GS01 0163
Analysis of Microarray Data

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Lecture 9: Exploring BioConductor

- How do we load CEL files into an AffyBatch? how can we merge batches? how can we partition batches?

- How do we check that it worked?

- How do we supply the associated phenoData?

- Given an AffyBatch, how do we look at it? boxplot, hist, ma-plots, ratio plots, PLM

- Given an AffyBatch, how do we fit it? expresso, justRMA

- Given an eset, what can we say about its contents?

- How can we get the probe level values for a probeset?
• How can we figure out what probeset corresponds to a given gene?

• How can we get the probe sequences for a probeset?
Loading CEL files into an AffyBatch

One theme for today is TMTOWTDI. We’re going to try to extend this from Perl over to BioConductor, and to the analysis of Affy data.

To begin with, let’s say that we’ve got a set of CEL files. How do we pull them in?

There are several options. How do I survey them?
Loading CEL files into an AffyBatch

One theme for today is TMTOWTDI. We’re going to try to extend this from Perl over to BioConductor, and to the analysis of Affy data.

To begin with, let’s say that we’ve got a set of CEL files. How do we pull them in?

There are several options. How do I survey them?

> library("affy");
> vignette("affy");

Don’t panic, it’s not really 271 pages...
Differential Expression

Reading the Fine Manual: Vignettes

```r
vignette {utils}

View or List Vignettes

Description

View a specified vignette, or list the available ones.

Usage

vignette(topic, package = NULL, lib.loc = NULL)

## S3 method for class 'vignette':
print(x, ...)
## S3 method for class 'vignette':
edit(name, ...)

Arguments

topic a character string giving the (base) name of the vignette to view. If omitted, all vignettes from
all installed packages are listed.

package a character vector with the names of packages to search through, or NULL in which case all
available packages in the library trees specified by lib.loc are searched.

lib.loc a character vector of directory names of R libraries, or NULL. The default value of NULL
corresponds to all libraries currently known.

x, name Object of class vignette.
...
Ignored by the print method, passed on to file.edit by the edit method.

Details
```

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GS01 0163: Analysis of Microarray Data
> vignette(package = "affy");
ReadAffy: Help from Top

read.affybatch {affy}  

Read CEL files into an AffyBatch

Description

Read CEL files into an AffyBatch

Usage

read.affybatch(..., filenames = character(0),
            phenoData = new("phenoData"),
            description = NULL,
            notes = "",
            compress = getOption("BioC")$affy$compress.cel,
            rm.mask = FALSE, rm.outliers = FALSE, rm.extra = FALSE,
            verbose = FALSE, sd=FALSE, cdfname = NULL)

ReadAffy(..., filenames=character(0),
           widget=getOption("BioC")$affy$use.widgets,
           compress=getOption("BioC")$affy$compress.cel,
           celfile.path=NULL,
           sampleNames=NULL,
           phenoData=NULL,
           description=NULL,
           notes="",
           rm.mask=FALSE, rm.outliers=FALSE, rm.extra=FALSE,
           verbose=FALSE, sd=FALSE, cdfname = NULL)

Arguments

...  file names separated by comma.
ReadAffy: ... to Bottom

obtain a MIAME instance. If left NULL but widget=TRUE then widgets are used. If left NULL and widget=FALSE then an empty instance of MIAME is created.

Value

An AffyBatch object.

Author(s)

Ben Bolstad bmb@bmbolstad.com (read.affybatch), Laurent Gautier, and Rafael A. Irizarry (ReadAffy)

See Also

AffyBatch

Examples

if(require(affydata)){
    celpath <- paste(.path.package("affydata"),"celfiles",sep="/"
    fns <- list.celfiles(path=celpath,full.names=TRUE)

    cat("Reading files:\n",paste(fns,collapse="\n"),"\n")
    ##read a binary celfile
    abatch <- ReadAffy(filenames=fns[1])
    ##read a text celfile
    abatch <- ReadAffy(filenames=fns[2])
    ##read all files in that dir
    abatch <- ReadAffy(celfile.path=celpath)
}

[Package affy version 1.10.0 Index]
The Affy Index

Methods for Affymetrix Oligonucleotide Arrays

Documentation for package `affy' version 1.10.0
User Guides and Package Vignettes

Read overview or browse directory.

Help Pages

A B C D E F G H I J L M N O P Q R S T U W X misc

$AffyBatch
Class AffyBatch

-- A --

affy-options
Options for the affy package

affy.scalevalue.exprSet
Scale normalization for exprSets

AffyBatch
Class AffyBatch

AffyBatch-class
Class AffyBatch

affybatch.example
AffyBatch instance affybatch.example

affybatch.example2
AffyBatch instance affybatch.example
**Differential Expression**

**R documentation: Sweave**

Sweave \{utils\}

**Automatic Generation of Reports**

**Description**

Sweave provides a flexible framework for mixing text and S code for automatic report generation. The basic idea is to replace the S code with its output, such that the final document only contains the text and the output of the statistical analysis.

**Usage**

Sweave(file, driver = RweaveLatex(),
       syntax = getOption("SweaveSyntax"), ...)

Stangle(file, driver = Rtangle(),
        syntax = getOption("SweaveSyntax"), ...)

**Arguments**

- **file** Name of Sweave source file.
- **driver** The actual workhorse, see details below.
- **syntax** An object of class SweaveSyntax or a character string with its name. The default installation provides SweaveSyntaxNoWeb and SweaveSyntaxLaTeX.
  
  ... Further arguments passed to the driver’s setup function.

**Details**

Automatic generation of reports by mixing word processing markup (like latex) and S code. The S code is executed during Sweave processing and its output is inserted into the Sweave text (via \texttt{Sweave}) or is written into a separate file (via \texttt{Stangle}). This allows Sweave to generate reproducible reports.
Reading a list of files

some_cels.txt:

../../DataSets/SinghProstate/N01_normal.CEL
../../DataSets/SinghProstate/N05_normal.CEL
../../DataSets/SinghProstate/N11_normal.CEL
../../DataSets/SinghProstate/N15_normal.CEL
../../DataSets/SinghProstate/N21_normal.CEL
../../DataSets/SinghProstate/N25_normal.CEL

> celList <- readTable("some_cels.txt");
> ABatch <- ReadAffy(celList);
The Evolution...
The Evolution...

oops...

> celList <- readTable("some_cels.txt");
> celList <- as.character(celList$V1);
> ABatch <- ReadAffy(celList);
The Evolution...

oops...

> celList <- readTable("some_cels.txt");
> celList <- as.character(celList$V1);
> ABatch <- ReadAffy(celList);

oops...

> celList <- readTable("some_cels.txt");
> celList <- as.character(celList$V1);
> ABatch <- ReadAffy(filenames = celList);

Ta Da!
Checking the Contents

> slotNames(ABatch)
[1] "cdfName"       "nrow"       "ncol"
[5] "se.exprs"     "description" "annotation"
[9] "reporterInfo" "phenoData"

> phenoData(ABatch)
phenoData object with 1 variables and 6 cases
varLabels
sample: arbitrary numbering
Looking at phenoData

```r
> slotNames(phenoData(ABatch))
[1] "pData" "varLabels" "varMetadata"
> (phenoData(ABatch))@pData
  sample
N01__normal.CEL  1
N05__normal.CEL  2
N11__normal.CEL  3
N15__normal.CEL  4
N21__normal.CEL  5
N25__normal.CEL  6
> (phenoData(ABatch))@varLabels
$sample
[1] "arbitrary numbering"
```
Assigning phenoData

some_pdata.txt:

<table>
<thead>
<tr>
<th>Sample name</th>
<th>Concocted</th>
</tr>
</thead>
<tbody>
<tr>
<td>N01_norm</td>
<td>A</td>
</tr>
<tr>
<td>N05_norm</td>
<td>A</td>
</tr>
<tr>
<td>N11_norm</td>
<td>A</td>
</tr>
<tr>
<td>N15_borm</td>
<td>B</td>
</tr>
<tr>
<td>N21_borm</td>
<td>B</td>
</tr>
<tr>
<td>N25_borm</td>
<td>B</td>
</tr>
</tbody>
</table>

> p1 <- read.phenoData("some_pdata.txt"); # error
Assigning phenoData, pt 2

```r
> p1 <- read.phenoData("some_pdata.txt",
>       sep="\t")

> p1

phenoData object with 2 variables and 7 cases

  varLabels
V1: read from file
V2: read from file

# Not quite what we want.
```
Assigning phenoData, pt 3

> p1 <- read.phenoData("some_pdata.txt",
                      sep="\t", header=TRUE)

> p1
phenoData object with 2 variables
    and 6 cases

  varLabels
Sample.name: read from file
Concocted: read from file
> phenoData(ABatch) <- p1
Other ways of Reading Data

Are they all in one directory?

What is the list of filenames?

read.affybatch vs ReadAffy

GUI?
Other ways of Reading Data 1

kabagg$ ls ../../../DataSets/SinghSmall
N60__normal.CEL N61__normal.CEL N62__normal.CEL

> ABSmall <- ReadAffy(celfile.path=
    "../../../DataSets/SinghSmall"); # works
Other ways of Reading Data 2

kabagg$ ls ../../DataSets/SinghSmall2
N60__normal.CEL.gz N61__normal.CEL.gz
N62__normal.CEL.gz

> ABSmall <- ReadAffy(celfile.path="../../DataSets/SinghSmall2",
compress=TRUE); # works

This takes only about 1/3 the space...
Other ways of Reading Data 3

```
kabagg$ ls ../../DataSets/SinghSmall3
N60.gz N61.gz N62.gz

> ABSmall <- ReadAffy(celfile.path="../../DataSets/SinghSmall3",
                      compress=TRUE); # fails

> ABSmall <- ReadAffy(filenames="../../DataSets/SinghSmall3/N60.gz",
                      compress=TRUE); # works
```

This still takes only about 1/3 the space...
Now let’s Quantify

t0 <- date();
eset0 <- expresso(ABatch,
        bgcorrect.method="rma",
        normalize.method="quantiles",
        pmcorrect.method="pmonly",
        summary.method="medianpolish");

t1 <- date(); # 151s
eset1 <- justRMA(filenames = celList);
t2 <- date(); # 10s

The customized routines are better if they do what you want to do...

(also note that justRMA didn’t build an AffyBatch.)
Just Because I’m Curious

> exprs(eset1)[1,]
N01__normal.CEL  N05__normal.CEL  N11__normal.CEL
  7.789481  7.314639  7.445363
N15__normal.CEL  N21__normal.CEL  N25__normal.CEL
  7.289881  7.503692  7.412608

Can we reconstruct this?

> ABatch.BG <- bg.correct.rma(ABatch)
> ABatch.BG.norm <-
  normalize.AffyBatch.quantiles(ABatch.BG)

These steps produce AffyBatch objects, with altered exprs.
What is the First Gene?

(well, ok, probeset)

> gn1 <- geneNames(ABatch.BG.norm)[1]
> gn1
[1] "1000_at"

Ok, now what are the values?

pr1 <- pm(ABatch.BG.norm, gn1);
Looking at it, Take 1

```
image(1:nrow(pr1), 1:ncol(pr1), pr1, xlab="Probes", ylab="Samples", main="PM Intensities for 1000_at")
```

Some parallelism, but we may be missing something...
Looking at it, Take 2

image(1:nrow(pr1), 1:ncol(pr1), log2(pr1),
xlab="Probes", ylab="Samples",
main="Log2 (PM Intensities) for 1000_at")

Logs!
Fitting the Probes

```r
> pr1Fit <- medpolish(log2(pr1))
1 : 45.72612
2 : 45.08797
Final: 45.03615
> names(pr1Fit)
[1] "overall" "row" "col" "residuals"
[5] "name"
> pr1Fit$overall + pr1Fit$col
  N01__normal.CEL  N05__normal.CEL  N11__normal.CEL
    7.789481     7.314639     7.445363
  N15__normal.CEL  N21__normal.CEL  N25__normal.CEL
    7.289881     7.503692     7.412608

This is what we found before!
```
We can Check the Code

```r
> medpolish
function (x, eps = 0.01, maxiter = 10,
       trace.iter = TRUE, na.rm = FALSE)
{
  z <- as.matrix(x)
  nr <- nrow(z)
  nc <- ncol(z)
  t <- 0
  r <- numeric(nr)
  c <- numeric(nc)
  oldsum <- 0
  for (iter in 1:maxiter) {
    rdelta <- apply(z, 1, median, na.rm = na.rm)
    z <- z - matrix(rdelta, nr = nr, nc = nc)
```
and Check the Residuals

image(1:nrow(prl), 1:ncol(prl), prlFit$residuals,
    xlab="Probes", ylab="Samples",
    main="RMA Residuals for 1000_at")

Trivia Q: Who introduced median polish?
One other Fitting Approach: PLM

PLM = “Probe Level Model”

```r
library("affyPLM");
plm1 <- fitPLM(ABatch); # takes a few minutes
par(mfrow=c(2,2));
image(ABatch[, 1],main="N01 Raw");
image(plm1, type="weights", which=1, main="N01 Weights");
image(plm1, type="resids", which=1, main="N01 Resids");
image(plm1, type="sign.resids", which=1, main="N01 sign(Resids)"学会。
```
Looking at N01
Looking at N05

R Graphics: Device 3 (ACTIVE)

N05 Raw

N05 Weights

N05 Resids

N05 sign(Resids)
> library("hgu95av2");
What Does This Package Contain?

> hgu95av2()

Quality control information for hgu95av2
Date built: Created: Sun Mar 26 00:53:27 2006

Number of probes: 12625
Probe number mismatch: None
Probe mismatch: None
Mappings found for probe based rda files:
  hgu95av2ACCNUM found 12625 of 12625
  hgu95av2CHRLOC found 11716 of 12625
  hgu95av2CHR found 12171 of 12625
  hgu95av2ENZYME found 1922 of 12625
  hgu95av2GENENAME found 11660 of 12625
DIFFERENTIAL EXPRESSION

hgu95av2GO found 11101 of 12625
hgu95av2LOCUSID found 12238 of 12625
hgu95av2MAP found 12140 of 12625
hgu95av2OMIM found 9978 of 12625
hgu95av2PATH found 4252 of 12625
hgu95av2PMID found 12136 of 12625
hgu95av2REFSEQ found 12039 of 12625
hgu95av2SUMFUNC found 0 of 12625
hgu95av2SYMBOL found 12184 of 12625
hgu95av2UNIGENE found 12127 of 12625

Mappings found for non-probe based rda files:

hgu95av2CHRLENGTHS found 25
hgu95av2ENZYME2PROBE found 660
hgu95av2GO2ALLPROBES found 6012
hgu95av2GO2PROBE found 4274
hgu95av2ORGANISM found 1
hgu95av2PATH2PROBE found 173
hgu95av2PFAM found 10412
hgu95av2PMID2PROBE found 107253
hgu95av2PROSITE found 8193

(we can also see this using ls("package:hgu95av2").)
What Does This Package Contain?

> hgu95av2GENENAME
<environment: 0x26519bdc>

Almost everything in this package is an “environment”, which is R’s fancy name for a hash table. We can access things by name.

> hgu95av2GENENAME"$1000_at"
[1] "mitogen-activated protein kinase 3"

We can access a lot of annotation!
What was Needed for Quantification?

```r
> library("hgu95av2cdf");
> hgu95av2cdf$"1000_at"

<table>
<thead>
<tr>
<th></th>
<th>pm</th>
<th>mm</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>358160</td>
<td>358800</td>
</tr>
<tr>
<td>2</td>
<td>118945</td>
<td>119585</td>
</tr>
<tr>
<td>3</td>
<td>323731</td>
<td>324371</td>
</tr>
<tr>
<td>4</td>
<td>223978</td>
<td>224618</td>
</tr>
<tr>
<td>...</td>
<td></td>
<td></td>
</tr>
<tr>
<td>15</td>
<td>317054</td>
<td>317694</td>
</tr>
<tr>
<td>16</td>
<td>404069</td>
<td>404709</td>
</tr>
</tbody>
</table>

These give the indices of the probes within the 409600-long vector of expression intensities.
What if We Want to Go in Reverse?

Given a probeset, I can find a gene name. What if I have a gene name, and I want something else?

Can we find “BAD”?

This is a gene symbol, so we probably want to work with the hgu95av2SYMBOL environment.

The key function for extracting items from an environment without the key is “contents”.

```r
> tempSYM <- contents(hgu95av2SYMBOL);
> tempSYM[1]
$'986_at'
[1] "CYP19A1"
```
Finding BAD in the Contents

```r
> tempSYM[tempSYM == "BAD"]
$'1861_at'
[1] "BAD"

> names(tempSYM[tempSYM == "BAD"])
[1] "1861_at"
```

This gives us the key!

Some of these queries are simplified if we invoke

```r
> library("annotate"); # for example,
> getLL("1861_at", "hgu95av2");
[1] 572
```
One More Thing...

sequences?

```r
> library("hgu95av2probe");
> data(hgu95av2probe); # a big file

> as.data.frame(hgu95av2probe[1,])

  sequence   x   y
1  TCTCCTTTGCTGAGGCCTCCAGCTT 399 559

Probe.Set.Name   Probe.Interrogation.Position
1000_at           1367

Target.Strandedness
Antisense
```
So, What’s BAD?

```r
> as.data.frame(hgu95av2probe[hgu95av2probe$Probe.Set.Name == "1861_at",])

<table>
<thead>
<tr>
<th>sequence</th>
<th>x</th>
<th>y</th>
<th>Probe.Set.Name</th>
<th>Probe.Interrogation.Position</th>
<th>Target.Strandedness</th>
</tr>
</thead>
<tbody>
<tr>
<td>CAACCTCTGGGCAGCACACAGCGCTAT</td>
<td>403</td>
<td>485</td>
<td>1861_at</td>
<td>384</td>
<td>Antisense</td>
</tr>
<tr>
<td>AACCTCTGGGCAGCACACAGCGCTATG</td>
<td>402</td>
<td>485</td>
<td>1861_at</td>
<td>385</td>
<td>Antisense</td>
</tr>
<tr>
<td>CCTCTGGGCAGCACACAGCGCTATGGC</td>
<td>207</td>
<td>491</td>
<td>1861_at</td>
<td>387</td>
<td>Antisense</td>
</tr>
<tr>
<td>TGGGCAGCACACACAGCGCTATGGCCGCG</td>
<td>436</td>
<td>421</td>
<td>1861_at</td>
<td>391</td>
<td>Antisense</td>
</tr>
<tr>
<td>GCAGCACACACAGCGCTATGGCCGCGAGC</td>
<td>285</td>
<td>599</td>
<td>1861_at</td>
<td>394</td>
<td>Antisense</td>
</tr>
</tbody>
</table>

... 

The midpoint of the first probe should be at position 384 within the cDNA sequence.