Introduction to Bioconductor

Useful Information

- **Web page: www.bioconductor.org**

- **Mailing list:**
  bioconductor@stat.math.ethz.ch

- **You can install from GUI or using install.packages**

Vignettes

- **Bioconductor has adopted a new documentation paradigm, the vignette.**

- **A vignette is an executable document consisting of a collection of documentation text and code chunks.**

- **Vignettes form dynamic, integrated, and reproducible statistical documents that can be automatically updated if either data or analyses are changed.**

- **Vignettes can be generated using the Sweave function from the R tools package.**

- **Use .find.package to get the original Rnw file**

Classes and Methods

- **Objects in R can be complicated. Example are lists**

- **We can also define classes - objects that follow a particular format**

- **Methods are functions, such as plot, that behave differently depending on class**

`exprSet` class

exprs — Matrix of expression measures, genes x samples

se.exprs — Matrix of SEs for expression measures, genes x samples

phenoData — Sample level covariates, instance of class **phenoData**

annotation — Name of annotation data

description — MIAME information

notes — Any notes

`phenoData` class

pData — Matrix of samples x covariates

varLabels — List describing each covariate