

# Package ‘beachmat’

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**Title** Compiling Bioconductor to Handle Each Matrix Type

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**Imports** methods, DelayedArray (>= 0.15.14), BiocGenerics, Matrix, Rcpp

**Suggests** testthat, BiocStyle, knitr, rmarkdown, rcmdcheck,  
BiocParallel, HDF5Array

**LinkingTo** Rcpp

**biocViews** DataRepresentation, DataImport, Infrastructure

**Description** Provides a consistent C++ class interface for reading from and writing data to a variety of commonly used matrix types. Ordinary matrices and several sparse/dense Matrix classes are directly supported, third-party S4 classes may be supported by external linkage, while all other matrices are handled by DelayedArray block processing.

**License** GPL-3

**NeedsCompilation** yes

**VignetteBuilder** knitr

**SystemRequirements** C++11

**RoxygenNote** 7.1.1

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## R topics documented:

colBlockApply	2
realizeFileBackedMatrix	4
toCsparse	5
whichNonZero	6

<b>Index</b>	<b>8</b>
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colBlockApply	<i>Apply over blocks of columns or rows</i>
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### Description

Apply a function over blocks of columns or rows using **DelayedArray**'s block processing mechanism.

### Usage

```
colBlockApply(
  x,
  FUN,
  ...,
  grid = NULL,
  coerce.sparse = TRUE,
  BPPARAM = getAutoBPPARAM()
)
```

```
rowBlockApply(
  x,
  FUN,
  ...,
  grid = NULL,
  coerce.sparse = TRUE,
  BPPARAM = getAutoBPPARAM()
)
```

### Arguments

x	A matrix-like object to be split into blocks and looped over. This can be of any class that respects the matrix contract.
FUN	A function that operates on columns or rows in x, for colBlockApply and rowBlockApply respectively. Ordinary matrices, <a href="#">CsparseMatrix</a> or <a href="#">SparseArraySeed</a> objects may be passed as the first argument.
...	Further arguments to pass to FUN.
grid	An <a href="#">ArrayGrid</a> object specifying how x should be split into blocks. For colBlockApply and rowBlockApply, blocks should consist of consecutive columns and rows, respectively. Alternatively, this can be set to TRUE or FALSE, see Details.

coerce.sparse	Logical scalar indicating whether blocks of a sparse <a href="#">DelayedMatrix</a> x should be automatically coerced into <a href="#">CsparseMatrix</a> objects.
BPPARAM	A <a href="#">BiocParallelParam</a> object from the <b>BiocParallel</b> package, specifying how parallelization should be performed across blocks.

## Details

This is a wrapper around [blockApply](#) that is dedicated to looping across rows or columns of x. The aim is to provide a simpler interface for the common task of [applying](#) across a matrix, along with a few modifications to improve efficiency for parallel processing and for natively supported x.

Note that the fragmentation of x into blocks is not easily predictable, meaning that FUN should be capable of operating on each row/column independently. Users can retrieve the current location of each block of x by calling [currentViewport](#) inside FUN.

If grid is not explicitly set to an [ArrayGrid](#) object, it can take several values:

- If TRUE, the function will choose a grid that (i) respects the memory limits in [getAutoBlockSize](#) and (ii) fragments x into sufficiently fine chunks that every worker in BPPARAM gets to do something. If FUN might make large allocations, this mode should be used to constrain memory usage.
- The default grid=NULL is very similar to TRUE except that that memory limits are ignored when x is of any type that can be passed directly to FUN. This avoids unnecessary copies of x and is best used when FUN itself does not make large allocations.
- If FALSE, the function will choose a grid that covers the entire x. This is provided for completeness and is only really useful for debugging.

The default of coerce.sparse=TRUE will generate [dgCMatrix](#) objects during block processing of a sparse [DelayedMatrix](#) x. This is convenient as it avoids the need for FUN to specially handle [SparseArraySeed](#) objects. If the coercion is not desired (e.g., to preserve integer values in x), it can be disabled with coerce.sparse=FALSE.

## Value

A list of length equal to the number of blocks, where each entry is the output of FUN for the results of processing each the rows/columns in the corresponding block.

## See Also

[blockApply](#), for the original **DelayedArray** implementation.

[toCsparse](#), to convert [SparseArraySeeds](#) to [CsparseMatrix](#) objects prior to further processing in FUN.

## Examples

```
x <- matrix(runif(10000), ncol=10)
str(colBlockApply(x, colSums))
str(rowBlockApply(x, rowSums))

library(Matrix)
y <- rsparsematrix(10000, 10000, density=0.01)
```

```
str(colBlockApply(y, colSums))
str(rowBlockApply(y, rowSums))

library(DelayedArray)
z <- DelayedArray(y) + 1
str(colBlockApply(z, colSums))
str(rowBlockApply(z, rowSums))

# We can also force multiple blocks:
library(BiocParallel)
BPPARAM <- SnowParam(2)
str(colBlockApply(x, colSums, BPPARAM=BPPARAM))
str(rowBlockApply(x, rowSums, BPPARAM=BPPARAM))
```

---

realizeFileBackedMatrix

*Realize a file-backed DelayedMatrix*

---

## Description

Realize a file-backed DelayedMatrix into its corresponding in-memory format.

## Usage

```
realizeFileBackedMatrix(x)
```

```
isFileBackedMatrix(x)
```

## Arguments

x                    A [DelayedMatrix](#) object.

## Details

A file-backed matrix representation is recognized based on whether it has a [path](#) method for any one of its seeds. If so, and the "beachmat.realizeFileBackedMatrix" option is not FALSE, we will load it into memory. This is intended for DelayedMatrix objects that have already been subsetted (e.g., to highly variable genes), which can be feasibly loaded into memory for rapid calculations.

## Value

For realizeFileBackedMatrix, an ordinary matrix or a [dgCMatrix](#), depending on whether [is\\_sparse\(x\)](#).

For isFileBackedMatrix, a logical scalar indicating whether x has file-backed components.

## Author(s)

Aaron Lun

## Examples

```
mat <- matrix(rnorm(50), ncol=5)
realizeFileBackedMatrix(mat) # no effect

library(HDF5Array)
mat2 <- as(mat, "HDF5Array")
realizeFileBackedMatrix(mat2) # realized into memory
```

---

toCsparse

*Convert a SparseArraySeed to a CsparseMatrix*

---

## Description

Exactly what it says in the title.

## Usage

```
toCsparse(x)
```

## Arguments

x Any object produced by block processing with [colBlockApply](#) or [rowBlockApply](#). This can be a matrix, sparse matrix or a two-dimensional [SparseArraySeed](#).

## Details

This is intended for use inside functions to be passed to [colBlockApply](#) or [rowBlockApply](#). The idea is to pre-process blocks for user-defined functions that don't know how to deal with [SparseArraySeed](#) objects, which is often the case for R-defined functions that do not benefit from **beachmat**'s C++ abstraction.

## Value

x is returned unless it was a [SparseArraySeed](#), in which case an appropriate [CsparseMatrix](#) object is returned instead.

## Author(s)

Aaron Lun

## Examples

```
library(DelayedArray)
out <- SparseArraySeed(c(10, 10),
  nzindex=cbind(1:10, sample(10)),
  nzdata=runif(10))
toCsparse(out)
```

---

whichNonZero                      *Find non-zero entries of a matrix*

---

### Description

Finds the non-zero entries of a matrix in the most efficient manner for each matrix representation. Not sure there's much more to say here.

### Usage

```
whichNonZero(x, ...)  
  
## S4 method for signature 'ANY'  
whichNonZero(x, ...)  
  
## S4 method for signature 'TsparseMatrix'  
whichNonZero(x, ...)  
  
## S4 method for signature 'CsparseMatrix'  
whichNonZero(x, ...)  
  
## S4 method for signature 'SparseArraySeed'  
whichNonZero(x, ...)  
  
## S4 method for signature 'DelayedMatrix'  
whichNonZero(x, BPPARAM = NULL, ...)
```

### Arguments

x	A numeric matrix-like object, usually sparse in content if not in representation.
...	For the generic, additional arguments to pass to the specific methods. For the methods, additional arguments that are currently ignored.
BPPARAM	A <b>BiocParallelParam</b> object from the <b>BiocParallel</b> package controlling how parallelization should be performed. Only used when x is a <a href="#">DelayedMatrix</a> object; defaults to no parallelization.

### Value

A list containing i, an integer vector of the row indices of all non-zero entries; j, an integer vector of the column indices of all non-zero entries; and x, a (usually atomic) vector of the values of the non-zero entries.

### Author(s)

Aaron Lun

**See Also**

[which](#), obviously.

**Examples**

```
x <- Matrix::rsparsematrix(1e6, 1e6, 0.000001)
out <- whichNonZero(x)
str(out)
```

# Index

apply, 3  
ArrayGrid, 2, 3  
  
blockApply, 3  
  
colBlockApply, 2, 5  
CsparseMatrix, 2, 3, 5  
currentViewport, 3  
  
DelayedMatrix, 3, 4, 6  
dgCMatrix, 3, 4  
  
getAutoBlockSize, 3  
  
is\_sparse, 4  
isFileBackedMatrix  
    (realizeFileBackedMatrix), 4  
  
path, 4  
  
realizeFileBackedMatrix, 4  
rowBlockApply, 5  
rowBlockApply (colBlockApply), 2  
  
SparseArraySeed, 2, 3, 5  
  
toCsparse, 3, 5  
  
which, 7  
whichNonZero, 6  
whichNonZero, ANY-method (whichNonZero),  
    6  
whichNonZero, CsparseMatrix-method  
    (whichNonZero), 6  
whichNonZero, DelayedMatrix-method  
    (whichNonZero), 6  
whichNonZero, SparseArraySeed-method  
    (whichNonZero), 6  
whichNonZero, TsparseMatrix-method  
    (whichNonZero), 6