



Installing R and Packages

INBRE Bioinformatics Core Training Programs
-Microarray Workshop I –

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Overview

- These slides step you through the process of installing the statistical analysis package, R, and the required packages for the microarray data analysis we will focus on in the course. Here is the list of things you will do.
 1. Install R
 2. Download and install Bioconductor packages
 3. Download and install R/maanova and R/qvalue packages
 4. Test whether the installation was successful
 5. Learn how to launch help from within R

Downloading R

- Enter the address for R's homepage in browser:



<http://www.r-project.org/index.html>

- Click '[CRAN](#)' located under the 'Download, Packages' section on the left-hand side of the webpage.

About R

[What is R?](#)

[Contributors](#)

[Screenshots](#)

[What's new?](#)

Download, Packages

[CRAN](#)

R Project

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Downloading R

- Scroll down to view a list of CRAN mirrors located in the USA, and click on one of the location links.

USA

<http://cran.cnr.Berkeley.edu>

<http://cran.stat.ucla.edu/>

<http://streaming.stat.iastate.edu/CRAN/>

<http://cran.mtu.edu/>

<http://cran.wustl.edu/>

<http://www.ibiblio.org/pub/languages/R/CRAN/>

<http://cran.case.edu/>

<http://lib.stat.cmu.edu/R/CRAN/>

<http://cran.mirrors.hoobly.com>

<http://www.revolution-computing.com/cran/>

<http://www.cyberuse.com/cran>

<http://cran.frcrc.org/>

University of California, Berkeley, CA

University of California, Los Angeles, CA

Iowa State University, Ames, IA

Michigan Technological University, Houghton, MI

Washington University, St. Louis, MO

University of North Carolina, Chapel Hill, NC

Case Western Reserve University, Cleveland, OH

Statlib, Carnegie Mellon University, Pittsburgh, PA

Hoobly Classifieds, Pittsburgh, PA

Revolution Computing, San Antonio, TX

CyberUse.com, Dallas, TX

Fred Hutchinson Cancer Research Center, Seattle, WA

Downloading R

- Select the operating system of the machine.

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:

- [Linux](#)
- [MacOS X](#)
- [Windows](#)






- Select the corresponding install program.

– Windows: [base](#) Binaries for base distribution (managed by Duncan Murdoch)

– MAC: [R 2.8.1.dmg](#) (latest version)
MD5-hash: c43581d6ebede51fee2da8fb5292b2c7
(ca. 63MB)

– Linux users will need to select the file depending upon

OS:

 Parent Directory		-
 debian/	17-Feb-2009 10:23	-
 redhat/	06-Jan-2009 09:04	-
 suse/	22-Dec-2008 23:54	-
 ubuntu/	24-Mar-2009 06:25	-

Installing R

- Windows:

[Download R 2.8.1 for Windows](#) (34 megabytes)

[Installation and other instructions](#)

New features in this version: [Windows specific](#), [all platforms](#).

- An installation guide link is located below the link to download the executable file.

Frequently asked questions

- [How do I install R when using Windows Vista?](#)
 - [How do I update packages in my previous version of R?](#)
- R installation should be as simple as clicking the downloaded executable file.

Installing R

- MAC:

Installation instructions are located to the right of the download link.

Universal binary of **R 2.8.1** for Mac OS X 10.4.4 and higher. This is a disk image containing the installer of R for Mac OS X 10.4.4 or higher. This image also contains Tcl/Tk libraries (for X11) and GNU Fortran 4.2.3 for both PowerPC and Intel Macs. This binary was tested on both Mac OS X 10.4 (Tiger) and Mac OS X 10.5 (Leopard).

Depending on your browser, you may need to press the control key and click on this link to download the file. To install R simply double-click on icon of the multi-package "R.mpkg" contained in the R-2.8.0.dmg disk image.

- Linux:

Installation instructions are located directly beneath the links to OS files.

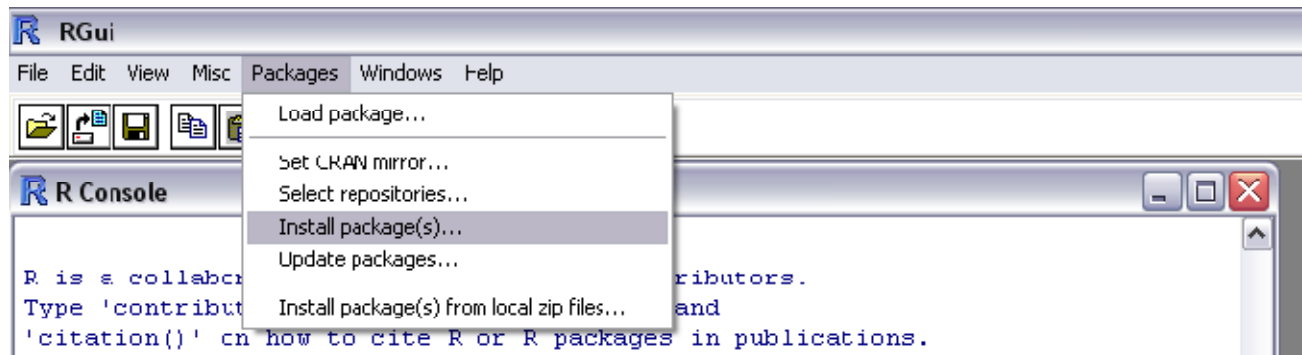
Installing Bioconductor Packages

- Not all packages are available on CRAN (Comprehensive R Archive Network)
 - Additional packages are available through Bioconductor
 - www.bioconductor.org
- R allows command line installation of packages supplied through Bioconductor
 - Install using the following commands
(<http://www.bioconductor.org/docs/install/>)

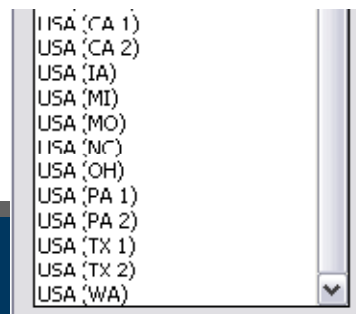
```
source("http://bioconductor.org/biocLite.R")  
biocLite()
```

Installing R/maanova and R/qvalue Packages

- Open R, and from the menu bar select 'Packages' -> Install Package(s)...

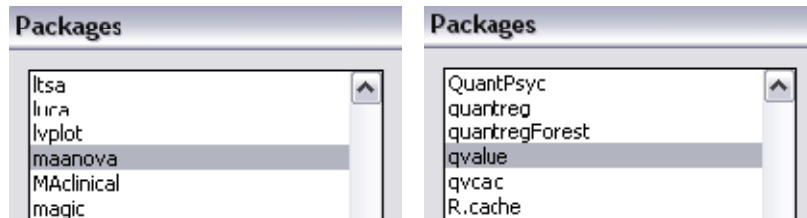


- Select a USA CRAN mirror.



Installing R/maanova and R/qvalue Packages

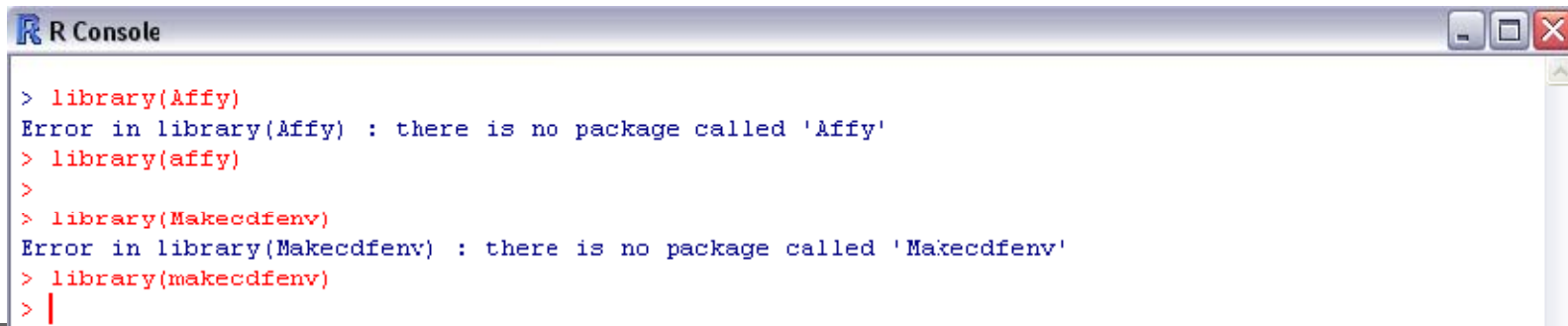
- Select the desired package for installation.
 - ‘maanova’ and ‘qvalue’ will be used in the analysis of the data



- Multiple packages can be selected by holding down the ‘control’ key and clicking on the desired packages.
- R will also install any additional packages required by the selected package(s).

Using And Testing Installed Packages

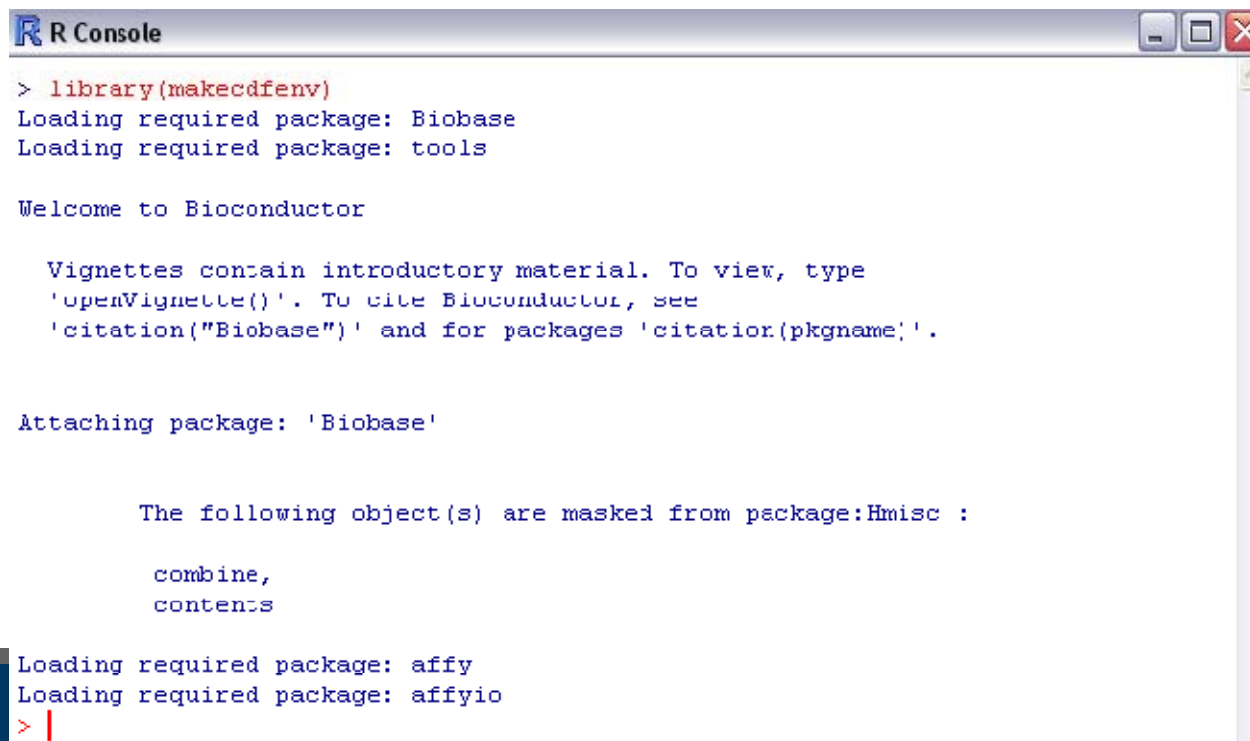
- Once a package has been downloaded, it must be loaded in R before its functions are available for use.
 - The **library()** function will load a package for use in the current R session.
 - As shown below, if the **library()** function returns an error, the package was not downloaded successfully or the name was misspelled (capitalization **is** important).



```
R Console
> library(Affy)
Error in library(Affy) : there is no package called 'Affy'
> library(affy)
>
> library(Makecdfenv)
Error in library(Makecdfenv) : there is no package called 'Makecdfenv'
> library(makecdfenv)
> |
```

Using And Testing Installed Packages

- If another package is required for a package to load successfully, R will also load that package.
 - ‘makecdfenv’ requires ‘affy’ to be loaded



```
R Console
> library(makecdfenv)
Loading required package: Biobase
Loading required package: tools

Welcome to Bioconductor

  Vignettes contain introductory material. To view, type
  'openVignette()'. To cite Bioconductor, see
  'citation("Biobase")' and for packages 'citation(pkgname)'.

Attaching package: 'Biobase'

  The following object(s) are masked from package:Hmisc :

      combine,
      contents

Loading required package: affy
Loading required package: affyio
> |
```

Accessing Help Within R

- For all functions there are associated help files
 - To view a help file use the **help()** function or **? character**.
 - For example, **library(makecdfenv)** makes the function **make.cdf.env()** available. To obtain more information on the function type either **help(make.cdf.env)** or **?make.cdf.env**.
- Help files are very informative, and typically contain helpful examples.

Additional Information

- An introductory guide to R is available at:
<http://cran.r-project.org/doc/manuals/R-intro.pdf>
- A complete list of CRAN R packages is available at:
<http://cran.r-project.org/web/packages/>
- A complete list of Bioconductor R packages is available at:
<http://www.bioconductor.org/packages/release/Software.html>