

# Package ‘spam’

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**Description** Set of function for sparse matrix algebra. Differences with SparseM/Matrix are: (1) we only support (essentially) one sparse matrix format, (2) based on transparent and simple structure(s), (3) tailored for MCMC calculations within GMRF. (4) S3 and S4 like-“compatible” ... and it is fast.

**LazyLoad** Yes

**LazyData** Yes

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---

. SPAM .

*SPArse Matrix Package*

---

## Description

spam is a collection of functions for sparse matrix algebra.

## General overview

What is spam and what is it not:

While `Matrix` seems an overshoot of classes and `SparseM` focuses mainly on regression type problem, we provide a minimal set of sparse matrix functions fully functional for everyday spatial statistics life. There is however some emphasize on Markov chain Monte Carlo type calculations within the framework of (Gaussian) Markov random fields.

Emphasis is given on a comprehensive, simple, tutorial structure of the code. The code is S4 based but (in a tutorial spirit) the functions are in a S3 structure visible to the user (exported via `NAMESPACE`).

There exist many methods for sparse matrices that work identically as in the case of ordinary matrices. All the methods are discussed in the help and can be accessed directly via a `*.spam` concatenation to the function. For example, `help{chol.spam}` calls the help directly, whereas with `help{chol}` the user has to choose first between the basis help and the help provided by `spam`.

Sparseness is used when handling large matrices. Hence, care has been used to provide efficient and fast routines. Essentially, the functions do not transform the sparse structure into full matrices to use standard (available) functionality, followed by a back transform. We agree, more operators, functions, etc. should eventually be implemented.

The packages `fields` and `spdep` use `spam` as a required package.

### Author(s)

Reinhard Furrer

### References

[www.mines.edu/~rfurrer/software/spam/](http://www.mines.edu/~rfurrer/software/spam/)

### See Also

See `spam.class` for a detailed class description, `spam` and `spam.ops` for creation, coercion and algebraic operations.

`demo(package='spam')` lists available demos.

Related packages are `fields`, `Matrix` and `SparseM.ontology`.

### Examples

```
## Not run:
## History of changes
file.show(system.file("NEWS", package = "spam"))
## End(Not run)
```

---

adiag

*Binds Arrays Corner-to-Corner*

---

### Description

Creates a sparse block-diagonal matrix.

### Usage

```
adiag.spam(...)
```

## Arguments

... Arrays to be binded together

## Details

This is a small helper function to create block diagonal sparse matrices. In the two matrix case, `adiag.spam(A, B)`, this is equivalent to a complicated `rbind(cbind(A, null), cbind(B, t(null)))`, where `null` is a null matrix of appropriate dimension.

It is recursively defined.

The arrays are coerced to sparse matrices first.

This function is similar to the function `adiag` from the package `magic`. However, here no padding is done and all the `dimnames` are stripped.

## Value

Returns a `spam` matrix as described above.

## Author(s)

Reinhard Furrer

## See Also

[diag.spam](#).

## Examples

```
A <- diag.spam(2, 4)           # 2*I4
B <- matrix(1, 3, 3)
AB <- adiaq.spam(A, B)

# equivalent to:
ABalt <- rbind(cbind( A, matrix(0, nrow(A), ncol(B))),
               cbind( matrix(0, nrow(B), ncol(A)), B))

norm(AB-ABalt)

# Matrices do not need to be square:
adiaq.spam(1, 2:5, 6)
```

---

allequal

*Test if Two 'spam' Objects are (Nearly) Equal*


---

**Description**

Utility to compare two `spam` objects testing 'near equality'. Depending on the type of difference, comparison is still made to some extent, and a report of the differences is returned.

**Usage**

```
all.equal.spam(target, current, tolerance = .Machine$double.eps^0.5,
               scale = NULL, check.attributes = FALSE, ...)
```

**Arguments**

<code>target</code>	a <code>spam</code> object.
<code>current</code>	another <code>spam</code> object to be compared with <code>target</code> .
<code>tolerance</code>	numeric $\geq 0$ . Differences smaller than <code>tolerance</code> are not considered.
<code>scale</code>	numeric scalar $> 0$ (or <code>NULL</code> ). See 'Details'.
<code>check.attributes</code>	currently not yet implemented.
<code>...</code>	Further arguments for different methods.

**Details**

Numerical comparisons for `scale = NULL` (the default) are done by first computing the mean absolute difference of the two numerical vectors. If this is smaller than `tolerance` or not finite, absolute differences are used, otherwise relative differences scaled by the mean absolute difference.

If `scale` is positive, absolute comparisons are made after scaling (dividing) by `scale`.

Don't use `all.equal.spam` directly in `if` expressions-either use `isTRUE(all.equal.spam(...))` or `identical` if appropriate.

Cholesky decomposition routines use this function to test for symmetry.

A method for `matrix-spam` objects is defined as well.

**Value**

Either `TRUE` or a vector of 'mode' "character" describing the differences between `target` and `current`.

**Author(s)**

Reinhard Furrer

**Examples**

```

obj <- diag.spam(2)
obj[1,2] <- .Machine$double.eps

all.equal( diag.spam(2), obj)

all.equal( t(obj), obj)

all.equal( t(obj), obj*1.1)

# We can compare a spam to a matrix
all.equal(diag(2),diag.spam(2))

# the opposite does often not make sense,
# hence, it is not implemented.
all.equal(diag.spam(2),diag(2))

```

---

 apply

*Apply Functions Over Sparse Matrix Margins*


---

**Description**

Returns a vector or array or list of values obtained by applying a function to margins of a sparse matrix.

**Usage**

```
apply.spam(X, MARGIN=NULL, FUN, ...)
```

**Arguments**

X	the spam matrix to be used.
MARGIN	a vector giving the subscripts which the function will be applied over. 1 indicates rows, 2 indicates columns, NULL or c(1, 2) indicates rows and columns.
FUN	the function to be applied.
...	optional arguments to FUN.

**Details**

This is a handy wrapper to apply a function to the (nonzero) elements of a sparse matrix. For example, it is possible to apply a covariance matrix to a distance matrix obtained by `nearest.dist`, see Examples.

A call to `apply` only coerces the sparse matrix to a regular one.

The basic principle is applying the function to `@entries`, or to the extracted columns or rows (`[,i,drop=F]` or `[i,,drop=F]`). It is important to note that an empty column contains at

least one zero value and may lead to non intuitive results.

This function may evolve over the next few releases.

### Value

Similar as a call to `apply` with a regular matrix. The most important cases are as follows. The result is a vector (`MARGIN` is length 1 and `FUN` is scalar) or a matrix (`MARGIN` is length 1 and `FUN` returns fixed length vectors, or `MARGIN` is length 2 and `FUN` is scalar) or a list (if `FUN` returns vectors of different lengths).

### Author(s)

Reinhard Furrer

### See Also

`base:apply` for more details on `Value`.

### Examples

```
S <- as.spam(dist(1:5))
S <- apply.spam(S/2, NULL, exp)
# instead of
# S@entries <- exp( S@entries/2)

# Technical detail, a null matrix consists
# of one zero element.
apply.spam(S, c(1,2), pmax)
apply.spam(S, 1, range)

# A similar example as for the base apply.
# However, no dimnames else we would warnings.
x <- as.spam(cbind(x1 = 3, x2 = c(0,0,0, 5:2)))
apply.spam(x, 2, mean, trim = .2)
col.sums <- apply.spam(x, 2, sum)
row.sums <- apply.spam(x, 1, sum)
rbind(cbind(x, row.sums), c(col.sums, sum(col.sums)))

apply.spam(x, 2, is.vector)

# Sort the columns of a matrix
# Notice that the result is a list due to the different
# lengths induced by the nonzero elements
apply.spam(x, 2, sort)

# Function with extra args:
cave <- function(x, c1, c2) c(mean(x[c1]), mean(x[c2]))
apply(x, 1, cave, c1=1, c2=c(1,2))

ma <- spam(c(1:4, 0, 0,0, 6), nrow = 2)
ma
```

```
apply.spam(ma, 1, table) #--> a list of length 2  
apply.spam(ma, 1, stats::quantile)# 5 x n matrix with rownames
```

---

cbind

*Combine spam Matrices by Rows or Columns*

---

## Description

Take a sequence of vector, matrix or `spam` object arguments and combine by columns or rows, respectively.

## Usage

```
cbind.spam(..., deparse.level = 0)  
rbind.spam(..., deparse.level = 0)
```

## Arguments

`...` vectors, matrices or `spam` objects. See Details and Value  
`deparse.level`  
for compatibility reason here. Only 0 is implemented.

## Details

`rbind` and `cbind` are not exactly symmetric in how the objects are processed. The former is essentially an concatenation of the slots due to the sparse storage format. Different types of inputs are handled differently. The former calls a Fortran routine after the input has been coerced to `spam` objects.

Only two objects at a time are processed. If more than two are present, a loop concatenates them successively.

A method is defined for a `spam` object as first argument.

## Value

a `spam` object combining the `...` arguments column-wise or row-wise. (Exception: if there are no inputs or all the inputs are `NULL`, the value is `NULL`.)

## Author(s)

Reinhard Furrer

## See Also

[cbind](#), [spam-method](#).

**Examples**

```
x <- cbind.spam(1:5,6)

y <- cbind(x, 7)

rbind(x, x)
# for some large matrices  t( cbind( t(x), t(x)))
# might be slightly faster:
```

chol

*Cholesky Factorization for Sparse Matrices***Description**

`chol` performs a Cholesky decomposition of a symmetric positive definite sparse matrix `x` of class `spam`.

**Usage**

```
chol(x, ...)
chol.spam(x, pivot = "MMD", method = 'NgPeyton', memory =
          list(), eps = .Spam$eps, ...)

update.spam.chol.NgPeyton(object, x, ...)
```

**Arguments**

<code>x</code>	symmetric positive definite matrix of class <code>spam</code> .
<code>pivot</code>	should the matrix be permuted, and if, with what algorithm, see Details below.
<code>method</code>	Currently, only <code>NgPeyton</code> is implemented.
<code>memory</code>	Parameters specific to the method, see Details below.
<code>eps</code>	threshold to test symmetry. Defaults to <code>.Spam\$eps</code> .
<code>...</code>	further arguments passed to or from other methods.
<code>object</code>	an object from a previous call to <code>chol</code> .

**Details**

`chol` performs a Cholesky decomposition of a symmetric positive definite sparse matrix `x` of class `spam`. Currently, there is only the block sparse Cholesky algorithm of Ng and Peyton (1993) implemented (`method=NgPeyton`).

To `pivot`/permute the matrix, you can choose between the multiple minimum degree (`pivot=MMD`) or reverse Cuthill-McKee (`pivot=RCM`) from George and Lui (1981). It is also possible to furnish a specific permutation in which case `pivot` is a vector. For compatibility reasons, `pivot` can also

take a logical in which for `FALSE` no permutation is done and for `TRUE` is equivalent to `MMD`.

Often the sparseness structure is fixed and does not change, but the entries do. In those cases, we can update the Cholesky factor with `update.spam.chol.NgPeyton` by supplying a Cholesky factor and the updated matrix.

The option `cholupdatesingular` determines how singular matrices are handled by `update`. The function hands back an error (`"error"`), a warning (`"warning"`) or the value `NULL` (`"null"`).

The Cholesky decompositions requires parameters, linked to memory allocation. If the default values are too small the Fortran routine returns an error to `R`, which allocates more space and calls the Fortran routine again. The user can also pass better estimates of the allocation sizes to `chol` with the argument `memory=list(nnzR=..., nnzcolindices=...)`. The minimal sizes for a fixed sparseness structure can be obtained from a `summary` call.

The output of `chol` can be used with `forwardsolve` and `backsolve` to solve a system of linear equations.

Notice that the Cholesky factorization of the package `SparseM` is also based on the algorithm of Ng and Peyton (1993). Whereas the Cholesky routine of the package `Matrix` are based on `CHOLMOD` by Timothy A. Davis (C code).

### Value

The function returns the Cholesky factor in an object of class `spam.chol.method`. Recall that the latter is the Cholesky factor of a reordered matrix `x`, see also [ordering](#).

### Note

Although the symmetric structure of `x` is needed, only the upper diagonal entries are used. By default, the code does check for symmetry (contrarily to `base::chol`). However, depending on the matrix size, this is a time consuming test. A test is ignored if `.spam.options("cholsymmetrycheck")` is set to `FALSE`.

If a permutation is supplied with `pivot`, `.spam.options("cholpivotcheck")` determines if the permutation is tested for validity (defaults to `TRUE`).

### Author(s)

Reinhard Furrer, based on Ng and Peyton (1993) Fortran routines

### References

Ng, E. G. and B. W. Peyton (1993) Block sparse Cholesky algorithms on advanced uniprocessor computers, *SIAM J. Sci. Comput.*, **14**, 1034–1056.

George, A. and Liu, J. (1981) *Computer Solution of Large Sparse Positive Definite Systems*, Prentice Hall.

**See Also**

[det](#), [solve](#), [forwardsolve](#), [backsolve](#) and [ordering](#).

**Examples**

```
# generate multivariate normals:
set.seed(13)
n <- 25      # dimension
N <- 1000    # sample size
Sigma <- .25^abs(outer(1:n,1:n,"-"))
Sigma <- as.spam(Sigma, eps=1e-4)

cholS <- chol(Sigma)
# cholS is the upper triangular part of the permuted matrix Sigma
iord <- ordering(cholS, inv=TRUE)

R <- as.spam(cholS)
mvsample <- ( array(rnorm(N*n),c(N,n)) %*% R)[,iord]
# It is often better to order the sample than the matrix
# R itself.

# 'mvsample' is of class 'spam'. We need to transform it to a
# regular matrix, as there is no method 'var' for 'spam' (should there?).
norm( var( as.matrix(mvsample)) - Sigma, type="HS")
norm( t(R) %*% R - Sigma, type="sup")
```

**Description**

A few results of computational complexities for selected sparse algorithms in `spam`

**Details**

`chol` performs a Cholesky decomposition of a symmetric positive definite sparse matrix `x` of class `spam`. Currently, there is only the block sparse Cholesky algorithm of Ng and Peyton (1993) implemented (`method=NgPeyton`).

To pivot/permute the matrix, you can choose between the multiple minimum degree (`pivot=MMD`) or reverse Cuthill-McKee (`pivot=RCM`) from George and Lui (1981). It is also possible to furnish a specific permutation in which case `pivot` is a vector. For compatibility reasons, `pivot` can also take a logical in which for `FALSE` no permutation is done and for `TRUE` is equivalent to `MMD`.

Often the sparseness structure is fixed and does not change, but the entries do. In those cases, we can update the Cholesky factor with `update.spam.chol.NgPeyton` by supplying a Cholesky factor and the updated matrix.

The Cholesky decompositions requires parameters, linked to memory allocation. If the default values are too small the Fortran routine returns an error to `R`, which allocates more space and calls the Fortran routine again. The user can also pass better estimates of the allocation sizes to `chol` with the argument `memory=list(nnzR=..., nnzcolindices=...)`. The minimal sizes for a fixed sparseness structure can be obtained from a `summary` call.

The output of `chol` can be used with `forwardsolve` and `backsolve` to solve a system of linear equations.

## References

Ng, E. G. and B. W. Peyton (1993) Block sparse Cholesky algorithms on advanced uniprocessor computers, *SIAM J. Sci. Comput.*, **14**, 1034–1056.

George, A. and Liu, J. (1981) *Computer Solution of Large Sparse Positive Definite Systems*, Prentice Hall.

## See Also

[det](#), [solve](#), [forwardsolve](#), [backsolve](#) and [ordering](#).

---

det

*Calculate the determinant of a positive definite Sparse Matrix*

---

## Description

`det` and `determinant` calculate the determinant of a positive definite sparse matrix. `determinant` returns separately the modulus of the determinant, optionally on the logarithm scale, and the sign of the determinant.

## Usage

```
#      det(x, ...)
determinant(x, logarithm = TRUE, ...)
```

## Arguments

<code>x</code>	sparse matrix of class <code>spam</code> or a Cholesky factor of class <code>spam.chol</code> . NgPeyton.
<code>logarithm</code>	logical; if <code>TRUE</code> (default) return the logarithm of the modulus of the determinant.
<code>...</code>	Optional arguments. Examples include <code>method</code> argument and additional parameters used by the method.

**Details**

If the matrix is not positive definite, the function issues a warning and returns NA.

The determinant is based on the product of the diagonal entries of a Cholesky factor, i.e. internally, a Cholesky decomposition is performed. By default, the NgPeyton algorithm with minimal degree ordering is used. To change the methods or supply additional parameters to the Cholesky factorization function, see the help for [chol](#).

The determinant of a Cholesky factor is also defined.

**Value**

For `det`, the determinant of `x`. For `determinant`, a list with components

<code>modulus</code>	a numeric value. The modulus (absolute value) of the determinant if <code>logarithm</code> is FALSE; otherwise the logarithm of the modulus.
<code>sign</code>	integer; either +1 or -1 according to whether the determinant is positive or negative.

**Author(s)**

Reinhard Furrer

**References**

Ng, E. G. and B. W. Peyton (1993) Block sparse Cholesky algorithms on advanced uniprocessor computers, *SIAM J. Sci. Comput.*, **14**, 1034–1056.

**See Also**

[chol](#)

**Examples**

```
x <- spam( c(4, 3, 0, 3, 5, 1, 0, 1, 4), 3)
det( x)
determinant( x)

det( chol( x))
```

---

diag

*Sparse Matrix diagonals*

---

**Description**

Extract or replace the diagonal of a matrix, or construct a diagonal matrix.

**Usage**

```
# diag(x)
diag(x=1, nrow, ncol)
diag(x) <- value

diag.spam(x=1, nrow, ncol)
diag.spam(x) <- value
```

**Arguments**

`x` a spam matrix, a vector or a scalar.  
`nrow, ncol` Optional dimensions for the result.  
`value` either a single value or a vector of length equal to that of the current diagonal.

**Details**

Using `diag(x)` can have unexpected effects if `x` is a vector that could be of length one. Use `diag(x, nrow = length(x))` for consistent behaviour.

**Value**

If `x` is a spam matrix then `diag(x)` returns the diagonal of `x`.

The assignment form sets the diagonal of the sparse matrix `x` to the given value(s).

`diag.spam` works as `diag` for spam matrices: If `x` is a vector (or 1D array) of length two or more, then `diag.spam(x)` returns a diagonal matrix whose diagonal is `x`.

If `x` is a vector of length one then `diag.spam(x)` returns an identity matrix of order the nearest integer to `x`. The dimension of the returned matrix can be specified by `nrow` and `ncol` (the default is square).

The assignment form sets the diagonal of the matrix `x` to the given value(s).

**Author(s)**

Reinhard Furrer

**See Also**

[upper.tri](#), [lower.tri](#).

**Examples**

```
diag.spam(2, 4)           # 2*I4
smat <- diag.spam(1:5)
diag(smat)
diag(smat) <- 5:1

# The last line is equivalent to
diag.spam(smat) <- 5:1
```

```
# Note that diag.spam( 1:5) <- 5:1 not work of course.
```

---

dim

*Dimensions of an Object*

---

### Description

Retrieve or set the dimension of an `spam` object.

### Usage

```
# dim(x)
# dim(x) <- value
"dim<- .spam" (x, value)
```

### Arguments

<code>x</code>	a <code>spam</code> matrix
<code>value</code>	A numeric two-vector, which is coerced to integer (by truncation).

### Details

It is important to notice the different behavior of the replacement method for ordinary arrays and `spam` objects (see ‘Examples’). Here, the elements are not simply rearranged but an entirely new matrix is constructed. If the new column dimension is smaller than the original, the matrix is also cleaned (with `spam.option("eps")` as filter).

For the same operation as with regular arrays, use `spam`

### Value

`dim` retrieves the `dimension` slot of the object. It is a vector of mode `integer`.

The replacement method changes the dimension of the object by truncation or extension (with zeros).

### Author(s)

Reinhard Furrer

### See Also

[dim.](#)

**Examples**

```
x <- diag(4)
dim(x) <- c(2,8)
x

s <- diag.spam(4)
dim(s) <- c(7,3) # any positive value can be used

s <- diag.spam(4)
dim(s) <- c(2,8) # result is different than x
```

---

display

*Graphially represent the nonzero entries*


---

**Description**

The function represents the nonzero entries in a simple bicolor plot.

**Usage**

```
display(x, ...)
```

**Arguments**

`x` matrix of class `spam` or `spam.chol.NgPeyton`.  
`...` any other arguments passed to `image.default/plot`.

**Details**

`spam.getOption('imagesize')` determines if the sparse matrix is coerced into a matrix and the plotted with `image.default` or if the matrix is simply represented as a scatterplot with `pch="."`. The points are scaled according to `cex*spam.getOption('cex')/(nrow+ncol)`. For some devices or for non-square matrices, `cex` needs probably some adjustment.

**Author(s)**

Reinhard Furrer

**See Also**

[image](#), [spam.options](#)

## Examples

```
set.seed(13)

nz <- 8
ln <- nz
smat <- spam(0,ln,ln)
smat[cbind(sample(ln,nz), sample(ln,nz))] <- 1:nz

par(mfcol=c(1,2),pty='s')
spam.options( imagesize=1000)
display(smat)
spam.options( imagesize=10)
display(smat)

# very large but very sparse matrix
nz <- 128
ln <- nz^2
smat <- spam(0,ln,ln)
smat[cbind(sample(ln,nz), sample(ln,nz))] <- 1:nz

par(mfcol=c(1,1),pty='s')
display(smat, cex=100)
```

---

foreign

*Transformation to other sparse formats*

---

## Description

Transform between the `spam` sparse format to the `matrix.csr` format of `SparseM` and `dgRMatrix` format of `Matrix`

## Usage

```
as.spam.matrix.csr(x)
# as.matrix.csr.spam(x)
as.dgRMatrix.spam(x)
as.dgCMatrix.spam(x)
as.spam.dgRMatrix(x)
as.spam.dgCMatrix(x)
```

## Arguments

`x` sparse matrix of class `spam`, `matrix.csr`, `dgRMatrix` or `dgCMatrix`.

**Details**

We do not provide any S4 methods and because of the existing mechanism a standard S3 does not work.

The functions are based on `require`.

Notice that `as.matrix.csr.spam` should read as `as."matrix.csr".spam`.

**Value**

According to the call, a sparse matrix of class `spam`, `matrix.csr`, `dgRMatrix` or `dgCMatrix`.

**Author(s)**

Reinhard Furrer

**See Also**

`triplet`, `Matrix` or `matrix.csr`

**Examples**

```
## Not run:
S <- diag.spam(4)
U <- as.matrix.csr.spam( S)
R <- as.dgRMatrix.spam( S)
C <- as.dgCMatrix.spam( S)
as.spam.dgCMatrix(C)
slotNames(U)
slotNames(R)
# For column oriented sparse formats a transpose does not the job,
# as the slot names change.

# as.spam(R) does not work.
## End(Not run)

## Not run:
# a dataset contained in Matrix
data(KNex)
as.spam.dgCMatrix(KNex$mm)

## End(Not run)
```

---

`image`*Display a spam Object as Color Image*

---

### Description

The function creates a grid of colored rectangles with colors corresponding to the values in `z`.

### Usage

```
image(x, ...)
```

### Arguments

`x` matrix of class `spam` or `spam.chol.NgPeyton`.  
`...` any other arguments passed to `image.default` and `plot`.

### Details

`getOption('imagesize')` determines if the sparse matrix is coerced into a matrix and the plotted similarly to `image.default` or if the matrix is simply represented as a scatterplot with `pch="."`. The points are scaled according to `cex*spam.getOption('cex')/(nrow+ncol)`. For some devices or for non-square matrices, `cex` needs probably some adjustment.  
The a zero matrix in `spam` format has as (1,1) entry the value zero and only missing entries are interpreted as NA in the scatter plot.

### Author(s)

Reinhard Furrer

### See Also

[display](#) and [spam.options](#).  
The code is based on [image](#) of `graphics`.

### Examples

```
set.seed(13)
nz <- 8
ln <- nz
smat <- spam(0, ln, ln)
smat[ cbind(sample(ln, nz), sample(ln, nz)) ] <- 1:nz

par(mfcol=c(1,2),pty='s')
spam.options( imagesize=1000)
image(smat)#better: col=tim.colors(nz)
spam.options( imagesize=10)
image(smat)#better: col=tim.colors(nz)
```

```
nz <- 128
ln <- nz^2
smat <- spam(0, ln, ln)
smat[cbind(sample(ln, nz), sample(ln, nz))] <- 1:nz

par(mfcol=c(1,1),pty='s')
image(smat, cex=100) #better:, col=tim.colors(nz)
```

---

import

*Read external matrix formats*

---

## Description

Read matrices stored in the Harwell-Boeing or MatrixMarket formats.

## Usage

```
read.HB(file)
read.MM(file)
```

## Arguments

`file` the name of the file to read, as a character scalar.  
Alternatively, `read.HB` and `read.MM` accept connection objects.

## Details

The names of files storing matrices in the Harwell-Boeing format usually end in ".rua" or ".rsa". Those storing matrices in the MatrixMarket format usually end in ".mtx".

Currently, only real assembled Harwell-Boeing can be read with `read.HB`. Reading MatrixMarket formats is more flexible. However, as entries of `spam` matrices are of mode `double`, integers matrices are coerced to doubles, patterns lead to matrices containing ones and complex are coerced to the real part thereof. In these aforementioned cases, a warning is issued.

MatrixMarket also defines an array format, in which case a (possibly) dense `spam` object is returned (retaining only elements which are larger than `spam.options('eps')`). A warning is issued.

## Value

A sparse matrix of class `spam`.

## Note

The functions are based on `readHB` and `readMM` from the library `Matrix` to build the connection and read the raw data. At present, `read.MM` is more flexible than `readMM`.

**Author(s)**

Reinhard Furrer based on `Matrix` functions by Douglas Bates (bates@stat.wisc.edu) and Martin Maechler (maechler@stat.math.ethz.ch)

**References**

<http://math.nist.gov/MatrixMarket>  
<http://www.cise.ufl.edu/research/sparse/matrices>

**Examples**

```
## Not run:
image(read.MM(gzcon(url(
  "ftp://math.nist.gov/pub/MatrixMarket2/Harwell-Boeing/bcspwr/bcspwr01.mtx.gz"))))
## End(Not run)

## Not run:
## Datasets supplied within Matrix
str(read.MM(system.file("external/pores_1.mtx", package = "Matrix")))
str(read.HB(system.file("external/utm300.rua", package = "Matrix")))
str(read.MM(system.file("external/lund_a.mtx", package = "Matrix")))
str(read.HB(system.file("external/lund_a.rsa", package = "Matrix")))
## End(Not run)
```

---

isSymmetric                      *Test if a spam matrix is Symmetric*

---

**Description**

Efficient function to test if 'object' is symmetric or not.

**Usage**

```
isSymmetric.spam(object, tol = 100 * .Machine$double.eps, ...)
```

**Arguments**

object                      a spam matrix.  
tol                          numeric scalar  $\geq 0$ . Smaller differences are not considered, see `all.equal.spam`.  
...                          further arguments passed to `all.equal.spam`.

**Details**

symmetry is assessed by comparing the sparsity structure of `object` and `t(object)` via the function `all.equal.spam`.

**Value**

logical indicating if `object` is symmetric or not.

**Author(s)**

Reinhard Furrer

**See Also**

[all.equal.spam](#).

**Examples**

```
obj <- diag.spam(2)
isSymmetric(obj)

obj[1,2] <- .Machine$double.eps
isSymmetric(obj)
```

---

kronecker

*Kronecker products on sparse matrices*


---

**Description**

Computes the generalised kronecker product of two arrays, `X` and `Y`.

**Usage**

```
kronecker.spam(X, Y, FUN = "+", make.dimnames = FALSE, ...)
```

**Arguments**

<code>X</code>	sparse matrix of class <code>spam</code> , a vector or a matrix.
<code>Y</code>	sparse matrix of class <code>spam</code> , a vector or a matrix.
<code>FUN</code>	a function; it may be a quoted string. See details
<code>make.dimnames</code>	Provide <code>dimnames</code> that are the product of the <code>dimnames</code> of <code>'X'</code> and <code>'Y'</code> .
<code>...</code>	optional arguments to be passed to <code>FUN</code> .

**Details**

The sparseness structure is determined by the ordinary `%x%`. Hence, the result of `kronecker(X, Y, FUN = "+")` is different depending on the input.

**Value**

An array `A` with dimensions `dim(X) * dim(Y)`.

**Author(s)**

Reinhard Furrer

**Examples**

```
# Starting with non-spam objects, we get a spam matrix
kronecker.spam( diag(2), array(1:4,c(2,2)))

kronecker( diag.spam(2), array(1:4,c(2,2)))

# Notice the preservation of sparseness structure:
kronecker( diag.spam(2), array(1:4,c(2,2)),FUN="+")
```

---

`lower.tri`*Lower and Upper Triangular Part of a Sparse Matrix*

---

**Description**

Returns the lower or upper triangular structure or entries of a sparse matrix.

**Usage**

```
lower.tri(x, diag = FALSE)
upper.tri(x, diag = FALSE)
```

**Arguments**

<code>x</code>	a sparse matrix of class <code>spam</code>
<code>diag</code>	logical. Should the diagonal be included?

**Details**

Often not only the structure of the matrix is required but the entries as well. For compatibility, the default is only a structure consisting of ones (representing TRUEs). Setting the flag `spam.getOption('trivalues')` to TRUE, the function returns the actual values.

**See Also**

[spam.options](#) and [diag](#)

**Examples**

```
smat <- spam( c( 1,2,0,3,0,0,0,4,5), 3)
upper.tri( smat)
upper.tri( smat, diag=TRUE)

spam.options( trivalues=TRUE)
upper.tri( smat)
```

---

Math

*Mathematical functions*

---

### Description

Applies the `Math` group functions to 'spam' objects

### Usage

```
# ceiling(x)
# floor(x)

# exp(x, base = exp(1))
# log(x, base = exp(1))
# sqrt(x)

# abs(x)
# cumprod(x)
# cumsum(x)

# cos(x)
# sin(x)
# tan(x)
# acosh(x)
...
```

### Arguments

<code>x</code>	spam object.
<code>base</code>	positive number. The base with respect to which logarithms are computed. Defaults to $e = \exp(1)$ .

### Details

It is important to note that the zero entries do not enter the evaluation. The operations are performed on the stored non-zero elements. This may lead to differences if compared with the same operation on a full matrix. For example, the cosine of sparse matrix is a (full) matrix with many ones.

Evaluating function resulting in NA/NaN/Inf is possible but the result cannot be used further as NA/NaN/Inf are not meaningful (yet).

### Value

All functions operate on the vector `x@entries` and return the result thereof.

### Author(s)

Reinhard Furrer

**See Also**[Math2](#)**Examples**

```
getGroupMembers("Math")

mat <- matrix(c( 1,2,0,3,0,0,0,4,5),3)
smat <- as.spam( mat)
cos( mat)
cos( smat)

sqrt( smat)
```

---

Math2

*Rounding of Numbers*

---

**Description**

Applies the Math2 group functions to 'spam' objects

**Usage**

```
# round(x, digits = 0)
# signif(x, digits = 6)
```

**Arguments**

x	spam object.
digits	integer indicating the precision to be used.

**Details**

For this generic class typical `na.rm` argument has no weight here as NA/NaN/Inf are not meaningful (yet).

**Value**

All functions operate on the vector `x@entries` and return the result thereof.

**Author(s)**

Reinhard Furrer

**See Also**

[Math](#)

**Examples**

```

getGroupMembers("Math2")

smat <- diag.spam( rnorm(15))
round(smat, 3)

```

---

nearestdist                      *Distance Matrix Computation*

---

**Description**

This function computes and returns specific elements of distance matrix computed by using the specified distance measure.

**Usage**

```

nearest.dist( x, y=NULL, method = "euclidean",
             delta = 1, upper = FALSE,
             p=2, miles=TRUE, R=NULL,
             eps = NULL, diag = NULL)

```

**Arguments**

x	Matrix of first set of locations where each row gives the coordinates of a particular point. See also Details.
y	Matrix of second set of locations where each row gives the coordinates of a particular point. If this is missing x is used. See also Details.
method	the distance measure to be used. This must be one of "euclidean", "maximum", "minkowski" or "greatcircle". Any unambiguous substring can be given.
delta	only distances smaller than delta are recorded.
upper	Should the entire matrix (NULL) or only the upper-triagonal (TRUE) or lower-triagonal (FALSE) values be calculated.
p	The power of the Minkowski distance.
miles	For great circle distance: If true distances are in statute miles if false distances in kilometers.
R	For great circle distance: Radius to use for sphere to find spherical distances. If NULL the radius is either in miles or kilometers depending on the values of the miles argument. If R=1 then distances are of course in radians.
eps	deprecated. Left for backwards consistency.
diag	deprecated. Left for backwards consistency. See details.

## Details

For great circle distance, the by 2 matrices `x` and `y` contain the degrees longitudes in the first and the degrees latitudes in the second column. `eps` and `delta` are in degrees. The distance is in single precision (I am still not sure where I loose the double in the Fortran code) and if calculating the entire matrix `upper=NULL` (instead of adding its transpose) it may not pass the symmetry checks, for example.

Default value of Earth's radius is 3963.34miles (6378.388km).

The arguments `eps` and `diag` do not have any effect and are left for compatibility reasons.  
`x` and `y` can be any object with an existing `as.matrix` method.

A quick scan reveiled distance functions in at least 7 packages. The argument names should be as general as possible and be coherend with many (but not all) available distance functions.

The Fortran code is based on a idea of Doug Nychka.

## Value

A `spam` object containing the distances spanned between zero and `delta`. The sparse matrix may contain many zeros (e.g., collocated data). However, to calculate covariances, these zeros are essential.

## Author(s)

Reinhard Furrer

## Examples

```
# Note that upper=T and using t(X)+X is quicker than upper=NULL;
#   upper=T marginally slower than upper=F.

# To compare nearest.dist with dist, use diag=FALSE, upper=TRUE
nx <- 4
x <- expand.grid(as.double(1:nx), as.double(1:nx))
sum( (nearest.dist( x, delta=nx*2, diag=FALSE, upper=TRUE)@entries-
      c(dist(x)))^2)

# Create nearest neighbor structures:
par(mfcol=c(1,2))
x <- expand.grid(1:nx, 1:(2*nx))
display( nearest.dist( x, delta=1))
x <- expand.grid(1:(2*nx), 1:nx)
display( nearest.dist( x, delta=1))
```

options

*Options Settings***Description**

Allow the user to set and examine a variety of *options* which affect the way in which R computes and displays sparse matrix results.

**Usage**

```
spam.options(...)
```

```
spam.getOption(x)
```

**Arguments**

- `...` any options can be defined, using `name = value` or by passing a list of such tagged values. However, only the ones below are used in `spam`. Further, `spam.options('name') == spam.options()['name']`, see the example.
- `x` a character string holding an option name.

**Details**

Invoking `spam.options()` with no arguments returns a list with the current values of the options. To access the value of a single option, one should use `spam.getOption("eps")`, e.g., rather than `spam.options("eps")` which is a *list* of length one.

Internally, the options are kept in the list `.Spam`.

Of course, printing is still subordinate to `getOption("max.print")` or similar options.

**Value**

For `spam.getOption`, the current value set for option `x`, or `NULL` if the option is unset.

For `spam.options()`, a list of all set options sorted by category. For `spam.options(name)`, a list of length one containing the set value, or `NULL` if it is unset. For uses setting one or more options, a list with the previous values of the options changed (returned invisibly).

**Options used**

A short description with the default values follows.

**eps=.Machine\$double.eps:** values smaller than this are considered as zero. This is only used when creating `spam` objects.

**drop=FALSE:** default parameter for `drop` when subsetting

**printsize=100:** the max number of elements of a matrix which we display as regular matrix.

**imagesize=10000:** the max number of elements of a matrix we display as regular matrix with `image` or `display`. Larger matrices are represented as dots only.

**trivalues=FALSE:** a flag whether to return the structure (`FALSE`) or the values themselves (`TRUE`) when returning the upper and lower triangular part of a matrix.

**cex=1200:** default dot size for `image` or `display`.

**dopivoting=TRUE:** default parameter for "solve" routines. `FALSE` would solve the system without using the permutation.

**safemode=c(TRUE, TRUE, TRUE):** The logicals are determine (1) verify double and integer formats when constructing `spam` objects (2) quick sanity check when constructing sparse matrices (3) testing for NAs in Fortran calls. `TRUE`s are safer but slightly slower. The most relevant speedup is the second flag.

**cholsymmetrycheck=TRUE:** for the Cholesky factorization, verify if the matrix is symmetric.

**cholpivotcheck=TRUE:** for the Cholesky factorization, when passing a permutation, should a minimum set of checks be performed?

**cholupdatesingular="warning":** for a Cholesky update, what happens if the matrix is singular: "warning" only and returning the not updated factor, "error" or return simply "NULL".

**cholincreasefactor=c(1.25, 1.25):** If not enough memory could be allocated, these are the steps to increase it.

**nnznearestdistnnz=c(400^2, 400):** Memory allocation parameters for `nearest.dist`.

**nearestdistincreasefactor=1.25:** If not enough memory could be allocated, this is the step to increase it.

### Author(s)

`spam.options` is essentially identical to `sm.options`.

### See Also

[print](#), [display](#), [image](#), [upper.tri](#), [chol](#), [nearest.dist](#), etc.  
[powerboost](#)

### Examples

```
op <- spam.options()

# two ways of representing the options nicely.
utils::str(op)
noquote(format(op) )

smat <- diag.spam( 1:8)
smat
spam.options( printsize=49)
```

```

smat

# Reset to default values:
spam.options( eps=.Machine$double.eps, drop=FALSE,
  printsize=100, imagesize=10000, cex=1200,
  trivalues=FALSE, safemode=c(TRUE,TRUE,TRUE),
  dopivoting=TRUE, cholsymmetrycheck=TRUE,
  cholpivotcheck=TRUE, cholupdatesingular="warning",
  cholincreasefactor=c(1.25,1.25),
  nearestdistincreasefactor=1.25,
  nearestdistnnz=c(400^2,400) )

```

---

 ordering

*Extract the permutation*


---

### Description

Extract the (inverse) permutation used by the Cholesky decomposition

### Usage

```
ordering( x, inv=FALSE)
```

### Arguments

`x` object of class `spam.chol.method` returned by the function `chol`.  
`inv` Return the permutation (default) or inverse thereof.

### Details

Recall that calculating a Cholesky factor from a sparse matrix consists of finding a permutation first, then calculating the factors of the permuted matrix. The ordering is important when working with the factors themselves.

The ordering from a full/regular matrix is `1:n`.

Note that there exists many different algorithms to find orderings.

See the examples, they speak more than 10 lines.

### Author(s)

Reinhard Furrer

### See Also

[chol](#), [solve](#).

**Examples**

```

# Construct a pd matrix S to work with (size n)
n <- 100      # dimension
S <- .25^abs(outer(1:n,1:n,"-"))
S <- as.spam( S, eps=1e-4)
I <- diag(n)  # Identity matrix

cholS <- chol( S)
ord <- ordering(cholS)
iord <- ordering(cholS, inv=TRUE)

R <- as.spam( cholS ) # R'R = P S P', with P=I[ord,],
  # a permutation matrix (rows permuted).
RtR <- t(R) %**% R

# the following are equivalent:
as.spam( RtR - S[ord,ord] )
as.spam( RtR[iord,iord] - S )
as.spam( t(R[,iord]) %**% R[,iord] - S )

# trivially:
as.spam( t(I[iord,]) - I[ord,]) # (P^-1)' = P
as.spam( t(I[ord,]) - I[,ord]) #
as.spam( I[iord,] - I[,ord])
as.spam( I[ord,]%**%S%**I[,ord] - S[ord,ord] )
  # pre and post multiplication with P and P' is ordering

```

---

powerboost

*Specific options Setting*


---

**Description**

Sets several options for speed-up.

**Usage**

```
powerboost(flag)
```

**Arguments**

```
flag          on or off
```

**Details**

The options turn checking off ("safemode", "cholsymmetrycheck" and "cholpivotcheck") and switch to single precision for "eps".

**Value**

NULL in any case.

**Author(s)**

Reinhard Furrer, after receiving too much C.mc.st adds.

**See Also**

[spam.options.](#)

---

 print

---

*Printing and summarizing sparse matrices*


---

**Description**

Printing (non-zero elements) of sparse matrices and summarizing the sparseness structure thereof.

**Usage**

```
print(x, ...)
summary(object, ...)
```

**Arguments**

x	matrix of class <code>spam</code> or <code>spam.chol.method</code> .
object	matrix of class <code>spam</code> or <code>spam.chol.method</code> .
...	any other arguments passed to <code>print.default</code> .

**Details**

`spam.getOption('printsize')` determines if the sparse matrix is coerced into a matrix and the printed as an array or if only the non-zero elements of the matrix are given.

**Value**

NULL for `print`, because the information is printed with `cat` there is no real need to pass any object back.

A list containing the non-zero elements and the density for `summary` for class `spam`.

A list containing the non-zero elements of the factor, the density and the fill-in for `summary` for class `spam.chol.NgPeyton`.

**Author(s)**

Reinhard Furrer

**See Also**

[spam.options](#)

**Examples**

```
set.seed(13)
nz <- 8
ln <- nz
smat <- spam(0, ln, ln)
smat[cbind(sample(ln, nz), sample(ln, nz))] <- 1:nz

par(mfcol=c(1,2),pty='s')
spam.options( printsize=1000)
print(smat)
spam.options( printsize=10)
print(smat)
summary(smat)
(summary(smat))
```

---

 rmvnorm

*Draw Multivariate Normals*


---

**Description**

Fast ways to draw multivariate normals when the variance or precision matrix is sparse.

**Usage**

```
rmvnorm.spam(n, mu=rep(0, nrow(Sigma)), Sigma, ...)
rmvnorm.prec(n, mu=rep(0, nrow(Q)), Q, ...)
rmvnorm.canonical(n, b, Q, ...)
```

**Arguments**

n	number of observations.
mu	mean vector.
Sigma	covariance matrix of class spam.
Q	precision matrix.
b	vector determining the mean.
...	arguments passed to chol.

**Note**

There is intentionally no S3 distinction between the classes `spam` and `spam.chol.method`.

**Author(s)**

Reinhard Furrer, based on Ng and Peyton (1993) Fortran routines

**References**

See references in [chol](#).

**See Also**

[chol](#) and [ordering](#).

**Examples**

```
# Generate multivariate form a covariance inverse:
# (usefull for GRMF)
set.seed(13)
n <- 25 # dimension
N <- 1000 # sample size
Sigmainv <- .25^abs(outer(1:n,1:n,"-"))
Sigmainv <- as.spam( Sigmainv, eps=1e-4)

Sigma <- solve( Sigmainv) # for verification
iidsample <- array(rnorm(N*n),c(n,N))

mvsample <- backsolve( chol(Sigmainv), iidsample)
norm( var(t(mvsample)) - Sigma, type="HS")

# compare with:
mvsample <- backsolve( chol(as.matrix( Sigmainv)), iidsample)
norm( var(t(mvsample)) - Sigma, type="HS")

# 'solve' step by step:
b <- rnorm( n)
R <- chol(Sigmainv)
norm( backsolve( R, forwardsolve( R, b))-
      solve( Sigmainv, b),type="HS")
norm( backsolve( R, forwardsolve( R, diag(n)))- Sigma,type="HS")
```

---

 spam

*Sparse Matrix Class*


---

**Description**

This group of functions evaluates and coerces changes in class structure.

**Usage**

```
spam(x, nrow = 1, ncol = 1, eps = .Spam$eps)

as.spam(x, eps = .Spam$eps)

is.spam(x)
```

**Arguments**

<code>x</code>	is a matrix (of either dense or sparse form), a list, vector object or a distance object
<code>nrow</code>	number of rows of matrix
<code>ncol</code>	number of columns of matrix
<code>eps</code>	A tolerance parameter: elements of <code>x</code> such that $\text{abs}(x) < \text{eps}$ set to zero. Defaults to <code>eps = .Spam\$eps</code>

**Details**

The functions `spam` and `as.spam` act like `matrix` and `as.matrix` to coerce an object to a sparse matrix object of class `spam`.

If `x` is a list, it should contain either two or three elements. In case of the former, the list should contain a `n` by two matrix of indices (called `ind`) and the values. In case of the latter, the list should contain three vectors containing the row, column indices (called `i` and `j`) and the values. In both cases partial matching is done.

`eps` should be at least as large as `.Machine$double.eps`.

**Value**

A valid `spam` object.  
`is.spam` returns TRUE if `x` is a `spam` object.

**Note**

The zero matrix has the element zero stored in (1,1).

The functions do not test the presence of `NA/NaN/Inf`. Virtually all call a Fortran routine with the `NAOK=! .Spam$safemode[3]` argument, which defaults to FALSE resulting in an error. Hence, the `NaN` do not always properly propagate through (i.e. `spam` is not IEEE-754 compliant).

**Author(s)**

Reinhard Furrer

**References**

[http://en.wikipedia.org/wiki/Sparse\\_matrix](http://en.wikipedia.org/wiki/Sparse_matrix) as a start.

**See Also**

`SPAM` general overview of the package. `spam.options` for details about the `safemode` flag. `read.MM` and `foreign` to create `spam` matrices from `MatrixMarket` files and from certain `Matrix/SparseM` formats.

**Examples**

```
# old message, do not loop, when you create a large sparse matrix
set.seed(13)
nz <- 128
ln <- nz^2
smat <- spam(0,ln,ln)
is <- sample(ln,nz)
js <- sample(ln,nz)
system.time(for (i in 1:nz) smat[is[i], js[i]] <- i)
system.time(smat[cbind(is,js)] <- 1:nz)

getClass("spam")

try(as.spam.numeric(NA))
```

---

spam operations      *Basic Linear Algebra for Sparse Matrices*

---

**Description**

Basic linear algebra operations for sparse matrices of class `spam`.

**Details**

Linear algebra operations for matrices of class `spam` are designed to behave exactly as for regular matrices. In particular, matrix multiplication, transpose, addition, subtraction and various logical operations should work as with the conventional dense form of matrix storage, as does indexing, `rbind`, `cbind`, and diagonal assignment and extraction (see for example `diag`). Further functions with identical behavior are `dim` and thus `nrow`, `ncol`.

The function `norm` calculates the (matrix-)norm of the argument. The argument `type` specifies the `l1` norm, `sup` or `max` norm (default), or the Frobenius or Hilbert-Schmidt (`frobenius/hs`) norm. Partial matching can be used. For example, `norm` is used to check for symmetry in the function `chol` by computing the norm of the difference between the matrix and its transpose

The operator `%d*%` efficiently multiplies a diagonal matrix (in vector form) and a sparse matrix and is used for compatibility with the package fields. More specifically, this method is used in the internal functions of `Krig` to make the code more readable. It avoids having a branch in the source code to handle the diagonal or nondiagonal cases. Note that this operator is not symmetric: a vector in the left argument is interpreted as a diagonal matrix and a vector in the right argument is kept as a column vector.

The operator `%d+%` efficiently adds a diagonal matrix (in vector form) and a sparse matrix, similarly to the operator `%d+%`.

**References**

Some Fortran functions are based on <http://www-users.cs.umn.edu/~saad/software/SPARSKIT/sparskit.html>

**See Also**

[spam](#) for coercion and other class relations involving the sparse matrix classes.

**Examples**

```
# create a weight matrix and scale it:
## Not run:
wij <- distmat
# with distmat from a nearest.dist(..., upper=TRUE) call

n <- dim(wij)[1]

wij@entries <- kernel( wij@entries, h) # for some function kernel
wij <- wij + t(wij) + diag.spam(n)    # adjust from diag=FALSE, upper=TRUE

sumwij <- wij %**% rep(1,n)
  # row scaling:
  #   wij@entries <- wij@entries/sumwij[ wij@colindices]
  # col scaling:
wij@entries <- wij@entries/sumwij[ rep(1:n, diff(wij@rowpointers))]
## End(Not run)
```

---

spam solve

---

*Linear Equation Solving for Sparse Matrices*


---

**Description**

`backsolve` and `forwardsolve` solve a system of linear equations where the coefficient matrix is upper or lower triangular.

`solve` solves a linear system or computes the inverse of a matrix if the right-hand-side is missing.

**Usage**

```
solve(a, b, ...)

backsolve(r, x, ...)
forwardsolve(l, x, ...)
```

**Arguments**

<code>a</code>	symmetric positive definite matrix of class <code>spam</code> or a Cholesky factor as the result of a <code>chol</code> call.
<code>l, r</code>	object of class <code>spam</code> or <code>spam.chol.method</code> returned by the function <code>chol</code> .
<code>x, b</code>	vector or regular matrix of right-hand-side(s) of a system of linear equations.
<code>...</code>	further arguments passed to or from other methods, see Details below.

## Details

We can solve  $A x = b$  by first computing the Cholesky decomposition  $A = t(R) \%*\%R$ , then solving  $t(R) \%*\%y = b$  for  $y$ , and finally solving  $R \%*\%x = y$  for  $x$ . `solve` combines `chol`, a Cholesky decomposition of a symmetric positive definite sparse matrix, with `forwardsolve` and then `backsolve`.

In case  $a$  is from a `chol`, then `solve` is an efficient way to calculate `backsolve(a, forwardsolve(t(a), b))`.

`forwardsolve` and `backsolve` solve a system of linear equations where the coefficient matrix is lower (`forwardsolve`) or upper (`backsolve`) triangular. Usually, the triangular matrix is result from a `chol` call and it is not required to transpose it for `forwardsolve`. Note that arguments of the default methods `k`, `upper.tri` and `transpose` do not have any effects here.

If the right-hand-side in `solve` is missing it will compute the inverse of a matrix. For details about the specific Cholesky decomposition, see [chol](#).

Recall that the Cholesky factors are from ordered matrices.

## Note

There is intentionally no S3 distinction between the classes `spam` and `spam.chol.method`.

## Author(s)

Reinhard Furrer, based on Ng and Peyton (1993) Fortran routines

## References

See references in [chol](#).

## See Also

[det](#), [chol](#) and [ordering](#).

## Examples

```
# Generate multivariate form a covariance inverse:
# (usefull for GRMF)
set.seed(13)
n <- 25 # dimension
N <- 1000 # sample size
Sigmainv <- .25^abs(outer(1:n,1:n,"-"))
Sigmainv <- as.spam( Sigmainv, eps=1e-4)

Sigma <- solve( Sigmainv) # for verification
iidsample <- array(rnorm(N*n),c(n,N))

mvsample <- backsolve( chol(Sigmainv), iidsample)
norm( var(t(mvsample)) - Sigma, type="HS")

# compare with:
```

```

mvsample <- backsolve( chol(as.matrix( Sigmainv)), iidsample)
norm( var(t(mvsample)) - Sigma, type="HS")

# 'solve' step by step:
b <- rnorm( n)
R <- chol(Sigmainv)
norm( backsolve( R, forwardsolve( R, b))-
      solve( Sigmainv, b),type="HS")
norm( backsolve( R, forwardsolve( R, diag(n)))- Sigma,type="HS")

```

---

spam-class	<i>Class "spam"</i>
------------	---------------------

---

## Description

The spam class is a representation of sparse matrices.

## Objects from the Class

Objects can be created by calls of the form `new("spam", entries, colindices, rowpointers, dimension)`. The standard "old Yale sparse format" is used to store sparse matrices.

The matrix `x` is stored in row form. The first element of row `i` is `x@rowpointers[i]`. The length of row `i` is determined by `x@rowpointers[i+1]-x@rowpointers[i]`. The column indices of `x` are stored in the `x@colindices` vector. The column index for element `x@entries[k]` is `x@colindices[k]`.

## Slots

**entries:** Object of class "numeric" contains the nonzero values

**colindices:** Object of class "integer" ordered indices of the nonzero values

**rowpointers:** Object of class "integer" pointer to the beginning of each row in the arrays `entries` and `colindices`

**dimension:** Object of class "integer" ~~

## Methods

**as.matrix** signature (`x = "spam"`): transforming a sparse matrix into a regular matrix.

**as.spam** signature (`x = "spam"`): cleaning of a sparse matrix.

**[<-** signature (`x = "spam", i, j, value`): assigning a sparse matrix. The negative vectors are not implemented yet.

**[** signature (`x = "spam", i, j`): subsetting a sparse matrix. The negative vectors are not implemented yet.

**%\*%** signature (`x, y`): matrix multiplication, all combinations of sparse with full matrices or vectors are implemented.

**c** signature(x = "spam"): vectorizes the sparse matrix and takes account of the zeros. Hence the length of the result is `prod(dim(x))`.

**cbind** signature(x = "spam"): binds sparse matrices.

**chol** signature(x = "spam"): see [chol](#) for details.

**diag** signature(x = "spam"): see [diag](#) for details.

**dim<-** signature(x = "spam"): truncates or augments the matrix see [dim](#) for details.

**dim** signature(x = "spam"): gives the dimension of the sparse matrix.

**image** signature(x = "spam"): see [image](#) for details.

**display** signature(x = "spam"): see [display](#) for details.

**length<-** signature(x = "spam"): Is not implemented and causes an error.

**length** signature(x = "spam"): gives the number of non-zero elements.

**lower.tri** signature(x = "spam"): see [lower.tri](#) for details.

**Math** signature(x = "spam"): see [Math](#) for details.

**Math2** signature(x = "spam"): see [Math2](#) for details.

**norm** signature(x = "spam"): calculates the norm of a matrix.

**plot** signature(x = "spam", y): same functionality as the ordinary `plot`.

**print** signature(x = "spam"): see [print](#) for details.

**rbind** signature(x = "spam"): binds sparse matrices.

**solve** signature(a = "spam"): see [solve](#) for details.

**summary** signature(object = "spam"): small summary statement of the sparse matrix.

**Summary** signature(x = "spam"): All functions of the `Summary` class (like `min`, `max`, `range`...) operate on the vector `x@entries` and return the result thereof. See [Examples](#) or [Summary](#) for details.

**t** signature(x = "spam"): transpose of a sparse matrix.

**upper.tri** signature(x = "spam"): see [lower.tri](#) for details.

## Details

The compressed sparse row (CSR) format is often described with the vectors `a`, `ia`, `ja`. To be a bit more comprehensive, we have chosen longer slot names.

## Note

The slots `colindices` and `rowpointers` are tested for proper integer assignments. This is not true for `entries`.

## Author(s)

Reinhard Furrer, some of the Fortran code is based on A. George, J. Liu, E. S. Ng, B.W Peyton and Y. Saad (alphabetical)

**Examples**

```
showMethods("as.spam")

smat <- diag.spam(runif(15))
range(smat)
cos(smat)
```

---

```
spam.chol.NgPeyton-class
      Class "spam.chol.NgPeyton"
```

---

**Description**

Result of a Cholesky decomposition with the NgPeyton method

**Objects from the Class**

Objects are created by calls of the form `chol(x, method="NgPeyton", ...)` and should not be created directly with a `new("spam.chol.NgPeyton", ...)` call.

At present, no proper print method is defined. However, the factor can be transformed into a spam object.

**Methods**

**as.spam** signature(x = "spam"): Transform the factor into a spam object

**length** signature(x = "spam"): ...

**backsolve** signature(r = "spam.chol.NgPeyton"): solving a triangular system, see [solve](#).

**forwardsolve** signature(l = "spam.chol.NgPeyton"): solving a triangular system, see [solve](#).

**dim** signature(x = "spam"): Retrieve the dimension. Note that "dim<-" is not implemented.

**length** signature(x = "spam"): Retrieve the dimension. Note that "dim<-" is not implemented.

**c** signature(x = "spam"): Coerce the factor into a vector .

**Author(s)**

Reinhard Furrer

**References**

Ng, E. G. and B. W. Peyton (1993), "Block sparse Cholesky algorithms on advanced uniprocessor computers", *SIAM J. Sci. Comput.*, **14**, pp. 1034-1056.

**See Also**

[print.spam ordering](#) and [chol](#)

**Examples**

```
x <- spam( c(4,3,0,3,5,1,0,1,4), 3)
cf <- chol( x)
cf
as.spam( cf)

# Modify at own risk...
slotNames(cf)
```

---

Summary

*Rounding of Numbers*

---

**Description**

Applies the `Math2` group functions to 'spam' objects

**Usage**

```
# max(x, ..., na.rm = FALSE)
```

**Arguments**

`x` spam object.

**Details**

For this generic class typical `na.rm` argument has no weight here as `NA/NaN/Inf` are not meaningful (yet).

**Value**

All functions operate on the vector `x@entries` and return the result thereof.

**Author(s)**

Reinhard Furrer

**See Also**

[Math](#) and [Math2](#).

**Examples**

```
getGroupMembers("Summary")

smat <- diag.spam( runif(15) )
range(smat)
```

triplet

*Transform a spam format to triplets***Description**

Returns a list containing the indices and elements of a `spam` object.

**Usage**

```
triplet(x, tri=FALSE)
```

**Arguments**

`x` sparse matrix of class `spam` or a matrix.  
`tri` Boolean indicating whether to create individual row and column indices vectors.

**Details**

The elements are row (column) first if `x` is a `spam` object (matrix).

**Value**

A list with elements

`indices` a by two matrix containing the indices if `tri=FALSE`.  
`i, j` vectors containing the row and column indices if `tri=TRUE`.  
`values` a vector containing the matrix elements

**Author(s)**

Reinhard Furrer

**See Also**

[spam.list](#) for the inverse operation and [foreign](#) for other transformations.

**Examples**

```
x <- diag.spam(1:4)
x[2,3] <- 5
triplet(x)
all.equal( spam(triplet(x, tri=TRUE)), x)
```

---

 UScounties

*Adjacency structure of the counties in the contiguous United States*


---

### Description

First and second order adjacency structure of the counties in the contiguous United States. We consider that two counties are neighbors if they share at least one edge of their polygon description in `maps`.

### Format

Two matrices of class `spam`

**UScounties.storder** Contains a one in the `i` and `j` element if county `i` is a neighbor of county `j`.

**UScounties.ndorder** Contains a one in the `i` and `j` element if counties `i` and `j` are a neighbors of county `k` and counties `i` and `j` are not neighbors.

### See Also

[map](#)

### Examples

```
# number of counties:
n <- nrow( UScounties.storder)

## Not run:
# make a precision matrix
Q <- diag.spam( n) + .2 * UScounties.storder + .1 * UScounties.ndorder
display( as.spam( chol( Q)))
## End(Not run)
```

---

 USprecip

*Monthly total precipitation (mm) for April 1948 in the contiguous United States*


---

### Description

This is a useful spatial data set of moderate to large size consisting of 11918 locations. See [www.image.ucar.edu/GSP/Data/US.monthly.met/](http://www.image.ucar.edu/GSP/Data/US.monthly.met/) for the source of these data.

**Format**

This data set is an array containing the following columns:

**lon,lat** Longitude-latitude position of monitoring stations

**raw** Monthly total precipitation in millimeters for April 1948

**anomaly** Preipitation anomaly for April 1948.

**infill** Indicator, which station values were observed (5906 out of the 11918) compared to which were estimated.

**Source**

[www.image.ucar.edu/GSP/Data/US.monthly.met/](http://www.image.ucar.edu/GSP/Data/US.monthly.met/)

**References**

Johns, C., Nychka, D., Kittel, T., and Daly, C. (2003) Infilling sparse records of spatial fields. *Journal of the American Statistical Association*, 98, 796–806.

**See Also**

[RMprecip](#)

**Examples**

```
# plot
## Not run:
library(fields)

data(USprecip)
par(mfcol=c(2,1))
quilt.plot(USprecip[,1:2],USprecip[,3])
US( add=TRUE, col=2, lty=2)
quilt.plot(USprecip[,1:2],USprecip[,4])
US( add=TRUE, col=2, lty=2)
## End(Not run)
```

---

version

*Spam Version Information*

---

**Description**

`spam.version` is a variable (list) holding detailed information about the version of `spam` loaded.

`spam.Version()` provides detailed information about the version of `spam` running.

**Usage**

```
spam.version
```

**Value**

`spam.version` is a list with character-string components

`status`            the status of the version (e.g., "beta")

`major`            the major version number

`minor`            the minor version number

`year`             the year the version was released

`month`            the month the version was released

`day`              the day the version was released

`version.string`  
                  a character string concatenating the info above, useful for plotting, etc.

`spam.version` is a list of class "simple.list" which has a `print` method.

**Author(s)**

Reinhard Furrer

**See Also**

See the R counterparts [R.version](#).

**Examples**

```
spam.version$version.string
```

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