Package ‘frma’

January 30, 2017

Version 1.26.0
Date 2015-09-22
Title Frozen RMA and Barcode
Description Preprocessing and analysis for single microarrays and microarray batches.
Author Matthew N. McCall <mccallm@gmail.com>, Rafael A. Irizarry <rafa@jhu.edu>, with contributions from Terry Therneau
Maintainer Matthew N. McCall <mccallm@gmail.com>
Depends R (>= 2.10.0), Biobase (>= 2.6.0)
Imports Biobase, MASS, DBI, affy, methods, oligo, oligoClasses, preprocessCore, utils, BiocGenerics
Suggests hgu133afmavecs, frmaExampleData
biocViews Software, Microarray, Preprocessing
License GPL (>= 2)
URL http://bioconductor.org
NeedsCompilation no

R topics documented:

barcode .................................................. 1
frma ....................................................... 2
frmaExpressionSet-class ................................. 3
GNUSE ................................................... 5

Index 6

<table>
<thead>
<tr>
<th>barcode</th>
<th>Gene Expression Barcode</th>
</tr>
</thead>
</table>

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 frmaExpression-
        Set 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 precom-
        puted 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(frmavecs)
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

```r
new("frmaExpressionSet", exprs = new("matrix"), se.exprs = new("matrix"), weights=new("matrix"), ...
```

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.

```r
new("frmaExpressionSet", assayData = assayDataNew(exprs=new("matrix"),se.exprs=new("matrix"))),
```

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**

```r
# create an instance of frmaExpressionSet
new("frmaExpressionSet")
```
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 frmavec 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")
Index

*Topic classes
   frmaExpressionSet-class, 3
*Topic manip
   barcode, 1
   frma, 2
   GNUSE, 5
   as.ExpressionSet, frmaExpressionSet-method
      (frmaExpressionSet-class), 3
   barcode, 1
   class:frmaExpressionSet
      (frmaExpressionSet-class), 3
   frma, 2
   frmaExpressionSet
      (frmaExpressionSet-class), 3
   frmaExpressionSet-class, 3
   frmaExpressionSet-methods
      (frmaExpressionSet-class), 3
   GNUSE, 5
   initialize, frmaExpressionSet-method
      (frmaExpressionSet-class), 3
   randomeffects
      (frmaExpressionSet-class), 3
   randomeffects, frmaExpressionSet-method
      (frmaExpressionSet-class), 3
   randomeffects<-
      (frmaExpressionSet-class), 3
   randomeffects<-, frmaExpressionSet-method
      (frmaExpressionSet-class), 3
   residuals, frmaExpressionSet-method
      (frmaExpressionSet-class), 3
   residuals<-
      (frmaExpressionSet-class), 3
   residuals<-, frmaExpressionSet-method
      (frmaExpressionSet-class), 3
   se.exprs, ExpressionSet-method
      (frmaExpressionSet-class), 3
   se.exprs<-
      (frmaExpressionSet-class), 3
   se.exprs<-, frmaExpressionSet-method
      (frmaExpressionSet-class), 3
   weights, frmaExpressionSet-method
      (frmaExpressionSet-class), 3
   weights<-
      (frmaExpressionSet-class), 3
   weights<-, frmaExpressionSet-method
      (frmaExpressionSet-class), 3

6