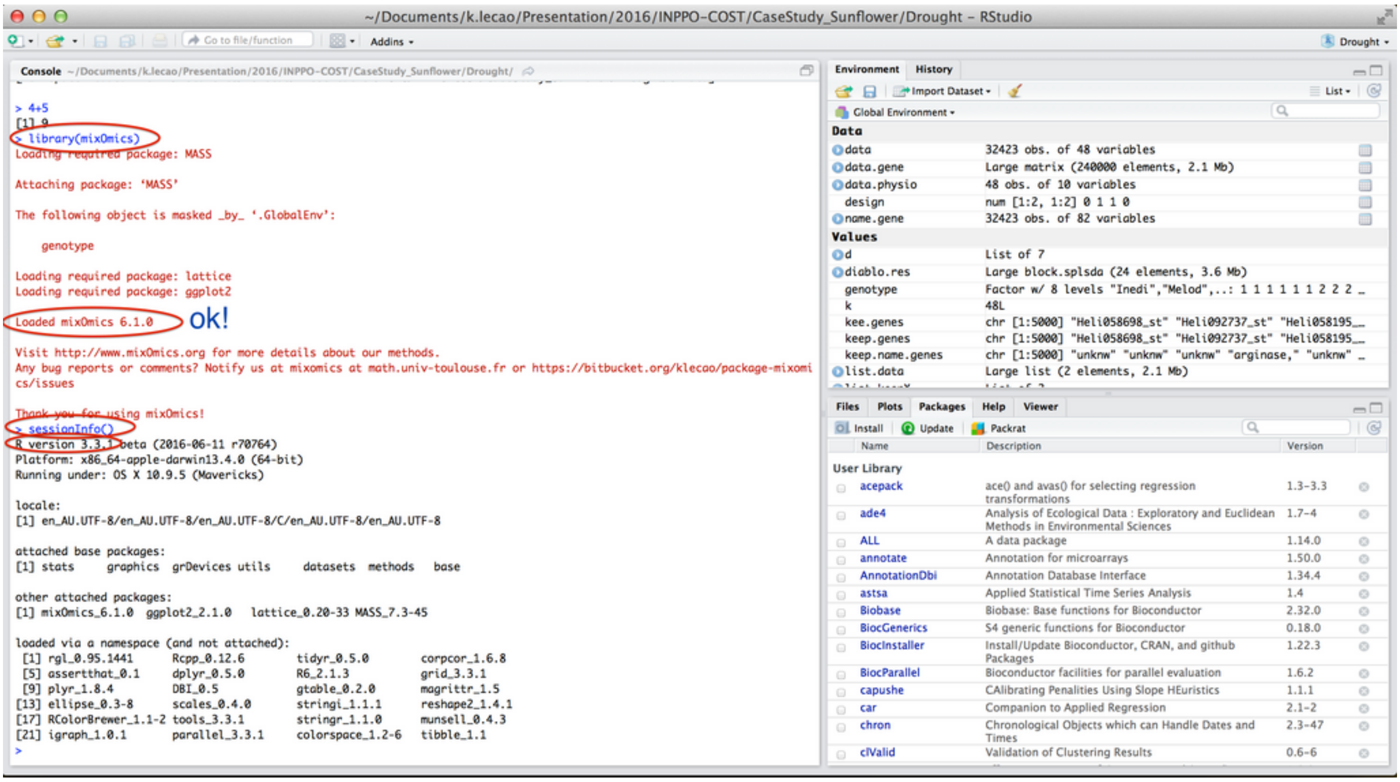
Install from: Repository (CRAN)

Packages (separate multiple with space or comma): mixOmics, mvtnorm, RColorBrewerm corrplot, igraph

Install to Library: /Users/klecao/Library/R/3.2/library [Default]

☑ Install dependencies

Figure 5. Specify the list of packages to be installed



```
> 4+5
[1] 9
> library(mixOmics)
Loading required package: MASS

Attaching package: ‘MASS’

The following object is masked _by_ ‘.GlobalEnv’:

    genotype

Loading required package: lattice
Loading required package: ggplot2

Loaded mixOmics 6.1.0

Visit http://www.mixOmics.org for more details about our methods.
Any bug reports or comments? Notify us at mixomics at math.univ-toulouse.fr or https://bitbucket.org/klecao/package-mixomi
cs/issues

Thank you for using mixOmics!
> sessionInfo()
R version 3.3.1 beta (2016-06-11 r70764)
Platform: x86_64-apple-darwin13.4.0 (64-bit)
Running under: OS X 10.9.5 (Mavericks)

locale:
[1] en_AU.UTF-8/en_AU.UTF-8/en_AU.UTF-8/C/en_AU.UTF-8/en_AU.UTF-8

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
[1] mixOmics_6.1.0  ggplot2_2.1.0   lattice_0.20-33 MASS_7.3-45

loaded via a namespace (and not attached):
 [1] rgl_0.95.1441      Rcpp_0.12.6        tidyr_0.5.0        corpcor_1.6.8
 [5] assertthat_0.1     dplyr_0.5.0        R6_2.1.3           grid_3.3.1
 [9] plyr_1.8.4         DBI_0.5            gtable_0.2.0       magrittr_1.5
[13] ellipse_0.3-8      scales_0.4.0       stringi_1.1.1      reshape2_1.4.1
[17] RColorBrewer_1.1-2 tools_3.3.1        stringr_1.1.0      munsell_0.4.3
[21] igraph_1.0.1       parallel_3.3.1     colorspace_1.2-6   tibble_1.1
>
```

Data	
data	32423 obs. of 48 variables
data.gene	Large matrix (240000 elements, 2.1 Mb)
data.physio	48 obs. of 10 variables
design	num [1:2, 1:2] 0 1 1 0
name.gene	32423 obs. of 82 variables
Values	
d	List of 7
diablo.res	Large block.splsda (24 elements, 3.6 Mb)
genotype	Factor w/ 8 levels "Inedi","Melod",..: 1 1 1 1 1 1 2 2 2 …
k	48L
kee.genes	chr [1:5000] "Heli058698_st" "Heli092737_st" "Heli058195_…
keep.genes	chr [1:5000] "Heli058698_st" "Heli092737_st" "Heli058195_…
keep.name.genes	chr [1:5000] "unknw" "unknw" "unknw" "arginase," "unknw" …
list.data	Large list (2 elements, 2.1 Mb)

	Name	Description	Version
User Library			
☐	acepack	ace() and avas() for selecting regression transformations	1.3-3.3
☐	ade4	Analysis of Ecological Data : Exploratory and Euclidean Methods in Environmental Sciences	1.7-4
☐	ALL	A data package	1.14.0
☐	annotate	Annotation for microarrays	1.50.0
☐	AnnotationDbi	Annotation Database Interface	1.34.4
☐	astsa	Applied Statistical Time Series Analysis	1.4
☐	Biobase	Biobase: Base functions for Bioconductor	2.32.0
☐	BiocGenerics	S4 generic functions for Bioconductor	0.18.0
☐	BiocInstaller	Install/Update Bioconductor, CRAN, and github Packages	1.22.3
☐	BiocParallel	Bioconductor facilities for parallel evaluation	1.6.2
☐	capushe	CAlibrating Penalities Using Slope HEuristics	1.1.1
☐	car	Companion to Applied Regression	2.1-2
☐	chron	Chronological Objects which can Handle Dates and Times	2.3-47
☐	clValid	Validation of Clustering Results	0.6-6

Figure 6. Check that the package mixOmics is installed and has the version 6.1.0.

That’s it, let’s get started!