Bioconductor overview

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Bioconductor Project

- The Bioconductor project started in 2001

Goal: make it easier to conduct reproducible consistent analysis of data from new high-throughput biological technologies

- Core maintainers of the Bioconductor website located at Fred Hutchinson Cancer Research Center
- Updated version released biannually coinciding with the release of R
- Many contributed software packages

Bioconductor packages

- Bioconductor software consists of R add-on packages.
- An R package is a structured collection of code (R, C, or other), documentation, and/or data for performing specific types of analyses.
- E.g. **affy**, **limma**, **sva** packages provide implementations of specialized statistical and graphical methods.

Goals of the Bioconductor Project

- Provide access to statistical and graphical tools for analysis of high-dimensional biological data

1. Microarray analysis
2. High-throughput 'omics' data

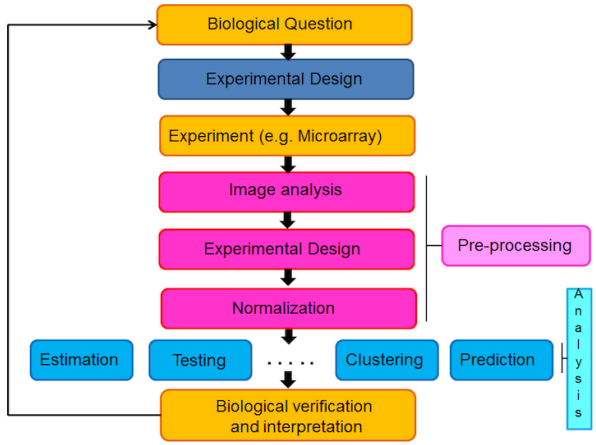
Goals of the Bioconductor Project

- Include comprehensive **documentation** describing and providing examples for packages
- Packages have associated **vignettes** that provide examples of how to use functions
- Have additional tools to work with publically available databases and other meta-data

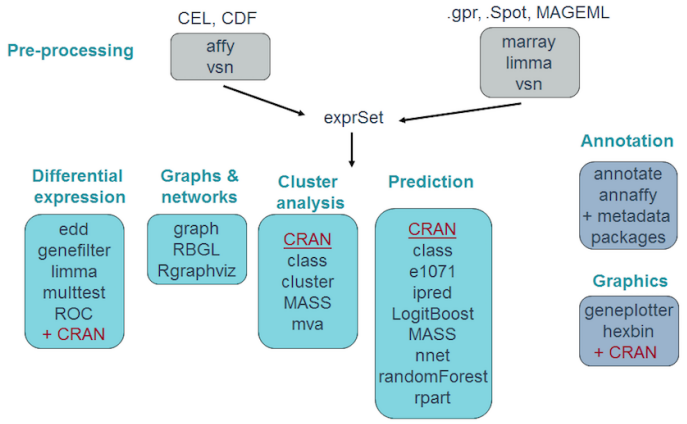
Vignettes

- 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 (or, `roxygen2` package)

Microarray data analysis



Microarray data analysis



Bioconductor website

Lets take a look at the website…

http://bioconductor.org/

marrayRaw class

Pre-normalization intensity data for a batch of arrays

`maRf`	`maGf`	Matrix of red and green foreground intensities
`maRb`	`maGb`	Matrix of red and green background intensities
`maW`		Matrix of spot quality weights
`maLayout`		Array layout parameters - `marrayLayout`
`maGnames`		Description of spotted probe sequences - `marrayInfo`
`maTargets`		Description of target samples - `marrayInfo`
`maNotes`		Any notes

AffyBatch class

Probe-level intensity data for a batch of arrays (same CDF)

`cdfName`		Name of `CDF` file for arrays in the batch
`nrow`	`ncol`	Dimensions of the array
`exprs`	`se.exprs`	Matrices of probe-level intensities and SEs rows → probe cells, columns → arrays.
`phenoData`		Sample level covariates, instance of class `phenoData`
`annotation`		Name of annotation data
`description`		MIAME information
`notes`		Any notes

ExpressionSet class

Processed Affymetrix or spotted array data

`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

MIAME

Minimum Information About a Microarray Experiment (MIAME)
http://fged.org/projects/miame/

The six most critical elements contributing towards MIAME are:

1 - The raw data for each hybridization (e.g., CEL or GPR files)

2 - The final processed (normalized) data for the set of hybridizations in the experiment (study) (e.g., the gene expression data matrix used to draw the conclusions from the study)

3 - The essential sample annotation including experimental factors and their values (e.g., compound and dose in a dose response experiment)

MIAME

Minimum Information About a Microarray Experiment (MIAME)
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4 - The experimental design including sample data relationships (e.g., which raw data file relates to which sample, which hybridizations are technical, which are biological replicates)

5 - Sufficient annotation of the array (e.g., gene identifiers, genomic coordinates, probe oligonucleotide sequences or reference commercial array catalog number)

6 - The essential laboratory and data processing protocols (e.g., what normalization method has been used to obtain the final processed data)

Pre-processing packages

1. `marray`: Spotted DNA microarrays.
2. `affy`: Affymetrix oligonucleotide chips.
3. `limma`: all, from spotted arrays to Affy to RNA-seq

- Reading in intensity data, diagnostic plots, normalization, computation of expression measures.
- The packages start with very different data structures, but produce similar objects of class `ExpressionSet`.
- One can then use other Bioconductor and CRAN packages for exploratory data analysis and visualization, differential expression detection