Package 'BufferedMatrixMethods'

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Type Package

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Suggests affyio, affy

LinkingTo BufferedMatrix

LazyLoad Yes

Description Microarray analysis methods that use BufferedMatrix objects

License GPL (>= 2)

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BufferedMatrix.justRMA

Use BufferedMatrix objects to facilitate RMA computation with low memory overhead

Description

Read CEL data into BufferedMatrix objects.

Usage

```
BufferedMatrix.justRMA(..., filenames=character(0),celfile.path=NULL,
                       phenoData=new("AnnotatedDataFrame"),
                       description=NULL,
                       notes="",
                       verbose=FALSE, background=TRUE, normalize=TRUE,
                       cdfname = NULL)
```

Arguments

...	file names separated by comma.
filenames	file names in a character vector.
celfile.path	path where CEL files are located
phenoData	a AnnotatedDataFrame object
description	a MIAME object
notes	notes
verbose	verbosity flag
normalize	logical value. If TRUE normalize data using quantile normalization
background	logical value. If TRUE background correct using RMA background correction
cdfname	Used to specify the name of an alternative cdf package. If set to NULL, the usual cdf package based on Affymetrix' mappings will be used.

Value

An ExpressionSet object, containing expression values identical to what one would get from running rma on an AffyBatch.

Author(s)

Ben Bolstad <bmb@bmbolstad.com>

See Also

BufferedMatrix, BufferedMatrix.read.probematrix

`BufferedMatrix.read.celfiles` *Read CEL file data into PM or MM BufferedMatrix*

Description

Read CEL data into `BufferedMatrix` objects.

Usage

```
BufferedMatrix.read.celfiles(..., filenames = character(0),celfile.path=NULL)
```

Arguments

`...`	file names separated by comma.
`filenames`	file names in a character vector.
`celfile.path`	path where CEL files are located

Value

A `BufferedMatrix` object containing the CEL file intensities.

Author(s)

Ben Bolstad <bmb@bmbolstad.com>

See Also

`BufferedMatrix`, `BufferedMatrix.read.probematrix`

`BufferedMatrix.read.probematrix` *Read CEL file data into PM or MM BufferedMatrix*

Description

Read CEL data into `BufferedMatrix` objects.

Usage

```
BufferedMatrix.read.probematrix(..., filenames = character(0),celfile.path=NULL,rm.mask = FALSE, rm.o
```

Arguments

...	file names separated by comma.
filenames	file names in a character vector.
celfile.path	path where CEL files are located
rm.mask	should the spots marked as 'MASKS' set to NA ?
rm.outliers	should the spots marked as 'OUTLIERS' set to NA
rm.extra	if TRUE, overrides what is in rm.mask and rm.oultiers
verbose	verbosity flag
which	should be either "pm", "mm" or "both"
cdfname	Used to specify the name of an alternative cdf package. If set to NULL, the usual cdf package based on Affymetrix' mappings will be used.

Value

A list of one or two BufferedMatrix objects. Each BufferedMatrix objects is either PM or MM data. No AffyBatch is created.

Author(s)

Ben Bolstad <bmb@bmbolstad.com>

See Also

AffyBatch, read.affybatch

RMA preprocess BufferedMatrix

RMA preprocessing functions that work on BufferedMatrix objects

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Description

This group of functions can be used to apply the RMA background correction, Quantile normalization and Median polish summarization to data stored in a BufferedMatrix object.

Usage

```
bg.correct.BufferedMatrix(x, copy=TRUE)
normalize.BufferedMatrix.quantiles(x, copy=TRUE)
BufferedMatrix.bg.correct.normalize.quantiles(x, copy=TRUE)
```

Arguments

x	a BufferedMatrix containing data to be processed
copy	should the BufferedMatrix be copied or should the input object be changed on output

Value

In the case of `normalize.BufferedMatrix.quantiles` and `bg.correct.BufferedMatrix` a `BufferedMatrix` is returned. The function `median.polish.summarize` returns a `matrix`.

The function `BufferedMatrix.bg.correct.normalize.quantiles` carries out both pre-processing steps with a single command.

Author(s)

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See Also

`rma`

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