

# Package ‘BufferedMatrixMethods’

June 15, 2025

**Type** Package

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

**Version** 1.72.0

**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** RELEASE\_3\_21

**git\_last\_commit** 62ad483

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-06-15

## 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

...	file names separated by comma.
filenames	file names in a character vector.
celfile.path	path where CEL files are located
phenoData	a <a href="#">AnnotatedDataFrame</a> object
description	a <a href="#">MIAME</a> 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](#)

---

`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, 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.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](mailto: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