

BufferedMatrixMethods

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R topics documented:

BufferedMatrix.read.probematrix	1
BufferedMatrix.justRMA	2
BufferedMatrix.read.celfiles	3
RMA preprocess BufferedMatrix	3

Index	5
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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,
```

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`

`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 <code>AnnotatedDataFrame</code> object
<code>description</code>	a <code>MIAME</code> 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

`...` 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)

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See Also

[BufferedMatrix](#), [BufferedMatrix.read.probematrix](#)

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

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.

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See Also

[rma](#)

Index

*Topic **manip**

- RMA preprocess
 - BufferedMatrix, [3](#)
- AffyBatch, [1](#), [2](#)
- AnnotatedDataFrame, [2](#)
- bg.correct.BufferedMatrix (RMA preprocess BufferedMatrix), [3](#)
- BufferedMatrix, [1-4](#)
- BufferedMatrix.bg.correct.normalize.quantiles (RMA preprocess BufferedMatrix), [3](#)
- BufferedMatrix.justRMA, [2](#)
- BufferedMatrix.read.celfiles, [3](#)
- BufferedMatrix.read.probematrix, [1](#), [2](#), [3](#)
- matrix, [4](#)
- median.polish.summarize (RMA preprocess BufferedMatrix), [3](#)
- median.polish.summarize, BufferedMatrix-method (RMA preprocess BufferedMatrix), [3](#)
- MIAME, [2](#)
- normalize.BufferedMatrix.quantiles (RMA preprocess BufferedMatrix), [3](#)
- read.affybatch, [2](#)
- rma, [2](#), [4](#)
- RMA preprocess BufferedMatrix, [3](#)