Package ‘bigmemory’

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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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- bigmemory-package ................................................. 2
- as.big.matrix-method ........................................... 5
- as.matrix,big.matrix-method ................................. 5
- big.matrix ......................................................... 6
- big.matrix-class ................................................. 10
- deepcopy ........................................................ 12
- describe,big.matrix-method ................................. 13
- descriptor-class ................................................ 14
- dim,big.matrix-method ........................................ 16
- dimnames,big.matrix-method ................................. 16
- Extract,big.matrix ............................................. 17
- flush .............................................................. 19
- GetMatrixSize ................................................... 20
- head,big.matrix-method ........................................ 20
- is.float .......................................................... 21
- is.float,numeric-method ....................................... 21
- is.sub.big.matrix .............................................. 21
- length,big.matrix-method ...................................... 23
- morder ............................................................ 23
- mwhich ............................................................ 25
- mwhich-methods .................................................. 26
- ncol,big.matrix-method ........................................ 27
- print,big.matrix-method ........................................ 28
- typeof,big.matrix-method ...................................... 28
- write.big.matrix ................................................. 29

**Index** 32

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**bigmemory-package**  
*Manage massive matrices with shared memory and memory-mapped files.*

**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 an S4 class whose interface is similar to that of a *matrix*. Use of these packages in parallel environments can provide substantial speed and memory efficiencies. **bigmemory** 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 ’s rich statistical programming environment. The package bigmemory and associated 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.

Memory considerations

For obvious reasons memory that the big.matrix uses is managed outside the R memory pool available to the garbage collector and the memory occupied by the big.matrix is not visible to the R. This has subtle implications:

- Memory usage is not visible via general R functions (e.g. the gc() function)
- Garbage collector is mislead by the very small memory footprint of the big.matrix object (which acts merely as a pointer to the external memory structure), which can result in much less eagerness to garbage-collect the unused big.memory objects. After removing a last reference to a big big.matrix, user should manually run gc() to reclaim the memory.
• Attaching the description of already finalized big.matrix and accessing this object will result in undefined behavior, which simply means it will crash the current R session with no hope of saving the data in it. To prevent R from de-allocating (finalizing) the matrices, user should keep at least one big.memory object somewhere in R memory in at least one R session on the current machine.

• Abruptly closed R (using e.g. task manager) will not have a chance to finalize the big.matrix objects, which will result in a memory leak, as the big.matrices will remain in the memory (perhaps under obfuscated names) with no easy way to reconnect R to them.

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" be default (a change in default behavior as of 4.1.1) but may be changed by the user.

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)

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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)
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()$bigmemory.default.type, init = NULL, 
dimnames = NULL, separated = FALSE, backingfile = NULL, 
backingpath = NULL, descriptorfile = NULL, binarydescriptor = FALSE, 
shared = options()$bigmemory.default.shared)

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 = options()$bigmemory.default.shared)

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'

```r
define(name = x)
define(name = x)
define(name = x)
define(name = x)
define(name = x)
define(name = x)
define(name = x)
define(name = x)
define(name = x)
define(name = x)
define(name = x)
define(name = x)
define(name = x)
```

### Arguments

- `nrow` number of rows.
- `ncol` number of columns.
- `type` the type of the atomic element (options()$bigmemory.default.type 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 of FALSE, the `dput()` file format is used.
- `shared` TRUE by default, and always TRUE if the big.matrix is file-backed. For a non-filebacked big.matrix, shared=FALSE uses non-shared memory, which can be more stable for large (say, >50 fails in such cases due to exhausted shared-memory resources in the system.
x a matrix, vector, or data.frame for \texttt{as.big.matrix}; if a vector, a one-column
\texttt{big.matrix} is created by \texttt{as.big.matrix}; if a data.frame, see details. For the
\texttt{is.*} functions, \texttt{x} is likely a \texttt{big.matrix}.

\texttt{address} an external\texttt{ptr}, so \texttt{is.nil(x@address)} might be a sensible thing to want to
check, but it's pretty obscure.

**Details**

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

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

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

If \texttt{x} has a huge number of rows and/or columns, then the use of \texttt{rownames} and/or \texttt{colnames}
will be extremely memory-intensive and should be avoided. If \texttt{x} has a huge number of columns and
\texttt{separated=TRUE} is used (this isn’t typically recommended), the user might want to store the trans-
pose as there is overhead of a pointer for each column in the matrix. If \texttt{separated} is \texttt{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 combina-
tions. If \texttt{separated} is \texttt{FALSE}, the matrix is stored in traditional column-major format. The function
\texttt{is.separated()} returns the separation type of the \texttt{big.matrix}.

When a \texttt{big.matrix}, \texttt{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 \texttt{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 \texttt{R} behavior.

A file-backed \texttt{big.matrix} may exceed available \texttt{RAM} in size by using a file cache (or possibly
multiple file caches, if \texttt{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 \texttt{attach.big.matrix}).

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

It should also be noted that a user can create an "anonymous" file-backed \texttt{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>>

References


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
**big.matrix-class**

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:

```r
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"): ...
```
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(rbmi.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**

```r
depthcopy(x, cols = NULL, rows = NULL, y = NULL, type = NULL, 
    separated = NULL, backingfile = NULL, backingpath = NULL, 
    descriptorfile = NULL, binarydescriptor = FALSE, 
    shared = options()$bigmemory.default.shared)
```

**Arguments**

- **x**: a big.matrix.
- **cols**: possible subset of columns for the deepcopy; could be numeric, named, or logical.
- **rows**: possible subset of rows for the deepcopy; could be numeric, named, or logical.
- **y**: optional destination object (matrix or big.matrix); if not specified, a big.matrix will be created.
- **type**: preferably specified, “integer” for example.
- **separated**: use separated column organization of the data instead of column-major organization; use with caution if the number of columns is large.
- **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**: we recommend specifying this for file-backing.
- **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.
- **shared**: TRUE by default, and always TRUE if the big.matrix is file-backed. For a non-filebacked big.matrix, shared=FALSE 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

```r
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)
```

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

```r
## 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.
Descriptor class

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] <- 2
z[,,]
zdescription <- describe(z)
zdescription
y <- attach.big.matrix(zdescription)
y[,,]
y
z
zz <- attach.resource(zdescription)
zz[1,1] <- -100
y[,,]
z[,,]
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
- **firstCol**  
  the first column of the submatrix
- **lastCol**  
  of the submatrix if not NULL
- **backingpath**  
  required path to the filebacked object, if applicable
- **obj**  
  The filename of the descriptor for a filebacked matrix, assumed to be in the directory specified
- **...**  
  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  Extract or Replace

Description

Extract or replace big.matrix elements

Usage

```r
## 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]

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Arguments

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

flush  Updating a big.matrix filebacking.

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 big.matrix.

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

```r
temp_dir = tempdir()
if (!dir.exists(temp_dir)) dir.create(temp_dir)
x <- big.matrix(nrow=3, ncol=3, backingfile='flushtest.bin',
    descriptorfile='flushdesc', backingpath=temp_dir,
    type='integer')
x[1,1] <- 0
flush(x)
```

---

GetMatrixSize  

Returns the size of the created matrix in bytes

Usage

```r
GetMatrixSize(bigMat)
```

Arguments

- **bigMat**  
a big.matrix object

---

head, big.matrix-method

Return First or Last Part of a big.matrix Object

Description

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

Usage

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

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

Arguments

- **x**  
  A big.matrix object
- **n**  
  A single integer for the number of rows to return
is.float  
*Check if Float*

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

**Usage**

```r
is.float(x)
```

**Arguments**

- `x`: An object to be evaluated if float

---

is.float.numeric-method  
*Is Float?*

**Description**
Check if R numeric value has float flag

**Usage**

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

**Arguments**

- `x`: A numeric value

---

is.sub.big.matrix  
*Submatrix support*

**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[,]
Length of a big.matrix object

Description
Get the length of a big.matrix object

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

Arguments
- `x`: A big.matrix object

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
```r
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, ...)
```
morder

Arguments

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

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 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

```r
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 \(\text{Inf} \) are allowed). If a scalar or vector of length 2 is provided instead of a list, it will be replicated length(cols) 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 length(cols) 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 \(\text{Inf} \) 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

```r
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')
```

---

`mwhich-methods` Expanded “which”-like functionality.
ncol, big.matrix-method

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

See Also

big.matrix, which, nwhich

--------------------------------------------------------------------------------
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

File interface for a “big.matrix”

Description

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

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 = options()$bigmemory.default.shared)

## 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 = options()$bigmemory.default.shared)

Arguments

x a big.matrix.
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 of 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.

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

```r
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[,] 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, 10
  describe, big.matrix-method, 13
  descriptor-class, 14

*Topic methods
  as.big.matrix-methods, 5
  big.matrix, 6
  deepcopy, 12
  describe, big.matrix-method, 13
  flush, 19
  is.sub.big.matrix, 21
  mwhich, 25
  mwhich-methods, 26
  write.big.matrix, 29

*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,matrix,missing,logical-method (Extract, big.matrix), 17
  [,big.matrix,matrix,missing,missing-method (Extract, big.matrix), 17
  [,big.matrix,matrix,missing,logical-method (Extract, big.matrix), 17
  [,big.matrix,matrix,missing,missing-method (Extract, big.matrix), 17
  [<-big.matrix,logical,character,ANY-method (Extract, big.matrix), 17
  [<-big.matrix,logical,logical,ANY-method (Extract, big.matrix), 17
  [<-big.matrix,logical,missing,matrix-method (Extract, big.matrix), 17
  [<-big.matrix,logical,missing,numeric-method (Extract, big.matrix), 17
  [<-big.matrix,missing,character,ANY-method (Extract, big.matrix), 17
  [<-big.matrix,missing,logical,ANY-method (Extract, big.matrix), 17
  [<-big.matrix,missing,missing,ANY-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, 16, 30
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, 4, 5, 6, 9, 11–14, 19, 22, 25–27, 29, 30
big.matrix-class, 10
big.matrix.descriptor-class (descriptor-class), 14
bigmemory, 9, 11, 14
bigmemory (bigmemory-package), 2
bigmemory-package, 2
data.frame, 5
decopy, 12
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
dir.name (big.matrix), 6
dir.name, big.matrix-method (big.matrix), 6
Extract, big.matrix, 17
file.name (big.matrix), 6
file.name, big.matrix-method (big.matrix), 6
filebacked, big.matrix (big.matrix), 6
flush, 19
flush, big.matrix-method (flush), 19
GetMatrixSize, 20
head, big.matrix-method, 20
intersect, 25
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, 21
is.float, numeric-method, 21
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, 21
is.sub.big.matrix, big.matrix-method (is.sub.big.matrix), 21
kmeans, 4
length, big.matrix-method, 23
lm, 4
matrix, 2, 6
morder, 23
morderCols (morder), 23
mpermute (morder), 23
mpermuteCols (morder), 23
mwhich, 4, 25, 27
mwhich, big.matrix, ANY, ANY, ANY, character-method (mwhich-methods), 26
mwhich, big.matrix, ANY, ANY, ANY, missing-method (mwhich-methods), 26
mwhich, matrix, ANY, ANY, ANY, character-method (mwhich-methods), 26
mwhich, matrix, ANY, ANY, ANY, missing-method (mwhich-methods), 26
mwhich-methods, 26
ncol, big.matrix-method, 27
nrow, big.matrix-method (ncol, big.matrix-method), 27
order, 24

print, big.matrix-method, 28

read.big.matrix, 4
read.big.matrix (write.big.matrix), 29
read.big.matrix, character-method
  (write.big.matrix), 29

shared.name (big.matrix), 6
shared.name, big.matrix-method
  (big.matrix), 6

split, 4
sub.big.matrix (is.sub.big.matrix), 21
sub.big.matrix, big.matrix-method
  (is.sub.big.matrix), 21
sub.big.matrix, big.matrix.descriptor-method
  (descriptor-class), 14

tail, big.matrix-method
  (head, big.matrix-method), 20
typeof, big.matrix-method, 28

union, 25

which, 25–27
write.big.matrix, 29
write.big.matrix, big.matrix, character-method
  (write.big.matrix), 29