

Package ‘bigmemory’

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Title Manage Massive Matrices with Shared Memory and Memory-Mapped Files

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Enhances biganalytics, bigtabulate, synchronicity

LinkingTo BH, Rcpp

Description Create, store, access, and manipulate massive matrices.
Matrices are allocated to shared memory and may use memory-mapped
files. Packages 'biganalytics', 'bigtabulate', 'synchronicity', and
'bigalgebra' provide advanced functionality.

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URL <http://www.bigmemory.org>

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R topics documented:

bigmemory-package	2
as.big.matrix-methods	5
as.matrix,big.matrix-method	5
big.matrix	6
big.matrix-class	9
deepcopy	11
describe,big.matrix-method	13
descriptor-class	14
dim,big.matrix-method	16
dimnames,big.matrix-method	16
Extract,big.matrix	17
flush	18
GetMatrixSize	19
head,big.matrix-method	19
is.float	20
is.float,numeric-method	20
is.sub.big.matrix	20
length,big.matrix-method	22
morder	22
mwhich	24
mwhich-methods	25
ncol,big.matrix-method	26
print,big.matrix-method	27
typeof,big.matrix-method	27
write.big.matrix	28
Index	31

bigmemory-package	<i>Manage massive matrices with shared memory and memory-mapped files.</i>
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Description

Create, store, access, and manipulate massive matrices. Matrices are, by default, allocated to shared memory and may use memory-mapped files. Packages **biganalytics**, **synchronicity**, **bigalgebra**, and **bigtabulate** provide advanced functionality. Access to and manipulation of a **big.matrix** object is exposed in by an S4 class whose interface is similar to that of an **matrix**. Use of these packages in parallel environments can provide substantial speed and memory efficiencies. **big-memory** also provides a C++ framework for the development of new tools that can work both with **big.matrix** and native **matrix** objects.

Details

Index of functions/methods (grouped in a friendly way):

`big.matrix`, `filebacked.big.matrix`, `as.big.matrix`
`is.big.matrix`, `is.separated`, `is.filebacked`
`describe`, `attach.big.matrix`, `attach.resource`
`sub.big.matrix`, `is.sub.big.matrix`
`dim`, `dimnames`, `nrow`, `ncol`, `print`, `head`, `tail`, `typeof`, `length`
`read.big.matrix`, `write.big.matrix`
`mwhich`
`morder`, `mpermute`
`deepcopy`
`flush`

Multi-gigabyte data sets challenge and frustrate users, even on well-equipped hardware. Use of C/C++ can provide efficiencies, but is cumbersome for interactive data analysis and lacks the flexibility and power of R's rich statistical programming environment. The package **bigmemory** and sister packages **biganalytics**, **synchronicity**, **bigtabulate**, and **bigalgebra** bridge this gap, implementing massive matrices and supporting their manipulation and exploration. The data structures may be allocated to shared memory, allowing separate processes on the same computer to share access to a single copy of the data set. The data structures may also be file-backed, allowing users to easily manage and analyze data sets larger than available RAM and share them across nodes of a cluster. These features of the Bigmemory Project open the door for powerful and memory-efficient parallel analyses and data mining of massive data sets.

This project (**bigmemory** and its sister packages) is still actively developed, although the design and current features can be viewed as "stable." Please feel free to email us with any questions: bigmemoryauthors@gmail.com.

Note

Various options are available. `options(bigmemory.typecast.warning)` can be set to avoid annoying warnings that might occur if, for example, you assign objects (typically type `double`) to `char`, `short`, or integer `big.matrix` objects. `options(bigmemory.print.warning)` protects against extracting and printing a massive matrix (which would involve the creation of a second massive copy of the matrix). `options(bigmemory.allow.dimnames)` by default prevents the setting of `dimnames` attributes, because they aren't allocated to shared memory and changes will not be visible across processes. `options(bigmemory.default.type)` is `"double"` by default (a change in default behavior as of 4.1.1) but may be changed by the user.

Versions ≥ 4.0 represent a major redesign, with the mutexes (locking) abstracted to package **synchronicity**, the exploratory data analysis functionality relocated to package **biganalytics**, and new linear algebra support available in package **bigalgebra**. Package **bigtabulate** extends the **bigmemory** package with table-, tapply-, and split-like behavior. The functions may also be used with regular matrices for speed and memory-efficiency gains. Package **bigmemory** itself is now minimalist, providing only the core functionality. As an example, the `apply()` method appears in **biganalytics**, supporting exploration and analysis, while `mwhich`, `morder` and `mpermute` appear in **bigmemory** as fundamental tools for data manipulation.

Note that you can't simply use a `big.matrix` with many (most) existing functions (e.g. `lm`, `kmeans`). One nice exception is `split`, because this function only accesses subsets of the matrix.

Author(s)

Michael J. Kane, John W. Emerson, Peter Haverty, and Charles Determan Jr.

Maintainers: Michael J. Kane <bigmemoryauthors@gmail.com>

References

<http://www.bigmemory.org>

See Also

For example, `big.matrix`, `mwhich`, `read.big.matrix`

Examples

```
# Our examples are all trivial in size, rather than burning huge amounts
# of memory.

x <- big.matrix(5, 2, type="integer", init=0,
               dimnames=list(NULL, c("alpha", "beta")))

x
x[1:2,]
x[,1] <- 1:5
x[, "alpha"]
colnames(x)
options(bigmemory.allow.dimnames=TRUE)
colnames(x) <- NULL
x[,]
```

as.big.matrix-methods *Create a “big.matrix” from a matrix or vector.*

Description

Create a `big.matrix` from a matrix or vector or `data.frame`; a vector will result in a `big.matrix` with one column. A data frame will have character vectors converted to factors, and then all factors converted to numeric factor levels. All labels or character values will be lost.

Methods

```
signature(x = "matrix") ...  
signature(x = "vector") ...  
signature(x = "data.frame") ...
```

as.matrix, big.matrix-method
 Convert to base R matrix

Description

Extract values from a `big.matrix` object and convert to a base R matrix object

Usage

```
## S4 method for signature 'big.matrix'  
as.matrix(x)
```

Arguments

x A `big.matrix` object

big.matrix

*The core "big.matrix" operations.***Description**

Create a big.matrix (or check to see if an object is a big.matrix, or create a big.matrix from a [matrix](#), and so on). The big.matrix may be file-backed.

Usage

```
big.matrix(nrow, ncol, type = options()$bigmemory.default.type, init = NULL,
  dimnames = NULL, separated = FALSE, backingfile = NULL,
  backingpath = NULL, descriptorfile = NULL, binarydescriptor = FALSE,
  shared = TRUE)
```

```
filebacked.big.matrix(nrow, ncol, type = options()$bigmemory.default.type,
  init = NULL, dimnames = NULL, separated = FALSE, backingfile = NULL,
  backingpath = NULL, descriptorfile = NULL, binarydescriptor = FALSE)
```

```
as.big.matrix(x, type = NULL, separated = FALSE, backingfile = NULL,
  backingpath = NULL, descriptorfile = NULL, binarydescriptor = FALSE,
  shared = TRUE)
```

```
is.big.matrix(x)
```

```
## S4 method for signature 'big.matrix'
is.big.matrix(x)
```

```
## S4 method for signature 'ANY'
is.big.matrix(x)
```

```
is.separated(x)
```

```
## S4 method for signature 'big.matrix'
is.separated(x)
```

```
is.filebacked(x)
```

```
## S4 method for signature 'big.matrix'
is.filebacked(x)
```

```
shared.name(x)
```

```
## S4 method for signature 'big.matrix'
shared.name(x)
```

```
file.name(x)
```

```
## S4 method for signature 'big.matrix'
file.name(x)

is.shared(x)

## S4 method for signature 'big.matrix'
is.shared(x)

is.readonly(x)

## S4 method for signature 'big.matrix'
is.readonly(x)

is.nil(address)
```

Arguments

nrow	number of rows.
ncol	number of columns.
type	the type of the atomic element (<code>options()\$bigmemory.default.type</code> by default – "double" – but can be changed by the user to "integer", "short", or "char").
init	a scalar value for initializing the matrix (NULL by default to avoid unnecessary time spent doing the initializing).
dimnames	a list of the row and column names; use with caution for large objects.
separated	use separated column organization of the data; see details.
backingfile	the root name for the file(s) for the cache of x.
backingpath	the path to the directory containing the file backing cache.
descriptorfile	the name of the file to hold the backingfile description, for subsequent use with attach.big.matrix ; if NULL, the backingfile is used as the root part of the descriptor file name. The descriptor file is placed in the same directory as the backing files.
binarydescriptor	the flag to specify if the binary RDS format should be used for the backingfile description, for subsequent use with attach.big.matrix ; if NULL or FALSE, the <code>dput()</code> file format is used.
shared	TRUE by default, and always TRUE if the big.matrix is file-backed. For a non-filebacked big.matrix, <code>shared=FALSE</code> uses non-shared memory, which can be more stable for large (say, >50) fail in such cases due to exhausted shared-memory resources in the system.
x	a matrix, vector, or data.frame for <code>as.big.matrix</code> ; if a vector, a one-column big.matrix is created by <code>as.big.matrix</code> ; if a data.frame, see details. For the <code>is.*</code> functions, x is likely a big.matrix.
address	an externalptr, so <code>is.nil(x@address)</code> might be a sensible thing to want to check, but it's pretty obscure.

Details

A `big.matrix` consists of an object in R that does nothing more than point to the data structure implemented in C++. The object acts much like a traditional R matrix, but helps protect the user from many inadvertant memory-consuming pitfalls of traditional R matrices and data frames.

There are two `big.matrix` types which manage data in different ways. A standard, shared `big.matrix` is constrained to available RAM, and may be shared across separate R processes. A file-backed `big.matrix` may exceed available RAM by using hard drive space, and may also be shared across processes. The atomic types of these matrices may be double, integer, short, or char (8, 4, 2, and 1 bytes, respectively).

If `x` is a `big.matrix`, then `x[1:5,]` is returned as an R matrix containing the first five rows of `x`. If `x` is of type double, then the result will be numeric; otherwise, the result will be an integer R matrix. The expression `x` alone will display information about the R object (e.g. the external pointer) rather than evaluating the matrix itself (the user should try `x[,]` with extreme caution, recognizing that a huge R matrix will be created).

If `x` has a huge number of rows and/or columns, then the use of `rownames` and/or `colnames` will be extremely memory-intensive and should be avoided. If `x` has a huge number of columns and `separated=TRUE` is used (this isn't typically recommended), the user might want to store the transpose as there is overhead of a pointer for each column in the matrix. If `separated` is `TRUE`, then the memory is allocated into separate vectors for each column. Use this option with caution if you have a large number of columns, as shared-memory segments are limited by OS and hardware combinations. If `separated` is `FALSE`, the matrix is stored in traditional column-major format. The function `is.separated()` returns the separation type of the `big.matrix`.

When a `big.matrix`, `x`, is passed as an argument to a function, it is essentially providing call-by-reference rather than call-by-value behavior. If the function modifies any of the values of `x`, the changes are not limited in scope to a local copy within the function. This introduces the possibility of side-effects, in contrast to standard R behavior.

A file-backed `big.matrix` may exceed available RAM in size by using a file cache (or possibly multiple file caches, if `separated=TRUE`). This can incur a substantial performance penalty for such large matrices, but less of a penalty than most other approaches for handling such large objects. A side-effect of creating a file-backed object is not only the file-backing(s), but a descriptor file (in the same directory) that is needed for subsequent attachments (see [attach.big.matrix](#)).

Note that we do not allow setting or changing the `dimnames` attributes by default; such changes would not be reflected in the descriptor objects or in shared memory. To override this, set `options(bigmemory.allow.dimnames=TRUE)`.

It should also be noted that a user can create an “anonymous” file-backed `big.matrix` by specifying `""` as the `filebacking` argument. In this case, the backing resides in the temporary directory and a descriptor file is not created. These should be used with caution since even anonymous backings use disk space which could eventually fill the hard drive. Anonymous backings are removed either manually, by a user, or automatically, when the operating system deems it appropriate.

Finally, note that `as.big.matrix` can coerce data frames. It does this by making any character columns into factors, and then making all factors numeric before forming the `big.matrix`. Level labels are not preserved and must be managed by the user if desired.

Value

A `big.matrix` is returned (for `big.matrix` and `filebacked.big.matrix`, and `as.big.matrix`), and `TRUE` or `FALSE` for `is.big.matrix` and the other functions.

Author(s)

John W. Emerson and Michael J. Kane <<bigmemoryauthors@gmail.com>>

See Also

[bigmemory](#), and perhaps the class documentation of [big.matrix](#); [attach.big.matrix](#) and [describe](#). Sister packages **biganalytics**, **bigtabulate**, **synchronicity**, and **bigalgebra** provide advanced functionality.

Examples

```
library(bigmemory)
x <- big.matrix(10, 2, type='integer', init=-5)
options(bigmemory.allow.dimnames=TRUE)
colnames(x) <- c("alpha", "beta")
is.big.matrix(x)
dim(x)
colnames(x)
rownames(x)
x[,]
x[1:8,1] <- 11:18
colnames(x) <- NULL
x[,]

# The following shared memory example is quite silly, as you wouldn't
# likely do this in a single R session. But if zdescription were
# passed to another R session via SNOW, foreach, or even by a
# simple file read/write, then the attach.big.matrix() within the
# second R process would give access to the same object in memory.
# Please see the package vignette for real examples.

z <- big.matrix(3, 3, type='integer', init=3)
z[,]
dim(z)
z[1,1] <- 2
z[,]
zdescription <- describe(z)
zdescription
y <- attach.big.matrix(zdescription)
y[,]
y
z
y[1,1] <- -100
y[,]
z[,]
```

Description

The `big.matrix` class is designed for matrices with elements of type double, integer, short, or char. A `big.matrix` acts much like a traditional R matrix, but helps protect the user from many inadvertent memory-consuming pitfalls of traditional R matrices and data frames. The objects are allocated to shared memory, and if file-backing is used they may exceed virtual memory in size. Sadly, 32-bit operating system constraints – largely Windows and some MacOS versions – will be a limiting factor with file-backed matrices; 64-bit operating systems are recommended.

Objects from the Class

Unlike many R objects, objects should not be created by calls of the form `new("big.matrix", ...)`. The functions `big.matrix()` and `filebacked.big.matrix()` are intended for the user.

Slots

address: Object of class "externalptr" points to the memory location of the C++ data structure.

Methods

As you would expect:

```
signature(x = "big.matrix", i = "ANY", j = "ANY"): ...
[<- signature(x = "big.matrix", i = "ANY", j = "missing"): ...
[<- signature(x = "big.matrix", i = "missing", j = "ANY"): ...
[<- signature(x = "big.matrix", i = "missing", j = "missing"): ...
[<- signature(x = "big.matrix", i = "matrix", j = "missing"): ...
[ signature(x = "big.matrix", i = "ANY", j = "ANY", drop = "missing"): ...
[ signature(x = "big.matrix", i = "ANY", j = "ANY", drop = "logical"): ...
[ signature(x = "big.matrix", i = "ANY", j = "missing", drop = "missing"): ...
[ signature(x = "big.matrix", i = "ANY", j = "missing", drop = "logical"): ...
[ signature(x = "big.matrix", i = "matrix", j = "missing", drop = "logical"): ...
[ signature(x = "big.matrix", i = "missing", j = "ANY", drop = "missing"): ...
[ signature(x = "big.matrix", i = "missing", j = "ANY", drop = "logical"): ...
[ signature(x = "big.matrix", i = "missing", j = "missing", drop = "missing"): ...
[ signature(x = "big.matrix", i = "missing", j = "missing", drop = "logical"): ...
```

The following are probably more interesting:

describe `signature(x = "big.matrix")`: provide necessary and sufficient information for the sharing or re-attaching of the object.

dim `signature(x = "big.matrix")`: returns the dimension of the `big.matrix`.

length `signature(x = "big.matrix")`: returns the product of the dimensions of the `big.matrix`.

dimnames<- `signature(x = "big.matrix", value = "list")`: set the row and column names, prohibited by default (see [bigmemory](#) to override).

dimnames `signature(x = "big.matrix")`: get the row and column names.

head signature(x = "big.matrix"): get the first 6 (or n) rows.

as.matrix signature(x = "big.matrix"): coerce a big.matrix to a matrix.

is.big.matrix signature(x = "big.matrix"): return TRUE if it's a big.matrix.

is.filebacked signature(x = "big.matrix"): return TRUE if there is a file-backing.

is.separated signature(x = "big.matrix") : return TRUE if the big.matrix is organized as a separated column vectors.

is.sub.big.matrix signature(x = "big.matrix"): return TRUE if this is a sub-matrix of a big.matrix.

ncol signature(x = "big.matrix"): returns the number of columns.

nrow signature(x = "big.matrix"): returns the number of rows.

print signature(x = "big.matrix"): a traditional print() is intentionally disabled, and returns head(x) unless options()\$bm.print.warning==FALSE; in this case, print(x[,]) is the result, which could be very big!

sub.big.matrix signature(x = "big.matrix"): for contiguous submatrices.

tail signature(x = "big.matrix"): returns the last 6 (or n) rows.

typeof signature(x = "big.matrix"): return the type of the atomic elements of the big.matrix.

write.big.matrix signature(bigMat = "big.matrix", fileName = "character"): produce an ASCII file from the big.matrix.

apply signature(x = "big.matrix"): apply() where MARGIN may only be 1 or 2, but otherwise conforming to what you would expect from apply().

Author(s)

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See Also

[big.matrix](#)

Examples

```
showClass("big.matrix")
```

deepcopy

Produces a physical copy of a "big.matrix"

Description

This is needed to make a duplicate of a big.matrix, with the new copy optionally filebacked.

Usage

```
deepcopy(x, cols = NULL, rows = NULL, y = NULL, type = NULL,
  separated = NULL, backingfile = NULL, backingpath = NULL,
  descriptorfile = NULL, binarydescriptor = FALSE, shared = TRUE)
```

Arguments

<code>x</code>	a <code>big.matrix</code> .
<code>cols</code>	possible subset of columns for the deepcopy; could be numeric, named, or logical.
<code>rows</code>	possible subset of rows for the deepcopy; could be numeric, named, or logical.
<code>y</code>	optional destination object (<code>matrix</code> or <code>big.matrix</code>); if not specified, a <code>big.matrix</code> will be created.
<code>type</code>	preferably specified, "integer" for example.
<code>separated</code>	use separated column organization of the data instead of column-major organization; use with caution if the number of columns is large.
<code>backingfile</code>	the root name for the file(s) for the cache of <code>x</code> .
<code>backingpath</code>	the path to the directory containing the file-backing cache.
<code>descriptorfile</code>	we recommend specifying this for file-backing.
<code>binarydescriptor</code>	the flag to specify if the binary RDS format should be used for the backingfile description, for subsequent use with <code>attach.big.matrix</code> ; if NULL or FALSE, the <code>dput()</code> file format is used.
<code>shared</code>	TRUE by default, and always TRUE if the <code>big.matrix</code> is file-backed. For a non-filebacked <code>big.matrix</code> , <code>shared=FALSE</code> uses non-shared memory, which can be more stable for large (say, >50% of RAM) objects. Shared memory allocation can sometimes fail in such cases due to exhausted shared-memory resources in the system.

Details

This is needed to make a duplicate of a `big.matrix`, because traditional syntax would only copy the object (the pointer to the `big.matrix` rather than the `big.matrix` itself). It can also make a copy of only a subset of columns.

Value

a `big.matrix`.

See Also

`big.matrix`

Examples

```
x <- as.big.matrix(matrix(1:30, 10, 3))
y <- deepcopy(x, -1)    # Don't include the first column.
x
y
head(x)
head(y)
```

describe, big.matrix-method

The basic “big.matrix” operations for sharing and re-attaching.

Description

The describe function returns the information needed by attach.big.matrix to reference a shared or file-backed big.matrix object. The attach.big.matrix and attach.resource functions create a new big.matrix object based on the descriptor information referencing previously allocated shared-memory or file-backed matrices.

Usage

```
## S4 method for signature 'big.matrix'
describe(x)

attach.big.matrix(obj, ...)
```

Arguments

x	a big.matrix object
obj	an object as returned by describe() or, optionally, the filename of the descriptor for a filebacked matrix, assumed to be in the directory specified by the path (if one is provided)
...	possibly path which gives the path where the descriptor and/or filebacking can be found

Details

The describe function returns a list of the information needed to attach to a big.matrix object. A descriptor file is automatically created when a new filebacked big.matrix is created.

Value

describe returns a list of the information needed to attach to a big.matrix object.

attach.big.matrix return a new instance of type big.matrix corresponding to a shared-memory or file-backed big.matrix.

Author(s)

Michael J. Kane and John W. Emerson <<bigmemoryauthors@gmail.com>>

See Also

[bigmemory](#), [big.matrix](#), or the class documentation [big.matrix](#).

Examples

```
# The example is quite silly, as you wouldn't likely do this in a
# single R session. But if zdescription were passed to another R session
# via SNOW, foreach, or even by a simple file read/write,
# then the attach of the second R process would give access to the
# same object in memory. Please see the package vignette for real examples.

z <- big.matrix(3, 3, type='integer', init=3)
z[,]
dim(z)
z[1,1] <- 2
z[,]
zdescription <- describe(z)
zdescription
y <- attach.big.matrix(zdescription)
y[,]
y
z
zz <- attach.resource(zdescription)
zz[1,1] <- -100
y[,]
z[,]
```

descriptor-class	<i>Class "big.matrix.descriptor"</i>
------------------	--------------------------------------

Description

An object of this class contains necessary and sufficient information to “attach” a shared or file-backed [big.matrix](#).

Usage

```
## S4 method for signature 'big.matrix.descriptor'
sub.big.matrix(x, firstRow = 1,
  lastRow = NULL, firstCol = 1, lastCol = NULL, backingpath = NULL)

## S4 method for signature 'character'
attach.resource(obj, ...)

## S4 method for signature 'big.matrix.descriptor'
attach.resource(obj, ...)
```

Arguments

x	A descriptor object
firstRow	the first row of the submatrix
lastRow	the last row of the submatrix if not NULL

<code>firstCol</code>	the first column of the submatrix
<code>lastCol</code>	of the submatrix if not NULL
<code>backingpath</code>	required path to the filebacked object, if applicable
<code>obj</code>	The filename of the descriptor for a filebacked matrix, assumed to be in the directory specified
<code>...</code>	possibly path which gives the path where the descriptor and/or filebacking can be found.

Objects from the Class

Objects should not be created by calls of the form `new("big.matrix.descriptor", ...)`, but should use the [describe](#) function.

Slots

description: Object of class "list"; details omitted.

Extends

Class ["descriptor"](#), directly.

Methods

attach.resource signature(`obj` = "big.matrix.descriptor"): ...

sub.big.matrix signature(`x` = "big.matrix.descriptor"): ...

Note

We provide `attach.resource` for convenience, but expect most users will prefer [attach.big.matrix](#).

Author(s)

John W. Emerson and Michael J. Kane

References

Other types of descriptors are defined in package **synchronicity**.

See Also

See also [attach.big.matrix](#).

Examples

```
showClass("big.matrix.descriptor")
```

dim, big.matrix-method *Dimensions of a big.matrix object*

Description

Retrieve the dimensions of a big.matrix object

Usage

```
## S4 method for signature 'big.matrix'
dim(x)
```

Arguments

x A big.matrix object

dimnames, big.matrix-method
 Dimnames of a big.matrix Object

Description

Retrieve or set the dimnames of an object

Usage

```
## S4 method for signature 'big.matrix'
dimnames(x)

## S4 replacement method for signature 'big.matrix,list'
dimnames(x) <- value
```

Arguments

x A big.matrix object
value A possible value for dimnames(x)

Extract, big.matrix	<i>Extract or Replace</i>
---------------------	---------------------------

Description

Extract or replace big.matrix elements

Usage

```
## S4 method for signature 'big.matrix,ANY,ANY,missing'
x[i, j, drop]

## S4 method for signature 'big.matrix,ANY,ANY,logical'
x[i, j, drop]

## S4 method for signature 'big.matrix,missing,ANY,missing'
x[i, j, drop]

## S4 method for signature 'big.matrix,missing,ANY,logical'
x[i, j, drop]

## S4 method for signature 'big.matrix,ANY,missing,missing'
x[i, j, drop]

## S4 method for signature 'big.matrix,ANY,missing,logical'
x[i, j, drop]

## S4 method for signature 'big.matrix,missing,missing,missing'
x[i, j, drop]

## S4 method for signature 'big.matrix,missing,missing,logical'
x[i, j, drop]

## S4 method for signature 'big.matrix,matrix,missing,missing'
x[i, j, drop]

## S4 replacement method for signature 'big.matrix,ANY,ANY'
x[i, j] <- value

## S4 replacement method for signature 'big.matrix,missing,ANY'
x[i, j] <- value

## S4 replacement method for signature 'big.matrix,ANY,missing'
x[i, j] <- value

## S4 replacement method for signature 'big.matrix,missing,missing'
x[i, j] <- value
```

```
## S4 replacement method for signature 'big.matrix,matrix,missing'
x[i, j] <- value
```

Arguments

x	A <code>big.matrix</code> object
i	Indices specifying the rows
j	Indices specifying the columns
drop	Logical indication if reduce to minimum dimensions
value	typically an array-like R object of similar class

flush	<i>Updating a <code>big.matrix</code> filebacking.</i>
-------	--

Description

For a file-backed `big.matrix` object, `flush()` forces any modified information to be written to the file-backing.

Usage

```
flush(con)

## S4 method for signature 'big.matrix'
flush(con)
```

Arguments

con	filebacked <code>big.matrix</code> .
-----	--------------------------------------

Details

This function flushes any modified data (in RAM) of a file-backed `big.matrix` to disk. This may be useful for improving performance in cases where allowing the operating system to decide on flushing creates a bottleneck (likely near the threshold of available RAM).

Value

TRUE or FALSE (invisible), indicating whether or not the flush was successful.

Author(s)

John W. Emerson and Michael J. Kane

Examples

```
temp_dir = tempdir()
if (!dir.exists(temp_dir)) dir.create(temp_dir)
x <- big.matrix(nrow=3, ncol=3, backingfile='flushtest.bin',
               descriptorfile='flushtest.desc', backingpath=temp_dir,
               type='integer')

x[1,1] <- 0
flush(x)
```

GetMatrixSize	<i>big.matrix</i> size
---------------	------------------------

Description

Returns the size of the created matrix in bytes

Usage

```
GetMatrixSize(bigMat)
```

Arguments

bigMat	a <i>big.matrix</i> object
--------	----------------------------

head, big.matrix-method	<i>Return First or Last Part of a big.matrix Object</i>
-------------------------	---

Description

Returns the first or last parts of a *big.matrix* object.

Usage

```
## S4 method for signature 'big.matrix'
head(x, n = 6)

## S4 method for signature 'big.matrix'
tail(x, n = 6)
```

Arguments

x	A <i>big.matrix</i> object
n	A single integer for the number of rows to return

is.float	<i>Check if Float</i>
----------	-----------------------

Description

Check to see if the elements of a big.matrix object are floats.

Usage

is.float(x)

Arguments

x An object to be evaluated if float

is.float,numeric-method	<i>Is Float?</i>
-------------------------	------------------

Description

Check if R numeric value has float flag

Usage

```
## S4 method for signature 'numeric'  
is.float(x)
```

Arguments

x A numeric value

is.sub.big.matrix	<i>Submatrix support</i>
-------------------	--------------------------

Description

This doesn't create a copy, it just provides a new version of the class which provides behavior for a contiguous submatrix of the big.matrix. Non-contiguous submatrices are not supported.

Usage

```
is.sub.big.matrix(x)

## S4 method for signature 'big.matrix'
is.sub.big.matrix(x)

sub.big.matrix(x, firstRow = 1, lastRow = NULL, firstCol = 1,
  lastCol = NULL, backingpath = NULL)

## S4 method for signature 'big.matrix'
sub.big.matrix(x, firstRow = 1, lastRow = NULL,
  firstCol = 1, lastCol = NULL, backingpath = NULL)
```

Arguments

x	either a big.matrix or a descriptor.
firstRow	the first row of the submatrix.
lastRow	the last row of the submatrix if not NULL.
firstCol	the first column of the submatrix.
lastCol	the last column of the submatrix if not NULL.
backingpath	required path to the filebacked object, if applicable.

Details

The `sub.big.matrix` function allows a user to create a `big.matrix` object that references a contiguous set of columns and rows of another `big.matrix` object.

The `is.sub.big.matrix` function returns TRUE if the specified argument is a `sub.big.matrix` object and return FALSE otherwise.

Value

A [big.matrix](#) which is actually a submatrix of a larger `big.matrix`. It is not a physical copy. Only contiguous blocks may form a submatrix.

Author(s)

John W. Emerson and Michael J. Kane

See Also

[big.matrix](#)

Examples

```
x <- big.matrix(10, 5, init=0, type="double")
x[,] <- 1:50
y <- sub.big.matrix(x, 2, 9, 2, 3)
y[,]
```

```

y[1,1] <- -99
x[, ]
rm(x)

```

length, big.matrix-method

Length of a big.matrix object

Description

Get the length of a big.matrix object

Usage

```

## S4 method for signature 'big.matrix'
length(x)

```

Arguments

x A big.matrix object

morder

Ordering and Permuting functions for “big.matrix” and “matrix” objects

Description

The morder function returns a permutation of row indices which can be used to rearrange an object according to the values in the specified columns (a multi-column ordering). The mpermute function actually reorders the rows of a big.matrix or matrix based on an order vector or a desired ordering on a set of columns.

Usage

```
morder(x, cols, na.last = TRUE, decreasing = FALSE)
```

```
morderCols(x, rows, na.last = TRUE, decreasing = FALSE)
```

```
mpermute(x, order = NULL, cols = NULL, allow.duplicates = FALSE, ...)
```

```
mpermuteCols(x, order = NULL, rows = NULL, allow.duplicates = FALSE, ...)
```

Arguments

<code>x</code>	A <code>big.matrix</code> or <code>matrix</code> object with numeric values.
<code>cols</code>	The columns of <code>x</code> to get the ordering for or reorder on
<code>na.last</code>	for controlling the treatment of NAs. If <code>TRUE</code> , missing values in the data are put last; if <code>FALSE</code> , they are put first; if <code>NA</code> , they are removed.
<code>decreasing</code>	logical. Should the sort order be increasing or decreasing?
<code>rows</code>	The rows of <code>x</code> to get the ordering for or reorder on
<code>order</code>	A vector specifying the reordering of rows, i.e. the result of a call to <code>order</code> or <code>morder</code> .
<code>allow.duplicates</code>	ff <code>TRUE</code> , allows a row to be duplicated in the resulting <code>big.matrix</code> or <code>matrix</code> (i.e. in this case, <code>order</code> would not need to be a permutation of <code>1:nrow(x)</code>).
<code>...</code>	optional parameters to pass to <code>morder</code> when <code>cols</code> is specified instead of just using <code>order</code> .

Details

The `morder` function behaves similar to `order`, returning a permutation of `1:nrow(x)` which rearranges objects according to the values in the specified columns. However, `morder` takes a `big.matrix` or an `R` matrix (with numeric type) and a set of columns (`cols`) with which to determine the ordering; `morder` does not incur the same memory overhead required by `order`, and runs more quickly.

The `mpermute` function changes the row ordering of a `big.matrix` or `matrix` based on a vector `order` or an ordering based on a set of columns specified by `cols`. It should be noted that this function has side-effects, that is `x` is changed when this function is called.

Value

`morder` returns an ordering vector. `mpermute` returns nothing but does change the contents of `x`. This type of a side-effect is generally frowned upon in `R`, but we “break” the rules here to avoid memory overhead and improve performance.

Author(s)

Michael J. Kane <<bigmemoryauthors@gmail.com>>

See Also

[order](#)

Examples

```
m = matrix(as.double(as.matrix(iris)), nrow=nrow(iris))
morder(m, 1)
order(m[,1])

m[order(m[,1]), 2]
mpermute(m, cols=1)
m[,2]
```

mwhich

Expanded “which”-like functionality.

Description

Implements [which](#)-like functionality for a [big.matrix](#), with additional options for efficient comparisons (executed in C++); also works for regular numeric matrices without the memory overhead.

Usage

```
mwhich(x, cols, vals, comps, op = "AND")
```

Arguments

x	a big.matrix (or a numeric matrix; see below).
cols	a vector of column indices or names.
vals	a list (one component for each of cols) of vectors of length 1 or 2; length 1 is used to test equality (or inequality), while vectors of length 2 are used for checking values in the range ($-\text{Inf}$ and Inf are allowed). If a scalar or vector of length 2 is provided instead of a list, it will be replicated <code>length(cols)</code> times.
comps	a list of operators (one component for each of cols), including 'eq', 'neq', 'le', 'lt', 'ge' and 'gt'. If a single operator, it will be replicated <code>length(cols)</code> times.
op	the comparison operator for combining the results of the individual tests, either 'AND' or 'OR'.

Details

To improve performance and avoid the creation of massive temporary vectors in R when doing comparisons, `mwhich()` efficiently executes column-by-column comparisons of values to the specified values or ranges, and then returns the row indices satisfying the comparison specified by the `op` operator. More advanced comparisons are then possible (and memory-efficient) in R by doing set operations ([union](#) and [intersect](#), for example) on the results of multiple `mwhich()` calls.

Note that NA is a valid argument in conjunction with 'eq' or 'neq', replacing traditional `is.na()` calls. And both $-\text{Inf}$ and Inf can be used for one-sided inequalities.

If `mwhich()` is used with a regular numeric R matrix, we access the data directly and thus incur no memory overhead. Interested developers might want to look at our code for this case, which uses a handy pointer trick (accessor) in C++.

Value

a vector of row indices satisfying the criteria.

Author(s)

John W. Emerson <<bigmemoryauthors@gmail.com>>

See Also[big.matrix](#), [which](#)**Examples**

```

x <- as.big.matrix(matrix(1:30, 10, 3))
options(bigmemory.allow.dimnames=TRUE)
colnames(x) <- c("A", "B", "C")
x[,]
x[mwhich(x, 1:2, list(c(2,3), c(11,17)),
          list(c('ge','le'), c('gt', 'lt')), 'OR'),]

x[mwhich(x, c("A","B"), list(c(2,3), c(11,17)),
          list(c('ge','le'), c('gt', 'lt')), 'AND'),]

# These should produce the same answer with a regular matrix:
y <- matrix(1:30, 10, 3)
y[mwhich(y, 1:2, list(c(2,3), c(11,17)),
          list(c('ge','le'), c('gt', 'lt')), 'OR'),]

y[mwhich(y, -3, list(c(2,3), c(11,17)),
          list(c('ge','le'), c('gt', 'lt')), 'AND'),]

x[1,1] <- NA
mwhich(x, 1:2, NA, 'eq', 'OR')
mwhich(x, 1:2, NA, 'neq', 'AND')

# Column 1 equal to 4 and/or column 2 less than or equal to 16:
mwhich(x, 1:2, list(4, 16), list('eq', 'le'), 'OR')
mwhich(x, 1:2, list(4, 16), list('eq', 'le'), 'AND')

# Column 2 less than or equal to 15:
mwhich(x, 2, 15, 'le')

# No NAs in either column, and column 2 strictly less than 15:
mwhich(x, c(1:2,2), list(NA, NA, 15), list('neq', 'neq', 'lt'), 'AND')

x <- big.matrix(4, 2, init=1, type="double")
x[1,1] <- Inf
mwhich(x, 1, Inf, 'eq')
mwhich(x, 1, 1, 'gt')
mwhich(x, 1, 1, 'le')

```

Description

Implements [which](#)-like functionality for a [big.matrix](#), with additional options for efficient comparisons (executed in C++); also works for regular numeric matrices without the memory overhead.

test

Methods

```
signature(x = "big.matrix=", cols = "ANY", vals = "ANY", " " comps = "ANY", op = "character")
...
signature(x = "big.matrix", cols = "ANY", vals = "ANY", " " comps = "ANY", op = "missing")
...
signature(x = "matrix", cols = "ANY", vals = "ANY", " " comps = "ANY", op = "character")
...
signature(x = "matrix", cols = "ANY", vals = "ANY", " " comps = "ANY", op = "missing")
...
```

See Also

[big.matrix](#), [which](#), [mwhich](#)

ncol, big.matrix-method

The Number of Rows/Columns of a big.matrix

Description

nrow and ncol return the number of rows or columns present in a big.matrix object.

Usage

```
## S4 method for signature 'big.matrix'
ncol(x)

## S4 method for signature 'big.matrix'
nrow(x)
```

Arguments

x A big.matrix object

Value

An integer of length 1

`print, big.matrix-method`*Print Values*

Description

print will print out the elements within a big.matrix object.

Usage

```
## S4 method for signature 'big.matrix'
print(x)
```

Arguments

x A big.matrix object

Note

By default, this will only return the head of a big.matrix to prevent console overflow. If you turn off the bigmemory.print.warning option then it will convert to a base R matrix and print all elements.

`typeof, big.matrix-method`*The Type of a big.matrix Object*

Description

typeof returns the storage type of a big.matrix object

Usage

```
## S4 method for signature 'big.matrix'
typeof(x)
```

Arguments

x A big.matrix object

write.big.matrix	<i>File interface for a “big.matrix”</i>
------------------	--

Description

Create a `big.matrix` by reading from a suitably-formatted ASCII file, or write the contents of a `big.matrix` to a file.

@importFrom stats na.omit

Usage

```
write.big.matrix(x, filename, row.names = FALSE, col.names = FALSE,
  sep = ",")

## S4 method for signature 'big.matrix,character'
write.big.matrix(x, filename,
  row.names = FALSE, col.names = FALSE, sep = ",")

read.big.matrix(filename, sep = ",", header = FALSE, col.names = NULL,
  row.names = NULL, has.row.names = FALSE, ignore.row.names = FALSE,
  type = NA, skip = 0, separated = FALSE, backingfile = NULL,
  backingpath = NULL, descriptorfile = NULL, binarydescriptor = FALSE,
  extraCols = NULL, shared = TRUE)

## S4 method for signature 'character'
read.big.matrix(filename, sep = ",", header = FALSE,
  col.names = NULL, row.names = NULL, has.row.names = FALSE,
  ignore.row.names = FALSE, type = NA, skip = 0, separated = FALSE,
  backingfile = NULL, backingpath = NULL, descriptorfile = NULL,
  binarydescriptor = FALSE, extraCols = NULL, shared = TRUE)
```

Arguments

x	a <code>big.matrix</code> .
filename	the name of an input/output file.
row.names	a vector of names, use them even if row names appear to exist in the file.
col.names	a vector of names, use them even if column names exist in the file.
sep	a field delimiter.
header	if TRUE, the first line (after a possible skip) should contain column names.
has.row.names	if TRUE, then the first column contains row names.
ignore.row.names	if TRUE when has.row.names==TRUE, the row names will be ignored.
type	preferably specified, "integer" for example.
skip	number of lines to skip at the head of the file.

separated	use separated column organization of the data instead of column-major organization.
backingfile	the root name for the file(s) for the cache of x.
backingpath	the path to the directory containing the file backing cache.
descriptorfile	the file to be used for the description of the filebacked matrix.
binarydescriptor	the flag to specify if the binary RDS format should be used for the backingfile description, for subsequent use with attach.big.matrix ; if NULL or FALSE, the dput() file format is used.
extraCols	the optional number of extra columns to be appended to the matrix for future use.
shared	if TRUE, the resulting big.matrix can be shared across processes.

Details

Files must contain only one atomic type (all integer, for example). You, the user, should know whether your file has row and/or column names, and various combinations of options should be helpful in obtaining the desired behavior.

When reading from a file, if type is not specified we try to make a reasonable guess for you without making any guarantees at this point. Unless you have really large integer values, we recommend you consider "short". If you have something that is essentially categorical, you might even be able use "char", with huge memory savings for large data sets.

Any non-numeric entry will be ignored and replaced with NA, so reading something that traditionally would be a data.frame won't cause an error. A warning is issued.

Wishlist: we'd like to provide an option to ignore specified columns while doing reads. Or perhaps to specify columns targeted for factor or character conversion to numeric values. Would you use such features? Email us and let us know!

Value

a [big.matrix](#) object is returned by read.big.matrix, while write.big.matrix creates an output file (a path could be part of filename).

Author(s)

John W. Emerson and Michael J. Kane <<bigmemoryauthors@gmail.com>>

See Also

[big.matrix](#)

Examples

```
# Without specifying the type, this big.matrix x will hold integers.

x <- as.big.matrix(matrix(1:10, 5, 2))
x[2,2] <- NA
```

```

x[,]
temp_dir = tempdir()
if (!dir.exists(temp_dir)) dir.create(temp_dir)
write.big.matrix(x, file.path(temp_dir, "foo.txt"))

# Just for fun, I'll read it back in as character (1-byte integers):
y <- read.big.matrix(file.path(temp_dir, "foo.txt"), type="char")
y[,]

# Other examples:
w <- as.big.matrix(matrix(1:10, 5, 2), type='double')
w[1,2] <- NA
w[2,2] <- -Inf
w[3,2] <- Inf
w[4,2] <- NaN
w[,]
write.big.matrix(w, file.path(temp_dir, "bar.txt"))
w <- read.big.matrix(file.path(temp_dir, "bar.txt"), type="double")
w[,]
w <- read.big.matrix(file.path(temp_dir, "bar.txt"), type="short")
w[,]

# Another example using row names (which we don't like).
x <- as.big.matrix(as.matrix(iris), type='double')
rownames(x) <- as.character(1:nrow(x))
head(x)
write.big.matrix(x, file.path(temp_dir, 'IrisData.txt'), col.names=TRUE,
                  row.names=TRUE)
y <- read.big.matrix(file.path(temp_dir, "IrisData.txt"), header=TRUE,
                    has.row.names=TRUE)
head(y)

# The following would fail with a dimension mismatch:
if (FALSE) y <- read.big.matrix(file.path(temp_dir, "IrisData.txt"),
                                header=TRUE)

```

Index

*Topic **classes**

- big.matrix, 6
- big.matrix-class, 9
- describe, big.matrix-method, 13
- descriptor-class, 14

*Topic **methods**

- as.big.matrix-methods, 5
- big.matrix, 6
- deepcopy, 11
- describe, big.matrix-method, 13
- flush, 18
- is.sub.big.matrix, 20
- mwhich, 24
- mwhich-methods, 25
- write.big.matrix, 28

*Topic **package**

- bigmemory-package, 2

- [, big.matrix, ANY, ANY, logical-method
(Extract, big.matrix), 17
- [, big.matrix, ANY, ANY, missing-method
(Extract, big.matrix), 17
- [, big.matrix, ANY, missing, logical-method
(Extract, big.matrix), 17
- [, big.matrix, ANY, missing, missing-method
(Extract, big.matrix), 17
- [, big.matrix, matrix, missing, missing-method
(Extract, big.matrix), 17
- [, big.matrix, missing, ANY, logical-method
(Extract, big.matrix), 17
- [, big.matrix, missing, ANY, missing-method
(Extract, big.matrix), 17
- [, big.matrix, missing, missing, logical-method
(Extract, big.matrix), 17
- [, big.matrix, missing, missing, missing-method
(Extract, big.matrix), 17
- [<-, big.matrix, ANY, ANY-method
(Extract, big.matrix), 17
- [<-, big.matrix, ANY, missing-method
(Extract, big.matrix), 17

- [<-, big.matrix, matrix, missing-method
(Extract, big.matrix), 17
- [<-, big.matrix, missing, ANY-method
(Extract, big.matrix), 17
- [<-, big.matrix, missing, missing-method
(Extract, big.matrix), 17

- as.big.matrix (big.matrix), 6
- as.big.matrix, data.frame-method
(as.big.matrix-methods), 5
- as.big.matrix, matrix-method
(as.big.matrix-methods), 5
- as.big.matrix, vector-method
(as.big.matrix-methods), 5
- as.big.matrix-methods, 5
- as.matrix, big.matrix-method, 5
- attach.big.matrix, 7–9, 12, 15, 29
- attach.big.matrix
(describe, big.matrix-method),
13
- attach.resource
(describe, big.matrix-method),
13
- attach.resource, big.matrix.descriptor-method
(descriptor-class), 14
- attach.resource, character-method
(descriptor-class), 14
- big.matrix, 2–5, 6, 9, 11–14, 18, 21, 24–26,
28, 29
- big.matrix-class, 9
- big.matrix.descriptor-class
(descriptor-class), 14
- bigmemory, 9, 10, 13
- bigmemory (bigmemory-package), 2
- bigmemory-package, 2
- data.frame, 5
- deepcopy, 11
- describe, 9, 15

- describe (describe,big.matrix-method),
13
- describe,big.matrix-method, 13
- descriptor, 15
- descriptor-class, 14
- dim,big.matrix-method, 16
- dimnames,big.matrix-method, 16
- dimnames<-,big.matrix,list-method
(dimnames,big.matrix-method),
16
- Extract,big.matrix, 17
- file.name (big.matrix), 6
- file.name,big.matrix-method
(big.matrix), 6
- filebacked.big.matrix (big.matrix), 6
- flush, 18
- flush,big.matrix-method (flush), 18
- GetMatrixSize, 19
- head,big.matrix-method, 19
- intersect, 24
- is.big.matrix (big.matrix), 6
- is.big.matrix,ANY-method (big.matrix), 6
- is.big.matrix,big.matrix-method
(big.matrix), 6
- is.filebacked (big.matrix), 6
- is.filebacked,big.matrix-method
(big.matrix), 6
- is.float, 20
- is.float,numeric-method, 20
- is.nil (big.matrix), 6
- is.readonly (big.matrix), 6
- is.readonly,big.matrix-method
(big.matrix), 6
- is.separated (big.matrix), 6
- is.separated,big.matrix-method
(big.matrix), 6
- is.shared (big.matrix), 6
- is.shared,big.matrix-method
(big.matrix), 6
- is.sub.big.matrix, 20
- is.sub.big.matrix,big.matrix-method
(is.sub.big.matrix), 20
- kmeans, 4
- length,big.matrix-method, 22
- lm, 4
- matrix, 2, 6
- morder, 4, 22
- morderCols (morder), 22
- mpermute, 4
- mpermute (morder), 22
- mpermuteCols (morder), 22
- mwhich, 4, 24, 26
- mwhich,big.matrix,ANY,ANY,ANY,character-method
(mwhich-methods), 25
- mwhich,big.matrix,ANY,ANY,ANY,missing-method
(mwhich-methods), 25
- mwhich,matrix,ANY,ANY,ANY,character-method
(mwhich-methods), 25
- mwhich,matrix,ANY,ANY,ANY,missing-method
(mwhich-methods), 25
- mwhich-methods, 25
- ncol,big.matrix-method, 26
- nrow,big.matrix-method
(ncol,big.matrix-method), 26
- order, 23
- print,big.matrix-method, 27
- read.big.matrix, 4
- read.big.matrix (write.big.matrix), 28
- read.big.matrix,character-method
(write.big.matrix), 28
- shared.name (big.matrix), 6
- shared.name,big.matrix-method
(big.matrix), 6
- split, 4
- sub.big.matrix (is.sub.big.matrix), 20
- sub.big.matrix,big.matrix-method
(is.sub.big.matrix), 20
- sub.big.matrix,big.matrix.descriptor-method
(descriptor-class), 14
- tail,big.matrix-method
(head,big.matrix-method), 19
- typeof,big.matrix-method, 27
- union, 24
- which, 24–26

`write.big.matrix`, [28](#)
`write.big.matrix`, `big.matrix`, character-method
 (`write.big.matrix`), [28](#)