Introduction to Bioconductor

Martin Morgan
Fred Hutchinson Cancer Research Center

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Bioconductor: Analysis and Comprehension of High Throughput Genetic Data

Goal	Help biologists understand their data
Focus	▸ Expression and other microarray; flow cytometry ▸ High-throughput sequencing
Themes	▸ Open source / open development ▸ Code reuse – statistics, visualization, domain-specific applications, e.g., *limma* ▸ Interoperability ▸ Reproducible – scripts, *vignettes*, packages
Success	$>$ 400 packages; very active mailing list; annual conferences (BioC2011, Seattle, July 27-29); courses; . . .

Representative Packages (Microarrays)

Pre-processing *affy*, *oligo*, *lumi*, *beadarray*, *limma*, *genefilter*, . . .

Machine learning *MLInterfaces*, *CMA*

Differential expression *limma*, . . .

Gene set enrichment *topGO*, *GOstats*, *GSEABase*, . . .

Annotation *AnnotationDbi*, ‘chip’, ‘org’ and *BSgenome* packages

‘Domain-specific’ *DNAcopy*, *snpMatrix*, . . .

Work Flow: Expression Microarrays

Prior to analysis

- Biological experimental design – treatments, replication, etc.
- Microarray preparation – especially two-channel

Analysis

1. Pre-processing (normalization); quality assessment; exploratory analysis
2. Differential expression; machine learning (clustering and classification)
3. Annotation
4. Gene set enrichment analysis
5. ...

`http://bioconductor.org/workflows` for common analyses.

Example Data

Chiaretti et al., 2005 [1]

- 128 adult patients, newly diagnosed for ALL
- B- and T-lineage; various molecular and cytological characteristics.
- HG-U95Av2
- Pre-processed (background correction, normalization, summarization into probe sets).

The ALL dataset

```
> library(ALL); data(ALL); ALL

ExpressionSet (storageMode: lockedEnvironment)
assayData: 12625 features, 128 samples
  element names: exprs
protocolData: none
phenoData
  sampleNames: 01005 01010 ... LAL4
    (128 total)
  varLabels: cod diagnosis ... date
    last seen (21 total)
  varMetadata: labelDescription
featureData: none
experimentData: use 'experimentData(object)'
  pubMedIds: 14684422 16243790
Annotation: hgu95av2
```

ExpressionSet

Example of an 'S4' class

- Coordinate different types of data (assay, phenotype, feature, experiment) into a single container
- Reduces clerical errors, enhances interoperability and reproducibility

Manipulate with *accessors* and *subsetting*

```
> m <- exprs(ALL)        # matrix of expression values
> adf <- phenoData(ALL) # data frame-like sample descriptio
> some <- ALL[,1:10]     # first 10 samples
```

Metadata, e.g., `adf`

- `pData(adf)`: 1 row per sample, columns representing measured attributes, e.g., sex, age, 'fusion protein'.
- Data about the columns, e.g., `varMetadata(adf)`

Warning: different S4 classes have different conventions

Pre-processing

Background correction

- One-channel: PM / MM probes
- Two-channel: background vs. foreground intensities

Normalization

- Key assumption: most probe sets not differentially expressed; distribution of intensities approxiamtely equal across arrays

Summarization

- One-channel: from probes to probesets (approxiamtely, genes)

One channel Affymetrix 3' expression arrays

- In practice:

```
> ## assume phenoData is an AnnotatedDataFrame
> ## "/celfile/directory" contains CEL files
> setwd("/your/celfile/directory")
> library(affy)
> eset <- just.rma(phenoData=phenoData)
```

- Other normalizatons, e.g., `just.gcrma`, `vsn2`; *affyPLM* for detailed probe models; *oligo* for recent arrays.
- *limma* for two-channel arrays.

Example: RMA (robust multi-chip average)

Background correction

- Observation: using MM probes is problematic when MM $>$ PM.
- Model PM probes as exponentially distributed signal, plus normal noise, $\exp(\alpha) + N(\mu, \sigma^2)$.

Normalization

- Quantile normalization – force the *distribution* of background-corrected expression values of each array to have exactly the same.

Summarization

- Estimate probeset effect by fitting a linear model to all probes in each probe set, across array.

Quality assessment

- In practice:

```
> library(arrayQualityMetrics)
> rpt <- arrayQualityMetrics(eset)
> ## or, as appropriate,
> ##   rpt <- arrayQualityMetrics(abatch)
> ##   rpt <- arrayQualityMetrics(rg)
> browseURL(rpt)
```

- QC summary statistics: acceptable ranges for ‘control’ probes
- Between-array distances: no unintended association with experimental conditions, e.g., run date.
- NUSE (normalized unscaled standard error) and RLE (relative log expression) plots: consistent expression and variablity across arrays.

Filtering probe sets

Use `nsFilter` from the *genefilter* package to filter out probes that:

- Lack variability
- Are without an Entrez Gene ID annotation
- Map to the same Entrez Gene ID
- Are not annotated to GO (or other) terms

```
> library(genefilter)
> filteredESet <- nsFilter(eset, require.entrez=TRUE,
+     remove.dupEntrez=TRUE, feature.exclude="^AFFX")
```

Lab activity

Goal: learn to work with S4 classes, especially *ExpressionSet*

1. Load and explore `ALL` object, including finding help on S4 objects.
2. Extract `mol.biol` `phenoData`, subset samples to include only BCR/ABL or NEG.
3. Perform quality assessment.
4. Filter (remove) probes without gene-level annotation

References

S. Chiaretti, X. Li, R. Gentleman, A. Vitale, K. S. Wang, F. Mandelli, R. Foa, and J. Ritz.
Gene expression profiles of B-lineage adult acute lymphocytic leukemia reveal genetic patterns that identify lineage derivation and distinct mechanisms of transformation.
Clin. Cancer Res., 11:7209–7219, Oct 2005.

sessionInfo

- R version 2.12.1 beta (2010-12-07 r53813), `i386-apple-darwin9.8.0`
- Locale: `C`
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Other packages: ALL 1.4.7, AnnotationDbi 1.12.0, Biobase 2.10.0, DBI 0.2-5, GO.db 2.4.5, RSQLite 0.9-4, SeattleIntro2010 0.0.33, biomaRt 2.6.0, genefilter 1.32.0, hgu95av2.db 2.4.5, org.Hs.eg.db 2.4.6
- Loaded via a namespace (and not attached): RCurl 1.4-3, XML 3.2-0, annotate 1.28.0, splines 2.12.1, survival 2.36-2, tools 2.12.1, xtable 1.5-6