Package 'frma'

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Title Frozen RMA and Barcode

Description Preprocessing and analysis for single microarrays and microarray batches.

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R topics documented:

barcode *Gene Expression Barcode*

Description

This function converts expression values produced via fRMA to a gene expression barcode.

Usage

```
barcode(object, platform=NULL, mu=NULL, tau=NULL, cutoff=6.5, output="binary")
```

Arguments

object	a vector or matrix of expression values or an ExpressionSet or frmaExpressionSet produced by frma
platform	the platform of the input data. One of GPL96, GPL570, GPL571, GPL1261, GPL6244, GPL6246. Required if object is a vector or matrix and either mu or tau is NULL.
mu	the mean of the unexpressed distribution. If NULL then precomputed values are used if possible.
tau	the standard deviation of the unexpressed distribution. If NULL then precomputed values are used if possible.
cutoff	the lod score cutoff used if output is binary.
output	the desired values to be returned. Options are: p-value, z-score, lod, or binary.

Value

A matrix containing the type of output specified by the output parameter. The option *binary* creates a gene expression barcode where 1s denote expressed genes and 0s denote unexpressed genes. The option *p-value* returns the p-values for the expression values under the unexpressed distribution. The option *lod* returns the LOD scores for expression values under the unexpressed distribution. The option *z-score* returns the z-scores for the expression values under the unexpressed distribution.

Author(s)

Matthew N. McCall

Examples

```
library(frma)
library(frmaExampleData)
data(AffyBatchExample)
object <- frma(AffyBatchExample)
bc <- barcode(object)
```

frma *Frozen Robust Multi-Array Analysis*

Description

This function preprocesses an AffyBatch, ExonFeatureSet, or GeneFeatureSet object using the fRMA method.

Usage

```
frma(object, background="rma", normalize="quantile",
    summarize="robust_weighted_average", target="probeset",
    input.vecs=NULL, output.param=NULL, verbose=FALSE)
```

Arguments

object	an AffyBatch, ExonFeatureSet, or GeneFeatureSet
background	type of background correction to perform: either "none" or "rma".
normalize	type of normalization to perform: either "none" or "quantile".
summarize	type of summarization to perform: one of "median_polish", "average", "median", "weighted_average", "robust_weighted_average", "random_effect".
target	summarization level for exon and gene arrays. Must be one of: probeset, core, full (exon only), extended (exon only).
input.vecs	a list of vectors to be used in preprocessing. If NULL, the correct package with pre-made vectors is loaded if it has been installed. These packages are of the form: <platform>frmavecs.
output.param	a vector of output elements to return. By default only the expression values and standard errors (if applicable) are returned. Additional options are: "residuals", "weights", "random_effects"
verbose	logical value. If TRUE then some messages are displayed while the function runs.

Value

The function returns an ExpressionSet if output.param=NULL or an frmaExpressionSet otherwise.

Author(s)

Matthew N. McCall

Examples

```
library(frmaExampleData)
data(AffyBatchExample)
object <- frma(AffyBatchExample)
```

frmaExpressionSet-class

Class to Contain and Describe High-Throughput Expression Level Assays preprocessed with fRMA

Description

This is a class representation for fRMA-preprocessed expression data. frmaExpressionSet class is derived from ExpressionSet, and requires a matrix named exprs and optionally matrices named se.exprs, weights, and residuals.

Extends

Extends class ExpressionSet.

Creating Objects

new("frmaExpressionSet",exprs = new("matrix"),se.exprs = new("matrix"),weights=new("matrix"),resid
= new("AnnotatedDataFrame"),featureData = new("AnnotatedDataFrame"),experimentData
= new("MIAME"),annotation = new("character"),...)

This creates a frmaExpressionSet with assayData implicitly created to contain exprs and se.exprs. The only required named arguments is exprs. Three optional named matrices, weights, residuals, and randomeffects can be added to the object.

new("frmaExpressionSet",assayData = assayDataNew(exprs=new("matrix"),se.exprs=new("matrix")),weig
= new("AnnotatedDataFrame"),featureData = new("AnnotatedDataFrame"),experimentData
= new("MIAME"),annotation = new("character"),...)

This creates a frmaExpressionSet with assayData provided explicitly. In this form, the only required named argument is assayData. Three optional named matrices, weights, residuals, and randomeffects can be added to the object.

Slots

se.exprs: standard errors for the expression estimates

weights: weights used in the summarization step

residuals: residuals from fitting the probe-level model

randomeffects: random effect estimates from fitting the probe-level model using random effect summarization

Inherited from ExpressionSet:

assayData: Contains matrices with equal dimensions, and with column number equal to nrow(phenoData). assayData must contain a matrix exprs with rows representing features and columns representing samples. It may also contain a matrix se.exprs containing standard errors.

phenoData: See eSet

annotation: See eSet

featureData: See eSet

experimentData: See eSet

Methods

Class-specific methods:

`se.exprs(frmaExpressionSet)` Access elements named `se.exprs` in the `AssayData-class` slot.

`weights(frmaExpressionSet)` Access elements named `weights`

`residuals(frmaExpressionSet)` Access elements named `residuals`

`randomeffects(frmaExpressionSet)` Access elements named `randomeffects`

For derived methods (see `ExpressionSet`).

See Also

`eSet-class`, `ExpressionSet-class`, `frma`.

Examples

```
# create an instance of frmaExpressionSet
new("frmaExpressionSet")
```

GNUSE *GNUSE*

Description

Computes the generalized normalized unscaled standard error (a measure of microarray quality).

Usage

```
GNUSE(object, medianSE=NULL, type=c("plot", "values", "stats", "density"), ...)
```

Arguments

`object`	an ExpressionSet or frmaExpressionSet containing standard errors produced by frma
`medianSE`	median standard errors to be used. If NULL, these are obtained from the correct frmavecs package.
`type`	the desired output
`...`	additional graphical parameters for types plot or density

Value

If type is plot, boxplots of GNUSE values are displayed. If type is values, the GNUSE values are returned. If type is stats, the median, IQR, 95th, and 99th percentiles are reported. If type is density, a density plots of GNUSE values are displayed.

Author(s)

Matthew N. McCall

Examples

```
library(frma)
library(frmaExampleData)
data(AffyBatchExample)
object <- frma(AffyBatchExample)
GNUSE(object, type="stats")
```

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