

INTRODUCTION TO R AND BIOCONDUCTOR

BST/STA 226 DISCUSSION – 5 FEBRUARY 2007

Getting Started with R

STA 141 Class Website (<http://eeyore.ucdavis.edu/stat141>) has lots of useful links for R.

Introductory Documents

“R for Beginners” by E. Paradis

“An Introduction to R” by W. Venables and D. Smith

Downloading and Installing R

1. Go to www.r-project.org
2. Select CRAN under downloads. Select a nearby site.
3. Select Precompiled Binary for your operating system
4. Download *.exe file and install

Packages

To get list of packages and download packages

1. Go to www.r-project.org
2. Select CRAN under downloads. Select a nearby site.
3. Select Packages under Software

Installing Packages

1. *To install a package directly from CRAN:*
 - In R GUI, select *Install packages* under *Packages*. Then select mirror. Then select desired packages
2. *To install a package from harddrive:*
 - Download desired package from CRAN. Select *Install package from local zip files* under *Packages*

Working with Packages

To see available packages – *library()*

To load an installed package – *library(package name)*

To get list of functions in a package – *library(help= package name)*

Getting Help

For help on a specific function, use

?mean or *help(“mean”)* or *help(mean)*

If you don't know the name of the function, use

apropos(“mean”) or *help.search(“mean”)*

Downloading and Installing BioConductor Packages

Bioconductor is a collection/repository of R packages for bioinformatics.

To obtain and install core BioConductor packages

1. Go to www.bioconductor.org
2. Select Install software
3. Follow directions for installing biocLite.R

This installs the following BioConductor packages.

affy	affydata	affyPLM
annaffy	annotate	Biobase
Biostrings	DynDoc	gcrma
genefilter	geneplotter	hgu95av2
limma	marray	matchprobes
multtest	reposTools	ROC
vsn	xtable	

To use a package, load it as described above for R packages. The main BioConductor package is `Biobase` but we will use several of the other packages as well. In subsequent classes, we will be using the estrogen data set which is available as the package `estrogen` under the experiment data heading under Browse Packages. You should install the estrogen package as well as the package `hgu95av2cdf` which is available under the annotation data heading.

In addition to these packages, the packages `tkWidgets` and `widgetTools` are helpful for using the vignettes. These packages are available on Bioconductor under Browse Packages. Install and load as any other package.

Vignettes

Most Bioconductor packages contain a *vignette*. A *vignette* is an executable document providing a step-by-step overview of the package functionality.

The function `vExplorer()` brings up a list of vignettes. You can then select a vignette and step through various code chunk. Through the graphical interface you can execute the code and see the results.

The function `openVignette()` lists available vignettes. Selecting a vignette pulls up a pdf file with information and code examples on the selected topic.