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**BIOINFORMATICS AND COMPUTATIONAL
BIOLOGY SOLUTIONS USING R AND
BIOCONDUCTOR**

**Biostatistics 140.688
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**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`




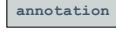


Vignettes

- 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

 <code>exprs</code>	Matrix of expression measures, genes x samples
 <code>se.exprs</code>	Matrix of SEs for expression measures, genes x samples
 <code>phenoData</code>	Sample level covariates, instance of class <code>phenoData</code>
 <code>annotation</code>	Name of annotation data
 <code>description</code>	MIAME information
 <code>notes</code>	Any notes

phenoData class

pData

Matrix of samples x covariates

varLabels

List describing each covariate
