Package ‘affycomp’

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Title Graphics Toolbox for Assessment of Affymetrix Expression Measures
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Description The package contains functions that can be used to compare expression
measures for Affymetrix Oligonucleotide Arrays.
License GPL (>= 2)
biocViews OneChannel, Microarray, Preprocessing
NeedsCompilation no

R topics documented:

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affycomp.compfigs.auxiliary

Auxiliary functions to create comparative Figures

Description
These functions are auxiliary function to affycompPlot. These Figures are used to compare expression measures. They take lists with components created by the assessDilution and assessSpikeIn functions.

Usage

affycomp.compfig2(l, method.names = as.character(1:length(l)),
  add.legend = TRUE, main = "Figure 2")

affycomp.compfig3(l, method.names = as.character(1:length(l)),
  main = "Figure 3")

affycomp.compfig4a(l, method.names = as.character(1:length(l)),
  add.legend = TRUE, main = "Figure 4a")

affycomp.compfig4b(l, method.names = as.character(1:length(l)),
  add.legend = TRUE, main = "Figure 4b")

affycomp.compfig4c(l, method.names = as.character(1:length(l)),
  add.legend = TRUE, rotate=TRUE, main = "Figure 4c")

affycomp.compfig5a(l, method.names = as.character(1:length(l)),
  add.legend = TRUE, main = "Figure 5a", maxfp=100)

affycomp.compfig5b(l, method.names = as.character(1:length(l)),
  add.legend = TRUE, main = "Figure 5b", maxfp=100)

affycomp.compfig5cde(l, method.names = as.character(1:length(l)),
  add.legend = TRUE, main = "Figure 5c", maxfp=100,
  type=c("low","med","high"))

affycomp.compfig5c(l, method.names = as.character(1:length(l)),
  add.legend = TRUE, main = "Figure 5c", maxfp=100)

affycomp.compfig5d(l, method.names = as.character(1:length(l)),
  add.legend = TRUE, main = "Figure 5d", maxfp=100)

affycomp.compfig5e(l, method.names = as.character(1:length(l)),
  add.legend = TRUE, main = "Figure 5e", maxfp=100)

Arguments

l a list of lists with the necessary components to create the Figure. See details.
method.names a character vector with the names of the expression measures methodologies being compared.

add.legend logical. If TRUE a legend is added.

main title of the Figure.

rotate in the case of compfig4c one can either show the actual local slopes or the bias (local slope minus 1).

maxfp range of the false positives in ROC will be from 0 to maxfp

type compfig5cdef is the engine for 5c, 5d, and 5e. type tells which of these 4 to run.

Details

These are similar to the functions defined in affycomp.figures.auxiliary. Main difference is that here you send lists with the result of the assessment functions as components.

Value

Figures are produced.

Author(s)

Rafael A. Irizarry

Examples

library(affycompData)
data(rma.assessment)
data(mas5.assessment)
affycomp.compfig2(list(rma.assessment$Dilution,mas5.assessment$Dilution))
affycomp.compfig3(list(rma.assessment$Dilution,mas5.assessment$Dilution))
affycomp.compfig4a(list(rma.assessment$Signal,mas5.assessment$Signal))
affycomp.compfig4b(list(rma.assessment$Dilution,mas5.assessment$Dilution))
affycomp.compfig5a(list(rma.assessment$FC,mas5.assessment$FC))
affycomp.compfig5b(list(rma.assessment$FC2,mas5.assessment$FC2))
Usage

```r
affycomp.figure1(l, main="Figure 1", xlim=NULL, ylim=NULL)
affycomp.figure1b(l, main="Figure 1b", xlim=NULL, ylim=NULL, cex=0.85, all=FALSE)
affycomp.figure2(l, main="Figure 2")
affycomp.figure2b(l, main="Figure 2b")
affycomp.figure3(l, main = "Figure 3")
affycomp.figure4a(l, main = "Figure 4a", equal.lims=FALSE)
affycomp.figure4b(l, main = "Figure 4b")
affycomp.figure4c(l, rotate=TRUE, main = "Figure 4c")
affycomp.figure5a(l, main = "Figure 5a", maxfp=100)
affycomp.figure5b(l, main = "Figure 5b", maxfp=100)
affycomp.figure5c(l, main = "Figure 5c", maxfp=100)
affycomp.figure5d(l, main = "Figure 5d", maxfp=100)
affycomp.figure5e(l, main = "Figure 5e", maxfp=100)
affycomp.figure6a(l, main = "Figure 6a", xlim = NULL, ylim = NULL)
affycomp.figure6b(l, main = "Figure 6b", xlim = NULL, ylim = NULL)
```

Arguments

- `l`: A list with the necessary components to create the Figure. See details.
- `main`: Title for the Figure.
- `maxfp`: range of the false positives in ROC will be from 0 to `maxfp`
- `xlim`: x-axis limits.
- `ylim`: y-axis limits.
- `cex`: size of numbers in figure 1b.
- `all`: logical. If TRUE all spikeins are shown. Otherwise, only those resulting in smaller, realistic, fold changes are shown.
- `equal.lims`: logical. If TRUE the limits of x-axis and y-axis will have same range.
- `rotate`: in the case of compfig4c one can either show the actual local slopes or the bias (local slope minus 1).

Details

Read the vignette for more details on what each Figure is. You can read `assessSpikeIn` and `assessDilution` to see which assessments are needed.

Value

Figures are produced.

Author(s)

Rafael A. Irizarry

Examples

```r
library(affycompData)
data(rma.assessment)
affycomp.figure1(rma.assessment$MA)
```
affycompPlot

affycomp.figure2(rma.assessment$Dilution)
affycomp.figure3(rma.assessment$Dilution)
affycomp.figure4a(rma.assessment$Signal)
affycomp.figure4b(rma.assessment$Dilution)
affycomp.figure5a(rma.assessment$FC)
affycomp.figure5b(rma.assessment$FC2)
affycomp.figure6a(rma.assessment$FC)
affycomp.figure6b(rma.assessment$FC)

affycompPlot

Description

Function that makes assessment plot

Usage

affycompPlot(..., assessment.list=NULL, method.names=NULL, figure1.xlim=c(-4,15), figure1 ylim=c(-10,12), figure1b.xlim=c(-2,14), figure1b.ylim=c(-6,5), figure6a.xlim=c(-12,12), figure6a.ylim=c(-12,12), figure6b.xlim=c(-3,3), figure6b.ylim=c(-6,6))

affycomp.compfigns(l, method.names = NULL, figure1.xlim = c(-4, 15), figure1.ylim = c(-10, 12), figure1b.xlim = c(-4, 15), figure1b.ylim = c(-4, 4), figure6a.xlim = c(-12, 12), figure6a.ylim = c(-12, 12), figure6b.xlim = c(-3, 3), figure6b.ylim = c(-6, 6))
affycomp.figures(l)
affycomp.compfigns.calls(what)
affycomp.compfigns.calls(what)

Arguments

... lists produced by the assessment functions (one for each method) separated by commas.
assessment.list

Alternatively, one can also send a list of lists produced by one of the assessment functions.
method.names A character vector with the names of the expression measure methodology.
figure1.xlim x-axis lim used for the plots in Figure 1.
figure1.ylim y-axis lim used for the plots in Figure 1.
figure1b.xlim x-axis lim used for the plots in Figure 1b.
figure1b.ylim y-axis lim used for the plots in Figure 1b.
figure6a.xlim x-axis lim used for the plots in Figure 6a.
figure6a.ylim y-axis lim used for the plots in Figure 6a.
figure6b.xlim x-axis lim used for the plots in Figure 6b.
figure6b.ylim y-axis lim used for the plots in Figure 6b.
l list with assessment lists as components.
what a dummy variable to know what function call to create.
affycompTable

Details
Read the vignette for more details on what each Figure is. Once an assessment is used this function
knows what to do. You can call any of the assessment functions described in `assessSpikeIn`,
`assessDilution` and `assessSD`.

`affycomp.figures`, `affycomp.figure.calls`, `affycomp.compfigs.calls` are auxiliary func-
tions.

Value
Figures are produced.

Author(s)
Rafael A. Irizarry

Examples
library(affycompData)
data(rma.assessment)
data(mas5.assessment)
affycompPlot(rma.assessment, mas5.assessment)
affycompPlot(rma.assessment$FC)
affycompPlot(rma.assessment$Dilution, mas5.assessment$Dilution)
affycompPlot(rma.assessment$Dilution, mas5.assessment$Dilution)
affycompPlot(rma.assessment$Signal, mas5.assessment$Signal)
affycompPlot(rma.assessment$Dilution, mas5.assessment$Dilution)
affycompPlot(rma.assessment$FC2, mas5.assessment$FC2)

Description
These functions take as an argument the output of the assessment functions.

Usage
affycompTable(..., Table=NULL, assessment.list=NULL, method.names=NULL)
tableAll(..., assessment.list=NULL, method.names=NULL)
tableDilution(l, method.names=NULL)
tableFC(l, method.names=NULL)
tableFC2(l, method.names=NULL)
tableSignal(l, method.names=NULL)
tableLS(l, method.names=NULL)
**Arguments**

- **...** lists produced by the assessment functions
- **Table** If TableAll was used one can send it through this argument
- **assessment.list** Alternatively, one can also send a list of lists produced by tableAll.
- **method.names** A character vector with the names of the expression measure methodology.
- **l** list of assessments.
- **rank** if TRUE tableRanks will present ranks instead of local slopes.
- **ngenes** when computing ranks, out of how many genes should we do it?

**Details**

Read the vignette for more details on what the entries of the table are. affycompTable has a few entries per graph. tableAll has more entries. Once an assessment is used this function knows what to do. You can call any of the assessment functions described in assessSpikeIn, assessDilution, assessSD, assessLS, assessMA2, and assessSpikeInSD.

Note tableRanks and tableOverallSNR work on the results from assessSpikeIn2.

**Value**

A matrix. One column per each method and one row for each comparison. tableOverallSNR is an exception. Where rows represent methods.

**Author(s)**

Rafael A. Irizarry

**Examples**

```r
library(affycompData)
data(rma.assessment) ##this was produced with affycomp.assess
data(mas5.assessment) ##this one too
tmp <- affycompTable(mas5.assessment,rma.assessment)
format(tmp,digit=2)
```
assessAll

Assessment functions

Description
Assessment functions. Takes a couple of ExpressionSet, one for spike in another for the dilution and returns a list with necessary information to create assessment plots.

Usage
assessAll(d, s, method.name=NULL, verbose=TRUE)

affycomp(d, s, method.name=NULL, verbose=TRUE, return.it=TRUE)

Arguments
d An ExpressionSet containing the expression measures for the Gene Logic’s dilution experiment.
s An ExpressionSet containing expression measures for the Affymetrix’s spike-in experiment.
method.name Name of expression measure being assessed.
verbose verbosity flag.
return.it if TRUE returns assessment lists.

Details
assessAll performs assessments for Figures 1-6. It is a wrapper for assessDilution and assessSpikeIn.
affycomp is a wrapper that does it all... including the plotting and creation of table.

Value
Lists with the necessary information to make the Figures.

Author(s)
Rafael A. Irizarry
assessSD

Arguments

exprset An ExpressionSet containing expression measures for GeneLogic’s dilution experiment.
method.name Name of expression measure being assessed.

Details

assessDilution performs the assessment for the plots related to Dilution (Figures 2, 3, 4b)

Value

Lists with the necessary information to make the Figures.

Author(s)

Rafael A. Irizarry

assessSD SD Assessment functions

Description

Assessment function for standard deviation estimates. Takes a dilution data ExpressionSet and returns a list with necessary information to create assessment plot.

Usage

assessSD(exprset, method.name=NULL, logx=FALSE)

Arguments

exprset An ExpressionSet containing expression measures for Affymetrix’s dilution experiment.
method.name Name of expression measure being assessed.
logx Logical indicating whether the average expression being computed should be logged, default no. See details.

Details

assessSD does the assessment for Figure 7. This requires the ExpressionSet to have standard error estimates for the expression measure. Some expression measures (e.g. dChip) will have SEs in original scale, where others (e.g. RMA) will have them in log scale. For the former, use logx=TRUE.

Value

Lists with the necessary information to make the Figures.

Author(s)

Rafael A. Irizarry
assessSpikeIn

Assessment functions for Spike In Data

Description

These functions are assessment functions. Each takes an ExpressionSet and returns a list with necessary information to create assessment plots.

Usage

assessSpikeIn(s, method.name=NULL, verbose=TRUE)
assessMA(exprset, method.name=NULL)
assessSignal(exprset, method.name=NULL)
assessFC(exprset, method.name=NULL)
assessFC2(exprset, method.name=NULL)

Arguments

s
An ExpressionSet containing expression measures for Affymetrix’s spike-in experiment.

exprset
An ExpressionSet containing expression measures for Affymetrix’s spike-in experiment.

method.name
Name of expression measure being assessed.

verbose
logical. If TRUE show messages.

Details

assessMA performs the assessment for the MA-plot (Figure 1), assessSignal performs the assessment for signal detection plot (Figure 4a), assessFC performs assessments used by fold-change related plots (Figures 5a, 6a, 6b). assessFC2 is for the ROC for genes with nominal fold changes of 2 (Figure 5b). assessSpikeIn is a wrapper for all these and returns a list of lists.

Value

Lists with the necessary information to make the Figures.

Author(s)

Rafael A. Irizarry
assessSpikeIn2

New Assessment functions for Spike In Data

Description

These functions are assessment functions. Each takes an ExpressionSet and returns a list with necessary information to create assessment plots.

Usage

assessSpikeIn2(s, method.name=NULL, verbose=TRUE)
assessSpikeInSD(exprset, method.name=NULL, span=1/3)
assessLS(exprset, method.name=NULL)
assessMA2(exprset, method.name=NULL)

Arguments

- **s**: An ExpressionSet containing expression measures for Affymetrix’s spike-in experiment.
- **exprset**: An ExpressionSet containing expression measures for Affymetrix’s spike-in experiment.
- **method.name**: Name of expression measure being assessed.
- **verbose**: logical. If TRUE show messages.
- **span**: span used in call to loess.

Details

assessMA2 performs the assessment for the second MA-plot (Figure 1b), and assessLS performs the assessment for signal detection plot (Figure 4c). assessMA2 also performs assessments used by fold-change related plots (Figures 5a,b) and the ROC plots (Figures 5c,d,e). assessSpikeInSD is for the standard deviation assessment in Figure 2b. assessSpikeIn2 is a wrapper for all these and returns a list of lists.

Value

Lists with the necessary information to make the Figures.

Author(s)

Rafael A. Irizarry
dilution.phenodata  Phenotypic Information for Dilution Study

**Description**

This object is of class `phenoData` with necessary information for the assessment.

**Usage**

```r
data(dilution.phenodata)
```

**Format**

An object of class `phenoData`

**Source**

Two sources of cRNA A (human liver tissue) and B (Central Nervous System cell line) have been hybridized to human array (HGU95Av2) in a range of proportions and dilutions. This object describes these.


exprset.log  Take log base 2 of Expression

**Description**

Take log base 2 of the expression matrix in an `ExpressionSet`

**Usage**

```r
eexprset.log(exprset)
```

**Arguments**

- `exprset`  `ExpressionSet`

**Details**

This function takes log base 2 of the expression matrix in an `ExpressionSet`. Negatives are converted to the smallest non-negative entry.

**Value**

An `ExpressionSet`

**Author(s)**

Rafael A. Irizarry
**hgu133a.spikein.phenodata**

*phenotypic information for HGU133A spike in study*

---

**Description**

This object is of class `phenoData` with necessary information for the assessments.

**Usage**

```r
data(hgu133a.spikein.phenodata)
```

**Format**

An object of class `phenoData`

**Source**

This comes from an experiment where 16 different cRNA fragments have been added to the hybridization mixture of the GeneChip arrays at different pM concentrations. For more information see Irizarry, R.A., et al. (2001) [http://www.biostat.jhsph.edu/~ririzarr/papers/index.html](http://www.biostat.jhsph.edu/~ririzarr/papers/index.html)

---

**hgu133a.spikein.xhyb**  *Cross hybridizers*

---

**Description**

Probe sets likely to crosshybridize to spiked-in probesets in the Affymetrix HGU133A spike in. This object is list. Each component of the list contains probeset names of possible crosshybridizers. The sequences of each spiked-in clone were collected and blasted against all HG-U133A target sequences. Target sequences are the ~600bp regions from which probes were selected. Thresholds of 100, 150 and 200bp were used and define the three components of the list.

**Usage**

```r
data(hgu133a.spikein.xhyb)
```

**Format**

A list

**Source**

Simon Cawley <simon_cawley@affymetrix.com>
**mas5.assessment**  
*Example of the result of assessments*

**Description**

The Dilution and both (HGU95 and HGU133) types of Spike-in data were processed with Affymetrix MAS 5.0 software, yielding three "MAS 5.0" ExpressionSet's. (These are available, in csv-format, at [http://affycomp.jhsph.edu/AFFY2/rafa@jhu.edu/030424.1033/](http://affycomp.jhsph.edu/AFFY2/rafa@jhu.edu/030424.1033/).) Then various assessment functions from the affycomp package (most recently, version 1.28.0) were applied. mas5.assessment resulted from assessAll on Dilution and HGU95. See mas5.assessment in affycompData for results of other assessments.

**Usage**

```r
data(mas5.assessment)
```

**Format**

A list of list.

---

**readin**  
*Read Expression Date Sets*

**Description**

Reads a comma-delimited file containing the expression values of the dilution and spike-in data sets and creates a ExpressionSet.

**Usage**

```r
read.dilution(filename)
read.spikein(filename, cdfName=c("hgu95a","hgu133a"), remove.xhyb=TRUE)
read.newspikein(filename)
```

**Arguments**

- `filename` character containing the filename to be read.
- `cdfName` are we reading data from the hgu95a or hgu133a spike-in experiment?
- `remove.xhyb` logical. If TRUE possible cross hybridizers are removed from the HGU133A spikein. See remove.hgu133a.xhyb.

**Details**

The file to be read must be comma-delimited with the first row containing the cel filenames (case sensitive). The first column must be the Affymetrix gene identifiers. read.dilution will put things in the right place.

read.newspikein is a wrapper to read results from the hgu133a spikein experiment.
Value
An `ExpressionSet`.

Author(s)
Rafael A. Irizarry

---

**remove.hgu133a.xhyb**  
*Remove crosshybridizers*

**Description**
This function removes possible cross hybridizers from Affymetrix HGU133A spike-in experiment.

**Usage**
```
remove.hgu133a.xhyb(s, bp = c("200", "150", "100"))
```

**Arguments**
- `s`: an `ExpressionSet` containing the HGU133A spike-in.
- `bp`: number of base pair matches needed to define a possible cross hybridizer.

**Details**
Some details are contained in the help file for `hgu133a.spikein.xhyb`.

**Value**
An `ExpressionSet` with probeset removed.

**See Also**
`hgu133a.spikein.xhyb`

---

**SD**  
*SD Assessment Functions*

**Description**
These functions create assessments, figures, and tables for expression standard errors.

**Usage**
```
affycomp.figure7(l, main="Figure 7")
affycomp.compfig7(l, method.names=as.character(1:length(l)), main="Figure 7")
tableSD(l, method.names=NULL)
```
spikein.phenodata

Arguments

- `l`: a list of lists with the necessary components to create the Figure. See details.
- `method.names`: a character vector with the names of the expression measures methodologies being compared.
- `main`: title of the Figure.

Details

This uses the dilution data. The exprsets need to have standard error estimates in the `assayDataElement(exprset,"se.exprs")`. Read the vignette for more details. The functions work similarly to those assessing expression measures.

All these files need the result of `assessSD`

Value

Depends on the call.

Author(s)

Rafael A. Irizarry

Examples

```r
library(affycompData)
data(rma.sd.assessment) # this was produced with affycomp.assess
data(lw.sd.assessment) # this one too
affycomp.compfig7(list(rma.sd.assessment,lw.sd.assessment))
affycomp.figure7(rma.sd.assessment)
```

---

**spikein.phenodata**  
*phenotypic information for spike in study*

Description

This object is of class `phenoData` with necessary information for the assessments.

Usage

```r
data(spikein.phenodata)
```

Format

An object of class `phenoData`

Source

This comes from an experiments where 16 different cRNA fragments have been added to the hybridization mixture of the GeneChip arrays at different pM concentrations. For more information see Irizarry, R.A., et al. (2001) [http://www.biostat.jhsph.edu/~ririzarr/papers/index.html](http://www.biostat.jhsph.edu/~ririzarr/papers/index.html)
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