# Package: BufferedMatrixMethods (via r-universe)

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**Type** Package

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

**Version** 1.76.0

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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.bom/bmbolstad/BufferedMatrixMethods

**biocViews** Infrastructure

**Repository** Bioconductor 3.23

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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

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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

| | |
|---|---|
| `...` | 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`

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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

| | |
|---|---|
| ... | 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

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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

| | |
|---|---|
| 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)

B. M. Bolstad `<bmb@bmbolstad.com>`

## See Also

`rma`

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