BioC Introduction

Chao-Jen Wong

Fred Hutchinson Cancer Research Center

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1. Getting Acquainted with Bioconductor

2. The ALL Dataset and ExpressionSet

3. BioC Introduction

4. Summary

5. Exercise

Outline

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Preparation

- Get acquainted with the Bioconductor website
  - biocView packages
    `http://bioconductor.org/download`
  - Getting help: mailing list
    `http://www.bioconductor.org/docs/mailList.html`
  - Searchable mailing list
    `http://dir.gmane.org/gmane.science.biology.informatics.conductor`
- Easy approach to install packages

```
source("http://bioconductor.org/biocLite.R")
biocLite()
biocLite(pkgs)
```

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The ALL ExpressionSet

Code

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

ExpressionSet (storageMode: lockedEnvironment)
assayData: 12625 features, 128 samples
  element names: exprs
phenoData
  sampleNames: 01005, 01010, ..., LAL4  (128 total)
  varLabels and varMetadata description:
    cod:  Patient ID
    diagnosis:  Date of diagnosis
    ...: ...
    date last seen:  date patient was la
  st seen
    (21 total)
featureData
  featureNames: 1000_at, 1001_at, ..., A
  FFX-YEL024w/RIP1_at  (12625 total)
  fvarLabels and fvarMetadata description: none
experimentData: use 'experimentData(object)'
  pubMedIds: 14684422 16243790
Annotation: hgu95av2
```

ExpressionSet

Structure for genomic data

- assayData: Expression data from microarray experiments.

```
> exprs(ALL)
```

- metadata: phenoData, featureData, annotation – A description of the samples and features in experiment.

```
> phenoData(ALL)
> sampleNames(ALL)
> featureData(ALL)
> head(featureNames(ALL))
> annotation(ALL)
```

- experimentData: A flexible structure to describe expeirment.

```
> experimentData(ALL)
> abstract(ALL)
```

- protocoldata: Equipment-generated variables describing sample phenotypes.

Some operations on ExpressionSet

Code

```
> class(ALL)

[1] "ExpressionSet"
attr(,"package")
[1] "Biobase"

> dim(ALL)

Features  Samples
   12625      128

> exprs(ALL)[1:3, 1:3]

             01005    01010    03002
1000_at   7.597323 7.479445 7.567593
1001_at   5.046194 4.932537 4.799294
1002_f_at 3.900466 4.208155 3.886169

> names(pData(ALL))
> varMetadata(ALL)[1:5,,drop=FALSE]
> colnames(exprs(ALL))
> table(ALL$BT) # dollar-sign returns phenodata selection
```

Some operations on ExpressionSet

Exercise

1. Get familiar with the generic functions to access the phenotypical data and meta-data associated with `ALL`.
2. Use pData, varLabels and VarMatedata to extract details of phenotype information of `ALL`.
3. Try to find covariates carrying the information of the molecular biology and cell types (B- and T-cells) of the `ALL` samples.

Data subsetting

Select samples originating from B-cell tumors (BT covariate) found to carry out BCR/ABL mutation and NEG with no cytogenetic abnormalities (mol.biol covariate).

Code: sebsetting

```
> bcell <- grep("^B", as.character(ALL$BT))
> types <- c("NEG", "BCR/ABL")
> moltyp <- which(as.character(ALL$mol.biol) %in% types)
> ALL_bcrneg <- ALL[, intersect(bcell, moltyp)]
```

Code: reshaping

```
> ALL_bcrneg$BT <- factor(ALL_bcrneg$BT)
> ALL_bcrneg$mol.biol <- factor(ALL_bcrneg$mol.biol)
```

Nonspecific filtering

`nsFilter` – filter out probe sets for a number of different criteria.

code: nsFilter

```
> library("genefilter")
> library("hgu95av2.db")
> #openVignette("genefilter")
> filt_bcrneg <- nsFilter(ALL_bcrneg,
+                      require.entrez=TRUE,
+                      require.GOBP=TRUE,
+                      remove.dupEntrez=TRUE,
+                      feature.exclude="^AFFX",
+                      var.cutoff=0.5)
> ALLfilt_bcrneg <- filt_bcrneg$eset
> dim(ALLfilt_bcrneg)

Features  Samples
    3842       79
```

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Finding help in R

- ? foo gets the manual page of function `foo`.
- class ? foo gets manual page of class `foo`.
- `help.start(foo)` gets html manual page of object `foo`.
- openVignette() provides interface for opening vignettes. Note that this function is in namespace of package *Biobase*.
- apropos finds objects in the search path that partially match the given character string.
- sessionInfo() prints version information of R and loaded packages.
- search() gives a list of attached packages in current working R session.

Finding help in R

Exercise:

1. There are many number of different plotting functions available. Can you find them?
2. Try to find function to use to perform a MannWhitney test.
3. Open the PDF version of the vignette "Bioconductor Overview" which is part of the *Biobase* package. Use either `biocLite()` or `install.packages()`.
4. What is the output of function `sessionInfo()`?
5. Try to install the *xtable* packages.

Annotation mapping

hgu95av2.db: mappings between Affymetrix IDs and various forms of biological annotation.

```
> hgu95av2()
> ls("package:hgu95av2.db")
```

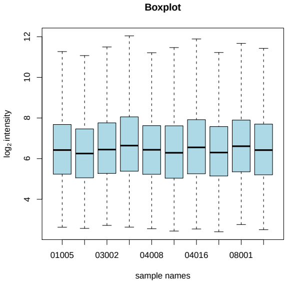
Code: mapping

```
> hgu95av2SYMBOL$"1001_at"

[1] "TIE1"

> mget("1001_at", hgu95av2SYMBOL)

$`1001_at`
[1] "TIE1"

> rmap <- revmap(hgu95av2SYMBOL) ## reverse mapping
> get("TIE1", rmap)

[1] "1001_at"
```

Graphics

Code: visualizing expression patterns

```
> apropos("plot")
> x <- exprs(ALLfilt_bcrneg)[, 1]
> y <- exprs(ALLfilt_bcrneg)[, 2]
> plot(x=x, y=y)
> smoothScatter(x=x, y=y)
> boxplot(exprs(ALLfilt_bcrneg)[, 1:10])
```



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Summary

- Logistics of access.
  - Install packages using biocLite().
  - Load packages into the session using library().
- ExpressionSet objects.
  - Fundamental facilities: exprs(), $.
  - Others: phenoData(), featureData(), varLabels(), annotation().
- Annotation mapping and remapping.
  - Fundamental facilities: get(), mget(), and revmap().
  - Annotation packages for certain platform *platfrom*.db.
- Visualization: boxplot(), heatmap().
- Session information: sessionInfo().

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Exercise

- hgu95avMAP *environment* contains the mappings between affymetrix identifiers and chromosome band locations.
- apply family of functions: apply(), sapply(), lapply(), and eapply().

eapply

1. Find the chromosome band to which the probe 1001_at maps.
2. Find all genes that map to the p arm of chromosome 17 (17p) using functions grep and eapply.