

Package ‘BufferedMatrixMethods’

May 5, 2024

Type Package

Title Microarray Data related methods that utilize BufferedMatrix objects

Version 1.68.0

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_19

git_last_commit 6b6ef58

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-05

Contents

| | |
|---|---|
| BufferedMatrix.justRMA | 2 |
| BufferedMatrix.read.celfiles | 3 |
| BufferedMatrix.read.probematrix | 3 |
| RMA preprocess BufferedMatrix | 4 |

| | |
|--------------|----------|
| Index | 6 |
|--------------|----------|

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](#)

`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(), 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(), 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 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](#)

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