

# Package ‘BufferedMatrixMethods’

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**Type** Package

**Title** Microarray Data related methods that utilize BufferedMatrix objects

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**Depends** R (>= 2.6.0), BufferedMatrix (>= 1.3.0), methods

**Suggests** affyio, affy

**LinkingTo** BufferedMatrix

**LazyLoad** Yes

**Description** Microarray analysis methods that use BufferedMatrix objects

**License** GPL (>= 2)

**URL** <https://github.com/bmbolstad/BufferedMatrixMethods>

**biocViews** Infrastructure

**git\_url** <https://git.bioconductor.org/packages/BufferedMatrixMethods>

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`BufferedMatrix.justRMA`*Use BufferedMatrix objects to facilitate RMA computation with low memory overhead*

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## 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 <a href="#">AnnotatedDataFrame</a> object                                                                                               |
| <code>description</code>  | a <a href="#">MIAME</a> 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)

Ben Bolstad <bmb@bmbolstad.com>

## See Also

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

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

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**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)**

Ben Bolstad <bmb@bmbolstad.com>

**See Also**

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

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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, 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)**

Ben Bolstad <bmb@bmbolstad.com>

**See Also**

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

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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**

|                   |                                                                                                     |
|-------------------|-----------------------------------------------------------------------------------------------------|
| <code>x</code>    | a <a href="#">BufferedMatrix</a> containing data to be processed                                    |
| <code>copy</code> | should the <a href="#">BufferedMatrix</a> 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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