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