

Package ‘BufferedMatrixMethods’

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Type Package

Title Microarray Data related methods that utilize BufferedMatrix objects

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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

<code>...</code>	file names separated by comma.
<code>filenames</code>	file names in a character vector.
<code>celfile.path</code>	path where CEL files are located
<code>phenoData</code>	a AnnotatedDataFrame object
<code>description</code>	a MIAME object
<code>notes</code>	notes
<code>verbose</code>	verbosity flag
<code>normalize</code>	logical value. If TRUE normalize data using quantile normalization
<code>background</code>	logical value. If TRUE background correct using RMA background correction
<code>cdfname</code>	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)

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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

<code>...</code>	file names separated by comma.
<code>filenames</code>	file names in a character vector.
<code>celfile.path</code>	path where CEL files are located

Value

A [BufferedMatrix](#) object containing the CEL file intensities.

Author(s)

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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

<code>...</code>	file names separated by comma.
<code>filenames</code>	file names in a character vector.
<code>celfile.path</code>	path where CEL files are located
<code>rm.mask</code>	should the spots marked as 'MASKS' set to NA ?
<code>rm.outliers</code>	should the spots marked as 'OUTLIERS' set to NA
<code>rm.extra</code>	if TRUE, overrides what is in <code>rm.mask</code> and <code>rm.outliers</code>
<code>verbose</code>	verbosity flag
<code>which</code>	should be either "pm", "mm" or "both"
<code>cdfname</code>	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)

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See Also

[AffyBatch](#), [read.affybatch](#)

RMA preprocess *BufferedMatrix*

RMA preprocessing functions that work on [BufferedMatrix](#) objects

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

<code>x</code>	a BufferedMatrix containing data to be processed
<code>copy</code>	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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* **manip**

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