

# Package ‘BufferedMatrixMethods’

April 24, 2025

**Type** Package  
**Title** Microarray Data related methods that utilize BufferedMatrix objects  
**Version** 1.73.0  
**Date** 2012-09-14  
**Author** Ben Bolstad <bmb@bmbolstad.com>  
**Maintainer** Ben Bolstad <bmb@bmbolstad.com>  
**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>  
**git\_branch** devel  
**git\_last\_commit** 57162b3  
**git\_last\_commit\_date** 2025-04-15  
**Repository** Bioconductor 3.22  
**Date/Publication** 2025-04-24

## Contents

|                                           |          |
|-------------------------------------------|----------|
| BufferedMatrix.justRMA . . . . .          | 2        |
| BufferedMatrix.read.celfiles . . . . .    | 3        |
| BufferedMatrix.read.probematrix . . . . . | 3        |
| RMA preprocess BufferedMatrix . . . . .   | 4        |
| <b>Index</b>                              | <b>6</b> |

---

`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 <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](#)

---

`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)

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, n
```

**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.outliers                                                                                     |
| 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*

---

**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 <a href="#">BufferedMatrix</a> containing data to be processed                                    |
| copy | 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)**

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

**See Also**

[rma](#)

# Index

- \* **manip**
  - RMA preprocess BufferedMatrix, [4](#)
- AffyBatch, [2](#), [4](#)
- AnnotatedDataFrame, [2](#)
- bg.correct.BufferedMatrix (RMA preprocess BufferedMatrix), [4](#)
- BufferedMatrix, [2–5](#)
- BufferedMatrix.bg.correct.normalize.quantiles (RMA preprocess BufferedMatrix), [4](#)
- BufferedMatrix.justRMA, [2](#)
- BufferedMatrix.read.celfiles, [3](#)
- BufferedMatrix.read.probematrix, [2](#), [3](#), [3](#)
- matrix, [5](#)
- median.polish.summarize (RMA preprocess BufferedMatrix), [4](#)
- median.polish.summarize, BufferedMatrix-method (RMA preprocess BufferedMatrix), [4](#)
- MIAME, [2](#)
- normalize.BufferedMatrix.quantiles (RMA preprocess BufferedMatrix), [4](#)
- read.affybatch, [4](#)
- rma, [2](#), [5](#)
- RMA preprocess BufferedMatrix, [4](#)