Introduction to R and Bioconductor

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LUMC

What is R?

- **Programming language for statistical computing and graphics**
  - **Based on S language (like S-Plus)**

- **Environment**
  - **Data handling**
  - **Tools integration**

Why R?

- **Flexible**
  - **can be extended via packages**

- **Open source and free**

The R Foundation for Statistical Computing

- **Non-profit organization**

- **Provides support for R project and Bioconductor i.a.**

Bioconductor

- **open source and open development software project for the analysis and comprehension of genomic data**

- **Has become undeclared standard in the literature**

  – **New methods are quickly implemented in R and made available via Bioconductor**

Bioconductor

- Gathers packages of R functions to analyse genomic data

- To have flexibility, users must know fundaments of the R language

The R project

- **Involves many collaborators from all over the world**
- **Flexible environment within which to perform statistical computations**
- **Homepage**

  ```
  – http://www.r-project.org
  ```

The R Project for Statistical Computing

PCA 5 vars
princomp(x = data, cor = cor)

Fertility
Catholic — Examination / Education
Agriculture
(1-3) 60%

Clustering 4 groups   Factor 1 [41%]   Factor 3 [19%]

Groups
28
16
1
2

Important News:

- The first R users conference useR! 2004 will take place in Vienna, Austria, from May 20-22, 2004.
- **R version 1.9.0** has been released on 2004-04-12.
- Eric Lecoutre has won the R homepage graphics competition (the result can be seen above) by submitting this R code.

Regular updates

- **Every six months or so the software is updated**

    - **Latest version is R 1.9.0 released 12-April-2004**

    – **Guarantees flexibility**

but

    – **Some code for older versions may no longer run**

Array Week – Bioinformatics Course LUMC

Overview

- **Installing R**

- **Getting started with R**

- **Installing Bioconductor**

- **Getting R and Bioconductor packages**

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Installing R

- **The R package and manuals can be obtained from**

  `http://cran.r-project.org`

  or a mirror

- **Just follow the instructions to install the base R package**

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CRAN Mirrors

The Comprehensive R Archive Network is available at the following URLs, please choose a location close to you:

Australia
    http://cran.au.r-project.org   PlanetMirror
    http://mirror.aarnet.edu.au/pub/CRAN   AARNet (accessible only from Australia and New Zealand)

Austria
    http://cran.at.r-project.org   Technische Universität Wien

Brasil
    http://cran.br.r-project.org   Universidade Federal do Paraná
    http://www.termix.ufv.br/CRAN   Federal University of Viçosa
    http://lmq.esalq.usp.br/CRAN   University of Sao Paulo, Piracicaba

Canada
    http://probability.ca/cran/   University of Toronto

Denmark
    http://cran.dk.r-project.org   SunSITE

France
    http://cran.fr.r-project.org   INRA, Toulouse

Hungary
    http://cran.hu.r-project.org   Semmelweis University

Italy
    http://microarrays.unife.it/CRAN/   Universita di Ferrara

Japan
    ftp://ftp.u-aizu.ac.jp/pub/lang/R/CRAN/   University of Aizu

Portugal
    http://neacm.fe.up.pt/CRAN/"   Universidade do Porto

About R
What is R?
Contributors
Screenshots
What's new?

Download
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CRAN
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Software
R Sources
R Binaries
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Related Projects
Bioconductor
Omega
gRaphical models
R GUIs
R spatial projects

Precompiled Binary Distributions

Base system and contributed packages. **Windows and Mac** users most likely want these versions of R.

- Linux

- MacOS X (10.2.x and above) This version of R for the Mac is actively maintained.
- MacOS (System 8.6 to 9.1 and MacOS X up to 10.1.x) Last supported version of R is 1.7.1, there will be no more updates.

- Windows (95 and later)

Source Code for all Platforms

Windows and Mac users most likely want 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!

- **Source code** of the latest release (2004-04-12): R-1.9.0.tgz (read what's new in the latest version).
- **Source code** of contributed packages
- Current patch set (daily snapshot): R-release.diff.gz.

What are R and CRAN?

R for Windows

This directory contains binaries for a base distribution and packages to run on Windows (NT, 95 and later) on Intel and clones (but not NT on Alpha and other platforms).

Note: CRAN does not have Windows systems and cannot check these binaries for viruses. Use the normal precautions with downloaded executables.

Subdirectories:

base   Binaries for base distribution (managed by Duncan Murdoch)

contrib   Binaries of contributed packages (managed by Uwe Ligges)

Please do not submit binaries to CRAN. Package developers might want to contact Duncan Murdoch or Uwe Ligges directly in case of questions / suggestions related to Windows binaries.

You may also want to read the R FAQ and R for Windows FAQ.

Last modified: April 4, 2004, by Friedrich Leisch

CRAN
Mirrors
What's new?
Search

About R
R Homepage

Software
R Sources
R Binaries
Packages
Other

Documentation
Manual
FAQs
Contributed
Newsletter

Related Projects
Bioconductor
Omega
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🏁Start | ⬚ ⬚ ⬚ | ⬚In... ⬚C:... ⬚C:... ⬚pr... ⬚\\... ⬚LF... ⬚In... ⬚C:... ⬚In... ⬚ex... ⬚T... | ⬚ ⬚ ⬚ ⬚ ⬚ ⬚ ⬚ ⬚ ⬚ ⬚ ⬚ ⬚ 13:42

Internet

Getting started

- **Upon starting, get a window where commands should be typed after a signal ">"**

- **Unless command involves printing out the results, R gives no output**
  - **silence from the package is normal**
  - **most of the time, when R gives a msg without having been asked to do so, it is an error msg**

Getting finished

- **Simply type**

    >q()

on a command line

File   Edit   Misc   Packages   Windows   Help

R Console

```
R : Copyright 2002, The R Development Core Team
Version 1.5.1  (2002-06-17)

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.

R is a collaborative project with many contributors.
Type `contributors()' for more information.

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

[Previously saved workspace restored]

>
```

Start   Inbox - Micro...   C:\Menezes\...   C:\Menezes\...   C:\Menezes\...   invgamma_c...   Introduction ...   RGui   11:38

```
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[Previously saved workspace restored]

> x<-2
>
```

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Type `q()' to quit R.

[Previously saved workspace restored]

> x<-2
> y<-x + 10
>
```

File   Edit   Misc   Packages   Windows   Help

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Type `q()' to quit R.

[Previously saved workspace restored]

> x<-2
> y<-x + 10
> print(x)
[1] 2
> print(y)
[1] 12
>
```

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`help.start()' for a HTML browser interface to help.
Type `q()' to quit R.

[Previously saved workspace restored]

> x<-2
> y<-x + 10
> print(x)
[1] 2
> print(y)
[1] 12
> # Finish the session
> q()
```

Getting help via command line

- **to get help for a command you know the name:**

  ```
  > help(command)
  ```

- **to get help about something you don't know the exact name:**

  ```
  > help.search("something")
  ```

  Also: get help via pull-down menus
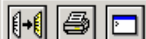
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File Edit Windows

R Console

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Type `demo()' for some demos, `help()'
`help.start()' for a HTML browser inter
Type `q()' to quit R.

[Previously saved workspace restored]

> help(plot)
>

R Information - Help for `plot'

about the graphical parameter arguments, see `par'.

Usage:

    plot(x, y, xlim=range(x), ylim=range(y), type="p",
        main, xlab, ylab, ...)

Arguments:

    x: the coordinates of points in the plot. Alternatively, a
        single plotting structure, function or any R object with a
        `plot' method can be provided.

    y: the y coordinates of points in the plot, optional if `x' is
        an appropriate structure.

xlim, ylim: the ranges to be encompassed by the x and y axes.

    type: what type of plot should be drawn. Possible types are

        * `"p"' for points,

        * `"l"' for lines,

        * `"b"' for both,
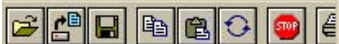
Start | Inbox - Micro... | C:\Menezes\... | C:\Menezes\... | C:\Menezes\... | invgamma_c... | Introduction ... | RGui   11:53

File Edit Misc Packages Windows Help

Console

FAQ on R
FAQ on R for Windows
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R functions (text)...
Html help
Search help...

Apropos...

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R Console

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'help.start()' for a HTML browser interface to help.
Type 'q()' to quit R.

>

Start   ... 15:11

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Type 'q()' to quit R.

>
```

Question

Help on

plot

OK   Cancel

Start ... Que... 15:12

RGui

File Edit Windows

R Console

```
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R is a collaborative p
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Type 'q()' to quit R.

> help("plot")
>
```

R `plot` help

```
plot                     package:base                   R Documentation

Generic X-Y Plotting

Description:

        Generic function for plotting of R objects.  For more details
        about the graphical parameter arguments, see 'par'.

Usage:

        plot(x, y, ...)

Arguments:

        x: the coordinates of points in the plot. Alternatively, a
           single plotting structure, function or _any R object with a
           'plot' method_ can be provided.

        y: the y coordinates of points in the plot, _optional_ if 'x' is
           an appropriate structure.

      ...: graphical parameters can be given as arguments to 'plot'.
           Many methods will also accept the following arguments:
```

Start   15:13

Reading datafiles

- **Point R out to your working directory**

```
> setwd("H:/Personal Folder/your name")
```

- **To read datafile with column names on first row, use**

```
> dataset <-
    read.table("exercise1.txt",header=TRUE)
```

File   Edit   View   Insert   Format   Help

probe.sets	control.1	control.2	treatment.1	treatment.2
221960_s_at	6.69811	6.745791	6.942202	6.85329
216261_at	6.615533	7.028536	7.060662	7.095305
217475_s_at	6.755857	7.026693	6.801845	6.843592
214284_s_at	6.845292	6.972958	6.768759	6.674566
212813_at	6.904793	7.1381	7.121685	6.958615
207555_s_at	7.696801	7.563247	7.366325	7.195175
216152_at	7.879939	8.001928	7.755341	7.55669
205636_at	7.396108	7.376154	7.07553	7.191523
217578_at	6.549701	6.542569	6.620866	6.801087
217270_s_at	7.313723	6.569656	6.987388	7.163664
1255_g_at	6.638923	6.622352	6.410462	6.769814
209824_s_at	8.680641	8.474756	8.135289	8.064454
220921_at	6.53055	6.770671	6.578218	6.985322
221778_at	7.544889	7.472731	7.318654	7.368969
215532_x_at	6.529508	6.645114	6.497584	6.468889
202341_s_at	7.248692	7.308284	7.351205	7.445675
217655_at	7.007951	6.897915	7.451917	7.179841
216440_at	6.815237	6.568643	6.884066	6.744207
215516_at	6.363936	6.588269	6.522675	6.405535
215132_at	6.55637	6.494841	6.687058	6.593364
215811_at	7.323681	7.283492	7.165731	7.235717
205994_at	6.516413	6.769349	6.808806	7.012297
214772_at	6.630682	6.784261	6.823488	6.969125
216123_x_at	6.898751	6.728207	6.690831	7.000961
214120_at	6.652872	6.926663	6.642945	6.563366
205505_at	7.558241	7.416128	7.322915	7.268548
208138_at	7.208544	7.150341	6.834189	6.79847
215859_at	6.527421	6.546691	6.691773	6.794099
209246_at	8.258085	8.168659	8.224383	8.218241
206930_at	6.790646	6.735447	7.225805	6.893898
221916_at	6.959618	6.60467	6.964193	6.918207
212823_s_at	7.640455	7.50883	7.487332	7.571327
204794_at	8.007472	7.482715	7.838908	8.410159
203125_x_at	8.643658	8.625826	8.685709	8.494766
206708_at	6.964255	6.913558	7.105168	7.263813
214786_at	6.476401	6.905958	6.400129	6.73557
205253_at	7.461251	7.439314	7.285351	6.908532
216086_at	6.58073	6.622352	6.735353	6.684993
216703_at	6.647597	6.647995	6.630721	6.739668

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Type `q()' to quit R.

[Previously saved workspace restored]

> help(plot)
> setwd("c:\\Menezes\\Microarray")
NULL
> lamin.vsn <-read.table("lamin.vsn.txt",header=TRUE)
>
```
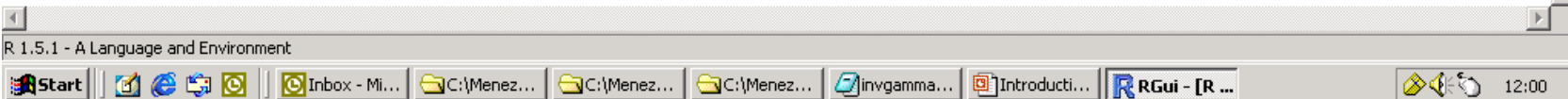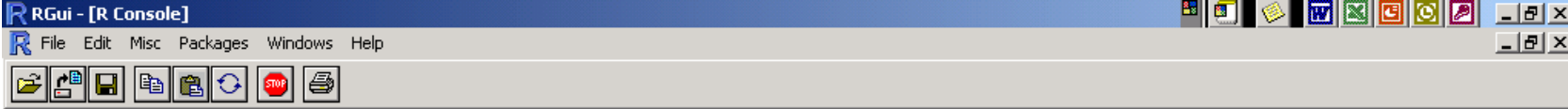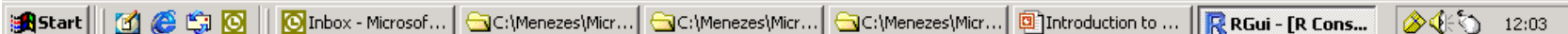
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Type `q()' to quit R.

[Previously saved workspace restored]

> help(plot)
> setwd("c:\\Menezes\\Microarray")
NULL
> lamin.vsn <-read.table("lamin.vsn.txt",header=TRUE)
> plot(control.1,control.2)
Error in plot(control.1, control.2) : Object "control.1" not found
> plot(lamin.vsn$control.1,lamin.vsn$control.2)
>
```

R R Console

```
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Type `demo()' for some demos, `help()'
`help.start()' for a HTML browser inte
Type `q()' to quit R.

[Previously saved workspace restored]

> help(plot)
> setwd("c:\\Menezes\\Microarray")
NULL
> lamin.vsn <-read.table("lamin.vsn.tx
> plot(control.1,control.2)
Error in plot(control.1, control.2) :
> plot(lamin.vsn$control.1,lamin.vsn$c
>
```

R R Graphics: Device 2 (ACTIVE)
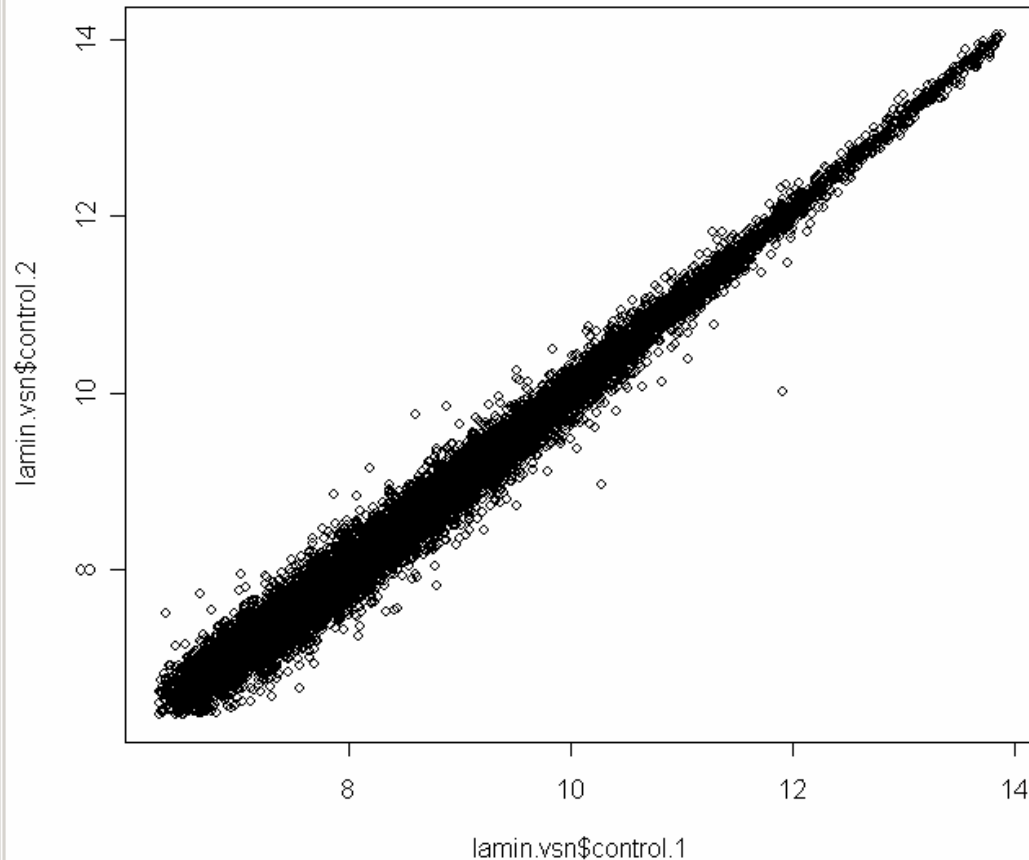
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Type `q()' to quit R.

[Previously saved workspace restored]

> setwd("c:\\Menezes\\Microarray")
NULL
> lamin.vsn <-read.table("lamin.vsn.txt",header=TRUE)
> plot(lamin.vsn$control.1,lamin.vsn$control.2)
> boxplot(lamin.vsn$control.1,lamin.vsn$control.2,lamin.vsn$treatment.1,lamin.vsn$treatment.2)
```
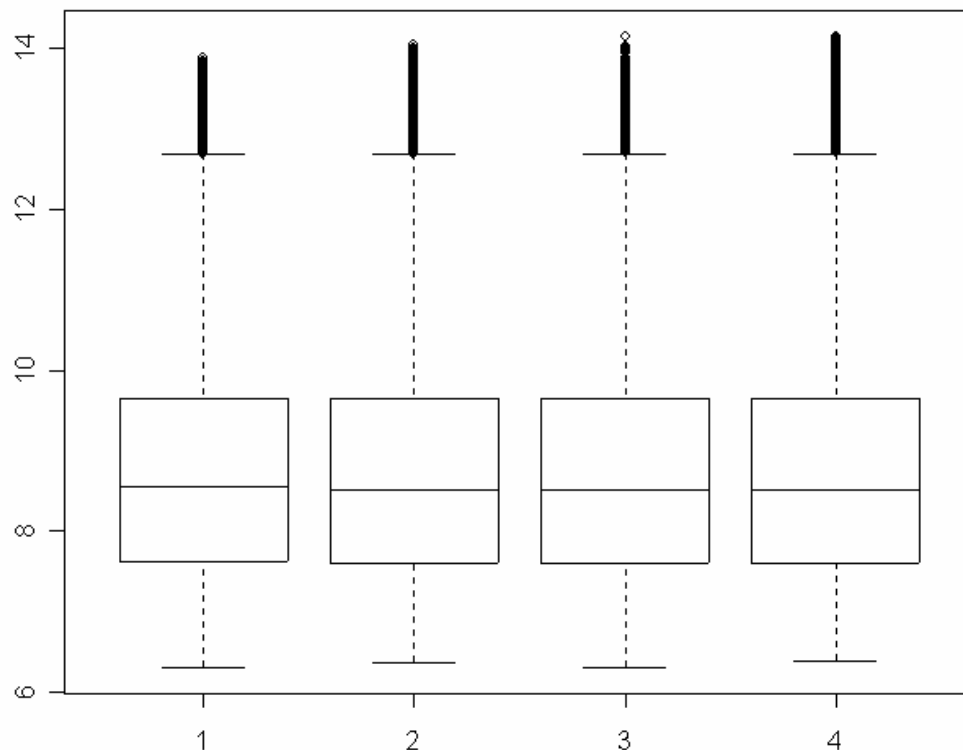
RGui

File   History   Resize   Windows

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[Previously saved workspace restored]

> setwd("c:\\Menezes\\Microarray")
NULL
> lamin.vsn <-read.table("lamin.vsn.txt
> plot(lamin.vsn$control.1,lamin.vsn$co
> boxplot(lamin.vsn$control.1,lamin.vsn
>

R Graphics: Device 2 (ACTIVE)

Start   Inbox - Micro...   C:\Menezes\...   C:\Menezes\...   C:\Menezes\...   Introduction ...   invgamma_la...   RGui   12:14

Reading datafiles

- In this example, the commands

```
> setwd("c:/Menezes/Microarray")
> lamin.vsn <-
  read.table("lamin.vsn.txt",header=TRUE)
```

will set the work directory and read the data file

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Using R packages

- **Loading to use**

  > `library(vsn)`

- **Getting help for a function**

  > `help("exprs",package=vsn)`

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Bioconductor

- `http://www.bioconductor.org`

- **Current release of packages**
  - **includes vsn, affy, limma, (gc)rma, multtest, global.test**

- **Developmental**
  - **Versions not yet fully tested**

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BioConductor: *open source software for bioinformatics*

The Bioconductor project is pleased to announce that it has won the **Insightful Innovation Award** from the Insightful Corporation for "excellence in deploying innovative, analyticial solutions that produce intelligence for data."

Bioconductor is an open source and open development software project for the analysis and comprehension of genomic data.

Released Bioconductor packages are described in the Bioconductor Packages section of the FAQ.

The broad goals of the projects are to

- provide access to a wide range of powerful statistical and graphical methods for the analysis of genomic data;
- facilitate the integration of biological metadata in the analysis of experimental data: e.g. literature data from PubMed, annotation data from LocusLink;
- allow the rapid development of extensible, scalable, and interoperable software;
- promote high-quality documentation and reproducible research;
- provide training in computational and statistical methods for the analysis of genomic data.

More detailed information about the project and our goals is found in the Bioconductor Basics section of the FAQ.

Bioconductor installation instructions

Bioconductor Release 1.3 is now available.

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Getting Bioconductor

Use the Bioconductor Install Script
- ## Simply type (in R):

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

then

```
getBioC(relLevel="release")
```

BioConductor: open source software for bioinformatics

About Bioconductor

- Main Page
- What is Bioconductor?
- Screenshots
- Citing Bioconductor
- Bioconductor FAQ
- Developers
- Mirrors
- Acknowledgements
- What's New?

Software

- How To
- Release 1.3 Packages
- Developmental Packages
- Previous Releases
- MetaData
- Experimental Data
- Change Log

Documentation

- Vignettes
- Short Courses
- Lab Materials
- Research Talks
- Publications

The Bioconductor project is pleased to announce that it has won the **Insightful Innovation Award** from the Insightful Corporation for "excellence in deploying innovative, analyticial solutions that produce intelligence for data."

Bioconductor is an open source and open development software project for the analysis and comprehension of genomic data.

Released Bioconductor packages are described in the Bioconductor Packages section of the FAQ.

The broad goals of the projects are to

- provide access to a wide range of powerful statistical and graphical methods for the analysis of genomic data;
- facilitate the integration of biological metadata in the analysis of experimental data: e.g. literature data from PubMed, annotation data from LocusLink;
- allow the rapid development of extensible, scalable, and interoperable software;
- promote high-quality documentation and reproducible research;
- provide training in computational and statistical methods for the analysis of genomic data.

More detailed information about the project and our goals is found in the Bioconductor Basics section of the FAQ.

Bioconductor **installation instructions**

Bioconductor **Release 1.3** is now available.

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BioConductor: open source software for bioinformatics

The Bioconductor Project Release 1.3 Package Index

Requires R-1.8.1: (Instructions for **downloading** R)

To use the Bioconductor Install Script:
Simply type (in R):
   source("http://www.bioconductor.org/getBioC.R")
Then
   getBioC(relLevel="release")
to install Bioconductor. There are several options available for **getBioC**. Users are encouraged to examine them
to see if any suit their needs.

Users should strongly consider using the **reposTools** package for installation and updating of packages. Using the **install
script** will set up the appropriate structure for the reposTools system.

Contributions from the community are welcome!

Package	Title	Version
AnnBuilder	Bioconductor annotation data package builder	1.3.3
Biobase	Biobase: Base functions for Bioconductor	1.4.0
DynDoc	Dynamic document tools	1.3.2
MAGEML	handling MAGEML documents	1.0.6
MeasurementError.cor	Measurement Error model estimate for correlation coefficient	1.0.2
RBGL	Test interface to boost C++ graph lib	1.1.14
ROC	utilities for ROC, with uarray focus	1.0.6
RdbiPgSQL	PostgreSQL access	1.0.2

Summary

- **What are R and Bioconductor**

- **Downloading and installing R and Bioconductor packages**

- **Getting started in R (very briefly)**

Apendices

- Package vs. library

- Getting R packages

- Getting Bioconductor packages

- Getting maanova

Package vs. library

- **A package is a bundle of functions**
- **A library is a directory containing installed packages**

  - **A package is loaded from a library by the function** `library()`.

Getting R packages

- **Downloading**

  ```
  > options(CRAN="http://cran.r-
    project.org")
  > install.packages("sma")
  ```

- **Loading to use**

  ```
  > library(sma)
  ```

- **Getting help for a function**

  ```
  > help(stat.bayesian,package=sma)
  ```

sma: Statistical Microarray Analysis

The package contains some simple functions for exploratory microarray analysis.

Version:	0.5.10
Depends:	R (>= 1.3.0)
Date:	2002/10/11
Author:	Sandrine Dudoit <sandrine@stat.berkeley.edu> Yee Hwa (Jean) Yang <yeehwa@stat.berkeley.edu> Benjamin Milo BOLSTAD <bolstad@stat.Berkeley.EDU>, with contributions from Natalie Thorne <thorne@wehi.edu.au> Ingrid Lönnstedt <ingrid@math.uu.se> Jessica Mar
Maintainer:	Yee Hwa (Jean) Yang and Benjamin Milo BOLSTAD <zarray@stat.Berkeley.EDU>
License:	GPL version 2 or newer
URL:	http://www.stat.berkeley.edu/users/terry/zarray/Html/smacode.html

Index of Contents (Text)
Reference Manual (PDF)

sn: The skew-normal and skew-t distributions

Functions for manipulating skew-normal and skew-t probability distributions, and for fitting them to data, in the scalar and the multivariate case.

Version:	0.30
Depends:	R (>= 1.0.1), mvtnorm
Date:	2002-06-30
Author:	Adelchi Azzalini <adelchi.azzalini@unipd.it>
Maintainer:	Adelchi Azzalini <adelchi.azzalini@unipd.it>
License:	GPL Version 2 or later.
URL:	http://azzalini.stat.unipd.it//SN

Index of Contents (Text)
Reference Manual (PDF)

Getting R packages

Using pull-down menu from the CRAN website

- Very easy
- Just check that you know what package you want before starting to download

File   Edit   Misc   Packages   Windows   Help

```
R : Copyright 2003, The R Development Core Team
Version 1.8.0  (2003-10-08)

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 det

R is a collaborative project with many contributors.
Type 'contributors()' for more information.

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

> local({a <- CRAN.packages()
+ install.packages(select.list(a[,1],,TRUE), .libPat
trying URL `http://cran.r-project.org/bin/windows/co
Content type `text/plain; charset=iso-8859-1' lengtk
opened URL
downloaded 15Kb
```
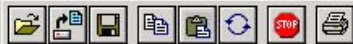
R Console

Select

- sandwich
- SASmixed
- sca
- scatterplot3d
- seacarb
- seao
- seao.gui
- segmented
- sem
- SenSrivastava
- serialize
- session
- sfsmisc
- sgeostat
- shapefiles
- shapes
- simpleboot
- skewt
- sm
- **sma**
- smoothSurv
- sn

OK   Cancel
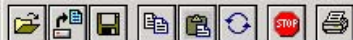
R 1.8.0 - A Language and Environment

Start | R-... Sri... C:\... Intr... exp... Fin... Wel... Inb... RGui Select   12:08

File   Edit   Misc   Packages   Windows   Help

```
R R Console                                                              _ | □ | X |

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'help.start()' for a HTML browser interface to help.
Type 'q()' to quit R.

> local({a <- CRAN.packages()
+ install.packages(select.list(a[,1],,TRUE), .libPaths()[1], available=a)})
trying URL `http://cran.r-project.org/bin/windows/contrib/1.8/PACKAGES'
Content type `text/plain; charset=iso-8859-1' length 16056 bytes
opened URL
downloaded 15Kb

trying URL `http://cran.r-project.org/bin/windows/contrib/1.8/sma_0.5.14.zip'
Content type `application/zip' length 3068799 bytes
opened URL
downloaded 2996Kb

package  sma  successfully unpacked and MD5 sums checked

Delete downloaded files (y/N)? y

updating HTML package descriptions
> ▮
```

```
Version 1.5.1   (2002-06-17)

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

[Previously saved workspace restored]

> options(CRAN="http://cran.r-project.org")
> install.packages("sma")
trying URL `http://cran.r-project.org/bin/windows/contrib/PACKAGES'
Content type `text/plain; charset=iso-8859-1' length 8202 bytes
opened URL
downloaded 8202 bytes

trying URL `http://cran.r-project.org/bin/windows/contrib/sma.zip'
Content type `application/zip' length 3100188 bytes
opened URL
downloaded 3027Kb


Delete downloaded files (y/N)? n
The packages are in C:\DOCUME~1\RXMENE~1\LOCALS~1\Temp\Rinstdir19169
updating HTML package descriptions
Warning message:
argument `lib' is missing: using C:/PROGRA~1/R/rw1051/library in: install.packages("sma")
> help(sma)
Error in help(sma) : No documentation for `sma' in specified packages and libraries:
  you could try `help.search("sma")'
> help(stat.bayesian,package=sma)
>
```
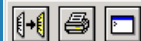
```
stat.bayesian              package:sma              R Documentation

Calculates an Odds Ratio of Each Gene in a Multi-slide microarray
Experiment

Description:

     This function takes the normalized expression estimates from a
     multi-slide microarray experiment (M-values output by stat.ma) and
     returns an odds ratio for each gene: log( Pr(the gene is
     differentially expressed) / Pr(the gene is not differentially
     expressed) ). The parameter estimates of the Bayesian model used,
     as well as some data structures which are useful when presenting
     the lodscore graphically are also in the output.

Usage:

          stat.bayesian(M=NULL, nb=NULL, nw=1, Xprep=NULL,
          para=list(p = 0.01, v = NULL, a = NULL, c = NULL, k = NULL))

Arguments:

       M: Matrix of (normalized) log expression ratios M = log_2 (R/G)
          (E.g. output from stat.ma())

      nb: Number of slides containing spots for a gene (common for all
          genes). Unnecessary argument if nw=1.

      nw: Number of spots for a gene within each slide (common to all
          genes).Default is 1.

   Xprep: Some data structures useful in graphical presentation. (This
          is calculated only if not already supplied as input. See
          details!)

    para: Estimates of the parameters used in the Bayesian
          calculations. (These are calculated only if not already
          supplied as input. See details!)
```
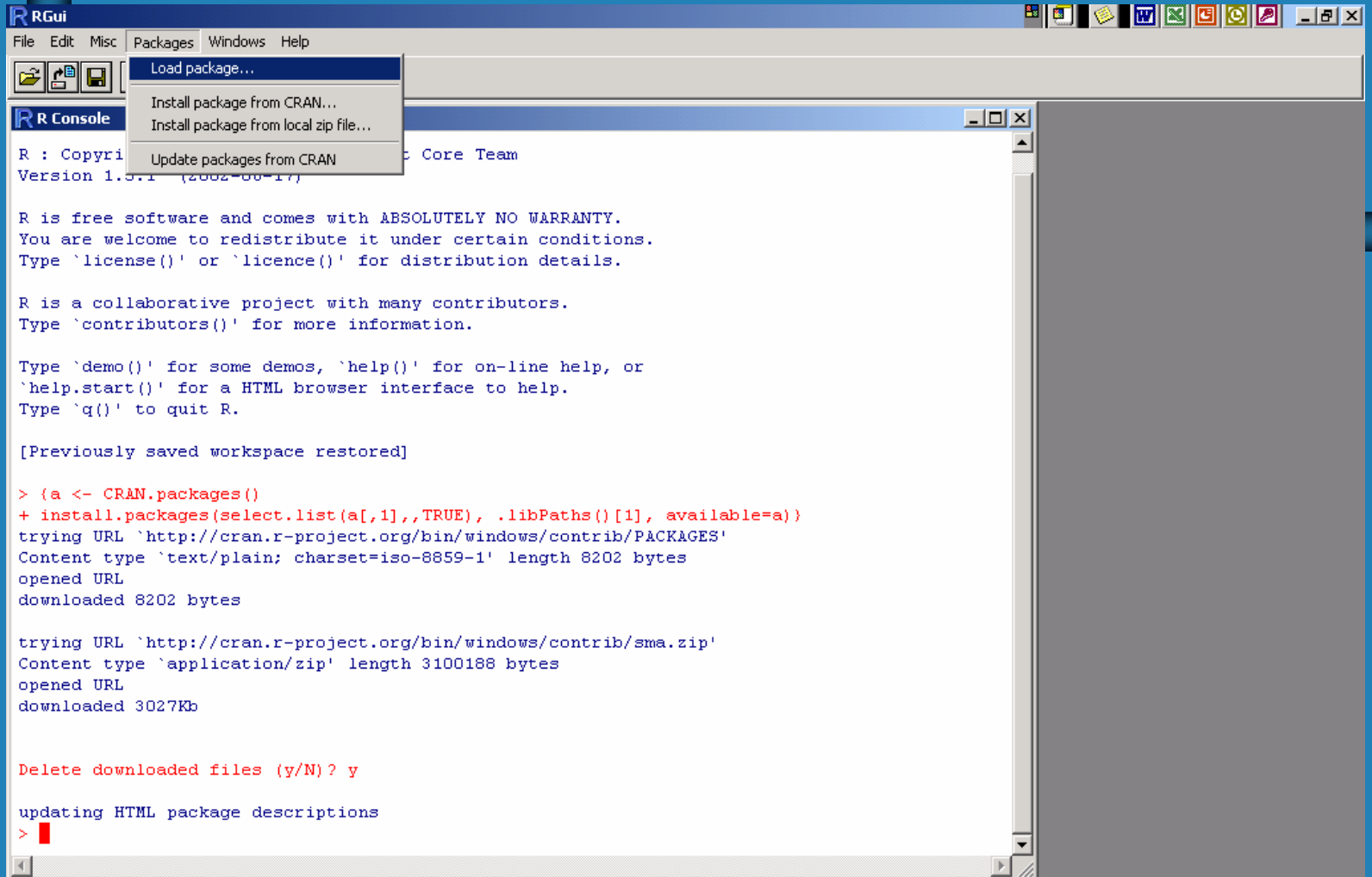
File Edit Misc Packages Windows Help

R Console

```
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`help.start()' for a HTML browser interface to help.
Type `q()' to quit R.

[Previously saved workspace restored]

> {a <- CRAN.packages()
+ install.packages(select.list(a[,1],,TRUE), .libPat
trying URL `http://cran.r-project.org/bin/windows/co
Content type `text/plain; charset=iso-8859-1' length
opened URL
downloaded 8202 bytes

trying URL `http://cran.r-project.org/bin/windows/co
Content type `application/zip' length 3100188 bytes
opened URL
downloaded 3027Kb


Delete downloaded files (y/N)? y

updating HTML package descriptions
> {pkg <- select.list(sort(.packages(all.available = TRUE)))
+ if(nchar(pkg)) library(pkg, character.only=TRUE)}
```

Select one

foreign
grid
KernSmooth
lattice
lqs
MASS
methods
mgcv
modreg
mva
nlme
nls
nnet
qvcalc
rpart
sma
spatial
splines
stepfun
survival
tcltk
tools

OK   Cancel

R Console

```
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`help.start()' for a HTML browser interface to help.
Type `q()' to quit R.

[Previously saved workspace restored]

> {a <- CRAN.packages()
+ install.packages(select.list(a[,1],,TRUE), .libPaths()[1], available=a)}
trying URL `http://cran.r-project.org/bin/windows/contrib/PACKAGES'
Content type `text/plain; charset=iso-8859-1' length 8202 bytes
opened URL
downloaded 8202 bytes

trying URL `http://cran.r-project.org/bin/windows/contrib/sma.zip'
Content type `application/zip' length 3100188 bytes
opened URL
downloaded 3027Kb


Delete downloaded files (y/N)? y

updating HTML package descriptions
> {pkg <- select.list(sort(.packages(all.available = TRUE)))
+ if(nchar(pkg)) library(pkg, character.only=TRUE)}
Warning message:
package sma was built under R version 1.6.0
>
```

Getting/using Bioconductor packages

- Same as with R packages

- Only needed if new package becomes available

Getting maanova

- **Go to the Jackson lab webpage**

  http://www.jax.org/research/churchill

- **Under "Software" you find "R/maanova"**

- **Follow the steps to download a zip file**

- **To install, follow instructions given in the Installation notes**