Package 'Matrix'

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Title Sparse and Dense Matrix Classes and Methods

Description A rich hierarchy of sparse and dense matrix classes, including general, symmetric, triangular, and diagonal matrices with numeric, logical, or pattern entries. Efficient methods for operating on such matrices, often wrapping the 'BLAS', 'LAPACK', and 'SuiteSparse' libraries.

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URL https://Matrix.R-forge.R-project.org

BugReports https://R-forge.R-project.org/tracker/?atid=294&group_id=61

Contact Matrix-authors@R-project.org

Depends R (>= 4.4), methods

Imports grDevices, graphics, grid, lattice, stats, utils

Suggests MASS, datasets, sfsmisc, tools

Enhances SparseM, graph

LazyData no

LazyDataNote not possible, since we use data/*.R and our S4 classes

BuildResaveData no

Encoding UTF-8

NeedsCompilation yes

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abIndex-class *Class "abIndex" of Abstract Index Vectors*

Description

The "abIndex" class, short for "Abstract Index Vector", is used for dealing with large index vectors more efficiently, than using integer (or numeric) vectors of the kind 2:1000000 or c(0:1e5, 1000:1e6).

Note that the current implementation details are subject to change, and if you consider working with these classes, please contact the package maintainers (packageDescription("Matrix")$Maintainer).

Objects from the Class

Objects can be created by calls of the form new("abIndex", ...), but more easily and typically either by as(x, "abIndex") where x is an integer (valued) vector, or directly by abIseq() and combination c(...) of such.

Slots

kind: a character string, one of ("int32", "double", "rleDiff"), denoting the internal structure of the abIndex object.

x: Object of class "numLike"; is used (i.e., not of length 0) only iff the object is *not* compressed, i.e., currently exactly when kind != "rleDiff".

rleD: object of class "rleDiff", used for compression via rle.

Methods

as.numeric, as.integer, as.vector signature(x = "abIndex"): ...

[signature(x = "abIndex", i = "index", j = "ANY", drop = "ANY"): ...

coerce signature(from = "numeric", to = "abIndex"): ...

coerce signature(from = "abIndex", to = "numeric"): ...

coerce signature(from = "abIndex", to = "integer"): ...

length signature(x = "abIndex"): ...

Ops signature(e1 = "numeric", e2 = "abIndex"): These and the following arithmetic and logic operations are **not yet implemented**; see Ops for a list of these (S4) group methods.

Ops signature(e1 = "abIndex", e2 = "abIndex"): ...

Ops signature(e1 = "abIndex", e2 = "numeric"): ...

Summary signature(x = "abIndex"): ...

show ("abIndex"): simple show method, building on show(<rleDiff>).

is.na ("abIndex"): works analogously to regular vectors.

is.finite, is.infinite ("abIndex"): ditto.

Note

This is currently experimental and not yet used for our own code. Please contact us (`packageDescription("Matrix")$Main`) if you plan to make use of this class.

Partly builds on ideas and code from Jens Oehlschlaegel, as implemented (around 2008, in the GPL'ed part of) package **ff**.

See Also

`rle` (**base**) which is used here; `numeric`

Examples

```
showClass("abIndex")
ii <- c(-3:40, 20:70)
str(ai <- as(ii, "abIndex"))# note
ai # -> show() method

stopifnot(identical(-3:20,
                    as(abIseq1(-3,20), "vector")))
```

`abIseq` *Sequence Generation of "abIndex", Abstract Index Vectors*

Description

Generation of abstract index vectors, i.e., objects of class `"abIndex"`.

`abIseq()` is designed to work entirely like `seq`, but producing `"abIndex"` vectors.
`abIseq1()` is its basic building block, where `abIseq1(n,m)` corresponds to `n:m`.

`c(x, ...)` will return an `"abIndex"` vector, when `x` is one.

Usage

```
abIseq1(from = 1, to = 1)
abIseq (from = 1, to = 1, by = ((to - from)/(length.out - 1)),
        length.out = NULL, along.with = NULL)

## S3 method for class 'abIndex'
c(...)
```

Arguments

`from`, `to`	the starting and (maximal) end value of the sequence.
`by`	number: increment of the sequence.
`length.out`	desired length of the sequence. A non-negative number, which for `seq` and `seq.int` will be rounded up if fractional.
`along.with`	take the length from the length of this argument.
`...`	in general an arbitrary number of R objects; here, when the first is an `"abIndex"` vector, these arguments will be concatenated to a new `"abIndex"` object.

Value

An abstract index vector, i.e., object of class "abIndex".

See Also

the class abIndex documentation; rep2abI() for another constructor; rle (**base**).

Examples

```
stopifnot(identical(-3:20,
                    as(abIseq1(-3,20), "vector")))

try( ## (arithmetic) not yet implemented
abIseq(1, 50, by = 3)
)
```

---

all.equal-methods *Matrix Package Methods for Function all.equal()*

Description

Methods for function all.equal() (from R package **base**) are defined for all Matrix classes.

Methods

target = "Matrix", current = "Matrix" \

target = "ANY", current = "Matrix" \

target = "Matrix", current = "ANY" these three methods are simply using all.equal.numeric directly and work via as.vector().

There are more methods, notably also for "sparseVector"'s, see showMethods("all.equal").

Examples

```
showMethods("all.equal")

(A <- spMatrix(3,3, i= c(1:3,2:1), j=c(3:1,1:2), x = 1:5))
ex <- expand(lu. <- lu(A))
stopifnot( all.equal(as(A[lu.@p + 1L, lu.@q + 1L], "CsparseMatrix"),
                     lu.@L %*% lu.@U),
           with(ex, all.equal(as(P %*% A %*% t(Q), "CsparseMatrix"),
                              L %*% U)),
           with(ex, all.equal(as(A, "CsparseMatrix"),
                              t(P) %*% L %*% U %*% Q)))
```

asUniqueT *Standardize a Sparse Matrix in Triplet Format*

Description

Detect or standardize a TsparseMatrix with unsorted or duplicated (i, j) pairs.

Usage

```
anyDuplicatedT(x, ...)
isUniqueT(x, byrow = FALSE, isT = is(x, "TsparseMatrix"))
asUniqueT(x, byrow = FALSE, isT = is(x, "TsparseMatrix"))
aggregateT(x)
```

Arguments

x	an R object. anyDuplicatedT and aggregateT require x inheriting from TsparseMatrix. asUniqueT requires x inheriting from Matrix and coerces x to TsparseMatrix if necessary.
...	optional arguments passed to the default method for generic function anyDuplicated.
byrow	a logical indicating if x should be sorted by row then by column.
isT	a logical indicating if x inherits from virtual class TsparseMatrix.

Value

anyDuplicatedT(x) returns the index of the first duplicated (i, j) pair in x (0 if there are no duplicated pairs).

isUniqueT(x) returns TRUE if x is a TsparseMatrix with sorted, nonduplicated (i, j) pairs and FALSE otherwise.

asUniqueT(x) returns the unique TsparseMatrix representation of x with sorted, nonduplicated (i, j) pairs. Values corresponding to identical (i, j) pairs are aggregated by addition, where in the logical case "addition" refers to logical OR.

aggregateT(x) aggregates without sorting.

See Also

Virtual class TsparseMatrix.

Examples

```
example("dgTMatrix-class", echo=FALSE)
## -> 'T2'  with (i,j,x) slots of length 5 each
T2u <- asUniqueT(T2)
stopifnot(## They "are" the same (and print the same):
          all.equal(T2, T2u, tol=0),
          ## but not internally:
```

```
          anyDuplicatedT(T2)  == 2,
          anyDuplicatedT(T2u) == 0,
          length(T2 @x) == 5,
          length(T2u@x) == 3)

isUniqueT(T2 ) # FALSE
isUniqueT(T2u) # TRUE

T3 <- T2u
T3[1, c(1,3)] <- 10; T3[2, c(1,5)] <- 20
T3u <- asUniqueT(T3)
str(T3u) # sorted in 'j', and within j, sorted in i
stopifnot(isUniqueT(T3u))

## Logical l.TMatrix and n.TMatrix :
(L2 <- T2 > 0)
validObject(L2u <- asUniqueT(L2))
(N2 <- as(L2, "nMatrix"))
validObject(N2u <- asUniqueT(N2))
stopifnot(N2u@i == L2u@i, L2u@i == T2u@i,  N2@i == L2@i, L2@i == T2@i,
          N2u@j == L2u@j, L2u@j == T2u@j,  N2@j == L2@j, L2@j == T2@j)
# now with a nasty NA  [partly failed in Matrix 1.1-5]:
L.0N <- L.1N <- L2
L.0N@x[1:2] <- c(FALSE, NA)
L.1N@x[1:2] <- c(TRUE, NA)
validObject(L.0N)
validObject(L.1N)
(m.0N <- as.matrix(L.0N))
(m.1N <- as.matrix(L.1N))
stopifnot(identical(10L, which(is.na(m.0N))), !anyNA(m.1N))
symnum(m.0N)
symnum(m.1N)
```

---

band-methods *Extract bands of a matrix*

Description

Return the matrix obtained by setting to zero elements below a diagonal (`triu`), above a diagonal (`tril`), or outside of a general band (band).

Usage

```
band(x, k1, k2, ...)
triu(x, k = 0L, ...)
tril(x, k = 0L, ...)
```

Arguments

x	a matrix-like object
k, k1, k2	integers specifying the diagonals that are not set to zero, k1 <= k2. These are interpreted relative to the main diagonal, which is k = 0. Positive and negative values of k indicate diagonals above and below the main diagonal, respectively.
...	optional arguments passed to methods, currently unused by package **Matrix**.

Details

`triu(x, k)` is equivalent to `band(x, k, dim(x)[2])`. Similarly, `tril(x, k)` is equivalent to `band(x, -dim(x)[1], k)`.

Value

An object of a suitable matrix class, inheriting from `triangularMatrix` where appropriate. It inherits from `sparseMatrix` if and only if x does.

Methods

x = "CsparseMatrix" method for compressed, sparse, column-oriented matrices.

x = "RsparseMatrix" method for compressed, sparse, row-oriented matrices.

x = "TsparseMatrix" method for sparse matrices in triplet format.

x = "diagonalMatrix" method for diagonal matrices.

x = "denseMatrix" method for dense matrices in packed or unpacked format.

x = "matrix" method for traditional matrices of implicit class `matrix`.

See Also

`bandSparse` for the *construction* of a banded sparse matrix directly from its non-zero diagonals.

Examples

```
## A random sparse matrix :
set.seed(7)
m <- matrix(0, 5, 5)
m[sample(length(m), size = 14)] <- rep(1:9, length=14)
(mm <- as(m, "CsparseMatrix"))

tril(mm)        # lower triangle
tril(mm, -1)    # strict lower triangle
triu(mm,  1)    # strict upper triangle
band(mm, -1, 2) # general band
(m5 <- Matrix(rnorm(25), ncol = 5))
tril(m5)        # lower triangle
tril(m5, -1)    # strict lower triangle
triu(m5, 1)     # strict upper triangle
band(m5, -1, 2) # general band
(m65 <- Matrix(rnorm(30), ncol = 5))  # not square
```

```
triu(m65)       # result not "dtrMatrix" unless square
(sm5 <- crossprod(m65)) # symmetric
   band(sm5, -1, 1)# "dsyMatrix": symmetric band preserves symmetry property
as(band(sm5, -1, 1), "sparseMatrix")# often preferable
(sm <- round(crossprod(triu(mm/2)))) # sparse symmetric ("dsC*")
band(sm, -1,1) # remains "dsC", *however*
band(sm, -2,1) # -> "dgC"
```

---

bandSparse *Construct Sparse Banded Matrix from (Sup-/Super-) Diagonals*

Description

Construct a sparse banded matrix by specifying its non-zero sup- and super-diagonals.

Usage

```
bandSparse(n, m = n, k, diagonals, symmetric = FALSE,
           repr = "C", giveCsparse = (repr == "C"))
```

Arguments

n, m	the matrix dimension $(n, m) = (nrow, ncol)$.
k	integer vector of "diagonal numbers", with identical meaning as in band(*, k), i.e., relative to the main diagonal, which is k=0.
diagonals	optional list of sub-/super- diagonals; if missing, the result will be a pattern matrix, i.e., inheriting from class nMatrix. diagonals can also be $n' \times d$ matrix, where d <- length(k) and $n' >= min(n, m)$. In that case, the sub-/super- diagonals are taken from the columns of diagonals, where only the first several rows will be used (typically) for off-diagonals.
symmetric	logical; if true the result will be symmetric (inheriting from class symmetricMatrix) and only the upper or lower triangle must be specified (via k and diagonals).
repr	character string, one of "C", "T", or "R", specifying the sparse *repr*esentation to be used for the result, i.e., one from the super classes CsparseMatrix, TsparseMatrix, or RsparseMatrix.
giveCsparse	(**deprecated**, replaced with repr): logical indicating if the result should be a CsparseMatrix or a TsparseMatrix, where the default was TRUE, and now is determined from repr; very often Csparse matrices are more efficient subsequently, but not always.

Value

a sparse matrix (of class CsparseMatrix) of dimension $n \times m$ with diagonal "bands" as specified.

See Also

band, for *extraction* of matrix bands; bdiag, diag, sparseMatrix, Matrix.

Examples

```
diags <- list(1:30, 10*(1:20), 100*(1:20))
s1 <- bandSparse(13, k = -c(0:2, 6), diag = c(diags, diags[2]), symm=TRUE)
s1
s2 <- bandSparse(13, k =  c(0:2, 6), diag = c(diags, diags[2]), symm=TRUE)
stopifnot(identical(s1, t(s2)), is(s1,"dsCMatrix"))

## a pattern Matrix of *full* (sub-)diagonals:
bk <- c(0:4, 7,9)
(s3 <- bandSparse(30, k = bk, symm = TRUE))

## If you want a pattern matrix, but with "sparse"-diagonals,
## you currently need to go via logical sparse:
lLis <- lapply(list(rpois(20, 2), rpois(20, 1), rpois(20, 3))[c(1:3, 2:3, 3:2)],
               as.logical)
(s4 <- bandSparse(20, k = bk, symm = TRUE, diag = lLis))
(s4. <- as(drop0(s4), "nsparseMatrix"))

n <- 1e4
bk <- c(0:5, 7,11)
bMat <- matrix(1:8, n, 8, byrow=TRUE)
bLis <- as.data.frame(bMat)
B  <- bandSparse(n, k = bk, diag = bLis)
Bs <- bandSparse(n, k = bk, diag = bLis, symmetric=TRUE)
B [1:15, 1:30]
Bs[1:15, 1:30]
## can use a list *or* a matrix for specifying the diagonals:
stopifnot(identical(B,  bandSparse(n, k = bk, diag = bMat)),
  identical(Bs, bandSparse(n, k = bk, diag = bMat, symmetric=TRUE))
          , inherits(B, "dtCMatrix") # triangular!
)
```

---

bdiag *Construct a Block Diagonal Matrix*

Description

Build a block diagonal matrix given several building block matrices.

Usage

```
bdiag(...)
.bdiag(lst)
```

Arguments

`...`	individual matrices or a `list` of matrices.
`lst`	non-empty `list` of matrices.

Details

For non-trivial argument list, `bdiag()` calls `.bdiag()`. The latter maybe useful to programmers.

Value

A *sparse* matrix obtained by combining the arguments into a block diagonal matrix.

The value of `bdiag()` inherits from class `CsparseMatrix`, whereas `.bdiag()` returns a `TsparseMatrix`.

Note

This function has been written and is efficient for the case of relatively few block matrices which are typically sparse themselves.

It is currently *inefficient* for the case of many small dense block matrices. For the case of *many* dense $k \times k$ matrices, the `bdiag_m()` function in the 'Examples' is an order of magnitude faster.

Author(s)

Martin Maechler, built on a version posted by Berton Gunter to R-help; earlier versions have been posted by other authors, notably Scott Chasalow to S-news. Doug Bates's faster implementation builds on `TsparseMatrix` objects.

See Also

`Diagonal` for constructing matrices of class `diagonalMatrix`, or `kronecker` which also works for `"Matrix"` inheriting matrices.

`bandSparse` constructs a *banded* sparse matrix from its non-zero sub-/super - diagonals.

Note that other CRAN R packages have own versions of `bdiag()` which return traditional matrices.

Examples

```
bdiag(matrix(1:4, 2), diag(3))
## combine "Matrix" class and traditional matrices:
bdiag(Diagonal(2), matrix(1:3, 3,4), diag(3:2))

mlist <- list(1, 2:3, diag(x=5:3), 27, cbind(1,3:6), 100:101)
bdiag(mlist)
stopifnot(identical(bdiag(mlist),
                    bdiag(lapply(mlist, as.matrix))))

ml <- c(as(matrix((1:24)%% 11 == 0, 6,4),"nMatrix"),
        rep(list(Diagonal(2, x=TRUE)), 3))
mln <- c(ml, Diagonal(x = 1:3))
stopifnot(is(bdiag(ml), "lsparseMatrix"),
          is(bdiag(mln),"dsparseMatrix") )
```

```
## random (diagonal-)block-triangular matrices:
rblockTri <- function(nb, max.ni, lambda = 3) {
   .bdiag(replicate(nb, {
         n <- sample.int(max.ni, 1)
         tril(Matrix(rpois(n * n, lambda = lambda), n, n)) }))
}

(T4 <- rblockTri(4, 10, lambda = 1))
image(T1 <- rblockTri(12, 20))


##' Fast version of Matrix :: .bdiag() -- for the case of *many*  (k x k) matrices:
##' @param lmat list(<mat1>, <mat2>, ....., <mat_N>)  where each mat_j is a  k x k 'matrix'
##' @return a sparse (N*k x N*k) matrix of class  \code{"\linkS4class{dgCMatrix}"}.
bdiag_m <- function(lmat) {
    ## Copyright (C) 2016 Martin Maechler, ETH Zurich
    if(!length(lmat)) return(new("dgCMatrix"))
    stopifnot(is.list(lmat), is.matrix(lmat[[1]]),
              (k <- (d <- dim(lmat[[1]]))[1]) == d[2], # k x k
              all(vapply(lmat, dim, integer(2)) == k)) # all of them
    N <- length(lmat)
    if(N * k > .Machine$integer.max)
        stop("resulting matrix too large; would be  M x M, with M=", N*k)
    M <- as.integer(N * k)
    ## result: an   M x M  matrix
    new("dgCMatrix", Dim = c(M,M),
        ## 'i :' maybe there's a faster way (w/o matrix indexing), but elegant?
        i = as.vector(matrix(0L:(M-1L), nrow=k)[, rep(seq_len(N), each=k)]),
        p = k * 0L:M,
        x = as.double(unlist(lmat, recursive=FALSE, use.names=FALSE)))
}

l12 <- replicate(12, matrix(rpois(16, lambda = 6.4), 4, 4),
                 simplify=FALSE)
dim(T12 <- bdiag_m(l12))# 48 x 48
T12[1:20, 1:20]
```

---

boolmatmult-methods *Boolean Arithmetic Matrix Products:* %&% *and Methods*

Description

For boolean or "patter**n**" matrices, i.e., R objects of class nMatrix, it is natural to allow matrix products using boolean instead of numerical arithmetic.

In package **Matrix**, we use the binary operator %&% (aka "infix") function) for this and provide methods for all our matrices and the traditional R matrices (see matrix).

Value

a pattern matrix, i.e., inheriting from "nMatrix", or an "ldiMatrix" in case of a diagonal matrix.

Methods

We provide methods for both the "traditional" (R base) matrices and numeric vectors and conceptually all matrices and sparseVectors in package **Matrix**.

`signature(x = "ANY", y = "ANY")`

`signature(x = "ANY", y = "Matrix")`

`signature(x = "Matrix", y = "ANY")`

`signature(x = "nMatrix", y = "nMatrix")`

`signature(x = "nMatrix", y = "nsparseMatrix")`

`signature(x = "nsparseMatrix", y = "nMatrix")`

`signature(x = "nsparseMatrix", y = "nsparseMatrix")`

`signature(x = "sparseVector", y = "sparseVector")`

Note

These boolean arithmetic matrix products had been newly introduced for **Matrix** 1.2.0 (March 2015). Its implementation has still not been tested extensively.

Originally, it was left unspecified how non-structural zeros, i.e., `0`'s as part of the `M@x` slot should be treated for numeric (`"dMatrix"`) and logical (`"lMatrix"`) sparse matrices. We now specify that boolean matrix products should behave as if applied to `drop0(M)`, i.e., as if dropping such zeros from the matrix before using it.
Equivalently, for all matrices `M`, boolean arithmetic should work as if applied to `M != 0` (or `M != FALSE`).

The current implementation ends up coercing both `x` and `y` to (virtual) class `nsparseMatrix` which may be quite inefficient for dense matrices. A future implementation may well return a matrix with **different** class, but the "same" content, i.e., the same matrix entries m_ij.

See Also

`%*%`, `crossprod()`, or `tcrossprod()`, for (regular) matrix product methods.

Examples

```
set.seed(7)
L <- Matrix(rnorm(20) > 1,    4,5)
(N <- as(L, "nMatrix"))
L. <- L; L.[1:2,1] <- TRUE; L.@x[1:2] <- FALSE; L. # has "zeros" to drop0()
D <- Matrix(round(rnorm(30)), 5,6) # -> values in -1:1 (for this seed)
L %&% D
stopifnot(identical(L %&% D, N %&% D),
          all(L %&% D == as((L %*% abs(D)) > 0, "sparseMatrix")))

## cross products , possibly with  boolArith = TRUE :
crossprod(N)     # -> sparse patter'n' (TRUE/FALSE : boolean arithmetic)
crossprod(N  +0) # -> numeric Matrix (with same "pattern")
stopifnot(all(crossprod(N) == t(N) %&% N),
          identical(crossprod(N), crossprod(N +0, boolArith=TRUE)),
```

```
          identical(crossprod(L), crossprod(N   , boolArith=FALSE)))
crossprod(D, boolArith =  TRUE) # pattern: "nsCMatrix"
crossprod(L, boolArith =  TRUE) #  ditto
crossprod(L, boolArith = FALSE) # numeric: "dsCMatrix"
```

BunchKaufman-class *Dense Bunch-Kaufman Factorizations*

Description

Classes BunchKaufman and pBunchKaufman represent Bunch-Kaufman factorizations of $n \times n$ real, symmetric matrices A, having the general form

$$A = UD_UU' = LD_LL'$$

where D_U and D_L are symmetric, block diagonal matrices composed of b_U and b_L 1×1 or 2×2 diagonal blocks; $U = \prod_{k=1}^{b_U} P_kU_k$ is the product of b_U row-permuted unit upper triangular matrices, each having nonzero entries above the diagonal in 1 or 2 columns; and $L = \prod_{k=1}^{b_L} P_kL_k$ is the product of b_L row-permuted unit lower triangular matrices, each having nonzero entries below the diagonal in 1 or 2 columns.

These classes store the nonzero entries of the $2b_U + 1$ or $2b_L + 1$ factors, which are individually sparse, in a dense format as a vector of length nn (BunchKaufman) or $n(n+1)/2$ (pBunchKaufman), the latter giving the "packed" representation.

Slots

Dim, Dimnames inherited from virtual class MatrixFactorization.

uplo a string, either "U" or "L", indicating which triangle (upper or lower) of the factorized symmetric matrix was used to compute the factorization and in turn how the x slot is partitioned.

x a numeric vector of length n*n (BunchKaufman) or n*(n+1)/2 (pBunchKaufman), where n=Dim[1]. The details of the representation are specified by the manual for LAPACK routines dsytrf and dsptrf.

perm an integer vector of length n=Dim[1] specifying row and column interchanges as described in the manual for LAPACK routines dsytrf and dsptrf.

Extends

Class BunchKaufmanFactorization, directly. Class MatrixFactorization, by class BunchKaufmanFactorization, distance 2.

Instantiation

Objects can be generated directly by calls of the form new("BunchKaufman", ...) or new("pBunchKaufman", ...), but they are more typically obtained as the value of BunchKaufman(x) for x inheriting from dsyMatrix or dspMatrix.

Methods

`coerce signature(from = "BunchKaufman", to = "dtrMatrix")`: returns a `dtrMatrix`, useful for inspecting the internal representation of the factorization; see 'Note'.

`coerce signature(from = "pBunchKaufman", to = "dtpMatrix")`: returns a `dtpMatrix`, useful for inspecting the internal representation of the factorization; see 'Note'.

`determinant signature(from = "p?BunchKaufman", logarithm = "logical")`: computes the determinant of the factorized matrix A or its logarithm.

`expand1 signature(x = "p?BunchKaufman")`: see `expand1-methods`.

`expand2 signature(x = "p?BunchKaufman")`: see `expand2-methods`.

`solve signature(a = "p?BunchKaufman", b = .)`: see `solve-methods`.

Note

In **Matrix** < `1.6-0`, class `BunchKaufman` extended `dtrMatrix` and class `pBunchKaufman` extended `dtpMatrix`, reflecting the fact that the internal representation of the factorization is fundamentally triangular: there are $n(n+1)/2$ "parameters", and these can be arranged systematically to form an $n \times n$ triangular matrix. **Matrix** `1.6-0` removed these extensions so that methods would no longer be inherited from `dtrMatrix` and `dtpMatrix`. The availability of such methods gave the wrong impression that `BunchKaufman` and `pBunchKaufman` represent a (singular) matrix, when in fact they represent an ordered set of matrix factors.

The coercions `as(., "dtrMatrix")` and `as(., "dtpMatrix")` are provided for users who understand the caveats.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dsytrf.f and https://netlib.org/lapack/double/dsptrf.f.

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class `dsyMatrix` and its packed counterpart.

Generic functions `BunchKaufman`, `expand1`, and `expand2`.

Examples

```
showClass("BunchKaufman")
set.seed(1)

n <- 6L
(A <- forceSymmetric(Matrix(rnorm(n * n), n, n)))

## With dimnames, to see that they are propagated :
dimnames(A) <- rep.int(list(paste0("x", seq_len(n))), 2L)

(bk.A <- BunchKaufman(A))
```

```
str(e.bk.A <- expand2(bk.A, complete = FALSE), max.level = 2L)
str(E.bk.A <- expand2(bk.A, complete =  TRUE), max.level = 2L)

## Underlying LAPACK representation
(m.bk.A <- as(bk.A, "dtrMatrix"))
stopifnot(identical(as(m.bk.A, "matrix"), `dim<-`(bk.A@x, bk.A@Dim)))

## Number of factors is 2*b+1, b <= n, which can be nontrivial ...
(b <- (length(E.bk.A) - 1L) %/% 2L)

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ U DU U', U := prod(Pk Uk) in floating point
stopifnot(exprs = {
    identical(names(e.bk.A), c("U", "DU", "U."))
    identical(e.bk.A[["U" ]], Reduce(`%*%`, E.bk.A[seq_len(b)]))
    identical(e.bk.A[["U."]], t(e.bk.A[["U"]]))
    ae1(A, with(e.bk.A, U %*% DU %*% U.))
})

## Factorization handled as factorized matrix
b <- rnorm(n)
stopifnot(identical(det(A), det(bk.A)),
          identical(solve(A, b), solve(bk.A, b)))
```

BunchKaufman-methods *Methods for Bunch-Kaufman Factorization*

Description

Computes the Bunch-Kaufman factorization of an $n \times n$ real, symmetric matrix A, which has the general form

$$A = U D_U U' = L D_L L'$$

where D_U and D_L are symmetric, block diagonal matrices composed of b_U and b_L 1×1 or 2×2 diagonal blocks; $U = \prod_{k=1}^{b_U} P_k U_k$ is the product of b_U row-permuted unit upper triangular matrices, each having nonzero entries above the diagonal in 1 or 2 columns; and $L = \prod_{k=1}^{b_L} P_k L_k$ is the product of b_L row-permuted unit lower triangular matrices, each having nonzero entries below the diagonal in 1 or 2 columns.

Methods are built on LAPACK routines `dsytrf` and `dsptrf`.

Usage

```
BunchKaufman(x, ...)
## S4 method for signature 'dsyMatrix'
BunchKaufman(x, warnSing = TRUE, ...)
## S4 method for signature 'dspMatrix'
BunchKaufman(x, warnSing = TRUE, ...)
```

```
## S4 method for signature 'matrix'
BunchKaufman(x, uplo = "U", ...)
```

Arguments

x	a finite symmetric matrix or Matrix to be factorized. If x is square but not symmetric, then it will be *treated* as symmetric; see uplo.
warnSing	a logical indicating if a warning should be signaled for singular x.
uplo	a string, either "U" or "L", indicating which triangle of x should be used to compute the factorization.
...	further arguments passed to or from methods.

Value

An object representing the factorization, inheriting from virtual class BunchKaufmanFactorization. The specific class is BunchKaufman unless x inherits from virtual class packedMatrix, in which case it is pBunchKaufman.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dsytrf.f and https://netlib.org/lapack/double/dsptrf.f.

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Classes BunchKaufman and pBunchKaufman and their methods.

Classes dsyMatrix and dspMatrix.

Generic functions expand1 and expand2, for constructing matrix factors from the result.

Generic functions Cholesky, Schur, lu, and qr, for computing other factorizations.

Examples

```
showMethods("BunchKaufman", inherited = FALSE)
set.seed(0)

data(CAex, package = "Matrix")
class(CAex) # dgCMatrix
isSymmetric(CAex) # symmetric, but not formally

A <- as(CAex, "symmetricMatrix")
class(A) # dsCMatrix

## Have methods for denseMatrix (unpacked and packed),
## but not yet sparseMatrix ...
## Not run:
(bk.A <- BunchKaufman(A))
```

```
## End(Not run)
(bk.A <- BunchKaufman(as(A, "unpackedMatrix")))

## A ~ U DU U' in floating point
str(e.bk.A <- expand2(bk.A), max.level = 2L)
stopifnot(all.equal(as(A, "matrix"), as(Reduce(`%*%`, e.bk.A), "matrix")))
```

CAex *Albers' example Matrix with "Difficult" Eigen Factorization*

Description

An example of a sparse matrix for which `eigen()` seemed to be difficult, an unscaled version of this has been posted to the web, accompanying an E-mail to R-help (https://stat.ethz.ch/mailman/listinfo/r-help), by Casper J Albers, Open University, UK.

Usage

```
data(CAex)
```

Format

This is a 72×72 symmetric matrix with 216 non-zero entries in five bands, stored as sparse matrix of class `dgCMatrix`.

Details

Historical note (2006-03-30): In earlier versions of R, `eigen(CAex)` fell into an infinite loop whereas `eigen(CAex, EISPACK=TRUE)` had been okay.

Examples

```
data(CAex, package = "Matrix")
str(CAex) # of class "dgCMatrix"

image(CAex)# -> it's a simple band matrix with 5 bands
## and the eigen values are basically 1 (42 times) and 0 (30 x):
zapsmall(ev <- eigen(CAex, only.values=TRUE)$values)
## i.e., the matrix is symmetric, hence
sCA <- as(CAex, "symmetricMatrix")
## and
stopifnot(class(sCA) == "dsCMatrix",
          as(sCA, "matrix") == as(CAex, "matrix"))
```

cbind2-methods *'cbind()' and 'rbind()' recursively built on cbind2/rbind2*

Description

The base functions `cbind` and `rbind` are defined for an arbitrary number of arguments and hence have the first formal argument `...`. Now, when S4 objects are found among the arguments, base `cbind()` and `rbind()` internally "dispatch" *recursively*, calling `cbind2` or `rbind2` respectively, where these have methods defined and so should dispatch appropriately.

`cbind2()` and `rbind2()` are from the **methods** package, i.e., standard R, and have been provided for binding together *two* matrices, where in **Matrix**, we have defined methods for these and the `'Matrix'` matrices.

Usage

```
## cbind(..., deparse.level = 1)
## rbind(..., deparse.level = 1)

## S4 method for signature 'Matrix,Matrix'
cbind2(x, y, ...)
## S4 method for signature 'Matrix,Matrix'
rbind2(x, y, ...)
```

Arguments

`...`	for `[cr]bind`, vector- or matrix-like R objects to be bound together; for `[cr]bind2`, further arguments passed to or from methods; see `cbind` and `cbind2`.
`deparse.level`	integer controlling the construction of labels in the case of non-matrix-like arguments; see `cbind`.
`x, y`	vector- or matrix-like R objects to be bound together.

Value

typically a 'matrix-like' object of a similar `class` as the first argument in `...`.

Note that sometimes by default, the result is a `sparseMatrix` if one of the arguments is (even in the case where this is not efficient). In other cases, the result is chosen to be sparse when there are more zero entries is than non-zero ones (as the default `sparse` in `Matrix()`).

Author(s)

Martin Maechler

See Also

`cbind`, `cbind2`.

Our class definition help pages mentioning `cbind2()` and `rbind2()` methods: `"denseMatrix"`, `"diagonalMatrix"`, `"indMatrix"`.

Examples

```
(a <- matrix(c(2:1,1:2), 2,2))

(M1 <- cbind(0, rbind(a, 7))) # a traditional matrix

D <- Diagonal(2)
(M2 <- cbind(4, a, D, -1, D, 0)) # a sparse Matrix

stopifnot(validObject(M2), inherits(M2, "sparseMatrix"),
          dim(M2) == c(2,9))
```

CHMfactor-class *Sparse Cholesky Factorizations*

Description

CHMfactor is the virtual class of sparse Cholesky factorizations of $n \times n$ real, symmetric matrices A, having the general form

$$P_1 A P_1' = L_1 D L_1' \overset{D_{jj} \geq 0}{=} LL'$$

or (equivalently)

$$A = P_1' L_1 D L_1' P_1 \overset{D_{jj} \geq 0}{=} P_1' L L' P_1$$

where P_1 is a permutation matrix, L_1 is a unit lower triangular matrix, D is a diagonal matrix, and $L = L_1\sqrt{D}$. The second equalities hold only for positive semidefinite A, for which the diagonal entries of D are non-negative and $\sqrt{D}$ is well-defined.

The implementation of class CHMfactor is based on CHOLMOD's C-level cholmod_factor_struct. Virtual subclasses CHMsimpl and CHMsuper separate the simplicial and supernodal variants. These have nonvirtual subclasses [dn]CHMsimpl and [dn]CHMsuper, where prefix 'd' and prefix 'n' are reserved for numeric and symbolic factorizations, respectively.

Usage

```
isLDL(x)
```

Arguments

x	an object inheriting from virtual class CHMfactor, almost always the result of a call to generic function Cholesky.

Value

isLDL(x) returns TRUE or FALSE: TRUE if x stores the lower triangular entries of $L_1 - I + D$, FALSE if x stores the lower triangular entries of L.

Slots

Of CHMfactor:

Dim, Dimnames inherited from virtual class MatrixFactorization.

colcount an integer vector of length Dim[1] giving an *estimate* of the number of nonzero entries in each column of the lower triangular Cholesky factor. If symbolic analysis was performed prior to factorization, then the estimate is exact.

perm a 0-based integer vector of length Dim[1] specifying the permutation applied to the rows and columns of the factorized matrix. perm of length 0 is valid and equivalent to the identity permutation, implying no pivoting.

type an integer vector of length 6 specifying details of the factorization. The elements correspond to members ordering, is_ll, is_super, is_monotonic, maxcsize, and maxesize of the original cholmod_factor_struct. Simplicial and supernodal factorizations are distinguished by is_super. Simplicial factorizations do not use maxcsize or maxesize. Supernodal factorizations do not use is_ll or is_monotonic.

Of CHMsimpl (all unused by nCHMsimpl):

nz an integer vector of length Dim[1] giving the number of nonzero entries in each column of the lower triangular Cholesky factor. There is at least one nonzero entry in each column, because the diagonal elements of the factor are stored explicitly.

p an integer vector of length Dim[1]+1. Row indices of nonzero entries in column j of the lower triangular Cholesky factor are obtained as i[p[j]+seq_len(nz[j])]+1.

i an integer vector of length greater than or equal to sum(nz) containing the row indices of nonzero entries in the lower triangular Cholesky factor. These are grouped by column and sorted within columns, but the columns themselves need not be ordered monotonically. Columns may be overallocated, i.e., the number of elements of i reserved for column j may exceed nz[j].

prv, nxt integer vectors of length Dim[1]+2 indicating the order in which the columns of the lower triangular Cholesky factor are stored in i and x. Starting from j <- Dim[1]+2, the recursion j <- nxt[j+1]+1 traverses the columns in forward order and terminates when nxt[j+1] = -1. Starting from j <- Dim[1]+1, the recursion j <- prv[j+1]+1 traverses the columns in backward order and terminates when prv[j+1] = -1.

Of dCHMsimpl:

x a numeric vector parallel to i containing the corresponding nonzero entries of the lower triangular Cholesky factor L *or* (if and only if type[2] is 0) of the lower triangular matrix $L_1 - I + D$.

Of CHMsuper:

super, pi, px integer vectors of length nsuper+1, where nsuper is the number of supernodes. super[j]+1 is the index of the leftmost column of supernode j. The row indices of supernode j are obtained as s[pi[j]+seq_len(pi[j+1]-pi[j])]+1. The numeric entries of supernode j are obtained as x[px[j]+seq_len(px[j+1]-px[j])]+1 (if slot x is available).

s an integer vector of length greater than or equal to Dim[1] containing the row indices of the supernodes. s may contain duplicates, but not within a supernode, where the row indices must be increasing.

Of dCHMsuper:

x a numeric vector of length less than or equal to prod(Dim) containing the numeric entries of the supernodes.

Extends

Class MatrixFactorization, directly.

Instantiation

Objects can be generated directly by calls of the form new("dCHMsimpl", ...), etc., but dCHMsimpl and dCHMsuper are more typically obtained as the value of Cholesky(x, ...) for x inheriting from sparseMatrix (often dsCMatrix).

There is currently no API outside of calls to new for generating nCHMsimpl and nCHMsuper. These classes are vestigial and may be formally deprecated in a future version of **Matrix**.

Methods

coerce signature(from = "CHMsimpl", to = "dtCMatrix"): returns a dtCMatrix representing the lower triangular Cholesky factor L *or* the lower triangular matrix $L_1 - I + D$, the latter if and only if from@type[2] is 0.

coerce signature(from = "CHMsuper", to = "dgCMatrix"): returns a dgCMatrix representing the lower triangular Cholesky factor L. Note that, for supernodes spanning two or more columns, the supernodal algorithm by design stores non-structural zeros above the main diagonal, hence dgCMatrix is indeed more appropriate than dtCMatrix as a coercion target.

determinant signature(from = "CHMfactor", logarithm = "logical"): behaves according to an optional argument sqrt. If sqrt = FALSE, then this method computes the determinant of the factorized matrix A or its logarithm. If sqrt = TRUE, then this method computes the determinant of the factor $L = L_1 sqrt(D)$ or its logarithm, giving NaN for the modulus when D has negative diagonal elements. For backwards compatibility, the default value of sqrt is TRUE, but that can be expected change in a future version of **Matrix**, hence defensive code will always set sqrt (to TRUE, if the code must remain backwards compatible with **Matrix** < 1.6-0). Calls to this method not setting sqrt may warn about the pending change. The warnings can be disabled with options(Matrix.warnSqrtDefault = 0).

diag signature(x = "CHMfactor"): returns a numeric vector of length n containing the diagonal elements of D, which (*if* they are all non-negative) are the squared diagonal elements of L.

expand signature(x = "CHMfactor"): see expand-methods.

expand1 signature(x = "CHMsimpl"): see expand1-methods.

expand1 signature(x = "CHMsuper"): see expand1-methods.

expand2 signature(x = "CHMsimpl"): see expand2-methods.

expand2 signature(x = "CHMsuper"): see expand2-methods.

image signature(x = "CHMfactor"): see image-methods.

nnzero signature(x = "CHMfactor"): see nnzero-methods.

solve signature(a = "CHMfactor", b = .): see solve-methods.

update signature(object = "CHMfactor"): returns a copy of object with the same nonzero pattern but with numeric entries updated according to additional arguments parent and mult, where parent is (coercible to) a dsCMatrix or a dgCMatrix and mult is a numeric vector of positive length.
The numeric entries are updated with those of the Cholesky factor of F(parent) + mult[1] * I, i.e., F(parent) plus mult[1] times the identity matrix, where F = identity for symmetric parent and F = tcrossprod for other parent. The nonzero pattern of F(parent) must match that of S if object = Cholesky(S, ...).

updown signature(update = ., C = ., object = "CHMfactor"): see updown-methods.

References

The CHOLMOD source code; see https://github.com/DrTimothyAldenDavis/SuiteSparse, notably the header file 'CHOLMOD/Include/cholmod.h' defining cholmod_factor_struct.

Chen, Y., Davis, T. A., Hager, W. W., & Rajamanickam, S. (2008). Algorithm 887: CHOLMOD, supernodal sparse Cholesky factorization and update/downdate. *ACM Transactions on Mathematical Software*, *35*(3), Article 22, 1-14. doi:10.1145/1391989.1391995

Amestoy, P. R., Davis, T. A., & Duff, I. S. (2004). Algorithm 837: AMD, an approximate minimum degree ordering algorithm. *ACM Transactions on Mathematical Software*, *17*(4), 886-905. doi:10.1145/1024074.1024081

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class dsCMatrix.

Generic functions Cholesky, updown, expand1 and expand2.

Examples

```
showClass("dCHMsimpl")
showClass("dCHMsuper")
set.seed(2)

m <- 1000L
n <- 200L
M <- rsparsematrix(m, n, 0.01)
A <- crossprod(M)

## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- rep.int(list(paste0("x", seq_len(n))), 2L)

(ch.A <- Cholesky(A)) # pivoted, by default
str(e.ch.A <- expand2(ch.A, LDL =  TRUE), max.level = 2L)
str(E.ch.A <- expand2(ch.A, LDL = FALSE), max.level = 2L)

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)
```

```
## A ~ P1' L1 D L1' P1 ~ P1' L L' P1 in floating point
stopifnot(exprs = {
    identical(names(e.ch.A), c("P1.", "L1", "D", "L1.", "P1"))
    identical(names(E.ch.A), c("P1.", "L" ,      "L." , "P1"))
    identical(e.ch.A[["P1"]],
              new("pMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
                  margin = 2L, perm = invertPerm(ch.A@perm, 0L, 1L)))
    identical(e.ch.A[["P1."]], t(e.ch.A[["P1"]]))
    identical(e.ch.A[["L1."]], t(e.ch.A[["L1"]]))
    identical(E.ch.A[["L." ]], t(E.ch.A[["L" ]]))
    identical(e.ch.A[["D"]], Diagonal(x = diag(ch.A)))
    all.equal(E.ch.A[["L"]], with(e.ch.A, L1 %*% sqrt(D)))
    ae1(A, with(e.ch.A, P1. %*% L1 %*% D %*% L1. %*% P1))
    ae1(A, with(E.ch.A, P1. %*% L  %*%         L.  %*% P1))
    ae2(A[ch.A@perm + 1L, ch.A@perm + 1L], with(e.ch.A, L1 %*% D %*% L1.))
    ae2(A[ch.A@perm + 1L, ch.A@perm + 1L], with(E.ch.A, L  %*%         L. ))
})

## Factorization handled as factorized matrix
## (in some cases only optionally, depending on arguments)
b <- rnorm(n)
stopifnot(identical(det(A), det(ch.A, sqrt = FALSE)),
          identical(solve(A, b), solve(ch.A, b, system = "A")))

u1 <- update(ch.A,   A , mult = sqrt(2))
u2 <- update(ch.A, t(M), mult = sqrt(2)) # updating with crossprod(M), not M
stopifnot(all.equal(u1, u2, tolerance = 1e-14))
```

`chol-methods` *Compute the Cholesky Factor of a Matrix*

Description

Computes the upper triangular Cholesky factor of an $n \times n$ real, symmetric, positive semidefinite matrix A, optionally after pivoting. That is the factor L' in

$$P_1 A P_1' = LL'$$

or (equivalently)

$$A = P_1' LL' P_1$$

where P_1 is a permutation matrix.

Methods for `denseMatrix` are built on LAPACK routines `dpstrf`, `dpotrf`, and `dpptrf`, The latter two do not permute rows or columns, so that P_1 is an identity matrix.

Methods for `sparseMatrix` are built on CHOLMOD routines `cholmod_analyze` and `cholmod_factorize_p`.

Usage

```
chol(x, ...)
## S4 method for signature 'dsyMatrix'
chol(x, pivot = FALSE, tol = -1, ...)
## S4 method for signature 'dspMatrix'
chol(x, ...)
## S4 method for signature 'dsCMatrix'
chol(x, pivot = FALSE, ...)
## S4 method for signature 'ddiMatrix'
chol(x, ...)
## S4 method for signature 'generalMatrix'
chol(x, uplo = "U", ...)
## S4 method for signature 'triangularMatrix'
chol(x, uplo = "U", ...)
```

Arguments

x	a finite, symmetric, positive semidefinite matrix or Matrix to be factorized. If x is square but not symmetric, then it will be *treated* as symmetric; see uplo. Methods for dense x require positive definiteness when pivot = FALSE. Methods for sparse (but not diagonal) x require positive definiteness unconditionally.
pivot	a logical indicating if the rows and columns of x should be pivoted. Methods for sparse x employ the approximate minimum degree (AMD) algorithm in order to reduce fill-in, i.e., without regard for numerical stability.
tol	a finite numeric tolerance, used only if pivot = TRUE. The factorization algorithm stops if the pivot is less than or equal to tol. Negative tol is equivalent to nrow(x) * .Machine$double.eps * max(diag(x)).
uplo	a string, either "U" or "L", indicating which triangle of x should be used to compute the factorization. The default is "U", even for lower triangular x, to be consistent with chol from **base**.
...	further arguments passed to or from methods.

Details

For x inheriting from diagonalMatrix, the diagonal result is computed directly and without pivoting, i.e., bypassing CHOLMOD.

For all other x, chol(x, pivot = value) calls Cholesky(x, perm = value, ...) under the hood. If you must know the permutation P_1 in addition to the Cholesky factor L', then call Cholesky directly, as the result of chol(x, pivot = TRUE) specifies L' but not P_1.

Value

A matrix, triangularMatrix, or diagonalMatrix representing the upper triangular Cholesky factor L'. The result is a traditional matrix if x is a traditional matrix, dense if x is dense, and sparse if x is sparse.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dpstrf.f, https://netlib.org/lapack/double/dpotrf.f, and https://netlib.org/lapack/double/dpptrf.f.

The CHOLMOD source code; see https://github.com/DrTimothyAldenDavis/SuiteSparse, notably the header file 'CHOLMOD/Include/cholmod.h' defining cholmod_factor_struct.

Chen, Y., Davis, T. A., Hager, W. W., & Rajamanickam, S. (2008). Algorithm 887: CHOLMOD, supernodal sparse Cholesky factorization and update/downdate. *ACM Transactions on Mathematical Software*, *35*(3), Article 22, 1-14. doi:10.1145/1391989.1391995

Amestoy, P. R., Davis, T. A., & Duff, I. S. (2004). Algorithm 837: AMD, an approximate minimum degree ordering algorithm. *ACM Transactions on Mathematical Software*, *17*(4), 886-905. doi:10.1145/1024074.1024081

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

The default method from **base**, chol, called for traditional matrices x.

Generic function Cholesky, for more flexibility notably when computing the Cholesky *factorization* and not only the *factor* L'.

Examples

```
showMethods("chol", inherited = FALSE)
set.seed(0)

## ---- Dense ------------------------------------------------------

## chol(x, pivot = value) wrapping Cholesky(x, perm = value)
selectMethod("chol", "dsyMatrix")

## Except in packed cases where pivoting is not yet available
selectMethod("chol", "dspMatrix")

## .... Positive definite ..................................................

(A1 <- new("dsyMatrix", Dim = c(2L, 2L), x = c(1, 2, 2, 5)))
(R1.nopivot <- chol(A1))
(R1 <- chol(A1, pivot = TRUE))

## In 2-by-2 cases, we know that the permutation is 1:2 or 2:1,
## even if in general 'chol' does not say ...

stopifnot(exprs = {
   all.equal(  A1           , as(crossprod(R1.nopivot), "dsyMatrix"))
   all.equal(t(A1[2:1, 2:1]), as(crossprod(R1        ), "dsyMatrix"))
   identical(Cholesky(A1)@perm, 2:1) # because 5 > 1
})
```

```
## .... Positive semidefinite but not positive definite .................

(A2 <- new("dpoMatrix", Dim = c(2L, 2L), x = c(1, 2, 2, 4)))
try(R2.nopivot <- chol(A2)) # fails as not positive definite
(R2 <- chol(A2, pivot = TRUE)) # returns, with a warning and ...

stopifnot(exprs = {
   all.equal(t(A2[2:1, 2:1]), as(crossprod(R2), "dsyMatrix"))
   identical(Cholesky(A2)@perm, 2:1) # because 4 > 1
})

## .... Not positive semidefinite ....................................

(A3 <- new("dsyMatrix", Dim = c(2L, 2L), x = c(1, 2, 2, 3)))
try(R3.nopivot <- chol(A3)) # fails as not positive definite
(R3 <- chol(A3, pivot = TRUE)) # returns, with a warning and ...

## _Not_ equal: see details and examples in help("Cholesky")
all.equal(t(A3[2:1, 2:1]), as(crossprod(R3), "dsyMatrix"))

## ---- Sparse ------------------------------------------------------------

## chol(x, pivot = value) wrapping
## Cholesky(x, perm = value, LDL = FALSE, super = FALSE)
selectMethod("chol", "dsCMatrix")

## Except in diagonal cases which are handled "directly"
selectMethod("chol", "ddiMatrix")

(A4 <- toeplitz(as(c(10, 0, 1, 0, 3), "sparseVector")))
(ch.A4.nopivot <- Cholesky(A4, perm = FALSE, LDL = FALSE, super = FALSE))
(ch.A4 <- Cholesky(A4, perm = TRUE, LDL = FALSE, super = FALSE))
(R4.nopivot <- chol(A4))
(R4 <- chol(A4, pivot = TRUE))

det4 <- det(A4)
b4 <- rnorm(5L)
x4 <- solve(A4, b4)

stopifnot(exprs = {
    identical(R4.nopivot, expand1(ch.A4.nopivot, "L."))
    identical(R4, expand1(ch.A4, "L."))
    all.equal(A4, crossprod(R4.nopivot))
    all.equal(A4[ch.A4@perm + 1L, ch.A4@perm + 1L], crossprod(R4))
    all.equal(diag(R4.nopivot), sqrt(diag(ch.A4.nopivot)))
    all.equal(diag(R4), sqrt(diag(ch.A4)))
    all.equal(sqrt(det4), det(R4.nopivot))
    all.equal(sqrt(det4), det(R4))
    all.equal(det4, det(ch.A4.nopivot, sqrt = FALSE))
    all.equal(det4, det(ch.A4, sqrt = FALSE))
    all.equal(x4, solve(R4.nopivot, solve(t(R4.nopivot), b4)))
    all.equal(x4, solve(ch.A4.nopivot, b4))
    all.equal(x4, solve(ch.A4, b4))
```

```
})
```

`chol2inv-methods` *Inverse from Cholesky Factor*

Description

Given *formally* upper and lower triangular matrices U and L, compute $(U'U)^{-1}$ and $(LL')^{-1}$, respectively.

This function can be seen as way to compute the inverse of a symmetric positive definite matrix given its Cholesky factor. Equivalently, it can be seen as a way to compute $(X'X)^{-1}$ given the R part of the QR factorization of X, if R is constrained to have positive diagonal entries.

Usage

```
chol2inv(x, ...)
## S4 method for signature 'dtrMatrix'
chol2inv(x, ...)
## S4 method for signature 'dtCMatrix'
chol2inv(x, ...)
## S4 method for signature 'generalMatrix'
chol2inv(x, uplo = "U", ...)
```

Arguments

`x`	a square matrix or `Matrix`, typically the result of a call to `chol`. If `x` is square but not (formally) triangular, then only the upper or lower triangle is considered, depending on optional argument `uplo` if `x` is a `Matrix`.
`uplo`	a string, either `"U"` or `"L"`, indicating which triangle of `x` contains the Cholesky factor. The default is `"U"`, to be consistent with `chol2inv` from **base**.
`...`	further arguments passed to or from methods.

Value

A matrix, `symmetricMatrix`, or `diagonalMatrix` representing the inverse of the positive definite matrix whose Cholesky factor is `x`. The result is a traditional matrix if `x` is a traditional matrix, dense if `x` is dense, and sparse if `x` is sparse.

See Also

The default method from **base**, `chol2inv`, called for traditional matrices `x`.

Generic function `chol`, for computing the upper triangular Cholesky factor L' of a symmetric positive semidefinite matrix.

Generic function `solve`, for solving linear systems and (as a corollary) for computing inverses more generally.

Examples

```
(A <- Matrix(cbind(c(1, 1, 1), c(1, 2, 4), c(1, 4, 16))))
(R <- chol(A))
(L <- t(R))
(R2i <- chol2inv(R))
(L2i <- chol2inv(R))
stopifnot(exprs = {
    all.equal(R2i, tcrossprod(solve(R)))
    all.equal(L2i,  crossprod(solve(L)))
    all.equal(as(R2i %*% A, "matrix"), diag(3L)) # the identity
    all.equal(as(L2i %*% A, "matrix"), diag(3L)) # ditto
})
```

Cholesky-class *Dense Cholesky Factorizations*

Description

Classes Cholesky and pCholesky represent dense, pivoted Cholesky factorizations of $n \times n$ real, symmetric, positive semidefinite matrices A, having the general form

$$P_1 A P_1' = L_1 D L_1' = L L'$$

or (equivalently)

$$A = P_1' L_1 D L_1' P_1 = P_1' L L' P_1$$

where P_1 is a permutation matrix, L_1 is a unit lower triangular matrix, D is a non-negative diagonal matrix, and $L = L_1 \sqrt{D}$.

These classes store the entries of the Cholesky factor L or its transpose L' in a dense format as a vector of length nn (Cholesky) or $n(n+1)/2$ (pCholesky), the latter giving the "packed" representation.

Slots

Dim, Dimnames inherited from virtual class MatrixFactorization.

uplo a string, either "U" or "L", indicating which triangle (upper or lower) of the factorized symmetric matrix was used to compute the factorization and in turn whether x stores L' or L.

x a numeric vector of length n*n (Cholesky) or n*(n+1)/2 (pCholesky), where n=Dim[1], listing the entries of the Cholesky factor L or its transpose L' in column-major order.

perm a 1-based integer vector of length Dim[1] specifying the permutation applied to the rows and columns of the factorized matrix. perm of length 0 is valid and equivalent to the identity permutation, implying no pivoting.

Extends

Class CholeskyFactorization, directly. Class MatrixFactorization, by class CholeskyFactorization, distance 2.

Instantiation

Objects can be generated directly by calls of the form `new("Cholesky", ...)` or `new("pCholesky", ...)`, but they are more typically obtained as the value of `Cholesky(x)` for `x` inheriting from `dsyMatrix` or `dspMatrix` (often the subclasses of those reserved for positive semidefinite matrices, namely `dpoMatrix` and `dppMatrix`).

Methods

`coerce signature(from = "Cholesky", to = "dtrMatrix")`: returns a `dtrMatrix` representing the Cholesky factor L or its transpose L'; see 'Note'.

`coerce signature(from = "pCholesky", to = "dtpMatrix")`: returns a `dtpMatrix` representing the Cholesky factor L or its transpose L'; see 'Note'.

`determinant signature(from = "p?Cholesky", logarithm = "logical")`: computes the determinant of the factorized matrix A or its logarithm.

`diag signature(x = "p?Cholesky")`: returns a numeric vector of length n containing the diagonal elements of D, which are the squared diagonal elements of L.

`expand1 signature(x = "p?Cholesky")`: see `expand1-methods`.

`expand2 signature(x = "p?Cholesky")`: see `expand2-methods`.

`solve signature(a = "p?Cholesky", b = .)`: see `solve-methods`.

Note

In **Matrix** < `1.6-0`, class `Cholesky` extended `dtrMatrix` and class `pCholesky` extended `dtpMatrix`, reflecting the fact that the factor L is indeed a triangular matrix. **Matrix** `1.6-0` removed these extensions so that methods would no longer be inherited from `dtrMatrix` and `dtpMatrix`. The availability of such methods gave the wrong impression that `Cholesky` and `pCholesky` represent a (singular) matrix, when in fact they represent an ordered set of matrix factors.

The coercions `as(., "dtrMatrix")` and `as(., "dtpMatrix")` are provided for users who understand the caveats.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dpstrf.f, https://netlib.org/lapack/double/dpotrf.f, and https://netlib.org/lapack/double/dpptrf.f.

Lucas, C. (2004). *LAPACK-style codes for level 2 and 3 pivoted Cholesky factorizations*. LAPACK Working Note, Number 161. https://www.netlib.org/lapack/lawnspdf/lawn161.pdf

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class `CHMfactor` for sparse Cholesky factorizations.

Classes `dpoMatrix` and `dppMatrix`.

Generic functions `Cholesky`, `expand1` and `expand2`.

Examples

```
showClass("Cholesky")
set.seed(1)

m <- 30L
n <- 6L
(A <- crossprod(Matrix(rnorm(m * n), m, n)))

## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- rep.int(list(paste0("x", seq_len(n))), 2L)

(ch.A <- Cholesky(A)) # pivoted, by default
str(e.ch.A <- expand2(ch.A, LDL =  TRUE), max.level = 2L)
str(E.ch.A <- expand2(ch.A, LDL = FALSE), max.level = 2L)

## Underlying LAPACK representation
(m.ch.A <- as(ch.A, "dtrMatrix")) # which is L', not L, because
A@uplo == "U"
stopifnot(identical(as(m.ch.A, "matrix"), `dim<-`(ch.A@x, ch.A@Dim)))

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ P1' L1 D L1' P1 ~ P1' L L' P1 in floating point
stopifnot(exprs = {
    identical(names(e.ch.A), c("P1.", "L1", "D", "L1.", "P1"))
    identical(names(E.ch.A), c("P1.", "L" ,      "L." , "P1"))
    identical(e.ch.A[["P1"]],
              new("pMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
                  margin = 2L, perm = invertPerm(ch.A@perm)))
    identical(e.ch.A[["P1."]], t(e.ch.A[["P1"]]))
    identical(e.ch.A[["L1."]], t(e.ch.A[["L1"]]))
    identical(E.ch.A[["L." ]], t(E.ch.A[["L" ]]))
    identical(e.ch.A[["D"]], Diagonal(x = diag(ch.A)))
    all.equal(E.ch.A[["L"]], with(e.ch.A, L1 %*% sqrt(D)))
    ae1(A, with(e.ch.A, P1. %*% L1 %*% D %*% L1. %*% P1))
    ae1(A, with(E.ch.A, P1. %*% L  %*%         L.  %*% P1))
    ae2(A[ch.A@perm, ch.A@perm], with(e.ch.A, L1 %*% D %*% L1.))
    ae2(A[ch.A@perm, ch.A@perm], with(E.ch.A, L  %*%         L. ))
})

## Factorization handled as factorized matrix
b <- rnorm(n)
all.equal(det(A), det(ch.A), tolerance = 0)
all.equal(solve(A, b), solve(ch.A, b), tolerance = 0)

## For identical results, we need the _unpivoted_ factorization
## computed by det(A) and solve(A, b)
(ch.A.nopivot <- Cholesky(A, perm = FALSE))
stopifnot(identical(det(A), det(ch.A.nopivot)),
          identical(solve(A, b), solve(ch.A.nopivot, b)))
```

Cholesky-methods *Methods for Cholesky Factorization*

Description

Computes the pivoted Cholesky factorization of an $n \times n$ real, symmetric matrix A, which has the general form

$$P_1 A P_1' = L_1 D L_1' \overset{D_{jj} \geq 0}{=} L L'$$

or (equivalently)

$$A = P_1' L_1 D L_1' P_1 \overset{D_{jj} \geq 0}{=} P_1' L L' P_1$$

where P_1 is a permutation matrix, L_1 is a unit lower triangular matrix, D is a diagonal matrix, and $L = L_1 \sqrt{D}$. The second equalities hold only for positive semidefinite A, for which the diagonal entries of D are non-negative and $\sqrt{D}$ is well-defined.

Methods for denseMatrix are built on LAPACK routines dpstrf, dpotrf, and dpptrf. The latter two do not permute rows or columns, so that P_1 is an identity matrix.

Methods for sparseMatrix are built on CHOLMOD routines cholmod_analyze and cholmod_factorize_p.

Usage

```
Cholesky(A, ...)
## S4 method for signature 'dsyMatrix'
Cholesky(A, perm = TRUE, tol = -1, ...)
## S4 method for signature 'dspMatrix'
Cholesky(A, ...)
## S4 method for signature 'dsCMatrix'
Cholesky(A, perm = TRUE, LDL = !super, super = FALSE,
    Imult = 0, ...)
## S4 method for signature 'ddiMatrix'
Cholesky(A, ...)
## S4 method for signature 'generalMatrix'
Cholesky(A, uplo = "U", ...)
## S4 method for signature 'triangularMatrix'
Cholesky(A, uplo = "U", ...)
## S4 method for signature 'matrix'
Cholesky(A, uplo = "U", ...)
```

Arguments

A	a finite, symmetric matrix or Matrix to be factorized. If A is square but not symmetric, then it will be *treated* as symmetric; see uplo. Methods for dense A require positive definiteness when perm = FALSE and positive semidefiniteness when perm = TRUE. Methods for sparse A require positive definiteness when LDL = TRUE and nonzero leading principal minors (after pivoting) when LDL = FALSE. Methods for sparse, *diagonal* A are an exception, requiring positive semidefiniteness unconditionally.

`perm` a logical indicating if the rows and columns of A should be pivoted. Methods for sparse `A` employ the approximate minimum degree (AMD) algorithm in order to reduce fill-in, i.e., without regard for numerical stability. Pivoting for sparsity may introduce nonpositive leading principal minors, causing the factorization to fail, in which case it may be necessary to set `perm = FALSE`.

`tol` a finite numeric tolerance, used only if `perm = TRUE`. The factorization algorithm stops if the pivot is less than or equal to `tol`. Negative `tol` is equivalent to `nrow(A) * .Machine$double.eps * max(diag(A))`.

`LDL` a logical indicating if the simplicial factorization should be computed as $P_1' L_1 D L_1' P_1$, such that the result stores the lower triangular entries of $L_1 - I + D$. The alternative is $P_1' L L' P_1$, such that the result stores the lower triangular entries of $L = L_1 \sqrt{D}$. This argument is ignored if `super = TRUE` (or if `super = NA` and the supernodal algorithm is chosen), as the supernodal code does not yet support the `LDL = TRUE` variant.

`super` a logical indicating if the factorization should use the supernodal algorithm. The alternative is the simplicial algorithm. Setting `super = NA` leaves the choice to a CHOLMOD-internal heuristic.

`Imult` a finite number. The matrix that is factorized is `A + Imult * diag(nrow(A))`, i.e., `A` plus `Imult` times the identity matrix. This argument is useful for symmetric, indefinite `A`, as `Imult > max(rowSums(abs(A)) - diag(abs(A)))` ensures that `A + Imult * diag(nrow(A))` is diagonally dominant. (Symmetric, diagonally dominant matrices are positive definite.)

`uplo` a string, either `"U"` or `"L"`, indicating which triangle of `A` should be used to compute the factorization. The default is `"U"`, even for lower triangular `A`, to be consistent with `chol` from **base**.

`...` further arguments passed to or from methods.

Details

Note that the result of a call to `Cholesky` inherits from `CholeskyFactorization` but not `Matrix`. Users who just want a matrix should consider using `chol`, whose methods are simple wrappers around `Cholesky` returning just the upper triangular Cholesky factor L', typically as a `triangularMatrix`. However, a more principled approach would be to construct factors as needed from the `CholeskyFactorization` object, e.g., with `expand1(x, "L")`, if `x` is the object.

The behaviour of `Cholesky(A, perm = TRUE)` for dense `A` is somewhat exceptional, in that it expects *without* checking that `A` is positive semidefinite. By construction, if A is positive semidefinite and the exact algorithm encounters a zero pivot, then the unfactorized trailing submatrix is the zero matrix, and there is nothing left to do. Hence when the finite precision algorithm encounters a pivot less than `tol`, it signals a warning instead of an error and zeros the trailing submatrix in order to guarantee that $P'LL'P$ is positive semidefinite even if A is not. It follows that one way to test for positive semidefiniteness of A in the event of a warning is to analyze the error

$$\frac{\|A - P'LL'P\|}{\|A\|}.$$

See the examples and LAPACK Working Note ("LAWN") 161 for details.

Value

An object representing the factorization, inheriting from virtual class CholeskyFactorization. For a traditional matrix A, the specific class is Cholesky. For A inheriting from unpackedMatrix, packedMatrix, and sparseMatrix, the specific class is Cholesky, pCholesky, and dCHMsimpl or dCHMsuper, respectively.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dpstrf.f, https://netlib.org/lapack/double/dpotrf.f, and https://netlib.org/lapack/double/dpptrf.f.

The CHOLMOD source code; see https://github.com/DrTimothyAldenDavis/SuiteSparse, notably the header file 'CHOLMOD/Include/cholmod.h' defining cholmod_factor_struct.

Lucas, C. (2004). *LAPACK-style codes for level 2 and 3 pivoted Cholesky factorizations*. LAPACK Working Note, Number 161. https://www.netlib.org/lapack/lawnspdf/lawn161.pdf

Chen, Y., Davis, T. A., Hager, W. W., & Rajamanickam, S. (2008). Algorithm 887: CHOLMOD, supernodal sparse Cholesky factorization and update/downdate. *ACM Transactions on Mathematical Software*, *35*(3), Article 22, 1-14. doi:10.1145/1391989.1391995

Amestoy, P. R., Davis, T. A., & Duff, I. S. (2004). Algorithm 837: AMD, an approximate minimum degree ordering algorithm. *ACM Transactions on Mathematical Software*, *17*(4), 886-905. doi:10.1145/1024074.1024081

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Classes Cholesky, pCholesky, dCHMsimpl and dCHMsuper and their methods.

Classes dpoMatrix, dppMatrix, and dsCMatrix.

Generic function chol, for obtaining the upper triangular Cholesky factor L' as a matrix or Matrix.

Generic functions expand1 and expand2, for constructing matrix factors from the result.

Generic functions BunchKaufman, Schur, lu, and qr, for computing other factorizations.

Examples

```
showMethods("Cholesky", inherited = FALSE)
set.seed(0)

## ---- Dense -------------------------------------------------------

## .... Positive definite ...............................................

n <- 6L
(A1 <- crossprod(Matrix(rnorm(n * n), n, n)))
(ch.A1.nopivot <- Cholesky(A1, perm = FALSE))
(ch.A1 <- Cholesky(A1))
stopifnot(exprs = {
    length(ch.A1@perm) == ncol(A1)
```

```
    isPerm(ch.A1@perm)
    is.unsorted(ch.A1@perm) # typically not the identity permutation
    length(ch.A1.nopivot@perm) == 0L
})

## A ~ P1' L D L' P1 ~ P1' L L' P1 in floating point
str(e.ch.A1 <- expand2(ch.A1, LDL =  TRUE), max.level = 2L)
str(E.ch.A1 <- expand2(ch.A1, LDL = FALSE), max.level = 2L)
stopifnot(exprs = {
    all.equal(as(A1, "matrix"), as(Reduce(`%*%`, e.ch.A1), "matrix"))
    all.equal(as(A1, "matrix"), as(Reduce(`%*%`, E.ch.A1), "matrix"))
})

## .... Positive semidefinite but not positive definite .................

A2 <- A1
A2[1L, ] <- A2[, 1L] <- 0
A2
try(Cholesky(A2, perm = FALSE)) # fails as not positive definite
ch.A2 <- Cholesky(A2) # returns, with a warning and ...
A2.hat <- Reduce(`%*%`, expand2(ch.A2, LDL = FALSE))
norm(A2 - A2.hat, "2") / norm(A2, "2") # 7.670858e-17

## .... Not positive semidefinite .....................................

A3 <- A1
A3[1L, ] <- A3[, 1L] <- -1
A3
try(Cholesky(A3, perm = FALSE)) # fails as not positive definite
ch.A3 <- Cholesky(A3) # returns, with a warning and ...
A3.hat <- Reduce(`%*%`, expand2(ch.A3, LDL = FALSE))
norm(A3 - A3.hat, "2") / norm(A3, "2") # 1.781568

## Indeed, 'A3' is not positive semidefinite, but 'A3.hat' _is_
ch.A3.hat <- Cholesky(A3.hat)
A3.hat.hat <- Reduce(`%*%`, expand2(ch.A3.hat, LDL = FALSE))
norm(A3.hat - A3.hat.hat, "2") / norm(A3.hat, "2") # 1.777944e-16

## ---- Sparse ------------------------------------------------------------

## Really just three cases modulo permutation :
##
##            type        factorization  minors of P1 A P1'
##   1  simplicial  P1 A P1' = L1 D L1'             nonzero
##   2  simplicial  P1 A P1' = L    L '            positive
##   3  supernodal  P1 A P2' = L    L '            positive

data(KNex, package = "Matrix")
A4 <- crossprod(KNex[["mm"]])

ch.A4 <-
list(pivoted =
     list(simpl1 = Cholesky(A4, perm =  TRUE, super = FALSE, LDL =  TRUE),
```

```
          simpl0 = Cholesky(A4, perm =  TRUE, super = FALSE, LDL = FALSE),
          super0 = Cholesky(A4, perm =  TRUE, super =  TRUE             )),
     unpivoted =
     list(simpl1 = Cholesky(A4, perm = FALSE, super = FALSE, LDL =  TRUE),
          simpl0 = Cholesky(A4, perm = FALSE, super = FALSE, LDL = FALSE),
          super0 = Cholesky(A4, perm = FALSE, super =  TRUE             )))
ch.A4

s <- simplify2array
rapply2 <- function(object, f, ...) rapply(object, f, , , how = "list", ...)

s(rapply2(ch.A4, isLDL))
s(m.ch.A4 <- rapply2(ch.A4, expand1, "L")) # giving L = L1 sqrt(D)

## By design, the pivoted and simplicial factorizations
## are more sparse than the unpivoted and supernodal ones ...
s(rapply2(m.ch.A4, object.size))

## Which is nicely visualized by lattice-based methods for 'image'
inm <- c("pivoted", "unpivoted")
jnm <- c("simpl1", "simpl0", "super0")
for(i in 1:2)
  for(j in 1:3)
    print(image(m.ch.A4[[c(i, j)]], main = paste(inm[i], jnm[j])),
          split = c(j, i, 3L, 2L), more = i * j < 6L)

simpl1 <- ch.A4[[c("pivoted", "simpl1")]]
stopifnot(exprs = {
    length(simpl1@perm) == ncol(A4)
    isPerm(simpl1@perm, 0L)
    is.unsorted(simpl1@perm) # typically not the identity permutation
})

## One can expand with and without D regardless of isLDL(.),
## but "without" requires L = L1 sqrt(D), which is conditional
## on min(diag(D)) >= 0, hence "with" is the default
isLDL(simpl1)
stopifnot(min(diag(simpl1)) >= 0)
str(e.ch.A4 <- expand2(simpl1, LDL =  TRUE), max.level = 2L) # default
str(E.ch.A4 <- expand2(simpl1, LDL = FALSE), max.level = 2L)
stopifnot(exprs = {
    all.equal(E.ch.A4[["L" ]], e.ch.A4[["L1" ]] %*% sqrt(e.ch.A4[["D"]]))
    all.equal(E.ch.A4[["L."]], sqrt(e.ch.A4[["D"]]) %*% e.ch.A4[["L1."]])
    all.equal(A4, as(Reduce(`%*%`, e.ch.A4), "symmetricMatrix"))
    all.equal(A4, as(Reduce(`%*%`, E.ch.A4), "symmetricMatrix"))
})

## The "same" permutation matrix with "alternate" representation
## [i, perm[i]] {margin=1} <-> [invertPerm(perm)[j], j] {margin=2}
alt <- function(P) {
    P@margin <- 1L + !(P@margin - 1L) # 1 <-> 2
    P@perm <- invertPerm(P@perm)
    P
```

```
}

## Expansions are elegant but inefficient (transposes are redundant)
## hence programmers should consider methods for 'expand1' and 'diag'
stopifnot(exprs = {
    identical(expand1(simpl1, "P1"), alt(e.ch.A4[["P1"]]))
    identical(expand1(simpl1, "L"), E.ch.A4[["L"]])
    identical(Diagonal(x = diag(simpl1)), e.ch.A4[["D"]])
})

## chol(A, pivot = value) is a simple wrapper around
## Cholesky(A, perm = value, LDL = FALSE, super = FALSE),
## returning L' = sqrt(D) L1' _but_ giving no information
## about the permutation P1
selectMethod("chol", "dsCMatrix")
stopifnot(all.equal(chol(A4, pivot = TRUE), E.ch.A4[["L."]]))

## Now a symmetric matrix with positive _and_ negative eigenvalues,
## hence _not_ positive semidefinite
A5 <- new("dsCMatrix",
          Dim = c(7L, 7L),
          p = c(0:1, 3L, 6:7, 10:11, 15L),
          i = c(0L, 0:1, 0:3, 2:5, 3:6),
          x = c(1, 6, 38, 10, 60, 103, -4, 6, -32, -247, -2, -16, -128, -2, -67))
(ev <- eigen(A5, only.values = TRUE)$values)
(t.ev <- table(factor(sign(ev), -1:1))) # the matrix "inertia"

ch.A5 <- Cholesky(A5)
isLDL(ch.A5)
(d.A5 <- diag(ch.A5)) # diag(D) is partly negative

## Sylvester's law of inertia holds here, but not in general
## in finite precision arithmetic
stopifnot(identical(table(factor(sign(d.A5), -1:1)), t.ev))

try(expand1(ch.A5, "L"))         # unable to compute L = L1 sqrt(D)
try(expand2(ch.A5, LDL = FALSE)) # ditto
try(chol(A5, pivot = TRUE))      # ditto

## The default expansion is "square root free" and still works here
str(e.ch.A5 <- expand2(ch.A5, LDL = TRUE), max.level = 2L)
stopifnot(all.equal(A5, as(Reduce(`%*%`, e.ch.A5), "symmetricMatrix")))

## Version of the SuiteSparse library, which includes CHOLMOD
Mv <- Matrix.Version()
Mv[["suitesparse"]]
```

---

coerce-methods-graph *Conversions "graph" <–> (sparse) Matrix*

Description

Since 2005, package **Matrix** has supported coercions to and from class graph from package **graph**. Since 2013, this functionality has been exposed via functions T2graph and graph2T, which, unlike methods for as(from, "<Class>"), support optional arguments.

Usage

```
graph2T(from, use.weights = )
T2graph(from, need.uniq = !isUniqueT(from), edgemode = NULL)
```

Arguments

from	for graph2T(), an R object of class "graph"; for T2graph(), a sparse matrix inheriting from "TsparseMatrix".
use.weights	logical indicating if weights should be used, i.e., equivalently the result will be numeric, i.e. of class dgTMatrix; otherwise the result will be ngTMatrix or nsTMatrix, the latter if the graph is undirected. The default looks if there are weights in the graph, and if any differ from 1, weights are used.
need.uniq	a logical indicating if from may need to be internally "uniqified"; do not set this and hence rather use the default, unless you know what you are doing!
edgemode	one of NULL, "directed", or "undirected". The default NULL looks if the matrix is symmetric and assumes "undirected" in that case.

Value

For graph2T(), a sparse matrix inheriting from "TsparseMatrix".

For T2graph() an R object of class "graph".

See Also

Package **igraph**, which provides similar coercions to and from its class igraph via functions graph_from_adjacency_matrix and as_adjacency_matrix.

Examples

```
if(requireNamespace("graph")) {
  n4 <- LETTERS[1:4]; dns <- list(n4,n4)
  show(a1 <- sparseMatrix(i= c(1:4),   j=c(2:4,1),   x = 2,    dimnames=dns))
  show(g1 <- as(a1, "graph")) # directed
  unlist(graph::edgeWeights(g1)) # all '2'

  show(a2 <- sparseMatrix(i= c(1:4,4), j=c(2:4,1:2), x = TRUE, dimnames=dns))
  show(g2 <- as(a2, "graph")) # directed
  # now if you want it undirected:
  show(g3  <- T2graph(as(a2,"TsparseMatrix"), edgemode="undirected"))
  show(m3 <- as(g3,"Matrix"))
  show( graph2T(g3) ) # a "pattern Matrix" (nsTMatrix)

  a. <- sparseMatrix(i=4:1, j=1:4, dimnames=list(n4, n4), repr="T") # no 'x'
```

```
  show(a.) # "ngTMatrix"
  show(g. <- as(a., "graph"))

}
```

`coerce-methods-SparseM` *Sparse Matrix Coercion from and to those from package* **SparseM**

Description

Methods for coercion from and to sparse matrices from package **SparseM** are provided here, for ease of porting functionality to the **Matrix** package, and comparing functionality of the two packages. All these work via the usual `as(., "<class>")` coercion,

```
as(from, Class)
```

Methods

from = "matrix.csr", to = "dgRMatrix" ...

from = "matrix.csc", to = "dgCMatrix" ...

from = "matrix.coo", to = "dgTMatrix" ...

from = "dgRMatrix", to = "matrix.csr" ...

from = "dgCMatrix", to = "matrix.csc" ...

from = "dgTMatrix", to = "matrix.coo" ...

from = "Matrix", to = "matrix.csr" ...

from = "matrix.csr", to = "dgCMatrix" ...

from = "matrix.coo", to = "dgCMatrix" ...

from = "matrix.csr", to = "Matrix" ...

from = "matrix.csc", to = "Matrix" ...

from = "matrix.coo", to = "Matrix" ...

See Also

The documentation in CRAN package **SparseM**, such as `SparseM.ontology`, and one important class, `matrix.csr`.

colSums-methods *Form Row and Column Sums and Means*

Description

Form row and column sums and means for objects, for sparseMatrix the result may optionally be sparse (sparseVector), too. Row or column names are kept respectively as for **base** matrices and colSums methods, when the result is numeric vector.

Usage

```
 colSums(x, na.rm = FALSE, dims = 1L, ...)
 rowSums(x, na.rm = FALSE, dims = 1L, ...)
colMeans(x, na.rm = FALSE, dims = 1L, ...)
rowMeans(x, na.rm = FALSE, dims = 1L, ...)

## S4 method for signature 'CsparseMatrix'
 colSums(x, na.rm = FALSE, dims = 1L,
         sparseResult = FALSE, ...)
## S4 method for signature 'CsparseMatrix'
 rowSums(x, na.rm = FALSE, dims = 1L,
         sparseResult = FALSE, ...)
## S4 method for signature 'CsparseMatrix'
colMeans(x, na.rm = FALSE, dims = 1L,
         sparseResult = FALSE, ...)
## S4 method for signature 'CsparseMatrix'
rowMeans(x, na.rm = FALSE, dims = 1L,
         sparseResult = FALSE, ...)
```

Arguments

x	a Matrix, i.e., inheriting from Matrix.
na.rm	logical. Should missing values (including NaN) be omitted from the calculations?
dims	completely ignored by the Matrix methods.
...	potentially further arguments, for method <-> generic compatibility.
sparseResult	logical indicating if the result should be sparse, i.e., inheriting from class sparseVector. Only applicable when x is inheriting from a sparseMatrix class.

Value

returns a numeric vector if sparseResult is FALSE as per default. Otherwise, returns a sparseVector.

dimnames(x) are only kept (as names(v)) when the resulting v is numeric, since sparseVectors do not have names.

See Also

colSums and the sparseVector classes.

Examples

```
(M <- bdiag(Diagonal(2), matrix(1:3, 3,4), diag(3:2))) # 7 x 8
colSums(M)
d <- Diagonal(10, c(0,0,10,0,2,rep(0,5)))
MM <- kronecker(d, M)
dim(MM) # 70 80
length(MM@x) # 160, but many are '0' ; drop those:
MM <- drop0(MM)
length(MM@x) # 32
  cm <- colSums(MM)
(scm <- colSums(MM, sparseResult = TRUE))
stopifnot(is(scm, "sparseVector"),
          identical(cm, as.numeric(scm)))
rowSums (MM, sparseResult = TRUE) # 14 of 70 are not zero
colMeans(MM, sparseResult = TRUE) # 16 of 80 are not zero
## Since we have no 'NA's, these two are equivalent :
stopifnot(identical(rowMeans(MM, sparseResult = TRUE),
                    rowMeans(MM, sparseResult = TRUE, na.rm = TRUE)),
  rowMeans(Diagonal(16)) == 1/16,
  colSums(Diagonal(7)) == 1)

## dimnames(x) -->  names( <value> ) :
dimnames(M) <- list(paste0("r", 1:7), paste0("V",1:8))
M
colSums(M)
rowMeans(M)
## Assertions :
stopifnot(exprs = {
    all.equal(colSums(M),
              structure(c(1,1,6,6,6,6,3,2), names = colnames(M)))
    all.equal(rowMeans(M),
              structure(c(1,1,4,8,12,3,2)/8, names = paste0("r", 1:7)))
})
```

`condest` *Compute Approximate CONDition number and 1-Norm of (Large) Matrices*

Description

"Estimate", i.e. compute approximately the CONDition number of a (potentially large, often sparse) matrix `A`. It works by apply a fast *randomized* approximation of the 1-norm, `norm(A,"1")`, through `onenormest(.)`.

Usage

```
condest(A, t = min(n, 5), normA = norm(A, "1"),
        silent = FALSE, quiet = TRUE)
```

```
onenormest(A, t = min(n, 5), A.x, At.x, n,
           silent = FALSE, quiet = silent,
           iter.max = 10, eps = 4 * .Machine$double.eps)
```

Arguments

A	a square matrix, optional for onenormest(), where instead of A, A.x and At.x can be specified, see there.
t	number of columns to use in the iterations.
normA	number; (an estimate of) the 1-norm of A, by default norm(A, "1"); may be replaced by an estimate.
silent	logical indicating if warning and (by default) convergence messages should be displayed.
quiet	logical indicating if convergence messages should be displayed.
A.x, At.x	when A is missing, these two must be given as functions which compute A %% x, or t(A) %% x, respectively.
n	== nrow(A), only needed when A is not specified.
iter.max	maximal number of iterations for the 1-norm estimator.
eps	the relative change that is deemed irrelevant.

Details

condest() calls lu(A), and subsequently onenormest(A.x = , At.x =) to compute an approximate norm of the *inverse* of A, A^{-1}, in a way which keeps using sparse matrices efficiently when A is sparse.

Note that onenormest() uses random vectors and hence *both* functions' results are random, i.e., depend on the random seed, see, e.g., set.seed().

Value

Both functions return a list; condest() with components,

est	a number > 0, the estimated (1-norm) condition number $\hat{\kappa}$; when $r :=$rcond(A), $1/\hat{\kappa} \approx r$.
v	the maximal Ax column, scaled to norm(v) = 1. Consequently, $norm(Av) = norm(A)/est$; when est is large, v is an approximate null vector.

The function onenormest() returns a list with components,

est	a number > 0, the estimated norm(A, "1").
v	0-1 integer vector length n, with an 1 at the index j with maximal column A[, j] in A.
w	numeric vector, the largest Ax found.
iter	the number of iterations used.

Author(s)

This is based on octave's `condest()` and `onenormest()` implementations with original author Jason Riedy, U Berkeley; translation to R and adaption by Martin Maechler.

References

Nicholas J. Higham and Françoise Tisseur (2000). A Block Algorithm for Matrix 1-Norm Estimation, with an Application to 1-Norm Pseudospectra. *SIAM J. Matrix Anal. Appl.* **21**, 4, 1185–1201.

William W. Hager (1984). Condition Estimates. *SIAM J. Sci. Stat. Comput.* **5**, 311–316.

See Also

`norm`, `rcond`.

Examples

```
data(KNex, package = "Matrix")
mtm <- with(KNex, crossprod(mm))
system.time(ce <- condest(mtm))
sum(abs(ce$v)) ## || v ||_1  == 1
## Prove that  || A v || = || A || / est  (as ||v|| = 1):
stopifnot(all.equal(norm(mtm %*% ce$v),
                    norm(mtm) / ce$est))

## reciprocal
1 / ce$est
system.time(rc <- rcond(mtm)) # takes ca  3 x  longer
rc
all.equal(rc, 1/ce$est) # TRUE -- the approximation was good

one <- onenormest(mtm)
str(one) ## est = 12.3
## the maximal column:
which(one$v == 1) # mostly 4, rarely 1, depending on random seed
```

`CsparseMatrix-class` *Class "CsparseMatrix" of Sparse Matrices in Column-compressed Form*

Description

The `"CsparseMatrix"` class is the virtual class of all sparse matrices coded in sorted compressed column-oriented form. Since it is a virtual class, no objects may be created from it. See `showClass("CsparseMatrix")` for its subclasses.

Slots

i: Object of class "integer" of length nnzero (number of non-zero elements). These are the *0-based* row numbers for each non-zero element in the matrix, i.e., i must be in 0:(nrow(.)-1).

p: integer vector for providing pointers, one for each column, to the initial (zero-based) index of elements in the column. .@p is of length ncol(.) + 1, with p[1] == 0 and p[length(p)] == nnzero, such that in fact, diff(.@p) are the number of non-zero elements for each column.

In other words, m@p[1:ncol(m)] contains the indices of those elements in m@x that are the first elements in the respective column of m.

Dim, Dimnames: inherited from the superclass, see the sparseMatrix class.

Extends

Class "sparseMatrix", directly. Class "Matrix", by class "sparseMatrix".

Methods

matrix products %*%, crossprod() and tcrossprod(), several solve methods, and other matrix methods available:

signature(e1 = "CsparseMatrix", e2 = "numeric"): ...

Arith signature(e1 = "numeric", e2 = "CsparseMatrix"): ...

Math signature(x = "CsparseMatrix"): ...

band signature(x = "CsparseMatrix"): ...

- signature(e1 = "CsparseMatrix", e2 = "numeric"): ...

- signature(e1 = "numeric", e2 = "CsparseMatrix"): ...

+ signature(e1 = "CsparseMatrix", e2 = "numeric"): ...

+ signature(e1 = "numeric", e2 = "CsparseMatrix"): ...

coerce signature(from = "CsparseMatrix", to = "TsparseMatrix"): ...

coerce signature(from = "CsparseMatrix", to = "denseMatrix"): ...

coerce signature(from = "CsparseMatrix", to = "matrix"): ...

coerce signature(from = "TsparseMatrix", to = "CsparseMatrix"): ...

coerce signature(from = "denseMatrix", to = "CsparseMatrix"): ...

diag signature(x = "CsparseMatrix"): ...

gamma signature(x = "CsparseMatrix"): ...

lgamma signature(x = "CsparseMatrix"): ...

log signature(x = "CsparseMatrix"): ...

t signature(x = "CsparseMatrix"): ...

tril signature(x = "CsparseMatrix"): ...

triu signature(x = "CsparseMatrix"): ...

Note

All classes extending CsparseMatrix have a common validity (see validObject) check function. That function additionally checks the i slot for each column to contain increasing row numbers. In earlier versions of **Matrix** (<= 0.999375-16), validObject automatically re-sorted the entries when necessary, and hence new() calls with somewhat permuted i and x slots worked, as new(...) (*with* slot arguments) automatically checks the validity.

Now, you have to use sparseMatrix to achieve the same functionality or know how to use .validateCsparse() to do so.

See Also

colSums, kronecker, and other such methods with own help pages.

Further, the super class of CsparseMatrix, sparseMatrix, and, e.g., class dgCMatrix for the links to other classes.

Examples

```
getClass("CsparseMatrix")

## The common validity check function (based on C code):
getValidity(getClass("CsparseMatrix"))
```

---

ddenseMatrix-class *Virtual Class "ddenseMatrix" of Numeric Dense Matrices*

Description

This is the virtual class of all dense numeric (i.e., **d**ouble, hence *"ddense"*) S4 matrices.

Its most important subclass is the dgeMatrix class.

Extends

Class "dMatrix" directly; class "Matrix", by the above.

Slots

the same slots at its subclass dgeMatrix, see there.

Methods

Most methods are implemented via as(*, "generalMatrix") and are mainly used as "fallbacks" when the subclass doesn't need its own specialized method.

Use showMethods(class = "ddenseMatrix", where = "package:Matrix") for an overview.

See Also

The virtual classes Matrix, dMatrix, and dsparseMatrix.

Examples

```
showClass("ddenseMatrix")

showMethods(class = "ddenseMatrix", where = "package:Matrix")
```

---

ddiMatrix-class *Class "ddiMatrix" of Diagonal Numeric Matrices*

Description

The class "ddiMatrix" of numerical diagonal matrices. Note that diagonal matrices now extend sparseMatrix, whereas they did extend dense matrices earlier.

Objects from the Class

Objects can be created by calls of the form new("ddiMatrix", ...) but typically rather via Diagonal.

Slots

x: numeric vector. For an $n \times n$ matrix, the x slot is of length n or 0, depending on the diag slot:

diag: "character" string, either "U" or "N" where "U" denotes unit-diagonal, i.e., identity matrices.

Dim,Dimnames: matrix dimension and dimnames, see the Matrix class description.

Extends

Class "diagonalMatrix", directly. Class "dMatrix", directly. Class "sparseMatrix", indirectly, see showClass("ddiMatrix").

Methods

%*% signature(x = "ddiMatrix", y = "ddiMatrix"): ...

See Also

Class diagonalMatrix and function Diagonal.

Examples

```
(d2 <- Diagonal(x = c(10,1)))
str(d2)
## slightly larger in internal size:
str(as(d2, "sparseMatrix"))

M <- Matrix(cbind(1,2:4))
M %*% d2 #> `fast' multiplication

chol(d2) # trivial
```

```
stopifnot(is(cd2 <- chol(d2), "ddiMatrix"),
          all.equal(cd2@x, c(sqrt(10),1)))
```

---

denseLU-class *Dense LU Factorizations*

Description

denseLU is the class of dense, row-pivoted LU factorizations of $m \times n$ real matrices A, having the general form

$$P_1 A = LU$$

or (equivalently)

$$A = P_1' LU$$

where P_1 is an $m \times m$ permutation matrix, L is an $m \times \min(m, n)$ unit lower trapezoidal matrix, and U is a $\min(m, n) \times n$ upper trapezoidal matrix. If $m = n$, then the factors L and U are triangular.

Slots

Dim, Dimnames inherited from virtual class MatrixFactorization.

x a numeric vector of length prod(Dim) storing the triangular L and U factors together in a packed format. The details of the representation are specified by the manual for LAPACK routine dgetrf.

perm an integer vector of length min(Dim) specifying the permutation P_1 as a product of transpositions. The corresponding permutation vector can be obtained as asPerm(perm).

Extends

Class LU, directly. Class MatrixFactorization, by class LU, distance 2.

Instantiation

Objects can be generated directly by calls of the form new("denseLU", ...), but they are more typically obtained as the value of lu(x) for x inheriting from denseMatrix (often dgeMatrix).

Methods

coerce signature(from = "denseLU", to = "dgeMatrix"): returns a dgeMatrix with the dimensions of the factorized matrix A, equal to L below the diagonal and equal to U on and above the diagonal.

determinant signature(from = "denseLU", logarithm = "logical"): computes the determinant of the factorized matrix A or its logarithm.

expand signature(x = "denseLU"): see expand-methods.

expand1 signature(x = "denseLU"): see expand1-methods.

expand2 signature(x = "denseLU"): see expand2-methods.

solve signature(a = "denseLU", b = "missing"): see solve-methods.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dgetrf.f.

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class sparseLU for sparse LU factorizations.

Class dgeMatrix.

Generic functions lu, expand1 and expand2.

Examples

```
showClass("denseLU")
set.seed(1)

n <- 3L
(A <- Matrix(round(rnorm(n * n), 2L), n, n))

## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- list(paste0("r", seq_len(n)),
                          paste0("c", seq_len(n)))

(lu.A <- lu(A))
str(e.lu.A <- expand2(lu.A), max.level = 2L)

## Underlying LAPACK representation
(m.lu.A <- as(lu.A, "dgeMatrix")) # which is L and U interlaced
stopifnot(identical(as(m.lu.A, "matrix"), `dim<-`(lu.A@x, lu.A@Dim)))

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ P1' L U in floating point
stopifnot(exprs = {
    identical(names(e.lu.A), c("P1.", "L", "U"))
    identical(e.lu.A[["P1."]],
              new(  "pMatrix", Dim = c(n, n), Dimnames = c(dn[1L], list(NULL)),
                  margin = 1L, perm = invertPerm(asPerm(lu.A@perm))))
    identical(e.lu.A[["L"]],
              new("dtrMatrix", Dim = c(n, n), Dimnames = list(NULL, NULL),
                  uplo = "L", diag = "U", x = lu.A@x))
    identical(e.lu.A[["U"]],
              new("dtrMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
                  uplo = "U", diag = "N", x = lu.A@x))
    ae1(A, with(e.lu.A, P1. %*% L %*% U))
    ae2(A[asPerm(lu.A@perm), ], with(e.lu.A, L %*% U))
})
```

```
## Factorization handled as factorized matrix
b <- rnorm(n)
stopifnot(identical(det(A), det(lu.A)),
          identical(solve(A, b), solve(lu.A, b)))
```

---

denseMatrix-class *Virtual Class "denseMatrix" of All Dense Matrices*

Description

This is the virtual class of all dense (S4) matrices. It partitions into two subclasses packedMatrix and unpackedMatrix. Alternatively into the (currently) three subclasses ddenseMatrix, ldenseMatrix, and ndenseMatrix.

denseMatrix is (hence) the direct superclass of these $(2 + 3 = 5)$ classes.

Extends

class "Matrix" directly.

Slots

exactly those of its superclass "Matrix", i.e., "Dim" and "Dimnames".

Methods

Use showMethods(class = "denseMatrix", where = "package:Matrix") for an overview of methods.

Extraction ("[") methods, see [-methods.

See Also

colSums, kronecker, and other such methods with own help pages.

Its superclass Matrix, and main subclasses, ddenseMatrix and sparseMatrix.

Examples

```
showClass("denseMatrix")
```

dgCMatrix-class *Compressed, sparse, column-oriented numeric matrices*

Description

The dgCMatrix class is a class of sparse numeric matrices in the compressed, sparse, column-oriented format. In this implementation the non-zero elements in the columns are sorted into increasing row order. dgCMatrix is the *"standard"* class for sparse numeric matrices in the **Matrix** package.

Objects from the Class

Objects can be created by calls of the form new("dgCMatrix", ...), more typically via as(*, "CsparseMatrix") or similar. Often however, more easily via Matrix(*, sparse = TRUE), or most efficiently via sparseMatrix().

Slots

x: Object of class "numeric" - the non-zero elements of the matrix.

... all other slots are inherited from the superclass "CsparseMatrix".

Methods

Matrix products (e.g., crossprod-methods), and (among other)

coerce signature(from = "matrix", to = "dgCMatrix")

diag signature(x = "dgCMatrix"): returns the diagonal of x

dim signature(x = "dgCMatrix"): returns the dimensions of x

image signature(x = "dgCMatrix"): plots an image of x using the levelplot function

solve signature(a = "dgCMatrix", b = "..."): see solve-methods, notably the extra argument sparse.

lu signature(x = "dgCMatrix"): computes the LU decomposition of a square dgCMatrix object

See Also

Classes dsCMatrix, dtCMatrix, lu

Examples

```
(m <- Matrix(c(0,0,2:0), 3,5))
str(m)
m[,1]
```

dgeMatrix-class *Class "dgeMatrix" of Dense Numeric (S4 Class) Matrices*

Description

A general numeric dense matrix in the S4 Matrix representation. `dgeMatrix` is the *"standard"* class for dense numeric matrices in the **Matrix** package.

Objects from the Class

Objects can be created by calls of the form `new("dgeMatrix", ...)` or, more commonly, by coercion from the `Matrix` class (see Matrix) or by `Matrix(..)`.

Slots

`x`: Object of class `"numeric"` - the numeric values contained in the matrix, in column-major order.

`Dim`: Object of class `"integer"` - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

`Dimnames`: a list of length two - inherited from class `Matrix`.

`factors`: Object of class `"list"` - a list of factorizations of the matrix.

Methods

The are group methods (see, e.g., `Arith`)

Arith `signature(e1 = "dgeMatrix", e2 = "dgeMatrix")`: ...

Arith `signature(e1 = "dgeMatrix", e2 = "numeric")`: ...

Arith `signature(e1 = "numeric", e2 = "dgeMatrix")`: ...

Math `signature(x = "dgeMatrix")`: ...

Math2 `signature(x = "dgeMatrix", digits = "numeric")`: ...

matrix products `%*%`, `crossprod()` and `tcrossprod()`, several `solve` methods, and other matrix methods available:

Schur `signature(x = "dgeMatrix", vectors = "logical")`: ...

Schur `signature(x = "dgeMatrix", vectors = "missing")`: ...

chol `signature(x = "dgeMatrix")`: see `chol`.

colMeans `signature(x = "dgeMatrix")`: columnwise means (averages)

colSums `signature(x = "dgeMatrix")`: columnwise sums

diag `signature(x = "dgeMatrix")`: ...

dim `signature(x = "dgeMatrix")`: ...

dimnames `signature(x = "dgeMatrix")`: ...

eigen `signature(x = "dgeMatrix", only.values= "logical")`: ...

eigen `signature(x = "dgeMatrix", only.values= "missing")`: ...

norm `signature(x = "dgeMatrix", type = "character")`: ...

norm `signature(x = "dgeMatrix", type = "missing")`: ...

rcond `signature(x = "dgeMatrix", norm = "character")` or `norm = "missing"`: the reciprocal condition number, `rcond()`.

rowMeans `signature(x = "dgeMatrix")`: rowwise means (averages)

rowSums `signature(x = "dgeMatrix")`: rowwise sums

t `signature(x = "dgeMatrix")`: matrix transpose

See Also

Classes `Matrix`, `dtrMatrix`, and `dsyMatrix`.

`dgRMatrix-class` *Sparse Compressed, Row-oriented Numeric Matrices*

Description

The `dgRMatrix` class is a class of sparse numeric matrices in the compressed, sparse, row-oriented format. In this implementation the non-zero elements in the rows are sorted into increasing column order.

Note: The column-oriented sparse classes, e.g., `dgCMatrix`, are preferred and better supported in the **Matrix** package.

Objects from the Class

Objects can be created by calls of the form `new("dgRMatrix", ...)`.

Slots

j: Object of class `"integer"` of length nnzero (number of non-zero elements). These are the column numbers for each non-zero element in the matrix.

p: Object of class `"integer"` of pointers, one for each row, to the initial (zero-based) index of elements in the row.

x: Object of class `"numeric"` - the non-zero elements of the matrix.

Dim: Object of class `"integer"` - the dimensions of the matrix.

Methods

diag `signature(x = "dgRMatrix")`: returns the diagonal of `x`

dim `signature(x = "dgRMatrix")`: returns the dimensions of `x`

image `signature(x = "dgRMatrix")`: plots an image of `x` using the `levelplot` function

See Also

the `RsparseMatrix` class, the virtual class of all sparse compressed **r**ow-oriented matrices, with its methods. The `dgCMatrix` class (**c**olumn compressed sparse) is really preferred.

dgTMatrix-class *Sparse matrices in triplet form*

Description

The "dgTMatrix" class is the class of sparse matrices stored as (possibly redundant) triplets. The internal representation is not at all unique, contrary to the one for class dgCMatrix.

Objects from the Class

Objects can be created by calls of the form new("dgTMatrix", ...), but more typically via spMatrix() or sparseMatrix(*, repr = "T").

Slots

i: integer row indices of non-zero entries *in 0-base*, i.e., must be in 0:(nrow(.)-1).

j: integer column indices of non-zero entries. Must be the same length as slot i and *0-based* as well, i.e., in 0:(ncol(.)-1).

x: numeric vector - the (non-zero) entry at position (i,j). Must be the same length as slot i. If an index pair occurs more than once, the corresponding values of slot x are added to form the element of the matrix.

Dim: Object of class "integer" of length 2 - the dimensions of the matrix.

Methods

+ signature(e1 = "dgTMatrix", e2 = "dgTMatrix")

image signature(x = "dgTMatrix"): plots an image of x using the levelplot function

t signature(x = "dgTMatrix"): returns the transpose of x

Note

Triplet matrices are a convenient form in which to construct sparse matrices after which they can be coerced to dgCMatrix objects.

Note that both new(.) and spMatrix constructors for "dgTMatrix" (and other "TsparseMatrix" classes) implicitly add x_k's that belong to identical (i_k, j_k) pairs.

However this means that a matrix typically can be stored in more than one possible "TsparseMatrix" representations. Use asUniqueT() in order to ensure uniqueness of the internal representation of such a matrix.

See Also

Class dgCMatrix or the superclasses dsparseMatrix and TsparseMatrix; asUniqueT.

Examples

```
m <- Matrix(0+1:28, nrow = 4)
m[-3,c(2,4:5,7)] <- m[ 3, 1:4] <- m[1:3, 6] <- 0
(mT <- as(m, "TsparseMatrix"))
str(mT)
mT[1,]
mT[4, drop = FALSE]
stopifnot(identical(mT[lower.tri(mT)],
                    m [lower.tri(m) ]))
mT[lower.tri(mT,diag=TRUE)] <- 0
mT

## Triplet representation with repeated (i,j) entries
## *adds* the corresponding x's:
T2 <- new("dgTMatrix",
          i = as.integer(c(1,1,0,3,3)),
          j = as.integer(c(2,2,4,0,0)), x=10*1:5, Dim=4:5)
str(T2) # contains (i,j,x) slots exactly as above, but
T2 ## has only three non-zero entries, as for repeated (i,j)'s,
   ## the corresponding x's are "implicitly" added
stopifnot(nnzero(T2) == 3)
```

`Diagonal` *Construct a Diagonal Matrix*

Description

Construct a formally diagonal `Matrix`, i.e., an object inheriting from virtual class `diagonalMatrix` (or, if desired, a *mathematically* diagonal `CsparseMatrix`).

Usage

```
Diagonal(n, x = NULL, names = FALSE)

.sparseDiagonal(n, x = NULL, uplo = "U", shape = "t", unitri = TRUE, kind, cols)
    .trDiagonal(n, x = NULL, uplo = "U", unitri = TRUE, kind)
   .symDiagonal(n, x = NULL, uplo = "U", kind)
```

Arguments

`n`	integer indicating the dimension of the (square) matrix. If missing, then `length(x)` is used.
`x`	numeric or logical vector listing values for the diagonal entries, to be recycled as necessary. If `NULL` (the default), then the result is a unit diagonal matrix. `.sparseDiagonal()` and friends ignore non-`NULL` `x` when `kind = "n"`.
`names`	either `logical` `TRUE` or `FALSE` or then a `character` vector of `length` `n`. If true *and* `names(x)` is not `NULL`, use that as both row and column names for the resulting matrix. When a character vector, use it for both dimnames.

uplo	one of c("U","L"), specifying the uplo slot of the result if the result is formally triangular of symmetric.
shape	one of c("t","s","g"), indicating if the result should be formally triangular, symmetric, or "general". The result will inherit from virtual class triangularMatrix, symmetricMatrix, or generalMatrix, respectively.
unitri	logical indicating if a formally triangular result with ones on the diagonal should be formally *unit* triangular, i.e., with diag slot equal to "U" rather than "N".
kind	one of c("d","l","n"), indicating the "mode" of the result: numeric, logical, or pattern. The result will inherit from virtual class dsparseMatrix, lsparseMatrix, or nsparseMatrix, respectively. Values other than "n" are ignored when x is non-NULL; in that case the mode is determined by typeof(x).
cols	optional integer vector with values in 0:(n-1), indexing columns of the specified diagonal matrix. If specified, then the result is (mathematically) D[, cols+1] rather than D, where D = Diagonal(n, x), and it is always "general" (i.e., shape is ignored).

Value

Diagonal() returns an object inheriting from virtual class diagonalMatrix.

.sparseDiagonal() returns a CsparseMatrix representation of Diagonal(n, x) or, if cols is given, of Diagonal(n, x)[, cols+1]. The precise class of the result depends on shape and kind.

.trDiagonal() and .symDiagonal() are simple wrappers, for .sparseDiagonal(shape = "t") and .sparseDiagonal(shape = "s"), respectively.

.sparseDiagonal() exists primarily to leverage efficient C-level methods available for CsparseMatrix.

Author(s)

Martin Maechler

See Also

the generic function diag for *extraction* of the diagonal from a matrix works for all "Matrices".

bandSparse constructs a *banded* sparse matrix from its non-zero sub-/super - diagonals. band(A) returns a band matrix containing some sub-/super - diagonals of A.

Matrix for general matrix construction; further, class diagonalMatrix.

Examples

```
Diagonal(3)
Diagonal(x = 10^(3:1))
Diagonal(x = (1:4) >= 2)#-> "ldiMatrix"

## Use Diagonal() + kronecker() for "repeated-block" matrices:
M1 <- Matrix(0+0:5, 2,3)
(M <- kronecker(Diagonal(3), M1))

(S <- crossprod(Matrix(rbinom(60, size=1, prob=0.1), 10,6)))
```

```
(SI <- S + 10*.symDiagonal(6)) # sparse symmetric still
stopifnot(is(SI, "dsCMatrix"))
(I4 <- .sparseDiagonal(4, shape="t"))# now (2012-10) unitriangular
stopifnot(I4@diag == "U", all(I4 == diag(4)))
```

`diagonalMatrix-class` *Class "diagonalMatrix" of Diagonal Matrices*

Description

Class "diagonalMatrix" is the virtual class of all diagonal matrices.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots

`diag`**:** `character` string, either `"U"` or `"N"`, where `"U"` means 'unit-diagonal'.

`Dim`**:** matrix dimension, and

`Dimnames`**:** the `dimnames`, a `list`, see the `Matrix` class description. Typically `list(NULL,NULL)` for diagonal matrices.

Extends

Class `"sparseMatrix"`, directly.

Methods

These are just a subset of the signature for which defined methods. Currently, there are (too) many explicit methods defined in order to ensure efficient methods for diagonal matrices.

coerce `signature(from = "matrix", to = "diagonalMatrix")`: ...

coerce `signature(from = "Matrix", to = "diagonalMatrix")`: ...

coerce `signature(from = "diagonalMatrix", to = "generalMatrix")`: ...

coerce `signature(from = "diagonalMatrix", to = "triangularMatrix")`: ...

coerce `signature(from = "diagonalMatrix", to = "nMatrix")`: ...

coerce `signature(from = "diagonalMatrix", to = "matrix")`: ...

coerce `signature(from = "diagonalMatrix", to = "sparseVector")`: ...

t `signature(x = "diagonalMatrix")`: ...
and many more methods

solve `signature(a = "diagonalMatrix", b, ...)`: is trivially implemented, of course; see also `solve-methods`.

which `signature(x = "nMatrix")`, semantically equivalent to **base** function `which(x, arr.ind)`.

"Math" `signature(x = "diagonalMatrix")`: all these group methods return a `"diagonalMatrix"`, apart from `cumsum()` etc which return a *vector* also for **base** `matrix`.

`* signature(e1 = "ddiMatrix", e2="denseMatrix")`: arithmetic and other operators from the `Ops` group have a few dozen explicit method definitions, in order to keep the results *diagonal* in many cases, including the following:

`/ signature(e1 = "ddiMatrix", e2="denseMatrix")`: the result is from class `ddiMatrix` which is typically very desirable. Note that when `e2` contains off-diagonal zeros or `NA`s, we implicitly use $0/x = 0$, hence differing from traditional R arithmetic (where $0/0 \mapsto$ NaN), in order to preserve sparsity.

summary `(object = "diagonalMatrix")`: Returns an object of S3 class `"diagSummary"` which is the summary of the vector `object@x` plus a simple heading, and an appropriate `print` method.

See Also

`Diagonal()` as constructor of these matrices, and `isDiagonal`. `ddiMatrix` and `ldiMatrix` are "actual" classes extending `"diagonalMatrix"`.

Examples

```
I5 <- Diagonal(5)
D5 <- Diagonal(x = 10*(1:5))
## trivial (but explicitly defined) methods:
stopifnot(identical(crossprod(I5), I5),
          identical(tcrossprod(I5), I5),
          identical(crossprod(I5, D5), D5),
          identical(tcrossprod(D5, I5), D5),
          identical(solve(D5), solve(D5, I5)),
          all.equal(D5, solve(solve(D5)), tolerance = 1e-12)
          )
solve(D5)# efficient as is diagonal

# an unusual way to construct a band matrix:
rbind2(cbind2(I5, D5),
       cbind2(D5, I5))
```

`diagU2N` *Transform Triangular Matrices from Unit Triangular to General Triangular and Back*

Description

Transform a triangular matrix `x`, i.e., of `class triangularMatrix`, from (internally!) unit triangular ("unitriangular") to "general" triangular (`diagU2N(x)`) or back (`diagN2U(x)`). Note that the latter, `diagN2U(x)`, also sets the diagonal to one in cases where `diag(x)` was not all one.

`.diagU2N(x)` and `.diagN2U(x)` assume *without* checking that `x` is a `triangularMatrix` with suitable `diag` slot (`"U"` and `"N"`, respectively), hence they should be used with care.

Usage

```
 diagU2N(x, cl = getClassDef(class(x)), checkDense = FALSE)
 diagN2U(x, cl = getClassDef(class(x)), checkDense = FALSE)

.diagU2N(x, cl = getClassDef(class(x)), checkDense = FALSE)
.diagN2U(x, cl = getClassDef(class(x)), checkDense = FALSE)
```

Arguments

x	a triangularMatrix, often sparse.
cl	(optional, for speedup only:) class (definition) of x.
checkDense	logical indicating if dense (see denseMatrix) matrices should be considered at all; i.e., when false, as per default, the result will be sparse even when x is dense.

Details

The concept of unit triangular matrices with a diag slot of "U" stems from LAPACK.

Value

a triangular matrix of the same class but with a different diag slot. For diagU2N (semantically) with identical entries as x, whereas in diagN2U(x), the off-diagonal entries are unchanged and the diagonal is set to all 1 even if it was not previously.

Note

Such internal storage details should rarely be of relevance to the user. Hence, these functions really are rather *internal* utilities.

See Also

"triangularMatrix", "dtCMatrix".

Examples

```
(T <- Diagonal(7) + triu(Matrix(rpois(49, 1/4), 7, 7), k = 1))
(uT <- diagN2U(T)) # "unitriangular"
(t.u <- diagN2U(10*T))# changes the diagonal!
stopifnot(all(T == uT), diag(t.u) == 1,
          identical(T, diagU2N(uT)))
T[upper.tri(T)] <- 5 # still "dtC"
T <- diagN2U(as(T,"triangularMatrix"))
dT <- as(T, "denseMatrix") # (unitriangular)
dT.n <- diagU2N(dT, checkDense = TRUE)
sT.n <- diagU2N(dT)
stopifnot(is(dT.n, "denseMatrix"), is(sT.n, "sparseMatrix"),
          dT@diag == "U", dT.n@diag == "N", sT.n@diag == "N",
          all(dT == dT.n), all(dT == sT.n))
```

dimScale *Scale the Rows and Columns of a Matrix*

Description

dimScale, rowScale, and colScale implement D1 %*% x %*% D2, D %*% x, and x %*% D for diagonal matrices D1, D2, and D with diagonal entries d1, d2, and d, respectively. Unlike the explicit products, these functions preserve dimnames(x) and symmetry where appropriate.

Usage

```
dimScale(x, d1 = sqrt(1/diag(x, names = FALSE)), d2 = d1)
rowScale(x, d)
colScale(x, d)
```

Arguments

x	a matrix, possibly inheriting from virtual class Matrix.
d1, d2, d	numeric vectors giving factors by which to scale the rows or columns of x; they are recycled as necessary.

Details

dimScale(x) (with d1 and d2 unset) is only roughly equivalent to cov2cor(x). cov2cor sets the diagonal entries of the result to 1 (exactly); dimScale does not.

Value

The result of scaling x, currently always inheriting from virtual class dMatrix.

It inherits from triangularMatrix if and only if x does. In the special case of dimScale(x, d1, d2) with identical d1 and d2, it inherits from symmetricMatrix if and only if x does.

Author(s)

Mikael Jagan

See Also

cov2cor

Examples

```
n <- 6L
(x <- forceSymmetric(matrix(1, n, n)))
dimnames(x) <- rep.int(list(letters[seq_len(n)]), 2L)

d <- seq_len(n)
(D <- Diagonal(x = d))
```

```
(scx <- dimScale(x, d)) # symmetry and 'dimnames' kept
(mmx <- D %*% x %*% D) # symmetry and 'dimnames' lost
stopifnot(identical(unname(as(scx, "generalMatrix")), mmx))

rowScale(x, d)
colScale(x, d)
```

---

dMatrix-class *(Virtual) Class "dMatrix" of "double" Matrices*

Description

The dMatrix class is a virtual class contained by all actual classes of numeric matrices in the **Matrix** package. Similarly, all the actual classes of logical matrices inherit from the lMatrix class.

Slots

Common to *all* matrix object in the package:

Dim: Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

Dimnames: list of length two; each component containing NULL or a character vector length equal the corresponding Dim element.

Methods

There are (relatively simple) group methods (see, e.g., Arith)

Arith signature(e1 = "dMatrix", e2 = "dMatrix"): ...

Arith signature(e1 = "dMatrix", e2 = "numeric"): ...

Arith signature(e1 = "numeric", e2 = "dMatrix"): ...

Math signature(x = "dMatrix"): ...

Math2 signature(x = "dMatrix", digits = "numeric"): this group contains round() and signif().

Compare signature(e1 = "numeric", e2 = "dMatrix"): ...

Compare signature(e1 = "dMatrix", e2 = "numeric"): ...

Compare signature(e1 = "dMatrix", e2 = "dMatrix"): ...

Summary signature(x = "dMatrix"): The "Summary" group contains the seven functions max(), min(), range(), prod(), sum(), any(), and all().

The following methods are also defined for all double matrices:

expm signature(x = "dMatrix"): computes the *"Matrix Exponential"*, see expm.

The following methods are defined for all logical matrices:

which signature(x = "lsparseMatrix") and many other subclasses of "lMatrix": as the **base** function which(x, arr.ind) returns the indices of the TRUE entries in x; if arr.ind is true, as a 2-column matrix of row and column indices. Since **Matrix** version 1.2-9, if useNames is true, as by default, with dimnames, the same as base::which.

See Also

The nonzero-pattern matrix class nMatrix, which can be used to store non-NA logical matrices even more compactly.

The numeric matrix classes dgeMatrix, dgCMatrix, and Matrix.

drop0(x, tol=1e-10) is sometimes preferable to (and more efficient than) zapsmall(x, digits=10).

Examples

```
showClass("dMatrix")

set.seed(101)
round(Matrix(rnorm(28), 4,7), 2)
M <- Matrix(rlnorm(56, sd=10), 4,14)
(M. <- zapsmall(M))
table(as.logical(M. == 0))
```

---

dmperm *Dulmage-Mendelsohn Permutation / Decomposition*

Description

For any $n \times m$ (typically) sparse matrix x compute the Dulmage-Mendelsohn row and columns permutations which at first splits the n rows and m columns into coarse partitions each; and then a finer one, reordering rows and columns such that the permutated matrix is "as upper triangular" as possible.

Usage

```
dmperm(x, nAns = 6L, seed = 0L)
```

Arguments

x	a typically sparse matrix; internally coerced to either "dgCMatrix" or "dtCMatrix".
nAns	an integer specifying the length of the resulting list. Must be 2, 4, or 6.
seed	an integer code in -1,0,1; determining the (initial) permutation; by default, seed = 0, no (or the identity) permutation; seed = -1 uses the "reverse" permutation k:1; for seed = 1, it is a *random* permutation (using R's RNG, seed, etc).

Details

See the book section by Tim Davis; page 122–127, in the References.

Value

a named list with (by default) 6 components,

p	integer vector with the permutation p, of length nrow(x).
q	integer vector with the permutation q, of length ncol(x).
r	integer vector of length nb+1, where block k is rows r[k] to r[k+1]-1 in A[p,q].
s	integer vector of length nb+1, where block k is cols s[k] to s[k+1]-1 in A[p,q].
rr5	integer vector of length 5, defining the coarse row decomposition.
cc5	integer vector of length 5, defining the coarse column decomposition.

Author(s)

Martin Maechler, with a lot of "encouragement" by Mauricio Vargas.

References

Section 7.4 *Dulmage-Mendelsohn decomposition*, pp. 122 ff of
Timothy A. Davis (2006) *Direct Methods for Sparse Linear Systems*, SIAM Series "Fundamentals of Algorithms".

See Also

Schur, the class of permutation matrices; "pMatrix".

Examples

```
set.seed(17)
(S9 <- rsparsematrix(9, 9, nnz = 10, symmetric=TRUE)) # dsCMatrix
str( dm9 <- dmperm(S9) )
(S9p <- with(dm9, S9[p, q]))
## looks good, but *not* quite upper triangular; these, too:
str( dm9.0 <- dmperm(S9, seed=-1)) # non-random too.
str( dm9_1 <- dmperm(S9, seed= 1)) # a random one
## The last two permutations differ, but have the same effect!
(S9p0 <- with(dm9.0, S9[p, q])) # .. hmm ..
stopifnot(all.equal(S9p0, S9p))# same as as default, but different from the random one


set.seed(11)
(M <- triu(rsparsematrix(9,11, 1/4)))
dM <- dmperm(M); with(dM, M[p, q])
(Mp <- M[sample.int(nrow(M)), sample.int(ncol(M))])
dMp <- dmperm(Mp); with(dMp, Mp[p, q])


set.seed(7)
(n7 <- rsparsematrix(5, 12, nnz = 10, rand.x = NULL))
str( dm.7 <- dmperm(n7) )
stopifnot(exprs = {
  lengths(dm.7[1:2]) == dim(n7)
```

```
  identical(dm.7,      dmperm(as(n7, "dMatrix")))
  identical(dm.7[1:4], dmperm(n7, nAns=4))
  identical(dm.7[1:2], dmperm(n7, nAns=2))
})
```

---

dpoMatrix-class *Positive Semi-definite Dense (Packed | Non-packed) Numeric Matrices*

Description

- The "dpoMatrix" class is the class of positive-semidefinite symmetric matrices in nonpacked storage.
- The "dppMatrix" class is the same except in packed storage. Only the upper triangle or the lower triangle is required to be available.
- The "corMatrix" and "copMatrix" classes represent correlation matrices. They extend "dpoMatrix" and "dppMatrix", respectively, with an additional slot sd allowing restoration of the original covariance matrix.

Objects from the Class

Objects can be created by calls of the form new("dpoMatrix", ...) or from crossprod applied to an "dgeMatrix" object.

Slots

uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

x: Object of class "numeric". The numeric values that constitute the matrix, stored in column-major order.

Dim: Object of class "integer". The dimensions of the matrix which must be a two-element vector of non-negative integers.

Dimnames: inherited from class "Matrix"

factors: Object of class "list". A named list of factorizations that have been computed for the matrix.

sd: (for "corMatrix" and "copMatrix") a numeric vector of length n containing the (original) $\sqrt{var(.)}$ entries which allow reconstruction of a covariance matrix from the correlation matrix.

Extends

Class "dsyMatrix", directly.
Classes "dgeMatrix", "symmetricMatrix", and many more by class "dsyMatrix".

Methods

chol `signature(x = "dpoMatrix")`: Returns (and stores) the Cholesky decomposition of `x`, see `chol`.

determinant `signature(x = "dpoMatrix")`: Returns the `determinant` of `x`, via `chol(x)`, see above.

rcond `signature(x = "dpoMatrix", norm = "character")`: Returns (and stores) the reciprocal of the condition number of `x`. The `norm` can be `"O"` for the one-norm (the default) or `"I"` for the infinity-norm. For symmetric matrices the result does not depend on the norm.

solve `signature(a = "dpoMatrix", b = "....")`, and

solve `signature(a = "dppMatrix", b = "....")` work via the Cholesky composition, see also the Matrix `solve-methods`.

Arith `signature(e1 = "dpoMatrix", e2 = "numeric")` (and quite a few other signatures): The result of ("elementwise" defined) arithmetic operations is typically *not* positive-definite anymore. The only exceptions, currently, are multiplications, divisions or additions with *positive* `length(.) == 1` numbers (or `logicals`).

Note

Currently the validity methods for these classes such as `getValidity(getClass("dpoMatrix"))` for efficiency reasons only check the diagonal entries of the matrix – they may not be negative. This is only necessary but not sufficient for a symmetric matrix to be positive semi-definite.

A more reliable (but often more expensive) check for positive semi-definiteness would look at the signs of `diag(BunchKaufman(.))` (with some tolerance for very small negative values), and for (strict) positive definiteness at something like `!inherits(tryCatch(chol(.), error=identity), "error")` . Indeed, when *coercing* to these classes, a version of `Cholesky()` or `chol()` is typically used, e.g., see `selectMethod("coerce", c(from="dsyMatrix", to="dpoMatrix"))` .

See Also

Classes `dsyMatrix` and `dgeMatrix`; further, `Matrix`, `rcond`, `chol`, `solve`, `crossprod`.

Examples

```
h6 <- Hilbert(6)
rcond(h6)
str(h6)
h6 * 27720 # is ``integer''
solve(h6)
str(hp6 <- pack(h6))

### Note that  as(*, "corMatrix")  *scales* the matrix
(ch6 <- as(h6, "corMatrix"))
stopifnot(all.equal(as(h6 * 27720, "dsyMatrix"), round(27720 * h6),
                    tolerance = 1e-14),
          all.equal(ch6@sd^(-2), 2*(1:6)-1,
                    tolerance = 1e-12))
chch <- Cholesky(ch6, perm = FALSE)
stopifnot(identical(chch, ch6@factors$Cholesky),
          all(abs(crossprod(as(chch, "dtrMatrix")) - ch6) < 1e-10))
```

drop0 *Drop Non-Structural Zeros from a Sparse Matrix*

Description

Deletes "non-structural" zeros (i.e., zeros stored explicitly, in memory) from a sparse matrix and returns the result.

Usage

```
drop0(x, tol = 0, is.Csparse = NA, give.Csparse = TRUE)
```

Arguments

x	a Matrix, typically inheriting from virtual class sparseMatrix. denseMatrix and traditional vectors and matrices are coerced to CsparseMatrix, with zeros dropped automatically, hence users passing such x should consider as(x, "CsparseMatrix") instead, notably in the tol = 0 case.
tol	a non-negative number. If x is numeric, then entries less than or equal to tol in absolute value are deleted.
is.Csparse	a logical used only if give.Csparse is TRUE, indicating if x already inherits from virtual class CsparseMatrix, in which case coercion is not attempted, permitting some (typically small) speed-up.
give.Csparse	a logical indicating if the result must inherit from virtual class CsparseMatrix. If FALSE and x inherits from RsparseMatrix, TsparseMatrix, or indMatrix, then the result preserves the class of x. The default value is TRUE only for backwards compatibility.

Value

A sparseMatrix, the result of deleting non-structural zeros from x, possibly after coercion.

Note

drop0 is sometimes called in conjunction with zapsmall, e.g., when dealing with sparse matrix products; see the example.

See Also

Function sparseMatrix, for constructing objects inheriting from virtual class sparseMatrix; nnzero.

Examples

```
(m <- sparseMatrix(i = 1:8, j = 2:9, x = c(0:2, 3:-1),
                   dims = c(10L, 20L)))
drop0(m)

## A larger example:
t5 <- new("dtCMatrix", Dim = c(5L, 5L), uplo = "L",
          x = c(10, 1, 3, 10, 1, 10, 1, 10, 10),
          i = c(0L,2L,4L, 1L, 3L,2L,4L, 3L, 4L),
          p = c(0L, 3L, 5L, 7:9))
TT <- kronecker(t5, kronecker(kronecker(t5, t5), t5))
IT <- solve(TT)
I. <- TT %*% IT ;  nnzero(I.) # 697 ( == 625 + 72 )
I.0 <- drop0(zapsmall(I.))
## which actually can be more efficiently achieved by
I.. <- drop0(I., tol = 1e-15)
stopifnot(all(I.0 == Diagonal(625)), nnzero(I..) == 625)
```

---

dsCMatrix-class *Numeric Symmetric Sparse (column compressed) Matrices*

Description

The dsCMatrix class is a class of symmetric, sparse numeric matrices in the compressed, **c**olumn-oriented format. In this implementation the non-zero elements in the columns are sorted into increasing row order.

The dsTMatrix class is the class of symmetric, sparse numeric matrices in **t**riplet format.

Objects from the Class

Objects can be created by calls of the form new("dsCMatrix", ...) or new("dsTMatrix", ...), or automatically via e.g., as(*, "symmetricMatrix"), or (for dsCMatrix) also from Matrix(.).

Creation "from scratch" most efficiently happens via sparseMatrix(*, symmetric=TRUE).

Slots

uplo: A character object indicating if the upper triangle ("U") or the lower triangle ("L") is stored.

i: Object of class "integer" of length nnZ (*half* number of non-zero elements). These are the row numbers for each non-zero element in the lower triangle of the matrix.

p: (only in class "dsCMatrix":) an integer vector for providing pointers, one for each column, see the detailed description in CsparseMatrix.

j: (only in class "dsTMatrix":) Object of class "integer" of length nnZ (as i). These are the column numbers for each non-zero element in the lower triangle of the matrix.

x: Object of class "numeric" of length nnZ – the non-zero elements of the matrix (to be duplicated for full matrix).

factors: Object of class "list" - a list of factorizations of the matrix.

Dim: Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

Extends

Both classes extend classes and symmetricMatrix dsparseMatrix directly; dsCMatrix further directly extends CsparseMatrix, where dsTMatrix does TsparseMatrix.

Methods

solve signature(a = "dsCMatrix", b = "...."): x <- solve(a,b) solves $Ax = b$ for x; see solve-methods.

chol signature(x = "dsCMatrix", pivot = "logical"): Returns (and stores) the Cholesky decomposition of x, see chol.

Cholesky signature(A = "dsCMatrix",...): Computes more flexibly Cholesky decompositions, see Cholesky.

determinant signature(x = "dsCMatrix", logarithm = "missing"): Evaluate the determinant of x on the logarithm scale. This creates and stores the Cholesky factorization.

determinant signature(x = "dsCMatrix", logarithm = "logical"): Evaluate the determinant of x on the logarithm scale or not, according to the logarithm argument. This creates and stores the Cholesky factorization.

t signature(x = "dsCMatrix"): Transpose. As for all symmetric matrices, a matrix for which the upper triangle is stored produces a matrix for which the lower triangle is stored and vice versa, i.e., the uplo slot is swapped, and the row and column indices are interchanged.

t signature(x = "dsTMatrix"): Transpose. The uplo slot is swapped from "U" to "L" or vice versa, as for a "dsCMatrix", see above.

See Also

Classes dgCMatrix, dgTMatrix, dgeMatrix and those mentioned above.

Examples

```
mm <- Matrix(toeplitz(c(10, 0, 1, 0, 3)), sparse = TRUE)
mm # automatically dsCMatrix
str(mm)
mT <- as(as(mm, "generalMatrix"), "TsparseMatrix")

## Either
(symM <- as(mT, "symmetricMatrix")) # dsT
(symC <- as(symM, "CsparseMatrix")) # dsC
## or
sT <- Matrix(mT, sparse=TRUE, forceCheck=TRUE) # dsT

sym2 <- as(symC, "TsparseMatrix")
## --> the same as 'symM', a "dsTMatrix"
```

dsparseMatrix-class *Virtual Class "dsparseMatrix" of Numeric Sparse Matrices*

Description

The Class "dsparseMatrix" is the virtual (super) class of all numeric sparse matrices.

Slots

Dim: the matrix dimension, see class "Matrix".

Dimnames: see the "Matrix" class.

x: a numeric vector containing the (non-zero) matrix entries.

Extends

Class "dMatrix" and "sparseMatrix", directly.
Class "Matrix", by the above classes.

See Also

the documentation of the (non virtual) sub classes, see showClass("dsparseMatrix"); in particular, dgTMatrix, dgCMatrix, and dgRMatrix.

Examples

```
showClass("dsparseMatrix")
```

dsRMatrix-class *Symmetric Sparse Compressed Row Matrices*

Description

The dsRMatrix class is a class of symmetric, sparse matrices in the compressed, row-oriented format. In this implementation the non-zero elements in the rows are sorted into increasing column order.

Objects from the Class

These "..RMatrix" classes are currently still mostly unimplemented!

Objects can be created by calls of the form new("dsRMatrix", ...).

Slots

`uplo`: A character object indicating if the upper triangle (`"U"`) or the lower triangle (`"L"`) is stored. At present only the lower triangle form is allowed.

`j`: Object of class `"integer"` of length `nnzero` (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.

`p`: Object of class `"integer"` of pointers, one for each row, to the initial (zero-based) index of elements in the row.

`factors`: Object of class `"list"` - a list of factorizations of the matrix.

`x`: Object of class `"numeric"` - the non-zero elements of the matrix.

`Dim`: Object of class `"integer"` - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

`Dimnames`: List of length two, see `Matrix`.

Extends

Classes `dsparseMatrix`, `symmetricMatrix`, and `RsparseMatrix`, directly.

Class `"dMatrix"`, by class `"dsparseMatrix"`; class `"sparseMatrix"`, by classes `"dsparseMatrix"` and `"RsparseMatrix"`.

Methods

forceSymmetric `signature(x = "dsRMatrix", uplo = "missing")`: a trivial method just returning `x`

forceSymmetric `signature(x = "dsRMatrix", uplo = "character")`: if `uplo == x@uplo`, this trivially returns `x`; otherwise `t(x)`.

See Also

the classes `dgCMatrix`, `dgTMatrix`, and `dgeMatrix`.

Examples

```
(m0 <- new("dsRMatrix"))
m2 <- new("dsRMatrix", Dim = c(2L,2L),
          x = c(3,1), j = c(1L,1L), p = 0:2)
m2
stopifnot(colSums(as(m2, "TsparseMatrix")) == 3:4)
str(m2)
(ds2 <- forceSymmetric(diag(2))) # dsy*
dR <- as(ds2, "RsparseMatrix")
dR # dsRMatrix
```

dsyMatrix-class *Symmetric Dense (Packed or Unpacked) Numeric Matrices*

Description

- The "dsyMatrix" class is the class of symmetric, dense matrices in *non-packed* storage and
- "dspMatrix" is the class of symmetric dense matrices in *packed* storage, see pack(). Only the upper triangle or the lower triangle is stored.

Objects from the Class

Objects can be created by calls of the form new("dsyMatrix", ...) or new("dspMatrix", ...), respectively.

Slots

uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

x: Object of class "numeric". The numeric values that constitute the matrix, stored in column-major order.

Dim,Dimnames: The dimension (a length-2 "integer") and corresponding names (or NULL), see the Matrix.

factors: Object of class "list". A named list of factorizations that have been computed for the matrix.

Extends

"dsyMatrix" extends class "dgeMatrix", directly, whereas
"dspMatrix" extends class "ddenseMatrix", directly.

Both extend class "symmetricMatrix", directly, and class "Matrix" and others, *in*directly, use showClass("dsyMatrix"), e.g., for details.

Methods

norm signature(x = "dspMatrix", type = "character"), or x = "dsyMatrix" or type = "missing": Computes the matrix norm of the desired type, see, norm.

rcond signature(x = "dspMatrix", type = "character"), or x = "dsyMatrix" or type = "missing": Computes the reciprocal condition number, rcond().

solve signature(a = "dspMatrix", b = "...."), and

solve signature(a = "dsyMatrix", b = "...."): x <- solve(a,b) solves $Ax = b$ for x; see solve-methods.

t signature(x = "dsyMatrix"): Transpose; swaps from upper triangular to lower triangular storage, i.e., the uplo slot from "U" to "L" or vice versa, the same as for all symmetric matrices.

See Also

The *positive (Semi-)definite* dense (packed or non-packed numeric matrix classes dpoMatrix, dppMatrix and corMatrix,

Classes dgeMatrix and Matrix; solve, norm, rcond, t

Examples

```
## Only upper triangular part matters (when uplo == "U" as per default)
(sy2 <- new("dsyMatrix", Dim = as.integer(c(2,2)), x = c(14, NA,32,77)))
str(t(sy2)) # uplo = "L", and the lower tri. (i.e. NA is replaced).

chol(sy2) #-> "Cholesky" matrix
(sp2 <- pack(sy2)) # a "dspMatrix"

## Coercing to dpoMatrix gives invalid object:
sy3 <- new("dsyMatrix", Dim = as.integer(c(2,2)), x = c(14, -1, 2, -7))
try(as(sy3, "dpoMatrix")) # -> error: not positive definite


## 4x4 example
m <- matrix(0,4,4); m[upper.tri(m)] <- 1:6
(sym <- m+t(m)+diag(11:14, 4))
(S1 <- pack(sym))
(S2 <- t(S1))
stopifnot(all(S1 == S2)) # equal "seen as matrix", but differ internally :
str(S1)
S2@x
```

---

dtCMatrix-class *Triangular, (compressed) sparse column matrices*

Description

The "dtCMatrix" class is a class of triangular, sparse matrices in the compressed, column-oriented format. In this implementation the non-zero elements in the columns are sorted into increasing row order.

The "dtTMatrix" class is a class of triangular, sparse matrices in triplet format.

Objects from the Class

Objects can be created by calls of the form new("dtCMatrix", ...) or calls of the form new("dtTMatrix", ...), but more typically automatically via Matrix() or coercions such as as(x, "triangularMatrix").

Slots

uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

`diag`: Object of class `"character"`. Must be either `"U"`, for unit triangular (diagonal is all ones), or `"N"`; see `triangularMatrix`.

`p`: (only present in `"dtCMatrix"`:) an `integer` vector for providing pointers, one for each column, see the detailed description in `CsparseMatrix`.

`i`: Object of class `"integer"` of length nnzero (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.

`j`: Object of class `"integer"` of length nnzero (number of non-zero elements). These are the column numbers for each non-zero element in the matrix. (Only present in the `dtTMatrix` class.)

`x`: Object of class `"numeric"` - the non-zero elements of the matrix.

`Dim`,`Dimnames`: The dimension (a length-2 `"integer"`) and corresponding names (or `NULL`), inherited from the `Matrix`, see there.

Extends

Class `"dgCMatrix"`, directly. Class `"triangularMatrix"`, directly. Class `"dMatrix"`, `"sparseMatrix"`, and more by class `"dgCMatrix"` etc, see the examples.

Methods

solve `signature(a = "dtCMatrix", b = "....")`: sparse triangular solve (aka "backsolve" or "forwardsolve"), see `solve-methods`.

t `signature(x = "dtCMatrix")`: returns the transpose of `x`

t `signature(x = "dtTMatrix")`: returns the transpose of `x`

See Also

Classes `dgCMatrix`, `dgTMatrix`, `dgeMatrix`, and `dtrMatrix`.

Examples

```
showClass("dtCMatrix")
showClass("dtTMatrix")
t1 <- new("dtTMatrix", x= c(3,7), i= 0:1, j=3:2, Dim= as.integer(c(4,4)))
t1
## from  0-diagonal to unit-diagonal {low-level step}:
tu <- t1 ; tu@diag <- "U"
tu
(cu <- as(tu, "CsparseMatrix"))
str(cu)# only two entries in @i and @x
stopifnot(cu@i == 1:0,
          all(2 * symmpart(cu) == Diagonal(4) + forceSymmetric(cu)))

t1[1,2:3] <- -1:-2
diag(t1) <- 10*c(1:2,3:2)
t1 # still triangular
(it1 <- solve(t1))
t1. <- solve(it1)
all(abs(t1 - t1.) < 10 * .Machine$double.eps)
```

```
## 2nd example
U5 <- new("dtCMatrix", i= c(1L, 0:3), p=c(0L,0L,0:2, 5L), Dim = c(5L, 5L),
          x = rep(1, 5), diag = "U")
U5
(iu <- solve(U5)) # contains one '0'
validObject(iu2 <- solve(U5, Diagonal(5)))# failed in earlier versions

I5 <- iu  %*% U5 # should equal the identity matrix
i5 <- iu2 %*% U5
m53 <- matrix(1:15, 5,3, dimnames=list(NULL,letters[1:3]))
asDiag <- function(M) as(drop0(M), "diagonalMatrix")
stopifnot(
   all.equal(Diagonal(5), asDiag(I5), tolerance=1e-14) ,
   all.equal(Diagonal(5), asDiag(i5), tolerance=1e-14) ,
   identical(list(NULL, dimnames(m53)[[2]]), dimnames(solve(U5, m53)))
)
```

`dtpMatrix-class` *Packed Triangular Dense Matrices - "dtpMatrix"*

Description

The `"dtpMatrix"` class is the class of triangular, dense, numeric matrices in packed storage. The `"dtrMatrix"` class is the same except in nonpacked storage.

Objects from the Class

Objects can be created by calls of the form `new("dtpMatrix", ...)` or by coercion from other classes of matrices.

Slots

`uplo`: Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular.

`diag`: Object of class `"character"`. Must be either `"U"`, for unit triangular (diagonal is all ones), or `"N"`; see `triangularMatrix`.

`x`: Object of class `"numeric"`. The numeric values that constitute the matrix, stored in column-major order. For a packed square matrix of dimension $d \times d$, `length(x)` is of length $d(d+1)/2$ (also when `diag == "U"`!).

`Dim`,`Dimnames`: The dimension (a length-2 `"integer"`) and corresponding names (or `NULL`), inherited from the `Matrix`, see there.

Extends

Class `"ddenseMatrix"`, directly. Class `"triangularMatrix"`, directly. Class `"dMatrix"` and more by class `"ddenseMatrix"` etc, see the examples.

Methods

%*% `signature(x = "dtpMatrix", y = "dgeMatrix")`: Matrix multiplication; ditto for several other signature combinations, see `showMethods("%*%", class = "dtpMatrix")`.

determinant `signature(x = "dtpMatrix", logarithm = "logical")`: the `determinant(x)` trivially is `prod(diag(x))`, but computed on log scale to prevent over- and underflow.

diag `signature(x = "dtpMatrix")`: ...

norm `signature(x = "dtpMatrix", type = "character")`: ...

rcond `signature(x = "dtpMatrix", norm = "character")`: ...

solve `signature(a = "dtpMatrix", b = "...")`: efficiently using internal backsolve or forwardsolve, see `solve-methods`.

t `signature(x = "dtpMatrix")`: `t(x)` remains a `"dtpMatrix"`, lower triangular if `x` is upper triangular, and vice versa.

See Also

Class `dtrMatrix`

Examples

```
showClass("dtrMatrix")

example("dtrMatrix-class", echo=FALSE)
(p1 <- pack(T2))
str(p1)
(pp <- pack(T))
ip1 <- solve(p1)
stopifnot(length(p1@x) == 3, length(pp@x) == 3,
          p1 @ uplo == T2 @ uplo, pp @ uplo == T @ uplo,
  identical(t(pp), p1), identical(t(p1), pp),
  all((l.d <- p1 - T2) == 0), is(l.d, "dtpMatrix"),
  all((u.d <- pp - T ) == 0), is(u.d, "dtpMatrix"),
  l.d@uplo == T2@uplo, u.d@uplo == T@uplo,
  identical(t(ip1), solve(pp)), is(ip1, "dtpMatrix"),
  all.equal(as(solve(p1,p1), "diagonalMatrix"), Diagonal(2)))
```

---

dtRMatrix-class *Triangular Sparse Compressed Row Matrices*

Description

The `dtRMatrix` class is a class of triangular, sparse matrices in the compressed, row-oriented format. In this implementation the non-zero elements in the rows are sorted into increasing columnd order.

Objects from the Class

This class is currently still mostly unimplemented!

Objects can be created by calls of the form `new("dtRMatrix", ...)`.

Slots

uplo: Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular. At present only the lower triangle form is allowed.

diag: Object of class `"character"`. Must be either `"U"`, for unit triangular (diagonal is all ones), or `"N"`; see `triangularMatrix`.

j: Object of class `"integer"` of length `nnzero(.)` (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.

p: Object of class `"integer"` of pointers, one for each row, to the initial (zero-based) index of elements in the row. (Only present in the `dsRMatrix` class.)

x: Object of class `"numeric"` - the non-zero elements of the matrix.

Dim: The dimension (a length-2 `"integer"`)

Dimnames: corresponding names (or `NULL`), inherited from the `Matrix`, see there.

Extends

Class `"dgRMatrix"`, directly. Class `"dsparseMatrix"`, by class `"dgRMatrix"`. Class `"dMatrix"`, by class `"dgRMatrix"`. Class `"sparseMatrix"`, by class `"dgRMatrix"`. Class `"Matrix"`, by class `"dgRMatrix"`.

Methods

No methods currently with class "dsRMatrix" in the signature.

See Also

Classes `dgCMatrix`, `dgTMatrix`, `dgeMatrix`

Examples

```
(m0 <- new("dtRMatrix"))
(m2 <- new("dtRMatrix", Dim = c(2L,2L),
                        x = c(5, 1:2), p = c(0L,2:3), j= c(0:1,1L)))
str(m2)
(m3 <- as(Diagonal(2), "RsparseMatrix"))# --> dtRMatrix
```

dtrMatrix-class *Triangular, dense, numeric matrices*

Description

The "dtrMatrix" class is the class of triangular, dense, numeric matrices in nonpacked storage. The "dtpMatrix" class is the same except in packed storage, see pack().

Objects from the Class

Objects can be created by calls of the form new("dtrMatrix", ...).

Slots

uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

diag: Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see triangularMatrix.

x: Object of class "numeric". The numeric values that constitute the matrix, stored in column-major order.

Dim: Object of class "integer". The dimensions of the matrix which must be a two-element vector of non-negative integers.

Extends

Class "ddenseMatrix", directly. Class "triangularMatrix", directly. Class "Matrix" and others, by class "ddenseMatrix".

Methods

Among others (such as matrix products, e.g. ?crossprod-methods),

norm signature(x = "dtrMatrix", type = "character"): ..

rcond signature(x = "dtrMatrix", norm = "character"): ..

solve signature(a = "dtrMatrix", b = "...."): efficiently use a "forwardsolve" or backsolve for a lower or upper triangular matrix, respectively, see also solve-methods.

+, -, *, ..., ==, >=, ... all the Ops group methods are available. When applied to two triangular matrices, these return a triangular matrix when easily possible.

See Also

Classes ddenseMatrix, dtpMatrix, triangularMatrix

Examples

```
(m <- rbind(2:3, 0:-1))
(M <- as(m, "generalMatrix"))

(T <- as(M, "triangularMatrix")) # formally upper triangular
(T2 <- as(t(M), "triangularMatrix"))
stopifnot(T@uplo == "U", T2@uplo == "L", identical(T2, t(T)))

m <- matrix(0,4,4); m[upper.tri(m)] <- 1:6
(t1 <- Matrix(m+diag(,4)))
str(t1p <- pack(t1))
(t1pu <- diagN2U(t1p))
stopifnot(exprs = {
   inherits(t1 , "dtrMatrix"); validObject(t1)
   inherits(t1p, "dtpMatrix"); validObject(t1p)
   inherits(t1pu,"dtCMatrix"); validObject(t1pu)
   t1pu@x == 1:6
   all(t1pu == t1p)
   identical((t1pu - t1)@x, numeric())# sparse all-0
})
```

---

expand-methods *Expand Matrix Factorizations*

Description

expand1 and expand2 construct matrix factors from objects specifying matrix factorizations. Such objects typically do not store the factors explicitly, employing instead a compact representation to save memory.

Usage

```
expand1(x, which, ...)
expand2(x, ...)

expand (x, ...)
```

Arguments

x	a matrix factorization, typically inheriting from virtual class MatrixFactorization.
which	a character string indicating a matrix factor.
...	further arguments passed to or from methods.

Details

Methods for expand are retained only for backwards compatibility with **Matrix** < 1.6-0. New code should use expand1 and expand2, whose methods provide more control and behave more consistently. Notably, expand2 obeys the rule that the product of the matrix factors in the returned list should reproduce (within some tolerance) the factorized matrix, *including* its dimnames.

Hence if x is a matrix and y is its factorization, then

```
all.equal(as(x, "matrix"), as(Reduce(`%*%`, expand2(y)), "matrix"))
```

should in most cases return TRUE.

Value

expand1 returns an object inheriting from virtual class Matrix, representing the factor indicated by which, always without row and column names.

expand2 returns a list of factors, typically with names using conventional notation, as in list(L=, U=). The first and last factors get the row and column names of the factorized matrix, which are preserved in the Dimnames slot of x.

Methods

The following table lists methods for expand1 together with allowed values of argument which.

class(x)	which
Schur	c("Q", "T", "Q.")
denseLU	c("P1", "P1.", "L", "U")
sparseLU	c("P1", "P1.", "P2", "P2.", "L", "U")
sparseQR	c("P1", "P1.", "P2", "P2.", "Q", "Q1", "R", "R1")
BunchKaufman, pBunchKaufman	c("U", "DU", "U.", "L", "DL", "L.")
Cholesky, pCholesky	c("P1", "P1.", "L1", "D", "L1.", "L", "L.")
CHMsimpl, CHMsimpl	c("P1", "P1.", "L1", "D", "L1.", "L", "L.")

Methods for expand2 and expand are described below. Factor names and classes apply also to expand1.

expand2 signature(x = "CHMsimpl"): expands the factorization $A = P_1' L_1 D L_1' P_1 = P_1' L L' P_1$ as list(P1., L1, D, L1., P1) (the default) or as list(P1., L, L., P1), depending on optional logical argument LDL. P1 and P1. are pMatrix, L1, L1., L, and L. are dtCMatrix, and D is a ddiMatrix.

expand2 signature(x = "CHMsuper"): as CHMsimpl, but the triangular factors are stored as dgCMatrix.

expand2 signature(x = "p?Cholesky"): expands the factorization $A = L_1 D L_1' = L L'$ as list(L1, D, L1.) (the default) or as list(L, L.), depending on optional logical argument LDL. L1, L1., L, and L. are dtrMatrix or dtpMatrix, and D is a ddiMatrix.

expand2 signature(x = "p?BunchKaufman"): expands the factorization $A = U D_U U' = L D_L L'$ where $U = \prod_{k=1}^{b_U} P_k U_k$ and $L = \prod_{k=1}^{b_L} P_k L_k$ as list(U, DU, U.) or list(L, DL, L.), depending on x@uplo. If optional argument complete is TRUE, then an unnamed list giving the full expansion with $2b_U + 1$ or $2b_L + 1$ matrix factors is returned instead. P_k are represented

as pMatrix, U_k and L_k are represented as dtCMatrix, and D_U and D_L are represented as dsCMatrix.

expand2 signature(x = "Schur"): expands the factorization $A = QTQ'$ as list(Q, T, Q.). Q and Q. are x@Q and t(x@Q) modulo Dimnames, and T is x@T.

expand2 signature(x = "sparseLU"): expands the factorization $A = P_1'LUP_2'$ as list(P1., L, U, P2.). P1. and P2. are pMatrix, and L and U are dtCMatrix.

expand2 signature(x = "denseLU"): expands the factorization $A = P_1'LU$ as list(P1., L, U). P1. is a pMatrix, and L and U are dtrMatrix if square and dgeMatrix otherwise.

expand2 signature(x = "sparseQR"): expands the factorization $A = P_1'QRP_2' = P_1'Q_1R_1P_2'$ as list(P1., Q, R, P2.) or list(P1., Q1, R1, P2.), depending on optional logical argument complete. P1. and P2. are pMatrix, Q and Q1 are dgeMatrix, R is a dgCMatrix, and R1 is a dtCMatrix.

expand signature(x = "CHMfactor"): as expand2, but returning list(P, L). expand(x)[["P"]] and expand2(x)[["P1"]] represent the same permutation matrix P_1 but have opposite margin slots and inverted perm slots. The components of expand(x) do not preserve x@Dimnames.

expand signature(x = "sparseLU"): as expand2, but returning list(P, L, U, Q). expand(x)[["Q"]] and expand2(x)[["P2."]] represent the same permutation matrix P_2' but have opposite margin slots and inverted perm slots. expand(x)[["P"]] represents the permutation matrix P_1 rather than its transpose P_1'; it is expand2(x)[["P1."]] with an inverted perm slot. expand(x)[["L"]] and expand2(x)[["L"]] represent the same unit lower triangular matrix L, but with diag slot equal to "N" and "U", respectively. expand(x)[["L"]] and expand(x)[["U"]] store the *permuted* first and second components of x@Dimnames in their Dimnames slots.

expand signature(x = "denseLU"): as expand2, but returning list(L, U, P). expand(x)[["P"]] and expand2(x)[["P1."]] are identical modulo Dimnames. The components of expand(x) do not preserve x@Dimnames.

See Also

The virtual class MatrixFactorization of matrix factorizations.

Generic functions Cholesky, BunchKaufman, Schur, lu, and qr for *computing* factorizations.

Examples

```
showMethods("expand1", inherited = FALSE)
showMethods("expand2", inherited = FALSE)
set.seed(0)

(A <- Matrix(rnorm(9L, 0, 10), 3L, 3L))
(lu.A <- lu(A))
(e.lu.A <- expand2(lu.A))
stopifnot(exprs = {
    is.list(e.lu.A)
    identical(names(e.lu.A), c("P1.", "L", "U"))
    all(sapply(e.lu.A, is, "Matrix"))
    all.equal(as(A, "matrix"), as(Reduce(`%*%`, e.lu.A), "matrix"))
})

## 'expand1' and 'expand2' give equivalent results modulo
```

```
## dimnames and representation of permutation matrices;
## see also function 'alt' in example("Cholesky-methods")
(a1 <- sapply(names(e.lu.A), expand1, x = lu.A, simplify = FALSE))
all.equal(a1, e.lu.A)

## see help("denseLU-class") and others for more examples
```

`expm-methods` *Matrix Exponential*

Description

Compute the exponential of a matrix.

Usage

```
expm(x)
```

Arguments

`x`	a matrix, typically inheriting from the `dMatrix` class.

Details

The exponential of a matrix is defined as the infinite Taylor series `expm(A) = I + A + A^2/2! + A^3/3! + ...` (although this is definitely not the way to compute it). The method for the `dgeMatrix` class uses Ward's diagonal Pade' approximation with three step preconditioning, a recommendation from Moler & Van Loan (1978) "Nineteen dubious ways...".

Value

The matrix exponential of `x`.

Author(s)

This is a translation of the implementation of the corresponding Octave function contributed to the Octave project by A. Scottedward Hodel `<A.S.Hodel@Eng.Auburn.EDU>`. A bug in there has been fixed by Martin Maechler.

References

https://en.wikipedia.org/wiki/Matrix_exponential

Cleve Moler and Charles Van Loan (2003) Nineteen dubious ways to compute the exponential of a matrix, twenty-five years later. *SIAM Review* **45**, 1, 3–49. doi:10.1137/S00361445024180

for historical reference mostly:
Moler, C. and Van Loan, C. (1978) Nineteen dubious ways to compute the exponential of a matrix. *SIAM Review* **20**, 4, 801–836. doi:10.1137/1020098

Eric W. Weisstein et al. (1999) *Matrix Exponential*. From MathWorld, https://mathworld.wolfram.com/MatrixExponential.html

See Also

Package **expm**, which provides newer (in some cases faster, more accurate) algorithms for computing the matrix exponential via its own (non-generic) function `expm()`. **expm** also implements `logm()`, `sqrtm()`, etc.

Generic function `Schur`.

Examples

```
(m1 <- Matrix(c(1,0,1,1), ncol = 2))
(e1 <- expm(m1)) ; e <- exp(1)
stopifnot(all.equal(e1@x, c(e,0,e,e), tolerance = 1e-15))
(m2 <- Matrix(c(-49, -64, 24, 31), ncol = 2))
(e2 <- expm(m2))
(m3 <- Matrix(cbind(0,rbind(6*diag(3),0))))# sparse!
(e3 <- expm(m3)) # upper triangular
```

---

externalFormats *Read and write external matrix formats*

Description

Read matrices stored in the Harwell-Boeing or MatrixMarket formats or write `sparseMatrix` objects to one of these formats.

Usage

```
readHB(file)
readMM(file)
writeMM(obj, file, ...)
```

Arguments

`obj`	a real sparse matrix
`file`	for `writeMM` - the name of the file to be written. For `readHB` and `readMM` the name of the file to read, as a character scalar. 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"`. Alternatively, `readHB` and `readMM` accept connection objects.
`...`	optional additional arguments. Currently none are used in any methods.

Value

The `readHB` and `readMM` functions return an object that inherits from the `"Matrix"` class. Methods for the `writeMM` generic functions usually return `NULL` and, as a side effect, the matrix `obj` is written to `file` in the MatrixMarket format (writeMM).

Note

The Harwell-Boeing format is older and less flexible than the MatrixMarket format. The function `writeHB` was deprecated and has now been removed. Please use `writeMM` instead.

Note that these formats do *not* know anything about `dimnames`, hence these are dropped by `writeMM()`.

A very simple way to export small sparse matrices `S`, is to use `summary(S)` which returns a `data.frame` with columns `i`, `j`, and possibly `x`, see `summary` in `sparseMatrix-class`, and an example below.

References

https://math.nist.gov/MatrixMarket/

https://sparse.tamu.edu/

Examples

```
str(pores <- readMM(system.file("external/pores_1.mtx", package = "Matrix")))
str(utm   <- readHB(system.file("external/utm300.rua" , package = "Matrix")))
str(lundA <- readMM(system.file("external/lund_a.mtx" , package = "Matrix")))
str(lundA <- readHB(system.file("external/lund_a.rsa" , package = "Matrix")))
## https://math.nist.gov/MatrixMarket/data/Harwell-Boeing/counterx/counterx.htm
str(jgl   <- readMM(system.file("external/jgl009.mtx" , package = "Matrix")))

## NOTE: The following examples take quite some time
## ----  even on a fast internet connection:
if(FALSE) {
## The URL has been corrected, but we need an untar step:
u. <- url("https://www.cise.ufl.edu/research/sparse/RB/Boeing/msc00726.tar.gz")
str(sm <- readHB(gzcon(u.)))
}

data(KNex, package = "Matrix")
## Store as MatrixMarket (".mtx") file, here inside temporary dir./folder:
(MMfile <- file.path(tempdir(), "mmMM.mtx"))
writeMM(KNex$mm, file=MMfile)
file.info(MMfile)[,c("size", "ctime")] # (some confirmation of the file's)

## very simple export - in triplet format - to text file:
data(CAex, package = "Matrix")
s.CA <- summary(CAex)
s.CA # shows  (i, j, x)  [columns of a data frame]
message("writing to ", outf <- tempfile())
write.table(s.CA, file = outf, row.names=FALSE)
## and read it back -- showing off  sparseMatrix():
str(dd <- read.table(outf, header=TRUE))
## has columns (i, j, x) -> we can use via do.call() as arguments to sparseMatrix():
mm <- do.call(sparseMatrix, dd)
stopifnot(all.equal(mm, CAex, tolerance=1e-15))
```

`facmul-methods` *Multiplication by Factors from Matrix Factorizations*

Description

Multiplies a matrix or vector on the left or right by a factor from a matrix factorization or its transpose.

Usage

```
facmul(x, factor, y, trans = FALSE, left = TRUE, ...)
```

Arguments

`x`	a `MatrixFactorization` object.
`factor`	a character string indicating a factor in the factorization represented by `x`, typically an element of `names(expand2(x, ...))`.
`y`	a matrix or vector to be multiplied on the left or right by the factor or its transpose.
`trans`	a logical indicating if the transpose of the factor should be used, rather than the factor itself.
`left`	a logical indicating if the `y` should be multiplied on the left by the factor, rather than on the right.
`...`	further arguments passed to or from methods.

Details

`facmul` is experimental and currently no methods are exported from **Matrix**.

Value

The value of `op(M) %*% y` or `y %*% op(M)`, depending on `left`, where `M` is the factor (always *without* `dimnames`) and `op(M)` is `M` or `t(M)`, depending on `trans`.

Examples

```
## Conceptually, methods for 'facmul' _would_ behave as follows ...
## Not run:
n <- 3L
x <- lu(Matrix(rnorm(n * n), n, n))
y <- rnorm(n)
L <- unname(expand2(x)[[nm <- "L"]])
stopifnot(exprs = {
    all.equal(facmul(x, nm, y, trans = FALSE, left =  TRUE), L %*% y)
    all.equal(facmul(x, nm, y, trans = FALSE, left = FALSE), y %*% L)
    all.equal(facmul(x, nm, y, trans =  TRUE, left =  TRUE),  crossprod(L, y))
    all.equal(facmul(x, nm, y, trans =  TRUE, left = FALSE), tcrossprod(y, L))
```

```
})

## End(Not run)
```

`fastMisc` *"Low Level" Coercions and Methods*

Description

"Semi-API" functions used internally by **Matrix**, often to bypass S4 dispatch and avoid the associated overhead. These are exported to provide this capability to expert users. Typical users should continue to rely on S4 generic functions to dispatch suitable methods, by calling, e.g., `as(., <class>)` for coercions.

Usage

```
.M2kind(from, kind = ".", sparse = NA)

.M2gen(from, kind = ".")
.M2sym(from, ...)
.M2tri(from, ...)
.M2diag(from)

.M2v(from)
.M2m(from)
.M2unpacked(from)
.M2packed(from)
.M2C(from)
.M2R(from)
.M2T(from)

.M2V(from)
.m2V(from, kind = ".")

.sparse2dense(from, packed = FALSE)
.diag2dense(from, kind = ".", shape = "t", packed = FALSE, uplo = "U")
.ind2dense(from, kind = "n")
.m2dense(from, class = ".ge", uplo = "U", diag = "N", trans = FALSE)

.dense2sparse(from, repr = "C")
.diag2sparse(from, kind = ".", shape = "t", repr = "C", uplo = "U")
.ind2sparse(from, kind = "n", repr = ".")
.m2sparse(from, class = ".gC", uplo = "U", diag = "N", trans = FALSE)

.tCRT(x, lazy = TRUE)

.diag.dsC(x, Chx = Cholesky(x, LDL = TRUE), res.kind = "diag")
```

```
.solve.dgC.lu  (a, b, tol = .Machine$double.eps, check = TRUE)
.solve.dgC.qr  (a, b, order = 3L, check = TRUE)
.solve.dgC.chol(a, b, check = TRUE)

.updateCHMfactor(object, parent, mult = 0)
```

Arguments

from, x, a, b	a Matrix, matrix, or vector.
kind	a string (".", ",", "n", "l", or "d") specifying the "kind" of the result. "." indicates that the kind of from should be preserved. "," is equivalent to "z" if from is complex and to "d" otherwise. "n" indicates that the result should inherit from nMatrix or nsparseVector (and so on).
shape	a string (".", "g", "s", or "t") specifying the "shape" of the result. "." indicates that the shape of from should be preserved. "g" indicates that the result should inherit from generalMatrix (and so on).
repr	a string (".", "C", "R", or "T") specifying the sparse representation of the result. "." is accepted only by .ind2sparse and indicates the most efficient representation, which is "C" ("R") for margin = 2 (1). "C" indicates that the result should inherit from CsparseMatrix (and so on).
packed	a logical indicating if the result should inherit from packedMatrix rather than from unpackedMatrix. It is ignored for from inheriting from generalMatrix.
sparse	a logical indicating if the result should inherit from sparseMatrix rather than from denseMatrix. If NA, then the result will be formally sparse if and only if from is.
uplo	a string ("U" or "L") indicating whether the result (if symmetric or triangular) should store the upper or lower triangle of from. The elements of from in the opposite triangle are ignored.
diag	a string ("N" or "U") indicating whether the result (if triangular) should be formally nonunit or unit triangular. In the unit triangular case, the diagonal elements of from are ignored.
trans	a logical indicating if the result should be a 1-row matrix rather than a 1-column matrix where from is a vector but not a matrix.
class	a string whose first three characters specify the class of the result. It should match the pattern "^[.nld](ge|sy|tr|sp|tp)" for .m2dense and "^[.nld][gst][CRT]" for .m2sparse, where "." in the first position is equivalent to "l" for logical arguments and "d" for numeric arguments.
...	optional arguments passed to isSymmetric or isTriangular.
lazy	a logical indicating if the transpose should be constructed with minimal allocation, but possibly *without* preserving representation.
Chx	optionally, the Cholesky(x, ...) factorization of x. If supplied, then x is unused.
res.kind	a string in c("trace", "sumLog", "prod", "min", "max", "range", "diag", "diagBack").

tol	see lu-methods.
order	see qr-methods.
check	a logical indicating if the first argument should be tested for inheritance from dgCMatrix and coerced if necessary. Set to FALSE for speed only if it is known to already inherit from dgCMatrix.
object	a Cholesky factorization inheriting from virtual class CHMfactor, almost always the result of a call to generic function Cholesky.
parent	an object of class dsCMatrix or class dgCMatrix.
mult	a numeric vector of postive length. Only the first element is used, and that must be finite.

Details

Functions with names of the form .<A>2<B> implement coercions from virtual class A to the "nearest" non-virtual subclass of virtual class B, where the virtual classes are abbreviated as follows:

M Matrix

V sparseVector

m matrix

v vector

dense denseMatrix

unpacked unpackedMatrix

packed packedMatrix

sparse CsparseMatrix, RsparseMatrix, or TsparseMatrix

C CsparseMatrix

R RsparseMatrix

T TsparseMatrix

gen generalMatrix

sym symmetricMatrix

tri triangularMatrix

diag diagonalMatrix

ind indMatrix

Abbreviations should be seen as a guide, rather than as an exact description of behaviour. Notably, .m2dense, .m2sparse, and .m2V accept vectors that are not matrices.

.tCRT(x): If lazy = TRUE, then .tCRT constructs the transpose of x using the most efficient representation, which for 'CRT' is 'RCT'. If lazy = FALSE, then .tCRT preserves the representation of x, behaving as the corresponding methods for generic function t.

.diag.dsC(x): .diag.dsC computes (or uses if Chx is supplied) the Cholesky factorization of x as LDL' in order to calculate one of several possible statistics from the diagonal entries of D. See res.kind under 'Arguments'.

`.solve.dgC.*(a, b)`: `.solve.dgC.lu(a, b)` needs a square matrix `a`. `.solve.dgC.qr(a, b)` needs a "long" matrix `a`, with `nrow(a) >= ncol(a)`. `.solve.dgC.chol(a, b)` needs a "wide" matrix `a`, with `nrow(a) <= ncol(a)`.

All three may be used to solve sparse linear systems directly. Only `.solve.dgC.qr` and `.solve.dgC.chol` be used to solve sparse *least squares* problems.

`.updateCHMfactor(object, parent, mult)`: `.updateCHMfactor` updates `object` with the result of Cholesky factorizing `F(parent) + mult[1] * diag(nrow(parent))`, i.e., `F(parent)` plus `mult[1]` times the identity matrix, where `F = identity` if `parent` is a `dsCMatrix` and `F = tcrossprod` if `parent` is a `dgCMatrix`. The nonzero pattern of `F(parent)` must match that of `S` if `object = Cholesky(S, ...)`.

Examples

```
D. <- diag(x = c(1, 1, 2, 3, 5, 8))
D.0 <- Diagonal(x = c(0, 0, 0, 3, 5, 8))
S. <- toeplitz(as.double(1:6))
C. <- new("dgCMatrix", Dim = c(3L, 4L),
          p = c(0L, 1L, 1L, 1L, 3L), i = c(1L, 0L, 2L), x = c(-8, 2, 3))

stopifnot(exprs = {
    identical(.M2tri (D.), as(D., "triangularMatrix"))
    identical(.M2sym (D.), as(D.,  "symmetricMatrix"))
    identical(.M2diag(D.), as(D.,   "diagonalMatrix"))
    identical(.M2kind(C., "l"),
              as(C., "lMatrix"))
    identical(.M2kind(.sparse2dense(C.), "l"),
              as(as(C., "denseMatrix"), "lMatrix"))
    identical(.diag2sparse(D.0, ".", "t", "C"),
              .dense2sparse(.diag2dense(D.0, ".", "t", TRUE), "C"))
    identical(.M2gen(.diag2dense(D.0, ".", "s", FALSE)),
              .sparse2dense(.M2gen(.diag2sparse(D.0, ".", "s", "T"))))
    identical(S.,
              .M2m(.m2sparse(S., ".sR")))
    identical(S. * lower.tri(S.) + diag(1, 6L),
              .M2m(.m2dense (S., ".tr", "L", "U")))
    identical(.M2R(C.), .M2R(.M2T(C.)))
    identical(.tCRT(C.), .M2R(t(C.)))
})

A <- tcrossprod(C.)/6 + Diagonal(3, 1/3); A[1,2] <- 3; A
stopifnot(exprs = {
    is.numeric( x. <- c(2.2, 0, -1.2) )
    all.equal(x., .solve.dgC.lu(A, c(1,0,0), check=FALSE))
    all.equal(x., .solve.dgC.qr(A, c(1,0,0), check=FALSE))
})

## Solving sparse least squares:

X <- rbind(A, Diagonal(3)) # design matrix X (for L.S.)
Xt <- t(X)                 # *transposed*  X (for L.S.)
(y <- drop(crossprod(Xt, 1:3)) + c(-1,1)/1000) # small rand.err.
```

```
str(solveCh <- .solve.dgC.chol(Xt, y, check=FALSE)) # Xt *is* dgC..
stopifnot(exprs = {
    all.equal(solveCh$coef, 1:3, tol = 1e-3)# rel.err ~ 1e-4
    all.equal(solveCh$coef, drop(solve(tcrossprod(Xt), Xt %*% y)))
    all.equal(solveCh$coef, .solve.dgC.qr(X, y, check=FALSE))
})
```

`forceSymmetric-methods` *Force a Matrix to 'symmetricMatrix' Without Symmetry Checks*

Description

Force a square matrix `x` to a `symmetricMatrix`, **without** a symmetry check as it would be applied for `as(x, "symmetricMatrix")`.

Usage

```
forceSymmetric(x, uplo)
```

Arguments

`x`	any square matrix (of numbers), either ""traditional"" (`matrix`) or inheriting from `Matrix`.
`uplo`	optional string, `"U"` or `"L"` indicating which "triangle" half of `x` should determine the result. The default is `"U"` unless `x` already has a `uplo` slot (i.e., when it is `symmetricMatrix`, or `triangularMatrix`), where the default will be `x@uplo`.

Value

a square matrix inheriting from class `symmetricMatrix`.

See Also

`symmpart` for the symmetric part of a matrix, or the coercions `as(x, <symmetricMatrix class>)`.

Examples

```
## Hilbert matrix
i <- 1:6
h6 <- 1/outer(i - 1L, i, "+")
sd <- sqrt(diag(h6))
hh <- t(h6/sd)/sd # theoretically symmetric
isSymmetric(hh, tol=0) # FALSE; hence
try( as(hh, "symmetricMatrix") ) # fails, but this works fine:
H6 <- forceSymmetric(hh)

## result can be pretty surprising:
(M <- Matrix(1:36, 6))
```

```
forceSymmetric(M) # symmetric, hence very different in lower triangle
(tm <- tril(M))
forceSymmetric(tm)
```

---

formatSparseM *Formatting Sparse Numeric Matrices Utilities*

Description

Utilities for formatting sparse numeric matrices in a flexible way. These functions are used by the format and print methods for sparse matrices and can be applied as well to standard R matrices. Note that *all* arguments but the first are optional.

formatSparseM() is the main "workhorse" of formatSpMatrix, the format method for sparse matrices.

.formatSparseSimple() is a simple helper function, also dealing with (short/empty) column names construction.

Usage

```
formatSparseM(x, zero.print = ".", align = c("fancy", "right"),
              m = as(x,"matrix"), asLogical=NULL, uniDiag=NULL,
              digits=NULL, cx, iN0, dn = dimnames(m))

.formatSparseSimple(m, asLogical=FALSE, digits=NULL,
    col.names, note.dropping.colnames = TRUE,
                  dn=dimnames(m))
```

Arguments

x	an R object inheriting from class sparseMatrix.
zero.print	character which should be used for *structural* zeroes. The default "." may occasionally be replaced by " " (blank); using "0" would look almost like print()ing of non-sparse matrices.
align	a string specifying how the zero.print codes should be aligned, see formatSpMatrix.
m	(optional) a (standard R) matrix version of x.
asLogical	should the matrix be formatted as a logical matrix (or rather as a numeric one); mostly for formatSparseM().
uniDiag	logical indicating if the diagonal entries of a sparse unit triangular or unit-diagonal matrix should be formatted as "I" instead of "1" (to emphasize that the 1's are "structural").
digits	significant digits to use for printing, see print.default.
cx	(optional) character matrix; a formatted version of x, still with strings such as "0.00" for the zeros.
iN0	(optional) integer vector, specifying the location of the *non*-zeroes of x.

col.names, note.dropping.colnames
: see formatSpMatrix.

dn
: dimnames to be used; a list (of length two) with row and column names (or NULL).

Value

a character matrix like cx, where the zeros have been replaced with (padded versions of) zero.print. As this is a *dense* matrix, do not use these functions for really large (really) sparse matrices!

Author(s)

Martin Maechler

See Also

formatSpMatrix which calls formatSparseM() and is the format method for sparse matrices.
printSpMatrix which is used by the (typically implicitly called) show and print methods for sparse matrices.

Examples

```
m <- suppressWarnings(matrix(c(0, 3.2, 0,0, 11,0,0,0,0,-7,0), 4,9))
fm <- formatSparseM(m)
noquote(fm)
## nice, but this is nicer {with "units" vertically aligned}:
print(fm, quote=FALSE, right=TRUE)
## and "the same" as :
Matrix(m)

## align = "right" is cheaper -->  the "." are not aligned:
noquote(f2 <- formatSparseM(m,align="r"))
stopifnot(f2 == fm   |   m == 0, dim(f2) == dim(m),
          (f2 == ".") == (m == 0))
```

---

generalMatrix-class *Class "generalMatrix" of General Matrices*

Description

Virtual class of "general" matrices; i.e., matrices that do not have a known property such as symmetric, triangular, or diagonal.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots

`Dim, Dimnames` inherited from virtual class `Matrix`.

`factors` a list of `MatrixFactorization` objects caching factorizations of the matrix. Typically, it is initialized as an empty list and updated "automagically" whenever a factorization is computed.

Extends

Class `"Matrix"`, directly.

See Also

Virtual classes `symmetricMatrix`, `triangularMatrix`, and `diagonalMatrix`.

`Hilbert` *Generate a Hilbert matrix*

Description

Generate the `n` by `n` symmetric Hilbert matrix. Because these matrices are ill-conditioned for moderate to large `n`, they are often used for testing numerical linear algebra code.

Usage

```
Hilbert(n)
```

Arguments

`n`	a non-negative integer.

Value

the `n` by `n` symmetric Hilbert matrix as a `"dpoMatrix"` object.

See Also

the class `dpoMatrix`

Examples

```
Hilbert(6)
```

image-methods *Methods for image() in Package 'Matrix'*

Description

Methods for function `image` in package **Matrix**. An image of a matrix simply color codes all matrix entries and draws the $n \times m$ matrix using an $n \times m$ grid of (colored) rectangles.

The **Matrix** package `image` methods are based on `levelplot()` from package **lattice**; hence these methods return an "object" of class `"trellis"`, producing a graphic when (auto-) `print()`ed.

Usage

```
## S4 method for signature 'dgTMatrix'
image(x,
      xlim = c(1, di[2]),
      ylim = c(di[1], 1), aspect = "iso",
      sub = sprintf("Dimensions: %d x %d", di[1], di[2]),
      xlab = "Column", ylab = "Row", cuts = 15,
      useRaster = FALSE,
      useAbs = NULL, colorkey = !useAbs,
      col.regions = NULL,
      lwd = NULL, border.col = NULL, ...)
```

Arguments

`x`	a Matrix object, i.e., fulfilling `is(x, "Matrix")`.
`xlim`, `ylim`	x- and y-axis limits; may be used to "zoom into" matrix. Note that x, y "feel reversed": `ylim` is for the rows (= 1st index) and `xlim` for the columns (= 2nd index). For convenience, when the limits are integer valued, they are both extended by `0.5`; also, `ylim` is always used decreasingly.
`aspect`	aspect ratio specified as number (y/x) or string; see `levelplot`.
`sub`, `xlab`, `ylab`	axis annotation with sensible defaults; see `plot.default`.
`cuts`	number of levels the range of matrix values would be divided into.
`useRaster`	logical indicating if raster graphics should be used (instead of the tradition rectangle vector drawing). If true, `panel.levelplot.raster` (from **lattice** package) is used, and the colorkey is also done via rasters, see also `levelplot` and possibly `grid.raster`. Note that using raster graphics may often be faster, but can be slower, depending on the matrix dimensions and the graphics device (dimensions).
`useAbs`	logical indicating if `abs(x)` should be shown; if `TRUE`, the former (implicit) default, the default `col.regions` will be `grey` colors (and no `colorkey` drawn). The default is `FALSE` unless the matrix has no negative entries.
`colorkey`	logical indicating if a color key aka 'legend' should be produced. Default is to draw one, unless `useAbs` is true. You can also specify a `list`, see `levelplot`, such as`list(raster=TRUE)` in the case of rastering.

col.regions	vector of gradually varying colors; see levelplot.
lwd	(only used when useRaster is false:) non-negative number or NULL (default), specifying the line-width of the rectangles of each non-zero matrix entry (drawn by grid.rect). The default depends on the matrix dimension and the device size.
border.col	color for the border of each rectangle. NA means no border is drawn. When NULL as by default, border.col <- if(lwd < .01) NA else NULL is used. Consider using an opaque color instead of NULL which corresponds to grid::get.gpar("col").
...	further arguments passed to methods and levelplot, notably at for specifying (possibly non equidistant) cut values for dividing the matrix values (superseding cuts above).

Value

as all **lattice** graphics functions, image(<Matrix>) returns a "trellis" object, effectively the result of levelplot().

Methods

All methods currently end up calling the method for the dgTMatrix class. Use showMethods(image) to list them all.

See Also

levelplot, and print.trellis from package **lattice**.

Examples

```
showMethods(image)
## And if you want to see the method definitions:
showMethods(image, includeDefs = TRUE, inherited = FALSE)

data(CAex, package = "Matrix")
image(CAex, main = "image(CAex)") -> imgC; imgC
stopifnot(!is.null(leg <- imgC$legend), is.list(leg$right)) # failed for 2 days ..
image(CAex, useAbs=TRUE, main = "image(CAex, useAbs=TRUE)")

cCA <- Cholesky(crossprod(CAex), Imult = .01)
## See  ?print.trellis --- place two image() plots side by side:
print(image(cCA, main="Cholesky(crossprod(CAex), Imult = .01)"),
      split=c(x=1,y=1,nx=2, ny=1), more=TRUE)
print(image(cCA, useAbs=TRUE),
      split=c(x=2,y=1,nx=2,ny=1))

data(USCounties, package = "Matrix")
image(USCounties)# huge
image(sign(USCounties))## just the pattern
    # how the result looks, may depend heavily on
    # the device, screen resolution, antialiasing etc
    # e.g. x11(type="Xlib") may show very differently than cairo-based
```

```
## Drawing borders around each rectangle;
    # again, viewing depends very much on the device:
image(USCounties[1:400,1:200], lwd=.1)
## Using (xlim,ylim) has advantage : matrix dimension and (col/row) indices:
image(USCounties, c(1,200), c(1,400), lwd=.1)
image(USCounties, c(1,300), c(1,200), lwd=.5 )
image(USCounties, c(1,300), c(1,200), lwd=.01)
## These 3 are all equivalent :
(I1 <- image(USCounties, c(1,100), c(1,100), useAbs=FALSE))
 I2 <- image(USCounties, c(1,100), c(1,100), useAbs=FALSE,        border.col=NA)
 I3 <- image(USCounties, c(1,100), c(1,100), useAbs=FALSE, lwd=2, border.col=NA)
stopifnot(all.equal(I1, I2, check.environment=FALSE),
          all.equal(I2, I3, check.environment=FALSE))
## using an opaque border color
image(USCounties, c(1,100), c(1,100), useAbs=FALSE, lwd=3, border.col = adjustcolor("skyblue", 1/2))

if(interactive() || nzchar(Sys.getenv("R_MATRIX_CHECK_EXTRA"))) {
## Using raster graphics: For PDF this would give a 77 MB file,
## however, for such a large matrix, this is typically considerably
## *slower* (than vector graphics rectangles) in most cases :
if(doPNG <- !dev.interactive())
   png("image-UScounties-raster.png", width=3200, height=3200)
image(USCounties, useRaster = TRUE) # should not suffer from anti-aliasing
if(doPNG)
   dev.off()
   ## and now look at the *.png image in a viewer you can easily zoom in and out
}#only if(doExtras)
```

`index-class` *Virtual Class "index" of Index Vectors*

Description

Class `index` is a virtual class designating index vectors, or "subscripts", for (possibly named) vectors and arrays. It is typically used in signatures of methods for the subscript and subassignment operators, namely `[` and `[<-`. It is implemented as a *union* of the atomic vector classes `numeric`, `logical`, and `character`.

See Also

`[`, `[-methods`, and `[<--methods`.

Examples

```
showClass("index")
```

indMatrix-class *Index Matrices*

Description

The indMatrix class is the class of row and column *index* matrices, stored as 1-based integer index vectors. A row (column) index matrix is a matrix whose rows (columns) are standard unit vectors. Such matrices are useful when mapping observations to discrete sets of covariate values.

Multiplying a matrix on the left by a row index matrix is equivalent to indexing its rows, i.e., sampling the rows "with replacement". Analogously, multiplying a matrix on the right by a column index matrix is equivalent to indexing its columns. Indeed, such products are implemented in **Matrix** as indexing operations; see 'Details' below.

A matrix whose rows *and* columns are standard unit vectors is called a *permutation* matrix. This special case is designated by the pMatrix class, a direct subclass of indMatrix.

Details

The transpose of an index matrix is an index matrix with identical perm but opposite margin. Hence the transpose of a row index matrix is a column index matrix, and vice versa.

The cross product of a row index matrix R and itself is a diagonal matrix whose diagonal entries are the the number of entries in each column of R.

Given a row index matrix R with perm slot p, a column index matrix C with perm slot q, and a matrix M with conformable dimensions, we have

RM	=	R %*% M	=	M[p,]
MC	=	M %*% C	=	M[, q]
$C'M$	=	crossprod(C, M)	=	M[q,]
MR'	=	tcrossprod(M, R)	=	M[, p]
$R'R$	=	crossprod(R)	=	Diagonal(x=tabulate(p, ncol(R)))
CC'	=	tcrossprod(C)	=	Diagonal(x=tabulate(q, nrow(C)))

Operations on index matrices that result in index matrices will accordingly return an indMatrix. These include products of two column index matrices and (equivalently) column-indexing of a column index matrix (when dimensions are not dropped). Most other operations on indMatrix treat them as sparse nonzero pattern matrices (i.e., inheriting from virtual class nsparseMatrix). Hence vector-valued subsets of indMatrix, such as those given by diag, are always of type "logical".

Objects from the Class

Objects can be created explicitly with calls of the form new("indMatrix", ...), but they are more commonly created by coercing 1-based integer index vectors, with calls of the form as(., "indMatrix"); see 'Methods' below.

Slots

`margin` an integer, either 1 or 2, specifying whether the matrix is a row (1) or column (2) index.

`perm` a 1-based integer index vector, i.e., a vector of length `Dim[margin]` with elements taken from `1:Dim[1+margin%%2]`.

`Dim`,`Dimnames` inherited from virtual superclass `Matrix`.

Extends

Classes `"sparseMatrix"` and `"generalMatrix"`, directly.

Methods

`%*% signature(x = "indMatrix", y = "Matrix")` and others listed by `showMethods("%*%", classes = "indMatrix")`: matrix products implemented where appropriate as indexing operations.

`coerce signature(from = "numeric", to = "indMatrix")`: supporting typical `indMatrix` construction from a vector of positive integers. Row indexing is assumed.

`coerce signature(from = "list", to = "indMatrix")`: supporting `indMatrix` construction for row *and* column indexing, including index vectors of length 0 and index vectors whose maximum is less than the number of rows or columns being indexed.

`coerce signature(from = "indMatrix", to = "matrix")`: coercion to a traditional `matrix` of logical type, with `FALSE` and `TRUE` in place of 0 and 1.

`t signature(x = "indMatrix")`: the transpose, which is an `indMatrix` with identical `perm` but opposite `margin`.

`rowSums`,`rowMeans`,`colSums`,`colMeans signature(x = "indMatrix")`: row and column sums and means.

`rbind2`,`cbind2 signature(x = "indMatrix", y = "indMatrix")`: row-wise catenation of two row index matrices with equal numbers of columns and column-wise catenation of two column index matrices with equal numbers of rows.

kronecker `signature(X = "indMatrix", Y = "indMatrix")`: Kronecker product of two row index matrices or two column index matrices, giving the row or column index matrix corresponding to their "interaction".

Author(s)

Fabian Scheipl at 'uni-muenchen.de', building on the existing class `pMatrix` after a nice hike's conversation with Martin Maechler. Methods for `crossprod(x, y)` and `kronecker(x, y)` with both arguments inheriting from `indMatrix` were made considerably faster thanks to a suggestion by Boris Vaillant. Diverse tweaks by Martin Maechler and Mikael Jagan, notably the latter's implementation of `margin`, prior to which the `indMatrix` class was designated only for row index matrices.

See Also

Subclass `pMatrix` of permutation matrices, a special case of index matrices; virtual class `nMatrix` of nonzero pattern matrices, and its subclasses.

Examples

```
p1 <- as(c(2,3,1), "pMatrix")
(sm1 <- as(rep(c(2,3,1), e=3), "indMatrix"))
stopifnot(all(sm1 == p1[rep(1:3, each=3),]))

## row-indexing of a <pMatrix> turns it into an <indMatrix>:
class(p1[rep(1:3, each=3),])

set.seed(12) # so we know '10' is in sample
## random index matrix for 30 observations and 10 unique values:
(s10 <- as(sample(10, 30, replace=TRUE),"indMatrix"))

## Sample rows of a numeric matrix :
(mm <- matrix(1:10, nrow=10, ncol=3))
s10 %*% mm

set.seed(27)
IM1 <- as(sample(1:20, 100, replace=TRUE), "indMatrix")
IM2 <- as(sample(1:18, 100, replace=TRUE), "indMatrix")
(c12 <- crossprod(IM1,IM2))
## same as cross-tabulation of the two index vectors:
stopifnot(all(c12 - unclass(table(IM1@perm, IM2@perm)) == 0))

# 3 observations, 4 implied values, first does not occur in sample:
as(2:4, "indMatrix")
# 3 observations, 5 values, first and last do not occur in sample:
as(list(2:4, 5), "indMatrix")

as(sm1, "nMatrix")
s10[1:7, 1:4] # gives an "ngTMatrix" (most economic!)
s10[1:4, ]  # preserves "indMatrix"-class

I1 <- as(c(5:1,6:4,7:3), "indMatrix")
I2 <- as(7:1, "pMatrix")
(I12 <- rbind(I1, I2))
stopifnot(is(I12, "indMatrix"),
          identical(I12, rbind(I1, I2)),
  colSums(I12) == c(2L,2:4,4:2))
```

`invertPerm` *Utilities for Permutation Vectors*

Description

`invertPerm` and `signPerm` compute the inverse and sign of a length-`n` permutation vector. `isPerm` tests if a length-`n` integer vector is a valid permutation vector. `asPerm` coerces a length-`m` transposition vector to a length-`n` permutation vector, where `m` <= `n`.

Usage

```
invertPerm(p, off = 1L, ioff = 1L)
signPerm(p, off = 1L)
isPerm(p, off = 1L)
asPerm(pivot, off = 1L, ioff = 1L, n = length(pivot))

invPerm(p, zero.p = FALSE, zero.res = FALSE)
```

Arguments

p	an integer vector of length n.
pivot	an integer vector of length m.
off	an integer offset, indicating that p is a permutation of off+0:(n-1) or that pivot contains m values sampled with replacement from off+0:(n-1).
ioff	an integer offset, indicating that the result should be a permutation of ioff+0:(n-1).
n	a integer greater than or equal to m, indicating the length of the result. Transpositions are applied to a permutation vector vector initialized as seq_len(n).
zero.p	a logical. Equivalent to off=0 if TRUE and off=1 if FALSE.
zero.res	a logical. Equivalent to ioff=0 if TRUE and ioff=1 if FALSE.

Details

invertPerm(p, off, ioff=1) is equivalent to order(p) or sort.list(p) for all values of off. For the default value off=1, it returns the value of p after p[p] <- seq_along(p).

invPerm is a simple wrapper around invertPerm, retained for backwards compatibility.

Value

By default, i.e., with off=1 and ioff=1:

invertPerm(p) returns an integer vector of length length(p) such that p[invertPerm(p)] and invertPerm(p)[p] are both seq_along(p), i.e., the identity permutation.

signPerm(p) returns 1 if p is an even permutation and -1 otherwise (i.e., if p is odd).

isPerm(p) returns TRUE if p is a permutation of seq_along(p) and FALSE otherwise.

asPerm(pivot) returns the result of transposing elements i and pivot[i] of a permutation vector initialized as seq_len(n), for i in seq_along(pivot).

See Also

Class pMatrix of permutation matrices.

Examples

```
p <- sample(10L) # a random permutation vector
ip <- invertPerm(p)
s <- signPerm(p)
```

```
## 'p' and 'ip' are indeed inverses:
stopifnot(exprs = {
    isPerm(p)
    isPerm(ip)
    identical(s, 1L) || identical(s, -1L)
    identical(s, signPerm(ip))
    identical(p[ip], 1:10)
    identical(ip[p], 1:10)
    identical(invertPerm(ip), p)
})

## Product of transpositions (1 2)(2 1)(4 3)(6 8)(10 1) = (3 4)(6 8)(1 10)
pivot <- c(2L, 1L, 3L, 3L, 5L, 8L, 7L, 8L, 9L, 1L)
q <- asPerm(pivot)
stopifnot(exprs = {
    identical(q, c(10L, 2L, 4L, 3L, 5L, 8L, 7L, 6L, 9L, 1L))
    identical(q[q], seq_len(10L)) # because the permutation is odd:
    signPerm(q) == -1L
})

invPerm # a less general version of 'invertPerm'
```

`is.na-methods` *is.na(), is.finite() Methods for 'Matrix' Objects*

Description

Methods for generic functions `anyNA()`, `is.na()`, `is.nan()`, `is.infinite()`, and `is.finite()`, for objects inheriting from virtual class `Matrix` or `sparseVector`.

Usage

```
## S4 method for signature 'denseMatrix'
is.na(x)
## S4 method for signature 'sparseMatrix'
is.na(x)
## S4 method for signature 'diagonalMatrix'
is.na(x)
## S4 method for signature 'indMatrix'
is.na(x)
## S4 method for signature 'sparseVector'
is.na(x)
## ...
## and likewise for anyNA, is.nan, is.infinite, is.finite
```

Arguments

x	an R object, here a sparse or dense matrix or vector.

Value

For `is.*()`, an `nMatrix` or `nsparseVector` matching the dimensions of `x` and specifying the positions in `x` of (some subset of) `NA`, `NaN`, `Inf`, and `-Inf`. For `anyNA()`, `TRUE` if `x` contains `NA` or `NaN` and `FALSE` otherwise.

See Also

`NA`, `NaN`, `Inf`

Examples

```
(M <- Matrix(1:6, nrow = 4, ncol = 3,
             dimnames = list(letters[1:4], LETTERS[1:3])))
stopifnot(!anyNA(M), !any(is.na(M)))

M[2:3, 2] <- NA
(inM <- is.na(M))
stopifnot(anyNA(M), sum(inM) == 2)

(A <- spMatrix(nrow = 10, ncol = 20,
               i = c(1, 3:8), j = c(2, 9, 6:10), x = 7 * (1:7)))
stopifnot(!anyNA(A), !any(is.na(A)))

A[2, 3] <- A[1, 2] <- A[5, 5:9] <- NA
(inA <- is.na(A))
stopifnot(anyNA(A), sum(inA) == 1 + 1 + 5)
```

---

is.null.DN *Are the Dimnames* dn *NULL-like ?*

Description

Are the `dimnames` dn `NULL`-like?

`is.null.DN(dn)` is less strict than `is.null(dn)`, because it is also true (`TRUE`) when the dimnames dn are "like" `NULL`, or `list(NULL,NULL)`, as they can easily be for the traditional R matrices (`matrix`) which have no formal `class` definition, and hence much freedom in how their `dimnames` look like.

Usage

```
is.null.DN(dn)
```

Arguments

dn	`dimnames()` of a `matrix`-like R object.

Value

`logical` `TRUE` or `FALSE`.

Note

This function is really to be used on "traditional" matrices rather than those inheriting from `Matrix`, as the latter will always have dimnames `list(NULL,NULL)` exactly, in such a case.

Author(s)

Martin Maechler

See Also

`is.null`, `dimnames`, `matrix`.

Examples

```
m1 <- m2 <- m3 <- m4 <- m <-
    matrix(round(100 * rnorm(6)), 2, 3)
dimnames(m1) <- list(NULL, NULL)
dimnames(m2) <- list(NULL, character())
dimnames(m3) <- rev(dimnames(m2))
dimnames(m4) <- rep(list(character()),2)

m4 # prints absolutely identically to m

c.o <- capture.output
cm <- c.o(m)
stopifnot(exprs = {
    m == m1; m == m2; m == m3; m == m4
identical(cm, c.o(m1)); identical(cm, c.o(m2))
identical(cm, c.o(m3)); identical(cm, c.o(m4))
})

hasNoDimnames <- function(.) is.null.DN(dimnames(.))
stopifnot(exprs = {
    hasNoDimnames(m)
    hasNoDimnames(m1); hasNoDimnames(m2)
    hasNoDimnames(m3); hasNoDimnames(m4)
    hasNoDimnames(Matrix(m) -> M)
    hasNoDimnames(as(M, "sparseMatrix"))
})
```

---

isSymmetric-methods *Methods for Function 'isSymmetric' in Package 'Matrix'*

Description

`isSymmetric` tests whether its argument is a symmetric square matrix, by default tolerating some numerical fuzz and requiring symmetric `[dD]imnames` in addition to symmetry in the mathematical sense. `isSymmetric` is a generic function in **base**, which has a method for traditional matrices of implicit `class "matrix"`. Methods are defined here for various proper and virtual classes in **Matrix**, so that `isSymmetric` works for all objects inheriting from virtual class `"Matrix"`.

Usage

```
## S4 method for signature 'denseMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'CsparseMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'RsparseMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'TsparseMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'diagonalMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'indMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'dgeMatrix'
isSymmetric(object, checkDN = TRUE, tol = 100 * .Machine$double.eps, tol1 = 8 * tol, ...)
## S4 method for signature 'dgCMatrix'
isSymmetric(object, checkDN = TRUE, tol = 100 * .Machine$double.eps, ...)
```

Arguments

object	a "Matrix".
checkDN	a logical indicating whether symmetry of the Dimnames slot of object should be checked.
tol, tol1	numerical tolerances allowing *approximate* symmetry of numeric (rather than logical) matrices. See also isSymmetric.matrix.
...	further arguments passed to methods (typically methods for all.equal).

Details

The Dimnames slot of object, say dn, is considered to be symmetric if and only if

- dn[[1]] and dn[[2]] are identical *or* one is NULL; *and*
- ndn <- names(dn) is NULL *or* ndn[1] and ndn[2] are identical *or* one is the empty string "".

Hence list(a=nms, a=nms) is considered to be *symmetric*, and so too are list(a=nms, NULL) and list(NULL, a=nms).

Note that this definition is *looser* than that employed by isSymmetric.matrix, which requires dn[1] and dn[2] to be identical, where dn is the dimnames attribute of a traditional matrix.

Value

A logical, either TRUE or FALSE (never NA).

See Also

forceSymmetric; symmpart and skewpart; virtual class "symmetricMatrix" and its subclasses.

Examples

```
isSymmetric(Diagonal(4)) # TRUE of course
M <- Matrix(c(1,2,2,1), 2,2)
isSymmetric(M) # TRUE (*and* of formal class "dsyMatrix")
isSymmetric(as(M, "generalMatrix")) # still symmetric, even if not "formally"
isSymmetric(triu(M)) # FALSE

## Look at implementations:
showMethods("isSymmetric", includeDefs = TRUE) # includes S3 generic from base
```

---

isTriangular-methods *Test whether a Matrix is Triangular or Diagonal*

Description

`isTriangular` and `isDiagonal` test whether their argument is a triangular or diagonal matrix, respectively. Unlike the analogous `isSymmetric`, these two functions are generically from **Matrix** rather than `base`. Hence **Matrix** defines methods for traditional matrices of implicit class `"matrix"` in addition to matrices inheriting from virtual class `"Matrix"`.

By our definition, triangular and diagonal matrices are *square*, i.e., they have the same number of rows and columns.

Usage

```
isTriangular(object, upper = NA, ...)

isDiagonal(object)
```

Arguments

`object`	an R object, typically a matrix.
`upper`	a logical, either `TRUE` or `FALSE`, in which case `TRUE` is returned only for upper or lower triangular `object`; or otherwise `NA` (the default), in which case `TRUE` is returned for any triangular `object`.
`...`	further arguments passed to methods (currently unused by **Matrix**).

Value

A logical, either `TRUE` or `FALSE` (never `NA`).

If `object` is triangular and `upper` is `NA`, then `isTriangular` returns `TRUE` with an attribute `kind`, either `"U"` or `"L"`, indicating that `object` is **u**pper or **l**ower triangular, respectively. Users should not rely on how `kind` is determined for diagonal matrices, which are both upper and lower triangular.

See Also

`isSymmetric`; virtual classes `"triangularMatrix"` and `"diagonalMatrix"` and their subclasses.

Examples

```
isTriangular(Diagonal(4))
## is TRUE: a diagonal matrix is also (both upper and lower) triangular
(M <- Matrix(c(1,2,0,1), 2,2))
isTriangular(M) # TRUE (*and* of formal class "dtrMatrix")
isTriangular(as(M, "generalMatrix")) # still triangular, even if not "formally"
isTriangular(crossprod(M)) # FALSE

isDiagonal(matrix(c(2,0,0,1), 2,2)) # TRUE

## Look at implementations:
showMethods("isTriangular", includeDefs = TRUE)
showMethods("isDiagonal", includeDefs = TRUE)
```

KhatriRao *Khatri-Rao Matrix Product*

Description

Computes Khatri-Rao products for any kind of matrices.

The Khatri-Rao product is a column-wise Kronecker product. Originally introduced by Khatri and Rao (1968), it has many different applications, see Liu and Trenkler (2008) for a survey. Notably, it is used in higher-dimensional tensor decompositions, see Bader and Kolda (2008).

Usage

```
KhatriRao(X, Y = X, FUN = "*", sparseY = TRUE, make.dimnames = FALSE)
```

Arguments

X, Y	matrices of with the same number of columns.
FUN	the (name of the) function to be used for the column-wise Kronecker products, see kronecker, defaulting to the usual multiplication.
sparseY	logical specifying if Y should be coerced and treated as sparseMatrix. Set this to FALSE, e.g., to distinguish structural zeros from zero entries.
make.dimnames	logical indicating if the result should inherit dimnames from X and Y in a simple way.

Value

a "CsparseMatrix", say R, the Khatri-Rao product of X ($n \times k$) and Y ($m \times k$), is of dimension $(n \cdot m) \times k$, where the j-th column, R[,j] is the kronecker product kronecker(X[,j], Y[,j]).

Note

The current implementation is efficient for large sparse matrices.

Author(s)

Original by Michael Cysouw, Univ. Marburg; minor tweaks, bug fixes etc, by Martin Maechler.

References

Khatri, C. G., and Rao, C. Radhakrishna (1968) Solutions to Some Functional Equations and Their Applications to Characterization of Probability Distributions. *Sankhya: Indian J. Statistics, Series A* **30**, 167–180.

Bader, Brett W, and Tamara G Kolda (2008) Efficient MATLAB Computations with Sparse and Factored Tensors. *SIAM J. Scientific Computing* **30**, 205–231.

See Also

kronecker.

Examples

```
## Example with very small matrices:
m <- matrix(1:12,3,4)
d <- diag(1:4)
KhatriRao(m,d)
KhatriRao(d,m)
dimnames(m) <- list(LETTERS[1:3], letters[1:4])
KhatriRao(m,d, make.dimnames=TRUE)
KhatriRao(d,m, make.dimnames=TRUE)
dimnames(d) <- list(NULL, paste0("D", 1:4))
KhatriRao(m,d, make.dimnames=TRUE)
KhatriRao(d,m, make.dimnames=TRUE)
dimnames(d) <- list(paste0("d", 10*1:4), paste0("D", 1:4))
(Kmd <- KhatriRao(m,d, make.dimnames=TRUE))
(Kdm <- KhatriRao(d,m, make.dimnames=TRUE))

nm <- as(m, "nsparseMatrix")
nd <- as(d, "nsparseMatrix")
KhatriRao(nm,nd, make.dimnames=TRUE)
KhatriRao(nd,nm, make.dimnames=TRUE)

stopifnot(dim(KhatriRao(m,d)) == c(nrow(m)*nrow(d), ncol(d)))
## border cases / checks:
zm <- nm; zm[] <- FALSE # all FALSE matrix
stopifnot(all(K1 <- KhatriRao(nd, zm) == 0), identical(dim(K1), c(12L, 4L)),
          all(K2 <- KhatriRao(zm, nd) == 0), identical(dim(K2), c(12L, 4L)))

d0 <- d; d0[] <- 0; m0 <- Matrix(d0[-1,])
stopifnot(all(K3 <- KhatriRao(d0, m) == 0), identical(dim(K3), dim(Kdm)),
  all(K4 <- KhatriRao(m, d0) == 0), identical(dim(K4), dim(Kmd)),
  all(KhatriRao(d0, d0) == 0), all(KhatriRao(m0, d0) == 0),
  all(KhatriRao(d0, m0) == 0), all(KhatriRao(m0, m0) == 0),
  identical(dimnames(KhatriRao(m, d0, make.dimnames=TRUE)), dimnames(Kmd)))

## a matrix with "structural" and non-structural zeros:
```

```
m01 <- new("dgCMatrix", i = c(0L, 2L, 0L, 1L), p = c(0L, 0L, 0L, 2L, 4L),
           Dim = 3:4, x = c(1, 0, 1, 0))
D4 <- Diagonal(4, x=1:4) # "as" d
DU <- Diagonal(4)# unit-diagonal: uplo="U"
(K5  <- KhatriRao( d, m01))
K5d  <- KhatriRao( d, m01, sparseY=FALSE)
K5Dd <- KhatriRao(D4, m01, sparseY=FALSE)
K5Ud <- KhatriRao(DU, m01, sparseY=FALSE)
(K6  <- KhatriRao(diag(3),     t(m01)))
K6D  <- KhatriRao(Diagonal(3), t(m01))
K6d  <- KhatriRao(diag(3),     t(m01), sparseY=FALSE)
K6Dd <- KhatriRao(Diagonal(3), t(m01), sparseY=FALSE)
stopifnot(exprs = {
    all(K5 == K5d)
    identical(cbind(c(7L, 10L), c(3L, 4L)),
              which(K5 != 0, arr.ind = TRUE, useNames=FALSE))
    identical(K5d, K5Dd)
    identical(K6, K6D)
    all(K6 == K6d)
    identical(cbind(3:4, 1L),
              which(K6 != 0, arr.ind = TRUE, useNames=FALSE))
    identical(K6d, K6Dd)
})
```

KNex *Koenker-Ng Example Sparse Model Matrix and Response Vector*

Description

A model matrix `mm` and corresponding response vector `y` used in an example by Koenker and Ng. The matrix `mm` is a sparse matrix with 1850 rows and 712 columns but only 8758 non-zero entries. It is a `"dgCMatrix"` object. The vector `y` is just `numeric` of length 1850.

Usage

```
data(KNex)
```

References

Roger Koenker and Pin Ng (2003). SparseM: A sparse matrix package for R; *J. of Statistical Software*, **8** (6), doi:10.18637/jss.v008.i06

Examples

```
data(KNex, package = "Matrix")
class(KNex$mm)
dim(KNex$mm)
image(KNex$mm)
str(KNex)
```

```
system.time( # a fraction of a second
  sparse.sol <- with(KNex, solve(crossprod(mm), crossprod(mm, y))))

head(round(sparse.sol,3))

## Compare with QR-based solution ("more accurate, but slightly slower"):
system.time(
  sp.sol2 <- with(KNex, qr.coef(qr(mm), y) ))

all.equal(sparse.sol, sp.sol2, tolerance = 1e-13) # TRUE
```

---

kronecker-methods *Methods for Function 'kronecker()' in Package 'Matrix'*

Description

Computes Kronecker products for objects inheriting from "Matrix".

In order to preserver sparseness, we treat `0 * NA` as `0`, not as NA as usually in R (and as used for the **base** function kronecker).

Methods

kronecker `signature(X = "Matrix", Y = "ANY")` .....

kronecker `signature(X = "ANY", Y = "Matrix")` .....

kronecker `signature(X = "diagonalMatrix", Y = "ANY")` .....

kronecker `signature(X = "sparseMatrix", Y = "ANY")` .....

kronecker `signature(X = "TsparseMatrix", Y = "TsparseMatrix")` .....

kronecker `signature(X = "dgTMatrix", Y = "dgTMatrix")` .....

kronecker `signature(X = "dtTMatrix", Y = "dtTMatrix")` .....

kronecker `signature(X = "indMatrix", Y = "indMatrix")` .....

Examples

```
(t1 <- spMatrix(5,4, x= c(3,2,-7,11), i= 1:4, j=4:1)) #  5 x  4
(t2 <- kronecker(Diagonal(3, 2:4), t1))               # 15 x 12

## should also work with special-cased logical matrices
l3 <- upper.tri(matrix(,3,3))
M <- Matrix(l3)
(N <- as(M, "nsparseMatrix")) # "ntCMatrix" (upper triangular)
N2 <- as(N, "generalMatrix")  # (lost "t"riangularity)
MM <- kronecker(M,M)
NN <- kronecker(N,N) # "dtTMatrix" i.e. did keep
NN2 <- kronecker(N2,N2)
stopifnot(identical(NN,MM),
          is(NN2, "sparseMatrix"), all(NN2 == NN),
          is(NN, "triangularMatrix"))
```

ldenseMatrix-class *Virtual Class "ldenseMatrix" of Dense Logical Matrices*

Description

ldenseMatrix is the virtual class of all dense **l**ogical (S4) matrices. It extends both denseMatrix and lMatrix directly.

Slots

x: logical vector containing the entries of the matrix.

Dim, Dimnames: see Matrix.

Extends

Class "lMatrix", directly. Class "denseMatrix", directly. Class "Matrix", by class "lMatrix". Class "Matrix", by class "denseMatrix".

Methods

as.vector signature(x = "ldenseMatrix", mode = "missing"): ...

which signature(x = "ndenseMatrix"), semantically equivalent to **base** function which(x, arr.ind); for details, see the lMatrix class documentation.

See Also

Class lgeMatrix and the other subclasses.

Examples

```
showClass("ldenseMatrix")

as(diag(3) > 0, "ldenseMatrix")
```

ldiMatrix-class *Class "ldiMatrix" of Diagonal Logical Matrices*

Description

The class "ldiMatrix" of logical diagonal matrices.

Objects from the Class

Objects can be created by calls of the form new("ldiMatrix", ...) but typically rather via Diagonal.

Slots

x: "logical" vector.

diag: "character" string, either "U" or "N", see ddiMatrix.

Dim,Dimnames: matrix dimension and dimnames, see the Matrix class description.

Extends

Class "diagonalMatrix" and class "lMatrix", directly.

Class "sparseMatrix", by class "diagonalMatrix".

See Also

Classes ddiMatrix and diagonalMatrix; function Diagonal.

Examples

```
(lM <- Diagonal(x = c(TRUE,FALSE,FALSE)))
str(lM)#> gory details (slots)

crossprod(lM) # numeric
(nM <- as(lM, "nMatrix"))
crossprod(nM) # pattern sparse
```

---

lgeMatrix-class *Class "lgeMatrix" of General Dense Logical Matrices*

Description

This is the class of general dense logical matrices.

Slots

x: Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

Dim,Dimnames: The dimension (a length-2 "integer") and corresponding names (or NULL), see the Matrix class.

factors: Object of class "list". A named list of factorizations that have been computed for the matrix.

Extends

Class "ldenseMatrix", directly. Class "lMatrix", by class "ldenseMatrix". Class "denseMatrix", by class "ldenseMatrix". Class "Matrix", by class "ldenseMatrix". Class "Matrix", by class "ldenseMatrix".

Methods

Currently, mainly `t()` and coercion methods (for `as(.)`); use, e.g., `showMethods(class="lgeMatrix")` for details.

See Also

Non-general logical dense matrix classes such as `ltrMatrix`, or `lsyMatrix`; *sparse* logical classes such as `lgCMatrix`.

Examples

```
showClass("lgeMatrix")
str(new("lgeMatrix"))
set.seed(1)
(lM <- Matrix(matrix(rnorm(28), 4,7) > 0))# a simple random lgeMatrix
set.seed(11)
(lC <- Matrix(matrix(rnorm(28), 4,7) > 0))# a simple random lgCMatrix
as(lM, "CsparseMatrix")
```

---

lsparseMatrix-class *Sparse logical matrices*

Description

The `lsparseMatrix` class is a virtual class of logical sparse matrices, i.e., sparse matrices with entries `TRUE`, `FALSE`, or `NA`.

These can be stored in the "triplet" form (class `TsparseMatrix`, subclasses `lgTMatrix`, `lsTMatrix`, and `ltTMatrix`) or in compressed column-oriented form (class `CsparseMatrix`, subclasses `lgCMatrix`, `lsCMatrix`, and `ltCMatrix`) or–*rarely*–in compressed row-oriented form (class `RsparseMatrix`, subclasses `lgRMatrix`, `lsRMatrix`, and `ltRMatrix`). The second letter in the name of these non-virtual classes indicates general, symmetric, or triangular.

Details

Note that triplet stored (`TsparseMatrix`) matrices such as `lgTMatrix` may contain duplicated pairs of indices (i, j) as for the corresponding numeric class `dgTMatrix` where for such pairs, the corresponding `x` slot entries are added. For logical matrices, the `x` entries corresponding to duplicated index pairs (i, j) are "added" as well if the addition is defined as logical *or*, i.e., "`TRUE + TRUE |-> TRUE`" and "`TRUE + FALSE |-> TRUE`". Note the use of `asUniqueT()` for getting an internally unique representation without duplicated (i, j) entries.

Objects from the Class

Objects can be created by calls of the form `new("lgCMatrix", ...)` and so on. More frequently objects are created by coercion of a numeric sparse matrix to the logical form, e.g. in an expression `x != 0`.

The logical form is also used in the symbolic analysis phase of an algorithm involving sparse matrices. Such algorithms often involve two phases: a symbolic phase wherein the positions of the non-zeros in the result are determined and a numeric phase wherein the actual results are calculated. During the symbolic phase only the positions of the non-zero elements in any operands are of interest, hence any numeric sparse matrices can be treated as logical sparse matrices.

Slots

`x`: Object of class `"logical"`, i.e., either `TRUE`, `NA`, or `FALSE`.

`uplo`: Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular. Present in the triangular and symmetric classes but not in the general class.

`diag`: Object of class `"character"`. Must be either `"U"`, for unit triangular (diagonal is all ones), or `"N"` for non-unit. The implicit diagonal elements are not explicitly stored when `diag` is `"U"`. Present in the triangular classes only.

`p`: Object of class `"integer"` of pointers, one for each column (row), to the initial (zero-based) index of elements in the column. Present in compressed column-oriented and compressed row-oriented forms only.

`i`: Object of class `"integer"` of length nnzero (number of non-zero elements). These are the row numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed column-oriented forms only.

`j`: Object of class `"integer"` of length nnzero (number of non-zero elements). These are the column numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed row-oriented forms only.

`Dim`: Object of class `"integer"` - the dimensions of the matrix.

Methods

coerce `signature(from = "dgCMatrix", to = "lgCMatrix")`

t `signature(x = "lgCMatrix")`: returns the transpose of `x`

which `signature(x = "lsparseMatrix")`, semantically equivalent to **base** function `which(x, arr.ind)`; for details, see the `lMatrix` class documentation.

See Also

the class `dgCMatrix` and `dgTMatrix`

Examples

```
(m <- Matrix(c(0,0,2:0), 3,5, dimnames=list(LETTERS[1:3],NULL)))
(lm <- (m > 1)) # lgC
!lm     # no longer sparse
stopifnot(is(lm,"lsparseMatrix"),
          identical(!lm, m <= 1))

data(KNex, package = "Matrix")
str(mmG.1 <- (KNex $ mm) > 0.1)# "lgC..."
table(mmG.1@x)# however with many ``non-structural zeros''
## from logical to nz_pattern -- okay when there are no NA's :
```

```
nmG.1 <- as(mmG.1, "nMatrix") # <<< has "TRUE" also where mmG.1 had FALSE
## from logical to "double"
dmG.1 <- as(mmG.1, "dMatrix") # has '0' and back:
lmG.1 <- as(dmG.1, "lMatrix")
stopifnot(identical(nmG.1, as((KNex $ mm) != 0,"nMatrix")),
          validObject(lmG.1),
          identical(lmG.1, mmG.1))

class(xnx <- crossprod(nmG.1))# "nsC.."
class(xlx <- crossprod(mmG.1))# "dsC.." : numeric
is0 <- (xlx == 0)
mean(as.vector(is0))# 99.3% zeros: quite sparse, but
table(xlx@x == 0)# more than half of the entries are (non-structural!) 0
stopifnot(isSymmetric(xlx), isSymmetric(xnx),
          ## compare xnx and xlx : have the *same* non-structural 0s :
          sapply(slotNames(xnx),
                 function(n) identical(slot(xnx, n), slot(xlx, n))))
```

`lsyMatrix-class` *Symmetric Dense Logical Matrices*

Description

The `"lsyMatrix"` class is the class of symmetric, dense logical matrices in non-packed storage and `"lspMatrix"` is the class of of these in packed storage. In the packed form, only the upper triangle or the lower triangle is stored.

Objects from the Class

Objects can be created by calls of the form `new("lsyMatrix", ...)`.

Slots

`uplo`: Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular.

`x`: Object of class `"logical"`. The logical values that constitute the matrix, stored in column-major order.

`Dim`,`Dimnames`: The dimension (a length-2 `"integer"`) and corresponding names (or `NULL`), see the `Matrix` class.

`factors`: Object of class `"list"`. A named list of factorizations that have been computed for the matrix.

Extends

Both extend classes `"ldenseMatrix"` and `"symmetricMatrix"`, directly; further, class `"Matrix"` and others, *ind*irectly. Use `showClass("lsyMatrix")`, e.g., for details.

Methods

Currently, mainly `t()` and coercion methods (for `as(.)`; use, e.g., `showMethods(class="lsyMatrix")` for details.

See Also

`lgeMatrix`, `Matrix`, `t`

Examples

```
(M2 <- Matrix(c(TRUE, NA, FALSE, FALSE), 2, 2)) # logical dense (ltr)
str(M2)
# can
(sM <- M2 | t(M2)) # "lge"
as(sM, "symmetricMatrix")
str(sM <- as(sM, "packedMatrix")) # packed symmetric
```

---

ltrMatrix-class *Triangular Dense Logical Matrices*

Description

The `"ltrMatrix"` class is the class of triangular, dense, logical matrices in nonpacked storage. The `"ltpMatrix"` class is the same except in packed storage.

Slots

x: Object of class `"logical"`. The logical values that constitute the matrix, stored in column-major order.

uplo: Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular.

diag: Object of class `"character"`. Must be either `"U"`, for unit triangular (diagonal is all ones), or `"N"`; see `triangularMatrix`.

Dim,Dimnames: The dimension (a length-2 `"integer"`) and corresponding names (or `NULL`), see the `Matrix` class.

factors: Object of class `"list"`. A named list of factorizations that have been computed for the matrix.

Extends

Both extend classes `"ldenseMatrix"` and `"triangularMatrix"`, directly; further, class `"Matrix"`, `"lMatrix"` and others, *in*directly. Use `showClass("ltrMatrix")`, e.g., for details.

Methods

Currently, mainly `t()` and coercion methods (for `as(.)`; use, e.g., `showMethods(class="ltrMatrix")` for details.

See Also

Classes lgeMatrix, Matrix; function t

Examples

```
showClass("ltrMatrix")

str(new("ltpMatrix"))
(lutr <- as(upper.tri(matrix(, 4, 4)), "ldenseMatrix"))
str(lutp <- pack(lutr)) # packed matrix: only 10 = 4*(4+1)/2 entries
!lutp # the logical negation (is *not* logical triangular !)
## but this one is:
stopifnot(all.equal(lutp, pack(!!lutp)))
```

---

lu-methods *Methods for LU Factorization*

Description

Computes the pivoted LU factorization of an $m \times n$ real matrix A, which has the general form

$$P_1 A P_2 = LU$$

or (equivalently)

$$A = P_1' L U P_2'$$

where P_1 is an $m \times m$ permutation matrix, P_2 is an $n \times n$ permutation matrix, L is an $m \times \min(m, n)$ unit lower trapezoidal matrix, and U is a $\min(m, n) \times n$ upper trapezoidal matrix.

Methods for denseMatrix are built on LAPACK routine dgetrf, which does not permute columns, so that P_2 is an identity matrix.

Methods for sparseMatrix are built on CXSparse routine cs_lu, which requires $m = n$, so that L and U are triangular matrices.

Usage

```
lu(x, ...)
## S4 method for signature 'dgeMatrix'
lu(x, warnSing = TRUE, ...)
## S4 method for signature 'dgCMatrix'
lu(x, errSing = TRUE, order = NA_integer_,
  tol = 1, ...)
## S4 method for signature 'dsyMatrix'
lu(x, cache = TRUE, ...)
## S4 method for signature 'dsCMatrix'
lu(x, cache = TRUE, ...)
## S4 method for signature 'matrix'
lu(x, ...)
```

Arguments

x	a finite matrix or Matrix to be factorized, which must be square if sparse.
warnSing	a logical indicating if a warning should be signaled for singular x. Used only by methods for dense matrices.
errSing	a logical indicating if an error should be signaled for singular x. Used only by methods for sparse matrices.
order	an integer in 0:3 passed to CXSparse routine cs_sqr, indicating a strategy for choosing the column permutation P_2. 0 means no column permutation. 1, 2, and 3 indicate a fill-reducing ordering of $A + A'$, $\tilde{A}'\tilde{A}$, and $A'A$, where $\tilde{A}$ is A with "dense" rows removed. NA (the default) is equivalent to 2 if tol == 1 and 1 otherwise. Do not set to 0 unless you know that the column order of A is already sensible.
tol	a number. The original pivot element is used if its absolute value exceeds tol * a, where a is the maximum in absolute value of the other possible pivot elements. Set tol < 1 only if you know what you are doing.
cache	a logical indicating if the result should be cached in x@factors[["LU"]]. Note that caching is experimental and that only methods for classes extending generalMatrix or symmetricMatrix will have this argument.
...	further arguments passed to or from methods.

Details

What happens when x is determined to be near-singular differs by method. The method for class dgeMatrix completes the factorization, warning if warnSing = TRUE and in any case returning a valid denseLU object. Users of this method can detect singular x with a suitable warning handler; see tryCatch. In contrast, the method for class dgCMatrix abandons further computation, throwing an error if errSing = TRUE and otherwise returning NA. Users of this method can detect singular x with an error handler or by setting errSing = FALSE and testing for a formal result with is(., "sparseLU").

Value

An object representing the factorization, inheriting from virtual class LU. The specific class is denseLU unless x inherits from virtual class sparseMatrix, in which case it is sparseLU.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dgetrf.f.

Davis, T. A. (2006). *Direct methods for sparse linear systems*. Society for Industrial and Applied Mathematics. doi:10.1137/1.9780898718881

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Classes denseLU and sparseLU and their methods.

Classes dgeMatrix and dgCMatrix.

Generic functions expand1 and expand2, for constructing matrix factors from the result.

Generic functions Cholesky, BunchKaufman, Schur, and qr, for computing other factorizations.

Examples

```
showMethods("lu", inherited = FALSE)
set.seed(0)

## ---- Dense -------------------------------------------------------

(A1 <- Matrix(rnorm(9L), 3L, 3L))
(lu.A1 <- lu(A1))

(A2 <- round(10 * A1[, -3L]))
(lu.A2 <- lu(A2))

## A ~ P1' L U in floating point
str(e.lu.A2 <- expand2(lu.A2), max.level = 2L)
stopifnot(all.equal(A2, Reduce(`%*%`, e.lu.A2)))

## ---- Sparse ------------------------------------------------------

A3 <- as(readMM(system.file("external/pores_1.mtx", package = "Matrix")),
         "CsparseMatrix")
(lu.A3 <- lu(A3))

## A ~ P1' L U P2' in floating point
str(e.lu.A3 <- expand2(lu.A3), max.level = 2L)
stopifnot(all.equal(A3, Reduce(`%*%`, e.lu.A3)))
```

---

mat2triplet *Map Matrix to its Triplet Representation*

Description

From an R object coercible to "TsparseMatrix", typically a (sparse) matrix, produce its triplet representation which may collapse to a "Duplet" in the case of binary aka pattern, such as "nMatrix" objects.

Usage

```
mat2triplet(x, uniqT = FALSE)
```

Arguments

x	any R object for which as(x, "TsparseMatrix") works; typically a matrix of one of the **Matrix** package matrices.
uniqT	logical indicating if the triplet representation should be 'unique' in the sense of asUniqueT(byrow=FALSE).

Value

A list, typically with three components,

i	vector of row indices for all non-zero entries of x
i	vector of columns indices for all non-zero entries of x
x	vector of all non-zero entries of x; exists **only** when as(x, "TsparseMatrix") is **not** a "nsparseMatrix".

Note that the order of the entries is determined by the coercion to "TsparseMatrix" and hence typically with increasing j (and increasing i within ties of j).

Note

The mat2triplet() utility was created to be a more efficient and more predictable substitute for summary(<sparseMatrix>). UseRs have wrongly expected the latter to return a data frame with columns i and j which however is wrong for a "diagonalMatrix".

See Also

The summary() method for "sparseMatrix", summary,sparseMatrix-method.

mat2triplet() is conceptually the *inverse* function of spMatrix and (one case of) sparseMatrix.

Examples

```
mat2triplet # simple definition

i <- c(1,3:8); j <- c(2,9,6:10); x <- 7 * (1:7)
(Ax <- sparseMatrix(i, j, x = x)) ##  8 x 10 "dgCMatrix"
str(trA <- mat2triplet(Ax))
stopifnot(i == sort(trA$i),  sort(j) == trA$j,  x == sort(trA$x))

D <- Diagonal(x=4:2)
summary(D)
str(mat2triplet(D))
```

matmult-methods *Matrix (Cross) Products (of Transpose)*

Description

The basic matrix product, `%*%` is implemented for all our `Matrix` and also for `sparseVector` classes, fully analogously to R's base `matrix` and vector objects.

The functions `crossprod` and `tcrossprod` are matrix products or "cross products", ideally implemented efficiently without computing `t(.)`'s unnecessarily. They also return `symmetricMatrix` classed matrices when easily detectable, e.g., in `crossprod(m)`, the one argument case.

`tcrossprod()` takes the cross-product of the transpose of a matrix. `tcrossprod(x)` is formally equivalent to, but faster than, the call `x %*% t(x)`, and so is `tcrossprod(x, y)` instead of `x %*% t(y)`.

Boolean matrix products are computed via either `%&%` or `boolArith = TRUE`.

Usage

```
## S4 method for signature 'CsparseMatrix,diagonalMatrix'
x %*% y

## S4 method for signature 'CsparseMatrix,diagonalMatrix'
crossprod(x, y = NULL, boolArith = NA, ...)
       ## .... and for many more signatures

## S4 method for signature 'TsparseMatrix,missing'
tcrossprod(x, y = NULL, boolArith = NA, ...)
       ## .... and for many more signatures
```

Arguments

`x`	a matrix-like object
`y`	a matrix-like object, or for `[t]crossprod()` `NULL` (by default); the latter case is formally equivalent to `y = x`.
`boolArith`	`logical`, i.e., `NA`, `TRUE`, or `FALSE`. If true the result is (coerced to) a pattern matrix, i.e., `"nMatrix"`, unless there are `NA` entries and the result will be a `"lMatrix"`. If false the result is (coerced to) numeric. When `NA`, currently the default, the result is a pattern matrix when `x` and `y` are `"nsparseMatrix"` and numeric otherwise.
`...`	potentially more arguments passed to and from methods.

Details

For some classes in the `Matrix` package, such as `dgCMatrix`, it is much faster to calculate the cross-product of the transpose directly instead of calculating the transpose first and then its cross-product.

`boolArith = TRUE` for regular ("non cross") matrix products, `%*%` cannot be specified. Instead, we provide the `%&%` operator for *boolean* matrix products.

Value

A Matrix object, in the one argument case of an appropriate *symmetric* matrix class, i.e., inheriting from symmetricMatrix.

Methods

%*% `signature(x = "dgeMatrix", y = "dgeMatrix")`: Matrix multiplication; ditto for several other signature combinations, see `showMethods("%*%", class = "dgeMatrix")`.

%*% `signature(x = "dtrMatrix", y = "matrix")` and other signatures (use `showMethods("%*%", class="dtrMatrix")`): matrix multiplication. Multiplication of (matching) triangular matrices now should remain triangular (in the sense of class triangularMatrix).

crossprod `signature(x = "dgeMatrix", y = "dgeMatrix")`: ditto for several other signatures, use `showMethods("crossprod", class = "dgeMatrix")`, matrix crossproduct, an efficient version of `t(x) %*% y`.

crossprod `signature(x = "CsparseMatrix", y = "missing")` returns `t(x) %*% x` as an `dsCMatrix` object.

crossprod `signature(x = "TsparseMatrix", y = "missing")` returns `t(x) %*% x` as an `dsCMatrix` object.

crossprod,tcrossprod `signature(x = "dtrMatrix", y = "matrix")` and other signatures, see `"%*%"` above.

Note

`boolArith = TRUE`, `FALSE` or `NA` has been newly introduced for **Matrix** 1.2.0 (March 2015). Its implementation has still not been tested extensively. Notably the behaviour for sparse matrices with `x` slots containing extra zeros had not been documented previously, see the %&% help page.

Currently, `boolArith = TRUE` is implemented via CsparseMatrix coercions which may be quite inefficient for dense matrices. Contributions for efficiency improvements are welcome.

See Also

tcrossprod in R's base, and crossprod and %*%. **Matrix** package %&% for boolean matrix product methods.

Examples

```
## A random sparse "incidence" matrix :
m <- matrix(0, 400, 500)
set.seed(12)
m[runif(314, 0, length(m))] <- 1
mm <- as(m, "CsparseMatrix")
object.size(m) / object.size(mm) # smaller by a factor of > 200

## tcrossprod() is very fast:
system.time(tCmm <- tcrossprod(mm))# 0   (PIII, 933 MHz)
system.time(cm <- crossprod(t(m))) # 0.16
system.time(cm. <- tcrossprod(m))  # 0.02
```

```
stopifnot(cm == as(tCmm, "matrix"))

## show sparse sub matrix
tCmm[1:16, 1:30]
```

`Matrix` *Construct a Classed Matrix*

Description

Construct a Matrix of a class that inherits from `Matrix`.

Usage

```
Matrix(data=NA, nrow=1, ncol=1, byrow=FALSE, dimnames=NULL,
       sparse = NULL, doDiag = TRUE, forceCheck = FALSE)
```

Arguments

`data`	an optional numeric data vector or matrix.
`nrow`	when `data` is not a matrix, the desired number of rows
`ncol`	when `data` is not a matrix, the desired number of columns
`byrow`	logical. If `FALSE` (the default) the matrix is filled by columns, otherwise the matrix is filled by rows.
`dimnames`	a `dimnames` attribute for the matrix: a `list` of two character components. They are set if not `NULL` (as per default).
`sparse`	logical or `NULL`, specifying if the result should be sparse or not. By default, it is made sparse when more than half of the entries are 0.
`doDiag`	logical indicating if a `diagonalMatrix` object should be returned when the resulting matrix is diagonal (*mathematically*). As class `diagonalMatrix` `extends` `sparseMatrix`, this is a natural default for all values of `sparse`. Otherwise, if `doDiag` is false, a dense or sparse (depending on `sparse`) *symmetric* matrix will be returned.
`forceCheck`	logical indicating if the checks for structure should even happen when `data` is already a `"Matrix"` object.

Details

If either of `nrow` or `ncol` is not given, an attempt is made to infer it from the length of `data` and the other parameter. Further, `Matrix()` makes efforts to keep `logical` matrices logical, i.e., inheriting from class `lMatrix`, and to determine specially structured matrices such as symmetric, triangular or diagonal ones. Note that a *symmetric* matrix also needs symmetric `dimnames`, e.g., by specifying `dimnames = list(NULL,NULL)`, see the examples.

Most of the time, the function works via a traditional (*full*) `matrix`. However, `Matrix(0, nrow,ncol)` directly constructs an "empty" sparseMatrix, as does `Matrix(FALSE, *)`.

Although it is sometime possible to mix unclassed matrices (created with `matrix`) with ones of class `"Matrix"`, it is much safer to always use carefully constructed ones of class `"Matrix"`.

Value

Returns matrix of a class that inherits from "Matrix". Only if data is not a matrix and does not already inherit from class Matrix are the arguments nrow, ncol and byrow made use of.

See Also

The classes Matrix, symmetricMatrix, triangularMatrix, and diagonalMatrix; further, matrix.

Special matrices can be constructed, e.g., via sparseMatrix (sparse), bdiag (block-diagonal), bandSparse (banded sparse), or Diagonal.

Examples

```
Matrix(0, 3, 2)             # 3 by 2 matrix of zeros -> sparse
Matrix(0, 3, 2, sparse=FALSE)# -> 'dense'

## 4 cases - 3 different results :
Matrix(0, 2, 2)              # diagonal !
Matrix(0, 2, 2, sparse=FALSE)# (ditto)
Matrix(0, 2, 2,               doDiag=FALSE)# -> sparse symm. "dsCMatrix"
Matrix(0, 2, 2, sparse=FALSE, doDiag=FALSE)# -> dense  symm. "dsyMatrix"

Matrix(1:6, 3, 2)           # a 3 by 2 matrix (+ integer warning)
Matrix(1:6 + 1, nrow=3)

## logical ones:
Matrix(diag(4) >  0) # -> "ldiMatrix" with diag = "U"
Matrix(diag(4) >  0, sparse=TRUE) #  (ditto)
Matrix(diag(4) >= 0) # -> "lsyMatrix" (of all 'TRUE')
## triangular
l3 <- upper.tri(matrix(,3,3))
(M <- Matrix(l3))   # -> "ltCMatrix"
Matrix(! l3)        # -> "ltrMatrix"
as(l3, "CsparseMatrix")# "lgCMatrix"

Matrix(1:9, nrow=3,
       dimnames = list(c("a", "b", "c"), c("A", "B", "C")))
(I3 <- Matrix(diag(3)))# identity, i.e., unit "diagonalMatrix"
str(I3) # note  'diag = "U"' and the empty 'x' slot

(A <- cbind(a=c(2,1), b=1:2))# symmetric *apart* from dimnames
Matrix(A)                    # hence 'dgeMatrix'
(As <- Matrix(A, dimnames = list(NULL,NULL)))# -> symmetric
forceSymmetric(A) # also symmetric, w/ symm. dimnames
stopifnot(is(As, "symmetricMatrix"),
          is(Matrix(0, 3,3), "sparseMatrix"),
          is(Matrix(FALSE, 1,1), "sparseMatrix"))
```

Matrix-class *Virtual Class "Matrix" of Matrices*

Description

The Matrix class is a class contained by all actual classes in the **Matrix** package. It is a "virtual" class.

Slots

Dim an integer vector of length 2 giving the dimensions of the matrix.

Dimnames a list of length 2. Each element must be NULL or a character vector of length equal to the corresponding element of Dim.

Methods

determinant signature(x = "Matrix", logarithm = "missing"): and

determinant signature(x = "Matrix", logarithm = "logical"): compute the (log) determinant of x. The method chosen depends on the actual Matrix class of x. Note that det also works for all our matrices, calling the appropriate determinant() method. The Matrix::det is an exact copy of base::det, but in the correct namespace, and hence calling the S4-aware version of determinant().

diff signature(x = "Matrix"): As diff() for traditional matrices, i.e., applying diff() to each column.

dim signature(x = "Matrix"): extract matrix dimensions dim.

dim<- signature(x = "Matrix", value = "ANY"): where value is integer of length 2. Allows to *reshape* Matrix objects, but only when prod(value) == prod(dim(x)).

dimnames signature(x = "Matrix"): extract dimnames.

dimnames<- signature(x = "Matrix", value = "list"): set the dimnames to a list of length 2, see dimnames<-.

length signature(x = "Matrix"): simply defined as prod(dim(x)) (and hence of mode "double").

show signature(object = "Matrix"): show method for printing. For printing *sparse* matrices, see printSpMatrix.

zapsmall signature(x = "Matrix"): typically used for "dMatrix": round() matrix entries such that (relatively) very small entries become zero exactly.

image signature(object = "Matrix"): draws an image of the matrix entries, using levelplot() from package **lattice**.

head signature(object = "Matrix"): return only the *"head"*, i.e., the first few rows.

tail signature(object = "Matrix"): return only the *"tail"*, i.e., the last few rows of the respective matrix.

as.matrix, as.array signature(x = "Matrix"): the same as as(x, "matrix"); see also the note below.

as.vector `signature(x = "Matrix", mode = "missing")`: `as.vector(m)` should be identical to `as.vector(as(m,"matrix"))`, implemented more efficiently for some subclasses.

as(x, "vector"), as(x, "numeric") etc, similarly.

coerce `signature(from = "ANY", to = "Matrix")`: This relies on a correct `as.matrix()` method for `from`.

There are many more methods that (conceptually should) work for all `"Matrix"` objects, e.g., `colSums`, `rowMeans`. Even **base** functions may work automagically (if they first call `as.matrix()` on their principal argument), e.g., `apply`, `eigen`, `svd` or `kappa` all do work via coercion to a "traditional" (dense) `matrix`.

Note

Loading the `Matrix` namespace "overloads" `as.matrix` and `as.array` in the **base** namespace by the equivalent of `function(x) as(x, "matrix")`. Consequently, `as.matrix(m)` or `as.array(m)` will properly work when `m` inherits from the `"Matrix"` class — *also* for functions in package **base** and other packages. E.g., `apply` or `outer` can therefore be applied to `"Matrix"` matrices.

Author(s)

Douglas Bates <bates@stat.wisc.edu> and Martin Maechler

See Also

the classes `dgeMatrix`, `dgCMatrix`, and function `Matrix` for construction (and examples).

Methods, e.g., for `kronecker`.

Examples

```
slotNames("Matrix")

cl <- getClass("Matrix")
names(cl@subclasses) # more than 40 ..

showClass("Matrix")#> output with slots and all subclasses

(M <- Matrix(c(0,1,0,0), 6, 4))
dim(M)
diag(M)
cm <- M[1:4,] + 10*Diagonal(4)
diff(M)
## can reshape it even :
dim(M) <- c(2, 12)
M
stopifnot(identical(M, Matrix(c(0,1,0,0), 2,12)),
          all.equal(det(cm),
                    determinant(as(cm,"matrix"), log=FALSE)$modulus,
                    check.attributes=FALSE))
```

Matrix-notyet *Virtual Classes Not Yet Really Implemented and Used*

Description

iMatrix is the virtual class of all integer (S4) matrices. It extends the Matrix class directly.

zMatrix is the virtual class of all complex (S4) matrices. It extends the Matrix class directly.

Examples

```
showClass("iMatrix")
showClass("zMatrix")
```

MatrixClass *The Matrix (Super-) Class of a Class*

Description

Return the (maybe super-)class of class cl from package **Matrix**, returning character(0) if there is none.

Usage

```
MatrixClass(cl, cld = getClassDef(cl), ...Matrix = TRUE,
            dropVirtual = TRUE, ...)
```

Arguments

cl	string, class name
cld	its class definition
...Matrix	logical indicating if the result must be of pattern "[dlniz]..Matrix" where the first letter "[dlniz]" denotes the content kind.
dropVirtual	logical indicating if virtual classes are included or not.
...	further arguments are passed to .selectSuperClasses().

Value

a character string

Author(s)

Martin Maechler, 24 Mar 2009

See Also

Matrix, the mother of all **Matrix** classes.

Examples

```
mkA <- setClass("A", contains="dgCMatrix")
(A <- mkA())
stopifnot(identical(
     MatrixClass("A"),
     "dgCMatrix"))
```

MatrixFactorization-class

Virtual Class "MatrixFactorization" of Matrix Factorizations

Description

MatrixFactorization is the virtual class of factorizations of $m \times n$ matrices A, having the general form

$$P_1 A P_2 = A_1 \cdots A_p$$

or (equivalently)

$$A = P_1' A_1 \cdots A_p P_2'$$

where P_1 and P_2 are permutation matrices. Factorizations requiring symmetric A have the constraint $P_2 = P_1'$, and factorizations without row or column pivoting have the constraints $P_1 = I_m$ and $P_2 = I_n$, where I_m and I_n are the $m \times m$ and $n \times n$ identity matrices.

CholeskyFactorization, BunchKaufmanFactorization, SchurFactorization, LU, and QR are the virtual subclasses of MatrixFactorization containing all Cholesky, Bunch-Kaufman, Schur, LU, and QR factorizations, respectively.

Slots

Dim an integer vector of length 2 giving the dimensions of the factorized matrix.

Dimnames a list of length 2 preserving the dimnames of the factorized matrix. Each element must be NULL or a character vector of length equal to the corresponding element of Dim.

Methods

determinant signature(x = "MatrixFactorization", logarithm = "missing"): sets logarithm = TRUE and recalls the generic function.

dim signature(x = "MatrixFactorization"): returns x@Dim.

dimnames signature(x = "MatrixFactorization"): returns x@Dimnames.

dimnames<- signature(x = "MatrixFactorization", value = "NULL"): returns x with x@Dimnames set to list(NULL, NULL).

dimnames<- signature(x = "MatrixFactorization", value = "list"): returns x with x@Dimnames set to value.

`length signature(x = "MatrixFactorization")`: returns `prod(x@Dim)`.

`show signature(object = "MatrixFactorization")`: prints the internal representation of the factorization using `str`.

`solve signature(a = "MatrixFactorization", b = .)`: see `solve-methods`.

`unname signature(obj = "MatrixFactorization")`: returns `obj` with `obj@Dimnames` set to `list(NULL, NULL)`.

See Also

Classes extending `CholeskyFactorization`, namely `Cholesky`, `pCholesky`, and `CHMfactor`.

Classes extending `BunchKaufmanFactorization`, namely `BunchKaufman` and `pBunchKaufman`.

Classes extending `SchurFactorization`, namely `Schur`.

Classes extending `LU`, namely `denseLU` and `sparseLU`.

Classes extending `QR`, namely `sparseQR`.

Generic functions `Cholesky`, `BunchKaufman`, `Schur`, `lu`, and `qr` for *computing* factorizations.

Generic functions `expand1` and `expand2` for constructing matrix factors from `MatrixFactorization` objects.

Examples

```
showClass("MatrixFactorization")
```

---

ndenseMatrix-class *Virtual Class "ndenseMatrix" of Dense Logical Matrices*

Description

`ndenseMatrix` is the virtual class of all dense **l**ogical (S4) matrices. It extends both `denseMatrix` and `lMatrix` directly.

Slots

`x`: logical vector containing the entries of the matrix.

`Dim`, `Dimnames`: see `Matrix`.

Extends

Class `"nMatrix"`, directly. Class `"denseMatrix"`, directly. Class `"Matrix"`, by class `"nMatrix"`. Class `"Matrix"`, by class `"denseMatrix"`.

Methods

%*% `signature(x = "nsparseMatrix", y = "ndenseMatrix")`: ...

%*% `signature(x = "ndenseMatrix", y = "nsparseMatrix")`: ...

crossprod `signature(x = "nsparseMatrix", y = "ndenseMatrix")`: ...

crossprod `signature(x = "ndenseMatrix", y = "nsparseMatrix")`: ...

as.vector `signature(x = "ndenseMatrix", mode = "missing")`: ...

diag `signature(x = "ndenseMatrix")`: extracts the diagonal as for all matrices, see the generic `diag()`.

which `signature(x = "ndenseMatrix")`, semantically equivalent to **base** function `which(x, arr.ind)`; for details, see the `lMatrix` class documentation.

See Also

Class `ngeMatrix` and the other subclasses.

Examples

```
showClass("ndenseMatrix")

as(diag(3) > 0, "ndenseMatrix")# -> "nge"
```

---

nearPD *Nearest Positive Definite Matrix*

Description

Compute the nearest positive definite matrix to an approximate one, typically a correlation or variance-covariance matrix.

Usage

```
nearPD(x, corr = FALSE, keepDiag = FALSE, base.matrix = FALSE,
       do2eigen = TRUE, doSym = FALSE,
       doDykstra = TRUE, only.values = FALSE,
       ensureSymmetry = !isSymmetric(x),
       eig.tol = 1e-06, conv.tol = 1e-07, posd.tol = 1e-08,
       maxit = 100, conv.norm.type = "I", trace = FALSE)
```

Arguments

x	numeric $n \times n$ approximately positive definite matrix, typically an approximation to a correlation or covariance matrix. If x is not symmetric (and ensureSymmetry is not false), `symmpart(x)` is used.
corr	logical indicating if the matrix should be a *correlation* matrix.

keepDiag	logical, generalizing corr: if TRUE, the resulting matrix should have the same diagonal (diag(x)) as the input matrix.
base.matrix	logical indicating if the resulting mat component should be a **base** matrix or (by default) a Matrix of class dpoMatrix.
do2eigen	logical indicating if a posdefify() eigen step should be applied to the result of the Higham algorithm.
doSym	logical indicating if X <- (X + t(X))/2 should be done, after X <- tcrossprod(Qd, Q); some doubt if this is necessary.
doDykstra	logical indicating if Dykstra's correction should be used; true by default. If false, the algorithm is basically the direct fixpoint iteration $Y_k = P_U(P_S(Y_{k-1}))$.
only.values	logical; if TRUE, the result is just the vector of eigenvalues of the approximating matrix.
ensureSymmetry	logical; by default, symmpart(x) is used whenever isSymmetric(x) is not true. The user can explicitly set this to TRUE or FALSE, saving the symmetry test. *Beware* however that setting it FALSE for an **a**symmetric input x, is typically nonsense!
eig.tol	defines relative positiveness of eigenvalues compared to largest one, λ_1. Eigenvalues λ_k are treated as if zero when $\lambda_k/\lambda_1 \leq eig.tol$.
conv.tol	convergence tolerance for Higham algorithm.
posd.tol	tolerance for enforcing positive definiteness (in the final posdefify step when do2eigen is TRUE).
maxit	maximum number of iterations allowed.
conv.norm.type	convergence norm type (norm(*, type)) used for Higham algorithm. The default is "I" (infinity), for reasons of speed (and back compatibility); using "F" is more in line with Higham's proposal.
trace	logical or integer specifying if convergence monitoring should be traced.

Details

This implements the algorithm of Higham (2002), and then (if do2eigen is true) forces positive definiteness using code from posdefify. The algorithm of Knol and ten Berge (1989) (not implemented here) is more general in that it allows constraints to (1) fix some rows (and columns) of the matrix and (2) force the smallest eigenvalue to have a certain value.

Note that setting corr = TRUE just sets diag(.) <- 1 within the algorithm.

Higham (2002) uses Dykstra's correction, but the version by Jens Oehlschlägel did not use it (accidentally), and still gave reasonable results; this simplification, now only used if doDykstra = FALSE, was active in nearPD() up to Matrix version 0.999375-40.

Value

If only.values = TRUE, a numeric vector of eigenvalues of the approximating matrix; Otherwise, as by default, an S3 object of class "nearPD", basically a list with components

mat	a matrix of class dpoMatrix, the computed positive-definite matrix.
eigenvalues	numeric vector of eigenvalues of mat.

corr	logical, just the argument corr.
normF	the Frobenius norm (norm(x-X, "F")) of the difference between the original and the resulting matrix.
iterations	number of iterations needed.
converged	logical indicating if iterations converged.

Author(s)

Jens Oehlschlägel donated a first version. Subsequent changes by the Matrix package authors.

References

Cheng, Sheung Hun and Higham, Nick (1998) A Modified Cholesky Algorithm Based on a Symmetric Indefinite Factorization; *SIAM J. Matrix Anal.\ Appl.*, **19**, 1097–1110.

Knol DL, ten Berge JMF (1989) Least-squares approximation of an improper correlation matrix by a proper one. *Psychometrika* **54**, 53–61.

Higham, Nick (2002) Computing the nearest correlation matrix - a problem from finance; *IMA Journal of Numerical Analysis* **22**, 329–343.

See Also

A first version of this (with non-optional corr=TRUE) has been available as nearcor(); and more simple versions with a similar purpose posdefify(), both from package **sfsmisc**.

Examples

```
## Higham(2002), p.334f - simple example
A <- matrix(1, 3,3); A[1,3] <- A[3,1] <- 0
n.A <- nearPD(A, corr=TRUE, do2eigen=FALSE)
n.A[c("mat", "normF")]
n.A.m <- nearPD(A, corr=TRUE, do2eigen=FALSE, base.matrix=TRUE)$mat
stopifnot(exprs = {                           #=--------------
  all.equal(n.A$mat[1,2], 0.760689917)
  all.equal(n.A$normF, 0.52779033, tolerance=1e-9)
  all.equal(n.A.m, unname(as.matrix(n.A$mat)), tolerance = 1e-15)# seen rel.d.= 1.46e-16
})
set.seed(27)
m <- matrix(round(rnorm(25),2), 5, 5)
m <- m + t(m)
diag(m) <- pmax(0, diag(m)) + 1
(m <- round(cov2cor(m), 2))

str(near.m <- nearPD(m, trace = TRUE))
round(near.m$mat, 2)
norm(m - near.m$mat) # 1.102 / 1.08

if(requireNamespace("sfsmisc")) {
   m2 <- sfsmisc::posdefify(m) # a simpler approach
   norm(m - m2)  # 1.185, i.e., slightly "less near"
}
```

```
 round(nearPD(m, only.values=TRUE), 9)

## A longer example, extended from Jens' original,
## showing the effects of some of the options:

pr <- Matrix(c(1,     0.477, 0.644, 0.478, 0.651, 0.826,
               0.477, 1,     0.516, 0.233, 0.682, 0.75,
               0.644, 0.516, 1,     0.599, 0.581, 0.742,
               0.478, 0.233, 0.599, 1,     0.741, 0.8,
               0.651, 0.682, 0.581, 0.741, 1,     0.798,
               0.826, 0.75,  0.742, 0.8,   0.798, 1),
             nrow = 6, ncol = 6)

nc.  <- nearPD(pr, conv.tol = 1e-7) # default
nc.$iterations  # 2
nc.1 <- nearPD(pr, conv.tol = 1e-7, corr = TRUE)
nc.1$iterations # 11 / 12 (!)
ncr   <- nearPD(pr, conv.tol = 1e-15)
str(ncr)# still 2 iterations
ncr.1 <- nearPD(pr, conv.tol = 1e-15, corr = TRUE)
ncr.1 $ iterations # 27 / 30 !

ncF <- nearPD(pr, conv.tol = 1e-15, conv.norm = "F")
stopifnot(all.equal(ncr, ncF))# norm type does not matter at all in this example

## But indeed, the 'corr = TRUE' constraint did ensure a better solution;
## cov2cor() does not just fix it up equivalently :
norm(pr - cov2cor(ncr$mat)) # = 0.09994
norm(pr -       ncr.1$mat)  # = 0.08746 / 0.08805

### 3) a real data example from a 'systemfit' model (3 eq.):
(load(system.file("external", "symW.rda", package="Matrix"))) # "symW"
dim(symW) #  24 x 24
class(symW)# "dsCMatrix": sparse symmetric
if(dev.interactive())  image(symW)
EV <- eigen(symW, only=TRUE)$values
summary(EV) ## looking more closely {EV sorted decreasingly}:
tail(EV)# all 6 are negative
EV2 <- eigen(sWpos <- nearPD(symW)$mat, only=TRUE)$values
stopifnot(EV2 > 0)
if(requireNamespace("sfsmisc")) {
    plot(pmax(1e-3,EV), EV2, type="o", log="xy", xaxt="n", yaxt="n")
    for(side in 1:2) sfsmisc::eaxis(side)
} else
    plot(pmax(1e-3,EV), EV2, type="o", log="xy")
abline(0, 1, col="red3", lty=2)
```

---

ngeMatrix-class *Class "ngeMatrix" of General Dense Nonzero-pattern Matrices*

Description

This is the class of general dense nonzero-pattern matrices, see nMatrix.

Slots

x: Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

Dim,Dimnames: The dimension (a length-2 "integer") and corresponding names (or NULL), see the Matrix class.

factors: Object of class "list". A named list of factorizations that have been computed for the matrix.

Extends

Class "ndenseMatrix", directly. Class "lMatrix", by class "ndenseMatrix". Class "denseMatrix", by class "ndenseMatrix". Class "Matrix", by class "ndenseMatrix". Class "Matrix", by class "ndenseMatrix".

Methods

Currently, mainly t() and coercion methods (for as(.)); use, e.g., showMethods(class="ngeMatrix") for details.

See Also

Non-general logical dense matrix classes such as ntrMatrix, or nsyMatrix; *sparse* logical classes such as ngCMatrix.

Examples

```
showClass("ngeMatrix")
## "lgeMatrix" is really more relevant
```

---

nMatrix-class *Class "nMatrix" of Non-zero Pattern Matrices*

Description

The nMatrix class is the virtual "mother" class of all ***n**on-zero pattern* (or simply *patter**n***) matrices in the **Matrix** package.

Slots

Common to *all* matrix object in the package:

Dim: Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

Dimnames: list of length two; each component containing NULL or a character vector length equal the corresponding Dim element.

Methods

coerce `signature(from = "matrix", to = "nMatrix")`: Note that these coercions (must) coerce NAs to non-zero, hence conceptually TRUE. This is particularly important when `sparseMatrix` objects are coerced to `"nMatrix"` and hence to `nsparseMatrix`.

— — —

Additional methods contain group methods, such as

Ops `signature(e1 = "nMatrix", e2 = "....")`, ...

Arith `signature(e1 = "nMatrix", e2 = "....")`, ...

Compare `signature(e1 = "nMatrix", e2 = "....")`, ...

Logic `signature(e1 = "nMatrix", e2 = "....")`, ...

Summary `signature(x = "nMatrix", "....")`, ...

See Also

The classes `lMatrix`, `nsparseMatrix`, and the mother class, `Matrix`.

Examples

```
getClass("nMatrix")

L3 <- Matrix(upper.tri(diag(3)))
L3 # an "ltCMatrix"
as(L3, "nMatrix") # -> ntC*

## similar, not using Matrix()
as(upper.tri(diag(3)), "nMatrix")# currently "ngTMatrix"
```

`nnzero-methods` *The Number of Non-Zero Values of a Matrix*

Description

Returns the number of non-zero values of a numeric-like R object, and in particular an object `x` inheriting from class `Matrix`.

Usage

```
nnzero(x, na.counted = NA)
```

Arguments

x	an R object, typically inheriting from class Matrix or numeric.
na.counted	a logical describing how NAs should be counted. There are three possible settings for na.counted:

TRUE NAs *are* counted as non-zero (since "they are not zero").

NA (default)the result will be NA if there are NA's in x (since "NA's are not known, i.e., *may be* zero").

FALSE NAs are *omitted* from x before the non-zero entries are counted.

For sparse matrices, you may often want to use na.counted = TRUE.

Value

the number of non zero entries in x (typically integer).

Note that for a *symmetric* sparse matrix S (i.e., inheriting from class symmetricMatrix), nnzero(S) is typically *twice* the length(S@x).

Methods

signature(x = "ANY") the default method for non-Matrix class objects, simply counts the number 0s in x, counting NA's depending on the na.counted argument, see above.

signature(x = "denseMatrix") conceptually the same as for traditional matrix objects, care has to be taken for "symmetricMatrix" objects.

signature(x = "diagonalMatrix"), **and** signature(x = "indMatrix") fast simple methods for these special "sparseMatrix" classes.

signature(x = "sparseMatrix") typically, the most interesting method, also carefully taking "symmetricMatrix" objects into account.

See Also

The Matrix class also has a length method; typically, length(M) is much larger than nnzero(M) for a sparse matrix M, and the latter is a better indication of the *size* of M.

drop0, zapsmall.

Examples

```
m <- Matrix(0+1:28, nrow = 4)
m[-3,c(2,4:5,7)] <- m[ 3, 1:4] <- m[1:3, 6] <- 0
(mT <- as(m, "TsparseMatrix"))
nnzero(mT)
(S <- crossprod(mT))
nnzero(S)
str(S) # slots are smaller than nnzero()
stopifnot(nnzero(S) == sum(as.matrix(S) != 0))# failed earlier

data(KNex, package = "Matrix")
M <- KNex$mm
class(M)
```

```
dim(M)
length(M); stopifnot(length(M) == prod(dim(M)))
nnzero(M) # more relevant than length
## the above are also visible from
str(M)
```

---

norm-methods *Matrix Norms*

Description

Computes a matrix norm of x, using Lapack for dense matrices. The norm can be the one ("O", or "1") norm, the infinity ("I") norm, the Frobenius ("F") norm, the maximum modulus ("M") among elements of a matrix, or the spectral norm or 2-norm ("2"), as determined by the value of type.

Usage

```
norm(x, type, ...)
```

Arguments

x	a real or complex matrix.
type	A character indicating the type of norm desired. "O", "o" **or** "1" specifies the one norm, (maximum absolute column sum); "I" **or** "i" specifies the infinity norm (maximum absolute row sum); "F" **or** "f" specifies the Frobenius norm (the Euclidean norm of x treated as if it were a vector); "M" **or** "m" specifies the maximum modulus of all the elements in x; and "2" specifies the "spectral norm" aka "2-norm", which is the largest singular value (svd) of x. The default is "O". Only the first character of type[1] is used.
...	further arguments passed to or from other methods.

Details

For dense matrices, the methods eventually call the Lapack functions dlange, dlansy, dlantr, zlange, zlansy, and zlantr.

Value

A numeric value of class "norm", representing the quantity chosen according to type.

References

Anderson, E., et al. (1994). *LAPACK User's Guide,* 2nd edition, SIAM, Philadelphia.

See Also

onenormest(), an *approximate* randomized estimate of the 1-norm condition number, efficient for large sparse matrices.

The norm() function from R's **base** package.

Examples

```
x <- Hilbert(9)
norm(x)# = "O" = "1"
stopifnot(identical(norm(x), norm(x, "1")))
norm(x, "I")# the same, because 'x' is symmetric

allnorms <- function(x) {
    ## norm(NA, "2") did not work until R 4.0.0
    do2 <- getRversion() >= "4.0.0" || !anyNA(x)
    vapply(c("1", "I", "F", "M", if(do2) "2"), norm, 0, x = x)
}
allnorms(x)
allnorms(Hilbert(10))

i <- c(1,3:8); j <- c(2,9,6:10); x <- 7 * (1:7)
A <- sparseMatrix(i, j, x = x)                      ##  8 x 10 "dgCMatrix"
(sA <- sparseMatrix(i, j, x = x, symmetric = TRUE)) ## 10 x 10 "dsCMatrix"
(tA <- sparseMatrix(i, j, x = x, triangular= TRUE)) ## 10 x 10 "dtCMatrix"
(allnorms(A) -> nA)
allnorms(sA)
allnorms(tA)
stopifnot(all.equal(nA, allnorms(as(A, "matrix"))),
  all.equal(nA, allnorms(tA))) # because tA == rbind(A, 0, 0)
A. <- A; A.[1,3] <- NA
stopifnot(is.na(allnorms(A.))) # gave error
```

---

nsparseMatrix-class *Sparse "pattern" Matrices*

Description

The nsparseMatrix class is a virtual class of sparse *"pattern"* matrices, i.e., binary matrices conceptually with TRUE/FALSE entries. Only the positions of the elements that are TRUE are stored.

These can be stored in the "triplet" form (TsparseMatrix, subclasses ngTMatrix, nsTMatrix, and ntTMatrix which really contain pairs, not triplets) or in compressed column-oriented form (class CsparseMatrix, subclasses ngCMatrix, nsCMatrix, and ntCMatrix) or–*rarely*–in compressed row-oriented form (class RsparseMatrix, subclasses ngRMatrix, nsRMatrix, and ntRMatrix). The second letter in the name of these non-virtual classes indicates general, symmetric, or triangular.

Objects from the Class

Objects can be created by calls of the form `new("ngCMatrix", ...)` and so on. More frequently objects are created by coercion of a numeric sparse matrix to the pattern form for use in the symbolic analysis phase of an algorithm involving sparse matrices. Such algorithms often involve two phases: a symbolic phase wherein the positions of the non-zeros in the result are determined and a numeric phase wherein the actual results are calculated. During the symbolic phase only the positions of the non-zero elements in any operands are of interest, hence numeric sparse matrices can be treated as sparse pattern matrices.

Slots

`uplo`: Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular. Present in the triangular and symmetric classes but not in the general class.

`diag`: Object of class `"character"`. Must be either `"U"`, for unit triangular (diagonal is all ones), or `"N"` for non-unit. The implicit diagonal elements are not explicitly stored when `diag` is `"U"`. Present in the triangular classes only.

`p`: Object of class `"integer"` of pointers, one for each column (row), to the initial (zero-based) index of elements in the column. Present in compressed column-oriented and compressed row-oriented forms only.

`i`: Object of class `"integer"` of length nnzero (number of non-zero elements). These are the row numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed column-oriented forms only.

`j`: Object of class `"integer"` of length nnzero (number of non-zero elements). These are the column numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed row-oriented forms only.

`Dim`: Object of class `"integer"` - the dimensions of the matrix.

Methods

coerce `signature(from = "dgCMatrix", to = "ngCMatrix")`, and many similar ones; typically you should coerce to `"nsparseMatrix"` (or `"nMatrix"`). Note that coercion to a sparse pattern matrix records all the potential non-zero entries, i.e., explicit ("non-structural") zeroes are coerced to `TRUE`, not `FALSE`, see the example.

t `signature(x = "ngCMatrix")`: returns the transpose of `x`

which `signature(x = "lsparseMatrix")`, semantically equivalent to **base** function `which(x, arr.ind)`; for details, see the `lMatrix` class documentation.

See Also

the class `dgCMatrix`

Examples

```
(m <- Matrix(c(0,0,2:0), 3,5, dimnames=list(LETTERS[1:3],NULL)))
## ``extract the nonzero-pattern of (m) into an nMatrix'':
nm <- as(m, "nsparseMatrix") ## -> will be a "ngCMatrix"
str(nm) # no 'x' slot
```

```
nnm <- !nm # no longer sparse
## consistency check:
stopifnot(xor(as( nm, "matrix"),
              as(nnm, "matrix")))

## low-level way of adding "non-structural zeros" :
nnm <- as(nnm, "lsparseMatrix") # "lgCMatrix"
nnm@x[2:4] <- c(FALSE, NA, NA)
nnm
as(nnm, "nMatrix") # NAs *and* non-structural 0  |--->  'TRUE'

data(KNex, package = "Matrix")
nmm <- as(KNex $ mm, "nMatrix")
str(xlx <- crossprod(nmm))# "nsCMatrix"
stopifnot(isSymmetric(xlx))
image(xlx, main=paste("crossprod(nmm) : Sparse", class(xlx)))
```

`nsyMatrix-class` *Symmetric Dense Nonzero-Pattern Matrices*

Description

The `"nsyMatrix"` class is the class of symmetric, dense nonzero-pattern matrices in non-packed storage and `"nspMatrix"` is the class of of these in packed storage. Only the upper triangle or the lower triangle is stored.

Objects from the Class

Objects can be created by calls of the form `new("nsyMatrix", ...)`.

Slots

`uplo`: Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular.

`x`: Object of class `"logical"`. The logical values that constitute the matrix, stored in column-major order.

`Dim`,`Dimnames`: The dimension (a length-2 `"integer"`) and corresponding names (or `NULL`), see the `Matrix` class.

`factors`: Object of class `"list"`. A named list of factorizations that have been computed for the matrix.

Extends

`"nsyMatrix"` extends class `"ngeMatrix"`, directly, whereas
`"nspMatrix"` extends class `"ndenseMatrix"`, directly.

Both extend class `"symmetricMatrix"`, directly, and class `"Matrix"` and others, *in*directly, use `showClass("nsyMatrix")`, e.g., for details.

Methods

Currently, mainly `t()` and coercion methods (for `as(.)`; use, e.g., `showMethods(class="nsyMatrix")` for details.

See Also

`ngeMatrix`, `Matrix`, `t`

Examples

```
(s0 <- new("nsyMatrix"))

(M2 <- Matrix(c(TRUE, NA, FALSE, FALSE), 2, 2)) # logical dense (ltr)
(sM <- M2 & t(M2))                       # -> "lge"
class(sM <- as(sM, "nMatrix"))           # -> "nge"
     (sM <- as(sM, "symmetricMatrix"))   # -> "nsy"
str(sM <- as(sM, "packedMatrix")) # -> "nsp", i.e., packed symmetric
```

---

ntrMatrix-class *Triangular Dense Logical Matrices*

Description

The `"ntrMatrix"` class is the class of triangular, dense, logical matrices in nonpacked storage. The `"ntpMatrix"` class is the same except in packed storage.

Slots

`x`: Object of class `"logical"`. The logical values that constitute the matrix, stored in column-major order.

`uplo`: Object of class `"character"`. Must be either "U", for upper triangular, and "L", for lower triangular.

`diag`: Object of class `"character"`. Must be either `"U"`, for unit triangular (diagonal is all ones), or `"N"`; see `triangularMatrix`.

`Dim`,`Dimnames`: The dimension (a length-2 `"integer"`) and corresponding names (or `NULL`), see the `Matrix` class.

`factors`: Object of class `"list"`. A named list of factorizations that have been computed for the matrix.

Extends

`"ntrMatrix"` extends class `"ngeMatrix"`, directly, whereas
`"ntpMatrix"` extends class `"ndenseMatrix"`, directly.

Both extend Class `"triangularMatrix"`, directly, and class `"denseMatrix"`, `"lMatrix"` and others, *in*directly, use `showClass("nsyMatrix")`, e.g., for details.

Methods

Currently, mainly t() and coercion methods (for as(.); use, e.g., showMethods(class="ntrMatrix") for details.

See Also

Classes ngeMatrix, Matrix; function t

Examples

```
showClass("ntrMatrix")

str(new("ntpMatrix"))
(nutr <- as(upper.tri(matrix(, 4, 4)), "ndenseMatrix"))
str(nutp <- pack(nutr)) # packed matrix: only 10 = 4*(4+1)/2 entries
!nutp # the logical negation (is *not* logical triangular !)
## but this one is:
stopifnot(all.equal(nutp, pack(!!nutp)))
```

---

pack-methods *Representation of Packed and Unpacked Dense Matrices*

Description

pack() coerces dense symmetric and dense triangular matrices from unpacked format (storing the full matrix) to packed format (storing only one of the upper and lower triangles). unpack() performs the reverse coercion. The two formats are formalized by the virtual classes "packedMatrix" and "unpackedMatrix".

Usage

```
pack(x, ...)
## S4 method for signature 'dgeMatrix'
pack(x, symmetric = NA, upperTri = NA, ...)
## S4 method for signature 'lgeMatrix'
pack(x, symmetric = NA, upperTri = NA, ...)
## S4 method for signature 'ngeMatrix'
pack(x, symmetric = NA, upperTri = NA, ...)
## S4 method for signature 'matrix'
pack(x, symmetric = NA, upperTri = NA, ...)

unpack(x, ...)
```

Arguments

x	A dense symmetric or dense triangular matrix. **For** pack(): typically an "unpackedMatrix" or a standard "matrix", though "packedMatrix" are allowed and returned unchanged. **For** unpack(): typically a "packedMatrix", though "unpackedMatrix" are allowed and returned unchanged.
symmetric	logical (including NA) optionally indicating whether x is symmetric (or triangular).
upperTri	(for triangular x only) logical (including NA) indicating whether x is upper (or lower) triangular.
...	further arguments passed to or from other methods.

Details

pack(x) checks matrices x *not* inheriting from one of the virtual classes "symmetricMatrix" "triangularMatrix" for symmetry (via isSymmetric()) then for upper and lower triangularity (via isTriangular()) in order to identify a suitable coercion. Setting one or both of symmetric and upperTri to TRUE or FALSE rather than NA allows skipping of irrelevant tests for large matrices known to be symmetric or (upper or lower) triangular.

Users should *not* assume that pack() and unpack() are inverse operations. Specifically, y <- unpack(pack(x)) may not reproduce an "unpackedMatrix" x in the sense of identical(). See the examples.

Value

For pack(): a "packedMatrix" giving the condensed representation of x.

For unpack(): an "unpackedMatrix" giving the full storage representation of x.

Examples

```
showMethods("pack")
(s <- crossprod(matrix(sample(15), 5,3))) # traditional symmetric matrix
(sp <- pack(s))
mt <- as.matrix(tt <- tril(s))
(pt <- pack(mt))
stopifnot(identical(pt, pack(tt)),
  dim(s ) == dim(sp), all(s  == sp),
  dim(mt) == dim(pt), all(mt == pt), all(mt == tt))

showMethods("unpack")
(cp4 <- chol(Hilbert(4))) # is triangular
tp4 <- pack(cp4) # [t]riangular [p]acked
str(tp4)
(unpack(tp4))
stopifnot(identical(tp4, pack(unpack(tp4))))

z1 <- new("dsyMatrix", Dim = c(2L, 2L), x = as.double(1:4), uplo = "U")
z2 <- unpack(pack(z1))
```

```
stopifnot(!identical(z1, z2), # _not_ identical
          all(z1 == z2)) # but mathematically equal
cbind(z1@x, z2@x) # (unused!) lower triangle is "lost" in translation
```

---

packedMatrix-class *Virtual Class* "packedMatrix" *of Packed Dense Matrices*

Description

Class "packedMatrix" is the *virtual* class of dense symmetric or triangular matrices in "packed" format, storing only the choose(n+1,2) == n*(n+1)/2 elements of the upper or lower triangle of an n-by-n matrix. It is used to define common methods for efficient subsetting, transposing, etc. of its *proper* subclasses: currently "[dln]spMatrix" (packed symmetric), "[dln]tpMatrix" (packed triangular), and subclasses of these, such as "dppMatrix".

Slots

uplo: "character"; either "U", for upper triangular, and "L", for lower.

Dim, Dimnames: as all Matrix objects.

Extends

Class "denseMatrix", directly. Class "Matrix", by class "denseMatrix", distance 2.

Methods

pack signature(x = "packedMatrix"): ...

unpack signature(x = "packedMatrix"): ...

isSymmetric signature(object = "packedMatrix"): ...

isTriangular signature(object = "packedMatrix"): ...

isDiagonal signature(object = "packedMatrix"): ...

t signature(x = "packedMatrix"): ...

diag signature(x = "packedMatrix"): ...

diag<- signature(x = "packedMatrix"): ...

Author(s)

Mikael Jagan

See Also

pack and unpack; its virtual "complement" "unpackedMatrix"; its proper subclasses "dspMatrix", "ltpMatrix", etc.

Examples

```
showClass("packedMatrix")
showMethods(classes = "packedMatrix")
```

pMatrix-class *Permutation matrices*

Description

The pMatrix class is the class of *permutation* matrices, stored as 1-based integer permutation vectors. A permutation matrix is a square matrix whose rows *and* columns are all standard unit vectors. It follows that permutation matrices are a special case of *index* matrices (hence pMatrix is defined as a direct subclass of indMatrix).

Multiplying a matrix on the left by a permutation matrix is equivalent to permuting its rows. Analogously, multiplying a matrix on the right by a permutation matrix is equivalent to permuting its columns. Indeed, such products are implemented in **Matrix** as indexing operations; see 'Details' below.

Details

By definition, a permutation matrix is both a row index matrix and a column index matrix. However, the perm slot of a pMatrix cannot be used interchangeably as a row index vector and column index vector. If margin=1, then perm is a row index vector, and the corresponding column index vector can be computed as invPerm(perm), i.e., by inverting the permutation. Analogously, if margin=2, then perm and invPerm(perm) are column and row index vectors, respectively.

Given an n-by-n row permutation matrix P with perm slot p and a matrix M with conformable dimensions, we have

PM	=	P %*% M	=	M[p,]
MP	=	M %*% P	=	M[, i(p)]
$P'M$	=	crossprod(P, M)	=	M[i(p),]
MP'	=	tcrossprod(M, P)	=	M[, p]
$P'P$	=	crossprod(P)	=	Diagonal(n)
PP'	=	tcrossprod(P)	=	Diagonal(n)

where i := invPerm.

Objects from the Class

Objects can be created explicitly with calls of the form new("pMatrix", ...), but they are more commonly created by coercing 1-based integer index vectors, with calls of the form as(., "pMatrix"); see 'Methods' below.

Slots

margin,perm inherited from superclass indMatrix. Here, perm is an integer vector of length Dim[1] and a permutation of 1:Dim[1].

Dim,Dimnames inherited from virtual superclass Matrix.

Extends

Class "indMatrix", directly.

Methods

`%*%` `signature(x = "pMatrix", y = "Matrix")` and others listed by `showMethods("%*%", classes = "pMatrix")`: matrix products implemented where appropriate as indexing operations.

`coerce` `signature(from = "numeric", to = "pMatrix")`: supporting typical `pMatrix` construction from a vector of positive integers, specifically a permutation of `1:n`. Row permutation is assumed.

t `signature(x = "pMatrix")`: the transpose, which is a `pMatrix` with identical `perm` but opposite `margin`. Coincides with the inverse, as permutation matrices are orthogonal.

solve `signature(a = "pMatrix", b = "missing")`: the inverse permutation matrix, which is a `pMatrix` with identical `perm` but opposite `margin`. Coincides with the transpose, as permutation matrices are orthogonal. See `showMethods("solve", classes = "pMatrix")` for more signatures.

determinant `signature(x = "pMatrix", logarithm = "logical")`: always returning 1 or -1, as permutation matrices are orthogonal. In fact, the result is exactly the *sign* of the permutation.

See Also

Superclass indMatrix of index matrices, for many inherited methods; invPerm, for computing inverse permutation vectors.

Examples

```
(pm1 <- as(as.integer(c(2,3,1)), "pMatrix"))
t(pm1) # is the same as
solve(pm1)
pm1 %*% t(pm1) # check that the transpose is the inverse
stopifnot(all(diag(3) == as(pm1 %*% t(pm1), "matrix")),
          is.logical(as(pm1, "matrix")))

set.seed(11)
## random permutation matrix :
(p10 <- as(sample(10),"pMatrix"))

## Permute rows / columns of a numeric matrix :
(mm <- round(array(rnorm(3 * 3), c(3, 3)), 2))
mm %*% pm1
pm1 %*% mm
try(as(as.integer(c(3,3,1)), "pMatrix"))# Error: not a permutation

as(pm1, "TsparseMatrix")
p10[1:7, 1:4] # gives an "ngTMatrix" (most economic!)

## row-indexing of a <pMatrix> keeps it as an <indMatrix>:
p10[1:3, ]
```

printSpMatrix *Format and Print Sparse Matrices Flexibly*

Description

Format and print sparse matrices flexibly. These are the "workhorses" used by the format, show and print methods for sparse matrices. If x is large, printSpMatrix2(x) calls printSpMatrix() twice, namely, for the first and the last few rows, suppressing those in between, and also suppresses columns when x is too wide.

printSpMatrix() basically prints the result of formatSpMatrix().

Usage

```
formatSpMatrix(x, digits = NULL, maxp = 1e9,
               cld = getClassDef(class(x)), zero.print = ".",
               col.names, note.dropping.colnames = TRUE, uniDiag = TRUE,
               align = c("fancy", "right"), ...)

printSpMatrix(x, digits = NULL, maxp = max(100L, getOption("max.print")),
              cld = getClassDef(class(x)),
              zero.print = ".", col.names, note.dropping.colnames = TRUE,
              uniDiag = TRUE, col.trailer = "",
              align = c("fancy", "right"), ...)

printSpMatrix2(x, digits = NULL, maxp = max(100L, getOption("max.print")),
              zero.print = ".", col.names, note.dropping.colnames = TRUE,
              uniDiag = TRUE, suppRows = NULL, suppCols = NULL,
              col.trailer = if(suppCols) "......" else "",
              align = c("fancy", "right"),
              width = getOption("width"), fitWidth = TRUE, ...)
```

Arguments

x	an R object inheriting from class sparseMatrix.
digits	significant digits to use for printing, see print.default, the default, NULL, corresponds to using getOption("digits").
maxp	integer, default from options(max.print), influences how many entries of large matrices are printed at all. Typically should not be smaller than around 1000; values smaller than 100 are silently "rounded up" to 100.
cld	the class definition of x; must be equivalent to getClassDef(class(x)) and exists mainly for possible speedup.
zero.print	character which should be printed for *structural* zeroes. The default "." may occasionally be replaced by " " (blank); using "0" would look almost like print()ing of non-sparse matrices.

`col.names` logical or string specifying if and how column names of `x` should be printed, possibly abbreviated. The default is taken from `options("sparse.colnames")` if that is set, otherwise `FALSE` unless there are less than ten columns. When `TRUE` the full column names are printed.
When `col.names` is a string beginning with `"abb"` or `"sub"` and ending with an integer `n` (i.e., of the form `"abb... <n>"`), the column names are `abbreviate()`d or `substring()`ed to (target) length `n`, see the examples.

`note.dropping.colnames`
logical specifying, when `col.names` is `FALSE` if the dropping of the column names should be noted, `TRUE` by default.

`uniDiag` logical indicating if the diagonal entries of a sparse unit triangular or unit-diagonal matrix should be formatted as `"I"` instead of `"1"` (to emphasize that the 1's are "structural").

`col.trailer` a string to be appended to the right of each column; this is typically made use of by `show(<sparseMatrix>)` only, when suppressing columns.

`suppRows, suppCols`
logicals or `NULL`, for `printSpMatrix2()` specifying if rows or columns should be suppressed in printing. If `NULL`, sensible defaults are determined from `dim(x)` and `options(c("width", "max.print"))`. Setting both to `FALSE` may be a very bad idea.

`align` a string specifying how the `zero.print` codes should be aligned, i.e., padded as strings. The default, `"fancy"`, takes some effort to align the typical `zero.print = "."` with the position of `0`, i.e., the first decimal (one left of decimal point) of the numbers printed, whereas `align = "right"` just makes use of `print(*, right = TRUE)`.

`width` number, a positive integer, indicating the approximately desired (line) width of the output, see also `fitWidth`.

`fitWidth` logical indicating if some effort should be made to match the desired `width` or temporarily enlarge that if deemed necessary.

`...` unused optional arguments.

Details

formatSpMatrix: If `x` is large, only the first rows making up the approximately first `maxp` entries is used, otherwise all of `x`. `.formatSparseSimple()` is applied to (a dense version of) the matrix. Then, `formatSparseM` is used, unless in trivial cases or for sparse matrices without `x` slot.

Value

`formatSpMatrix()`
returns a character matrix with possibly empty column names, depending on `col.names` etc, see above.

`printSpMatrix*()`
return `x` *invisibly*, see `invisible`.

Author(s)

Martin Maechler

See Also

the virtual class sparseMatrix and the classes extending it; maybe sparseMatrix or spMatrix as simple constructors of such matrices.

The underlying utilities formatSparseM and .formatSparseSimple() (on the same page).

Examples

```
f1 <- gl(5, 3, labels = LETTERS[1:5])
X <- as(f1, "sparseMatrix")
X ## <==>  show(X)  <==>  print(X)
t(X) ## shows column names, since only 5 columns

X2 <- as(gl(12, 3, labels = paste(LETTERS[1:12],"c",sep=".")),
         "sparseMatrix")
X2
## less nice, but possible:
print(X2, col.names = TRUE) # use [,1] [,2] .. => does not fit

## Possibilities with column names printing:
      t(X2) # suppressing column names
print(t(X2), col.names=TRUE)
print(t(X2), zero.print = "", col.names="abbr. 1")
print(t(X2), zero.print = "-", col.names="substring 2")
```

---

qr-methods *Methods for QR Factorization*

Description

Computes the pivoted QR factorization of an $m \times n$ real matrix A, which has the general form

$$P_1 A P_2 = QR$$

or (equivalently)

$$A = P_1' Q R P_2'$$

where P_1 and P_2 are permutation matrices, $Q = \prod_{j=1}^{n} H_j$ is an $m \times m$ orthogonal matrix equal to the product of n Householder matrices H_j, and R is an $m \times n$ upper trapezoidal matrix.

denseMatrix use the default method implemented in **base**, namely qr.default. It is built on LINPACK routine dqrdc and LAPACK routine dgeqp3, which do not pivot rows, so that P_1 is an identity matrix.

Methods for sparseMatrix are built on CXSparse routines cs_sqr and cs_qr, which require $m \geq n$.

Usage

```
qr(x, ...)
## S4 method for signature 'dgCMatrix'
qr(x, order = 3L, ...)
```

Arguments

x	a finite matrix or Matrix to be factorized, satisfying nrow(x) >= ncol(x) if sparse.
order	an integer in 0:3 passed to CXSparse routine cs_sqr, indicating a strategy for choosing the column permutation P_2. 0 means no column permutation. 1, 2, and 3 indicate a fill-reducing ordering of $A + A'$, $\tilde{A}'\tilde{A}$, and $A'A$, where $\tilde{A}$ is A with "dense" rows removed. Do not set to 0 unless you know that the column order of A is already sensible.
...	further arguments passed to or from methods.

Details

If x is sparse and structurally rank deficient, having structural rank $r < n$, then x is augmented with $(n - r)$ rows of (partly non-structural) zeros, such that the augmented matrix has structural rank n. This augmented matrix is factorized as described above:

$$P_1 A P_2 = P_1 \begin{bmatrix} A_0 \\ 0 \end{bmatrix} P_2 = QR$$

where A_0 denotes the original, user-supplied $(m - (n - r)) \times n$ matrix.

Value

An object representing the factorization, inheriting from virtual S4 class QR or S3 class qr. The specific class is qr unless x inherits from virtual class sparseMatrix, in which case it is sparseQR.

References

Davis, T. A. (2006). *Direct methods for sparse linear systems*. Society for Industrial and Applied Mathematics. doi:10.1137/1.9780898718881

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class sparseQR and its methods.

Class dgCMatrix.

Generic function qr from **base**, whose default method qr.default "defines" the S3 class qr of dense QR factorizations.

Generic functions expand1 and expand2, for constructing matrix factors from the result.

Generic functions Cholesky, BunchKaufman, Schur, and lu, for computing other factorizations.

Examples

```
showMethods("qr", inherited = FALSE)

## Rank deficient: columns 3 {b2} and 6 {c3} are "extra"
M <- as(cbind(a1 = 1,
              b1 = rep(c(1, 0), each = 3L),
              b2 = rep(c(0, 1), each = 3L),
              c1 = rep(c(1, 0, 0), 2L),
              c2 = rep(c(0, 1, 0), 2L),
              c3 = rep(c(0, 0, 1), 2L)),
        "CsparseMatrix")
rownames(M) <- paste0("r", seq_len(nrow(M)))
b <- 1:6
eps <- .Machine$double.eps

## .... [1] full rank .............................................
## ===> a least squares solution of A x = b exists
##      and is unique _in exact arithmetic_

(A1 <- M[, -c(3L, 6L)])
(qr.A1 <- qr(A1))

stopifnot(exprs = {
    rankMatrix(A1) == ncol(A1)
    { d1 <- abs(diag(qr.A1@R)); sum(d1 < max(d1) * eps) == 0L }
    rcond(crossprod(A1)) >= eps
    all.equal(qr.coef(qr.A1, b), drop(solve(crossprod(A1), crossprod(A1, b))))
    all.equal(qr.fitted(qr.A1, b) + qr.resid(qr.A1, b), b)
})

## .... [2] numerically rank deficient with full structural rank .......
## ===> a least squares solution of A x = b does not
##      exist or is not unique _in exact arithmetic_

(A2 <- M)
(qr.A2 <- qr(A2))

stopifnot(exprs = {
    rankMatrix(A2) == ncol(A2) - 2L
    { d2 <- abs(diag(qr.A2@R)); sum(d2 < max(d2) * eps) == 2L }
    rcond(crossprod(A2)) < eps

    ## 'qr.coef' computes unique least squares solution of "nearby" problem
    ## Z x = b for some full rank Z ~ A, currently without warning {FIXME} !
    tryCatch({ qr.coef(qr.A2, b); TRUE }, condition = function(x) FALSE)

    all.equal(qr.fitted(qr.A2, b) + qr.resid(qr.A2, b), b)
})

## .... [3] numerically and structurally rank deficient ................
## ===> factorization of _augmented_ matrix with
##      full structural rank proceeds as in [2]
```

```
##  NB: implementation details are subject to change; see (*) below

A3 <- M
A3[, c(3L, 6L)] <- 0
A3
(qr.A3 <- qr(A3)) # with a warning ... "additional 2 row(s) of zeros"

stopifnot(exprs = {
    ## sparseQR object preserves the unaugmented dimensions (*)
    dim(qr.A3  ) == dim(A3)
    dim(qr.A3@V) == dim(A3) + c(2L, 0L)
    dim(qr.A3@R) == dim(A3) + c(2L, 0L)

    ## The augmented matrix remains numerically rank deficient
    rankMatrix(A3) == ncol(A3) - 2L
    { d3 <- abs(diag(qr.A3@R)); sum(d3 < max(d3) * eps) == 2L }
    rcond(crossprod(A3)) < eps
})

## Auxiliary functions accept and return a vector or matrix
## with dimensions corresponding to the unaugmented matrix (*),
## in all cases with a warning
qr.coef  (qr.A3, b)
qr.fitted(qr.A3, b)
qr.resid (qr.A3, b)

## .... [4] yet more examples ......................................

## By disabling column pivoting, one gets the "vanilla" factorization
## A = Q~ R, where Q~ := P1' Q is orthogonal because P1 and Q are

(qr.A1.pp <- qr(A1, order = 0L)) # partial pivoting

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

stopifnot(exprs = {
    length(qr.A1   @q) == ncol(A1)
    length(qr.A1.pp@q) == 0L # indicating no column pivoting
    ae2(A1[, qr.A1@q + 1L], qr.Q(qr.A1   ) %*% qr.R(qr.A1   ))
    ae2(A1                , qr.Q(qr.A1.pp) %*% qr.R(qr.A1.pp))
})
```

`rankMatrix` *Rank of a Matrix*

Description

Compute 'the' matrix rank, a well-defined functional in theory(*), somewhat ambiguous in practice. We provide several methods, the default corresponding to Matlab's definition.

(*) The rank of a $n \times m$ matrix A, $rk(A)$, is the maximal number of linearly independent columns (or rows); hence $rk(A) \leq min(n, m)$.

Usage

```
rankMatrix(x, tol = NULL,
           method = c("tolNorm2", "qr.R", "qrLINPACK", "qr",
                      "useGrad", "maybeGrad"),
           sval = svd(x, 0, 0)$d, warn.t = TRUE, warn.qr = TRUE)

qr2rankMatrix(qr, tol = NULL, isBqr = is.qr(qr), do.warn = TRUE)
```

Arguments

x	numeric matrix, of dimension $n \times m$, say.
tol	nonnegative number specifying a (relative, "scalefree") tolerance for testing of "practically zero" with specific meaning depending on method; by default, max(dim(x)) * .Machine$double.eps is according to Matlab's default (for its only method which is our method="tolNorm2").
method	a character string specifying the computational method for the rank, can be abbreviated: "tolNorm2": the number of singular values >= tol * max(sval); "qrLINPACK": for a dense matrix, this is the rank of qr(x, tol, LAPACK=FALSE) (which is qr(...)$rank); This ("qr*", dense) version used to be *the* recommended way to compute a matrix rank for a while in the past. For sparse x, this is equivalent to "qr.R". "qr.R": this is the rank of triangular matrix R, where qr() uses LAPACK or a "sparseQR" method (see qr-methods) to compute the decomposition QR. The rank of R is then defined as the number of "non-zero" diagonal entries d_i of R, and "non-zero"s fulfill $\lvert d_i \rvert \geq \mathrm{tol} \cdot \max(\lvert d_i \rvert)$. "qr": is for back compatibility; for dense x, it corresponds to "qrLINPACK", whereas for sparse x, it uses "qr.R". For all the "qr*" methods, singular values sval are not used, which may be crucially important for a large sparse matrix x, as in that case, when sval is not specified, the default, computing svd() currently coerces x to a dense matrix. "useGrad": considering the "gradient" of the (decreasing) singular values, the index of the *smallest* gap. "maybeGrad": choosing method "useGrad" only when that seems *reasonable*; otherwise using "tolNorm2".
sval	numeric vector of non-increasing singular values of x; typically unspecified and computed from x when needed, i.e., unless method = "qr".
warn.t	logical indicating if rankMatrix() should warn when it needs t(x) instead of x. Currently, for method = "qr" only, gives a warning by default because the caller often could have passed t(x) directly, more efficiently.

warn.qr	in the QR cases (i.e., if method starts with "qr"), rankMatrix() calls qr2rankMarix(.., do.warn = warn.qr), see below.
qr	an R object resulting from qr(x,..), i.e., typically inheriting from class "qr" or "sparseQR".
isBqr	logical indicating if qr is resulting from **base** qr(). (Otherwise, it is typically from **Matrix** package sparse qr.)
do.warn	logical; if true, warn about non-finite diagonal entries in the R matrix of the QR decomposition. Do not change lightly!

Details

qr2rankMatrix() is typically called from rankMatrix() for the "qr"* methods, but can be used directly - much more efficiently in case the qr-decomposition is available anyway.

Value

If x is a matrix of all 0 (or of zero dimension), the rank is zero; otherwise, typically a positive integer in 1:min(dim(x)) with attributes detailing the method used.

There are rare cases where the sparse QR decomposition "fails" in so far as the diagonal entries of R, the d_i (see above), end with non-finite, typically NaN entries. Then, a warning is signalled (unless warn.qr / do.warn is not true) and NA (specifically, NA_integer_) is returned.

Note

For large sparse matrices x, unless you can specify sval yourself, currently method = "qr" may be the only feasible one, as the others need sval and call svd() which currently coerces x to a denseMatrix which may be very slow or impossible, depending on the matrix dimensions.

Note that in the case of sparse x, method = "qr", all non-strictly zero diagonal entries d_i where counted, up to including **Matrix** version 1.1-0, i.e., that method implicitly used tol = 0, see also the set.seed(42) example below.

Author(s)

Martin Maechler; for the "*Grad" methods building on suggestions by Ravi Varadhan.

See Also

qr, svd.

Examples

```
rankMatrix(cbind(1, 0, 1:3)) # 2

(meths <- eval(formals(rankMatrix)$method))

## a "border" case:
H12 <- Hilbert(12)
rankMatrix(H12, tol = 1e-20) # 12;  but  11  with default method & tol.
sapply(meths, function(.m.) rankMatrix(H12, method = .m.))
```

```
## tolNorm2   qr.R  qrLINPACK   qr  useGrad maybeGrad
##       11     11         12   12       11        11
## The meaning of 'tol' for method="qrLINPACK" and *dense* x is not entirely "scale free"
rMQL <- function(ex, M) rankMatrix(M, method="qrLINPACK",tol = 10^-ex)
rMQR <- function(ex, M) rankMatrix(M, method="qr.R",     tol = 10^-ex)
sapply(5:15, rMQL, M = H12) # result is platform dependent
##  7  7  8 10 10 11 11 11 12 12 12  {x86_64}
sapply(5:15, rMQL, M = 1000 * H12) # not identical unfortunately
##  7  7  8 10 11 11 12 12 12 12 12
sapply(5:15, rMQR, M = H12)
##  5  6  7  8  8  9  9 10 10 11 11
sapply(5:15, rMQR, M = 1000 * H12) # the *same*


## "sparse" case:
M15 <- kronecker(diag(x=c(100,1,10)), Hilbert(5))
sapply(meths, function(.m.) rankMatrix(M15, method = .m.))
#--> all 15, but 'useGrad' has 14.
sapply(meths, function(.m.) rankMatrix(M15, method = .m., tol = 1e-7)) # all 14

## "large" sparse
n <- 250000; p <- 33; nnz <- 10000
L <- sparseMatrix(i = sample.int(n, nnz, replace=TRUE),
                  j = sample.int(p, nnz, replace=TRUE),
                  x = rnorm(nnz))
(st1 <- system.time(r1 <- rankMatrix(L)))                # warning+ ~1.5 sec (2013)
(st2 <- system.time(r2 <- rankMatrix(L, method = "qr"))) # considerably faster!
r1[[1]] == print(r2[[1]]) ## -->  ( 33  TRUE )

## another sparse-"qr" one, which ``failed'' till 2013-11-23:
set.seed(42)
f1 <- factor(sample(50, 1000, replace=TRUE))
f2 <- factor(sample(50, 1000, replace=TRUE))
f3 <- factor(sample(50, 1000, replace=TRUE))
D <- t(do.call(rbind, lapply(list(f1,f2,f3), as, 'sparseMatrix')))
dim(D); nnzero(D) ## 1000 x 150 // 3000 non-zeros (= 2%)
stopifnot(rankMatrix(D,           method='qr') == 148,
  rankMatrix(crossprod(D),method='qr') == 148)

## zero matrix has rank 0 :
stopifnot(sapply(meths, function(.m.)
                        rankMatrix(matrix(0, 2, 2), method = .m.)) == 0)
```

---

rcond-methods *Estimate the Reciprocal Condition Number*

Description

Estimate the reciprocal of the condition number of a matrix.

This is a generic function with several methods, as seen by `showMethods(rcond)`.

Usage

```
rcond(x, norm, ...)

## S4 method for signature 'sparseMatrix,character'
rcond(x, norm, useInv=FALSE, ...)
```

Arguments

x	an R object that inherits from the Matrix class.
norm	character string indicating the type of norm to be used in the estimate. The default is "O" for the 1-norm ("O" is equivalent to "1"). For sparse matrices, when useInv=TRUE, norm can be any of the kinds allowed for norm; otherwise, the other possible value is "I" for the infinity norm, see also norm.
useInv	logical (or "Matrix" containing solve(x)). If not false, compute the reciprocal condition number as $1/(\|x\| \cdot \|x^{-1}\|)$, where x^{-1} is the inverse of x, solve(x). This may be an efficient alternative (only) in situations where solve(x) is fast (or known), e.g., for (very) sparse or triangular matrices. Note that the *result* may differ depending on useInv, as per default, when it is false, an *approximation* is computed.
...	further arguments passed to or from other methods.

Value

An estimate of the reciprocal condition number of x.

BACKGROUND

The condition number of a regular (square) matrix is the product of the norm of the matrix and the norm of its inverse (or pseudo-inverse).

More generally, the condition number is defined (also for non-square matrices A) as

$$\kappa(A) = \frac{\max_{\|v\|=1} \|Av\|}{\min_{\|v\|=1} \|Av\|}.$$

Whenever x is *not* a square matrix, in our method definitions, this is typically computed via rcond(qr.R(qr(X)), ...) where X is x or t(x).

The condition number takes on values between 1 and infinity, inclusive, and can be viewed as a factor by which errors in solving linear systems with this matrix as coefficient matrix could be magnified.

rcond() computes the *reciprocal* condition number $1/\kappa$ with values in $[0, 1]$ and can be viewed as a scaled measure of how close a matrix is to being rank deficient (aka "singular").

Condition numbers are usually estimated, since exact computation is costly in terms of floating-point operations. An (over) estimate of reciprocal condition number is given, since by doing so overflow is avoided. Matrices are well-conditioned if the reciprocal condition number is near 1 and ill-conditioned if it is near zero.

References

Golub, G., and Van Loan, C. F. (1989). *Matrix Computations,* 2nd edition, Johns Hopkins, Baltimore.

See Also

norm, kappa() from package **base** computes an *approximate* condition number of a "traditional" matrix, even non-square ones, with respect to the $p = 2$ (Euclidean) norm. solve.

condest, a newer *approximate* estimate of the (1-norm) condition number, particularly efficient for large sparse matrices.

Examples

```
x <- Matrix(rnorm(9), 3, 3)
rcond(x)
## typically "the same" (with more computational effort):
1 / (norm(x) * norm(solve(x)))
rcond(Hilbert(9))  # should be about 9.1e-13

## For non-square matrices:
rcond(x1 <- cbind(1,1:10))# 0.05278
rcond(x2 <- cbind(x1, 2:11))# practically 0, since x2 does not have full rank

## sparse
(S1 <- Matrix(rbind(0:1,0, diag(3:-2))))
rcond(S1)
m1 <- as(S1, "denseMatrix")
all.equal(rcond(S1), rcond(m1))

## wide and sparse
rcond(Matrix(cbind(0, diag(2:-1))))

## Large sparse example ----------
m <- Matrix(c(3,0:2), 2,2)
M <- bdiag(kronecker(Diagonal(2), m), kronecker(m,m))
36*(iM <- solve(M)) # still sparse
MM <- kronecker(Diagonal(10), kronecker(Diagonal(5),kronecker(m,M)))
dim(M3 <- kronecker(bdiag(M,M),MM)) # 12'800 ^ 2
if(interactive()) ## takes about 2 seconds if you have >= 8 GB RAM
  system.time(r <- rcond(M3))
## whereas this is *fast* even though it computes  solve(M3)
system.time(r. <- rcond(M3, useInv=TRUE))
if(interactive()) ## the values are not the same
  c(r, r.)  # 0.05555 0.013888
## for all 4 norms available for sparseMatrix :
cbind(rr <- sapply(c("1","I","F","M"),
             function(N) rcond(M3, norm=N, useInv=TRUE)))
```

rep2abI *Replicate Vectors into 'abIndex' Result*

Description

`rep2abI(x, times)` conceptually computes `rep.int(x, times)` but with an `abIndex` class result.

Usage

```
rep2abI(x, times)
```

Arguments

`x`	numeric vector
`times`	integer (valued) scalar: the number of repetitions

Value

a vector of `class abIndex`

See Also

`rep.int()`, the base function; `abIseq`, `abIndex`.

Examples

```
(ab <- rep2abI(2:7, 4))
stopifnot(identical(as(ab, "numeric"),
   rep(2:7, 4)))
```

rleDiff-class *Class "rleDiff" of rle(diff(.)) Stored Vectors*

Description

Class `"rleDiff"` is for compactly storing long vectors which mainly consist of *linear* stretches. For such a vector `x`, `diff(x)` consists of *constant* stretches and is hence well compressable via `rle()`.

Objects from the Class

Objects can be created by calls of the form `new("rleDiff", ...)`.

Currently experimental, see below.

Slots

`first`: A single number (of class `"numLike"`, a class union of `"numeric"` and `"logical"`).

`rle`: Object of class `"rle"`, basically a `list` with components `"lengths"` and `"values"`, see `rle()`. As this is used to encode potentially huge index vectors, `lengths` may be of type `double` here.

Methods

There is a simple `show` method only.

Note

This is currently an *experimental* auxiliary class for the class `abIndex`, see there.

See Also

`rle`, `abIndex`.

Examples

```
showClass("rleDiff")

ab <- c(abIseq(2, 100), abIseq(20, -2))
ab@rleD  # is "rleDiff"
```

---

rsparsematrix *Random Sparse Matrix*

Description

Generate a random sparse matrix efficiently. The default has rounded gaussian non-zero entries, and `rand.x = NULL` generates random patter**n** matrices, i.e. inheriting from `nsparseMatrix`.

Usage

```
rsparsematrix(nrow, ncol, density, nnz = round(density * maxE),
              symmetric = FALSE,
              rand.x = function(n) signif(rnorm(n), 2), ...)
```

Arguments

`nrow`, `ncol`	number of rows and columns, i.e., the matrix dimension (`dim`).
`density`	optional number in $[0, 1]$, the density is the proportion of non-zero entries among all matrix entries. If specified it determines the default for `nnz`, otherwise `nnz` needs to be specified.
`nnz`	number of non-zero entries, for a sparse matrix typically considerably smaller than `nrow*ncol`. Must be specified if `density` is not.

symmetric	logical indicating if result should be a matrix of class symmetricMatrix. Note that in the symmetric case, nnz denotes the number of non zero entries of the upper (or lower) part of the matrix, including the diagonal.
rand.x	NULL or the random number generator for the x slot, a function such that rand.x(n) generates a numeric vector of length n. Typical examples are rand.x = rnorm, or rand.x = runif; the default is nice for didactical purposes.
...	optionally further arguments passed to sparseMatrix(), notably repr.

Details

The algorithm first samples "encoded" (i, j)s without replacement, via one dimensional indices, if not symmetric sample.int(nrow*ncol, nnz), then—if rand.x is not NULL—gets x <- rand.x(nnz) and calls sparseMatrix(i=i, j=j, x=x, ..). When rand.x=NULL, sparseMatrix(i=i, j=j, ..) will return a patter**n** matrix (i.e., inheriting from nsparseMatrix).

Value

a sparseMatrix, say M of dimension (nrow, ncol), i.e., with dim(M) == c(nrow, ncol), if symmetric is not true, with nzM <- nnzero(M) fulfilling nzM <= nnz and typically, nzM == nnz.

Author(s)

Martin Maechler

Examples

```
set.seed(17)# to be reproducible
M <- rsparsematrix(8, 12, nnz = 30) # small example, not very sparse
M
M1 <- rsparsematrix(1000, 20,  nnz = 123,  rand.x = runif)
summary(M1)

## a random *symmetric* Matrix
(S9 <- rsparsematrix(9, 9, nnz = 10, symmetric=TRUE)) # dsCMatrix
nnzero(S9)# ~ 20: as 'nnz' only counts one "triangle"

## a random patter*n* aka boolean Matrix (no 'x' slot):
(n7 <- rsparsematrix(5, 12, nnz = 10, rand.x = NULL))

## a [T]riplet representation sparseMatrix:
T2 <- rsparsematrix(40, 12, nnz = 99, repr = "T")
head(T2)
```

RsparseMatrix-class *Class "RsparseMatrix" of Sparse Matrices in Row-compressed Form*

Description

The "RsparseMatrix" class is the virtual class of all sparse matrices coded in sorted compressed row-oriented form. Since it is a virtual class, no objects may be created from it. See showClass("RsparseMatrix") for its subclasses.

Slots

j: Object of class "integer" of length nnzero (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.

p: Object of class "integer" of pointers, one for each row, to the initial (zero-based) index of elements in the row.

Dim, Dimnames: inherited from the superclass, see sparseMatrix.

Extends

Class "sparseMatrix", directly. Class "Matrix", by class "sparseMatrix".

Methods

Originally, **few** methods were defined on purpose, as we rather use the CsparseMatrix in **Matrix**. Then, more methods were added but *beware* that these typically do *not* return "RsparseMatrix" results, but rather Csparse* or Tsparse* ones; e.g., R[i, j] <- v for an "RsparseMatrix" R works, but after the assignment, R is a (triplet) "TsparseMatrix".

t signature(x = "RsparseMatrix"): ...

coerce signature(from = "RsparseMatrix", to = "CsparseMatrix"): ...

coerce signature(from = "RsparseMatrix", to = "TsparseMatrix"): ...

See Also

its superclass, sparseMatrix, and, e.g., class dgRMatrix for the links to other classes.

Examples

```
showClass("RsparseMatrix")
```

`Schur-class` *Schur Factorizations*

Description

`Schur` is the class of Schur factorizations of $n \times n$ real matrices A, having the general form

$$A = QTQ'$$

where Q is an orthogonal matrix and T is a block upper triangular matrix with 1×1 or 2×2 diagonal blocks specifying the real and complex conjugate eigenvalues of A. The column vectors of Q are the Schur vectors of A, and T is the Schur form of A.

The Schur factorization generalizes the spectral decomposition of normal matrices A, whose Schur form is block diagonal, to arbitrary square matrices.

Details

The matrix A and its Schur form T are *similar* and thus have the same spectrum. The eigenvalues are computed trivially as the eigenvalues of the diagonal blocks of T.

Slots

`Dim`, `Dimnames` inherited from virtual class `MatrixFactorization`.

`Q` an orthogonal matrix, inheriting from virtual class `Matrix`.

`T` a block upper triangular matrix, inheriting from virtual class `Matrix`. The diagonal blocks have dimensions 1-by-1 or 2-by-2.

`EValues` a numeric or complex vector containing the eigenvalues of the diagonal blocks of `T`, which are the eigenvalues of `T` and consequently of the factorized matrix.

Extends

Class `SchurFactorization`, directly. Class `MatrixFactorization`, by class `SchurFactorization`, distance 2.

Instantiation

Objects can be generated directly by calls of the form `new("Schur", ...)`, but they are more typically obtained as the value of `Schur(x)` for `x` inheriting from `Matrix` (often `dgeMatrix`).

Methods

`determinant signature(from = "Schur", logarithm = "logical")`: computes the determinant of the factorized matrix A or its logarithm.

`expand1 signature(x = "Schur")`: see `expand1-methods`.

`expand2 signature(x = "Schur")`: see `expand2-methods`.

`solve signature(a = "Schur", b = .)`: see `solve-methods`.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dgees.f.

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class dgeMatrix.

Generic functions Schur, expand1 and expand2.

Examples

```
showClass("Schur")
set.seed(0)

n <- 4L
(A <- Matrix(rnorm(n * n), n, n))

## With dimnames, to see that they are propagated :
dimnames(A) <- list(paste0("r", seq_len(n)),
                    paste0("c", seq_len(n)))

(sch.A <- Schur(A))
str(e.sch.A <- expand2(sch.A), max.level = 2L)

## A ~ Q T Q' in floating point
stopifnot(exprs = {
    identical(names(e.sch.A), c("Q", "T", "Q."))
    all.equal(A, with(e.sch.A, Q %*% T %*% Q.))
})

## Factorization handled as factorized matrix
b <- rnorm(n)
stopifnot(all.equal(det(A), det(sch.A)),
          all.equal(solve(A, b), solve(sch.A, b)))

## One of the non-general cases:
Schur(Diagonal(6L))
```

Schur-methods *Methods for Schur Factorization*

Description

Computes the Schur factorization of an $n \times n$ real matrix A, which has the general form

$$A = QTQ'$$

where Q is an orthogonal matrix and T is a block upper triangular matrix with 1×1 and 2×2 diagonal blocks specifying the real and complex conjugate eigenvalues of A. The column vectors of Q are the Schur vectors of A, and T is the Schur form of A.

Methods are built on LAPACK routine dgees.

Usage

```
Schur(x, vectors = TRUE, ...)
```

Arguments

x	a finite square matrix or Matrix to be factorized.
vectors	a logical. If TRUE (the default), then Schur vectors are computed in addition to the Schur form.
...	further arguments passed to or from methods.

Value

An object representing the factorization, inheriting from virtual class SchurFactorization if vectors = TRUE. Currently, the specific class is always Schur in that case. An exception is if x is a traditional matrix, in which case the result is a named list containing Q, T, and EValues slots of the Schur object.

If vectors = FALSE, then the result is the same named list but without Q.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dgees.f.

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class Schur and its methods.

Class dgeMatrix.

Generic functions expand1 and expand2, for constructing matrix factors from the result.

Generic functions Cholesky, BunchKaufman, lu, and qr, for computing other factorizations.

Examples

```
showMethods("Schur", inherited = FALSE)
set.seed(0)

Schur(Hilbert(9L)) # real eigenvalues

(A <- Matrix(round(rnorm(25L, sd = 100)), 5L, 5L))
(sch.A <- Schur(A)) # complex eigenvalues
```

```
## A ~ Q T Q' in floating point
str(e.sch.A <- expand2(sch.A), max.level = 2L)
stopifnot(all.equal(A, Reduce(`%*%`, e.sch.A)))

(e1 <- eigen(sch.A@T, only.values = TRUE)$values)
(e2 <- eigen(    A  , only.values = TRUE)$values)
(e3 <- sch.A@EValues)

stopifnot(exprs = {
    all.equal(e1, e2, tolerance = 1e-13)
    all.equal(e1, e3[order(Mod(e3), decreasing = TRUE)], tolerance = 1e-13)
    identical(Schur(A, vectors = FALSE),
              list(T = sch.A@T, EValues = e3))
    identical(Schur(as(A, "matrix")),
              list(Q = as(sch.A@Q, "matrix"),
                   T = as(sch.A@T, "matrix"), EValues = e3))
})
```

---

solve-methods *Methods in Package* **Matrix** *for Function* solve

---

Description

Methods for generic function solve for solving linear systems of equations, i.e., for X in $AX = B$, where A is a square matrix and X and B are matrices with dimensions consistent with A.

Usage

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

## S4 method for signature 'dgeMatrix,ANY'
solve(a, b, tol = .Machine$double.eps, ...)

## S4 method for signature 'dgCMatrix,missing'
solve(a, b, sparse = TRUE, ...)
## S4 method for signature 'dgCMatrix,matrix'
solve(a, b, sparse = FALSE, ...)
## S4 method for signature 'dgCMatrix,denseMatrix'
solve(a, b, sparse = FALSE, ...)
## S4 method for signature 'dgCMatrix,sparseMatrix'
solve(a, b, sparse = TRUE, ...)

## S4 method for signature 'denseLU,dgeMatrix'
solve(a, b, ...)
## S4 method for signature 'BunchKaufman,dgeMatrix'
solve(a, b, ...)
## S4 method for signature 'Cholesky,dgeMatrix'
solve(a, b, ...)
```

```
## S4 method for signature 'sparseLU,dgCMatrix'
solve(a, b, tol = .Machine$double.eps, ...)
## S4 method for signature 'sparseQR,dgCMatrix'
solve(a, b, ...)
## S4 method for signature 'CHMfactor,dgCMatrix'
solve(a, b, system = c("A", "LDLt", "LD", "DLt", "L", "Lt", "D", "P", "Pt"), ...)
```

Arguments

a	a finite square matrix or Matrix containing the coefficients of the linear system, or otherwise a MatrixFactorization, in which case methods behave (by default) as if the factorized matrix were specified.
b	a vector, sparseVector, matrix, or Matrix satisfying NROW(b) == nrow(a), giving the right-hand side(s) of the linear system. Vectors b are treated as length(b)-by-1 matrices. If b is missing, then methods take b to be an identity matrix.
tol	a non-negative number. For a inheriting from denseMatrix, an error is signaled if the reciprocal one-norm condition number (see rcond) of a is less than tol, indicating that a is near-singular. For a of class sparseLU, an error is signaled if the ratio min(d)/max(d) is less than tol, where d = abs(diag(a@U)). (Interpret with care, as this ratio is a cheap heuristic and *not* in general equal to or even proportional to the reciprocal one-norm condition number.) Setting tol = 0 disables the test.
sparse	a logical indicating if the result should be formally sparse, i.e., if the result should inherit from virtual class sparseMatrix. Only methods for sparse a and missing or matrix b have this argument. Methods for missing or sparse b use sparse = TRUE by default. Methods for dense b use sparse = FALSE by default.
system	a string specifying a linear system to be solved. Only methods for a inheriting from CHMfactor have this argument. See 'Details'.
...	further arguments passed to or from methods.

Details

Methods for general and symmetric matrices a compute a triangular factorization (LU, Bunch-Kaufman, or Cholesky) and call the method for the corresponding factorization class. The factorization is sparse if a is. Methods for sparse, symmetric matrices a attempt a Cholesky factorization and perform an LU factorization only if that fails (typically because a is not positive definite).

Triangular, diagonal, and permutation matrices do not require factorization (they are already "factors"), hence methods for those are implemented directly. For triangular a, solutions are obtained by forward or backward substitution; for diagonal a, they are obtained by scaling the rows of b; and for permutations a, they are obtained by permuting the rows of b.

Methods for dense a are built on 14 LAPACK routines: class d..Matrix, where ..=(ge|tr|tp|sy|sp|po|pp), uses routines d..tri and d..trs for missing and non-missing b, respectively. A corollary is that these methods always give a dense result.

Methods for sparse a are built on CXSparse routines cs_lsolve, cs_usolve, and cs_spsolve and CHOLMOD routines cholmod_solve and cholmod_spsolve. By default, these methods give a

vector result if b is a vector, a sparse matrix result if b is missing or a sparse matrix, and a dense matrix result if b is a dense matrix. One can override this behaviour by setting the sparse argument, where available, but that should be done with care. Note that a sparse result may be sparse only in the formal sense and not at all in the mathematical sense, depending on the nonzero patterns of a and b. Furthermore, whereas dense results are fully preallocated, sparse results must be "grown" in a loop over the columns of b.

Methods for a of class sparseQR are simple wrappers around qr.coef, giving the *least squares* solution in overdetermined cases.

Methods for a inheriting from CHMfactor can solve systems other than the default one $AX = B$. The correspondence between its system argument the system actually solved is outlined in the table below. See CHMfactor-class for a definition of notation.

system	isLDL(a)=TRUE	isLDL(a)=FALSE
"A"	$AX = B$	$AX = B$
"LDLt"	$L_1DL_1'X = B$	$LL'X = B$
"LD"	$L_1DX = B$	$LX = B$
"DLt"	$DL_1'X = B$	$L'X = B$
"L"	$L_1X = B$	$LX = B$
"Lt"	$L_1'X = B$	$L'X = B$
"D"	$DX = B$	$X = B$
"P"	$X = P_1B$	$X = P_1B$
"Pt"	$X = P_1'B$	$X = P_1'B$

See Also

Virtual class MatrixFactorization and its subclasses.

Generic functions Cholesky, BunchKaufman, Schur, lu, and qr for *computing* factorizations.

Generic function solve from **base**.

Function qr.coef from **base** for computing least squares solutions of overdetermined linear systems.

Examples

```
## A close to symmetric example with "quite sparse" inverse:
n1 <- 7; n2 <- 3
dd <- data.frame(a = gl(n1,n2), b = gl(n2,1,n1*n2))# balanced 2-way
X <- sparse.model.matrix(~ -1+ a + b, dd)# no intercept --> even sparser
XXt <- tcrossprod(X)
diag(XXt) <- rep(c(0,0,1,0), length.out = nrow(XXt))

n <- nrow(ZZ <- kronecker(XXt, Diagonal(x=c(4,1))))
image(a <- 2*Diagonal(n) + ZZ %*% Diagonal(x=c(10, rep(1, n-1))))
isSymmetric(a) # FALSE
image(drop0(skewpart(a)))
image(ia0 <- solve(a, tol = 0)) # checker board, dense [but really, a is singular!]
try(solve(a, sparse=TRUE))##-> error [ TODO: assertError ]
ia. <- solve(a, sparse=TRUE, tol = 1e-19)##-> *no* error
if(R.version$arch == "x86_64")
  ## Fails on 32-bit [Fedora 19, R 3.0.2] from Matrix 1.1-0 on [FIXME ??] only
```

```
  stopifnot(all.equal(as.matrix(ia.), as.matrix(ia0)))
a <- a + Diagonal(n)
iad <- solve(a)
ias <- solve(a, sparse=FALSE)
stopifnot(all.equal(as(iad,"denseMatrix"), ias, tolerance=1e-14))
I. <- iad %*% a          ; image(I.)
I0 <- drop0(zapsmall(I.)); image(I0)
.I <- a %*% iad
.I0 <- drop0(zapsmall(.I))
stopifnot( all.equal(as(I0, "diagonalMatrix"), Diagonal(n)),
           all.equal(as(.I0,"diagonalMatrix"), Diagonal(n)) )
```

`sparse.model.matrix` *Construct Sparse Design / Model Matrices*

Description

Construct a sparse model or "design" matrix, from a formula and data frame (`sparse.model.matrix`) or a single factor (`fac2sparse`).

The `fac2[Ss]parse()` functions are utilities, also used internally in the principal user level function `sparse.model.matrix()`.

Usage

```
sparse.model.matrix(object, data = environment(object),
    contrasts.arg = NULL, xlev = NULL, transpose = FALSE,
    drop.unused.levels = FALSE, row.names = TRUE,
    sep = "", verbose = FALSE, ...)

fac2sparse(from, to = c("d", "l", "n"),
   drop.unused.levels = TRUE, repr = c("C", "R", "T"), giveCsparse)
fac2Sparse(from, to = c("d", "l", "n"),
   drop.unused.levels = TRUE, repr = c("C", "R", "T"), giveCsparse,
   factorPatt12, contrasts.arg = NULL)
```

Arguments

`object`	an object of an appropriate class. For the default method, a model formula or terms object.
`data`	a data frame created with `model.frame`. If another sort of object, `model.frame` is called first.
`contrasts.arg`	**for** `sparse.model.matrix()`**:** A list, whose entries are contrasts suitable for input to the `contrasts` replacement function and whose names are the names of columns of `data` containing `factor`s. **for** `fac2Sparse()`**:** character string or `NULL` or (coercable to) `"sparseMatrix"`, specifying the contrasts to be applied to the factor levels.

xlev	to be used as argument of model.frame if data has no "terms" attribute.
transpose	logical indicating if the *transpose* should be returned; if the transposed is used anyway, setting transpose = TRUE is more efficient.
drop.unused.levels	should factors have unused levels dropped? The default for sparse.model.matrix has been changed to FALSE, 2010-07, for compatibility with R's standard (dense) model.matrix().
row.names	logical indicating if row names should be used.
sep	character string passed to paste() when constructing column names from the variable name and its levels.
verbose	logical or integer indicating if (and how much) progress output should be printed.
...	further arguments passed to or from other methods.
from	(for fac2sparse():) a factor.
to	a character indicating the "kind" of sparse matrix to be returned. The default, "d" is for double.
giveCsparse	**deprecated**, replaced with repr; logical indicating if the result must be a CsparseMatrix.
repr	character string, one of "C", "T", or "R", specifying the sparse *repr*esentation to be used for the result, i.e., one from the super classes CsparseMatrix, TsparseMatrix, or RsparseMatrix.
factorPatt12	logical vector, say fp, of length two; when fp[1] is true, return "contrasted" t(X); when fp[2] is true, the original ("dummy") t(X), i.e, the result of fac2sparse().

Value

a sparse matrix, extending CsparseMatrix (for fac2sparse() if repr = "C" as per default; a TsparseMatrix or RsparseMatrix, otherwise).

For fac2Sparse(), a list of length two, both components with the corresponding transposed model matrix, where the corresponding factorPatt12 is true.

fac2sparse(), the basic workhorse of sparse.model.matrix(), returns the *transpose* (t) of the model matrix.

Note

model.Matrix(sparse = TRUE) from package **MatrixModels** may be nowadays be preferable to sparse.model.matrix, as model.Matrix returns an object of class modelMatrix with additional slots assign and contrasts relating to the model variables.

Author(s)

Doug Bates and Martin Maechler, with initial suggestions from Tim Hesterberg.

See Also

model.matrix in package **stats**, part of base R.

model.Matrix in package **MatrixModels**; see 'Note'.

as(f, "sparseMatrix") (see coerce(from = "factor", ..) in the class doc sparseMatrix) produces the *transposed* sparse model matrix for a single factor f (and *no* contrasts).

Examples

```
dd <- data.frame(a = gl(3,4), b = gl(4,1,12))# balanced 2-way
options("contrasts") # the default:  "contr.treatment"
sparse.model.matrix(~ a + b, dd)
sparse.model.matrix(~ -1+ a + b, dd)# no intercept --> even sparser
sparse.model.matrix(~ a + b, dd, contrasts = list(a="contr.sum"))
sparse.model.matrix(~ a + b, dd, contrasts = list(b="contr.SAS"))

## Sparse method is equivalent to the traditional one :
stopifnot(all(sparse.model.matrix(~    a + b, dd) ==
          Matrix(model.matrix(~    a + b, dd), sparse=TRUE)),
      all(sparse.model.matrix(~0 + a + b, dd) ==
          Matrix(model.matrix(~0 + a + b, dd), sparse=TRUE)))

(ff <- gl(3,4,, c("X","Y", "Z")))
fac2sparse(ff) #  3 x 12 sparse Matrix of class "dgCMatrix"
##
##  X  1 1 1 1 . . . . . . . .
##  Y  . . . . 1 1 1 1 . . . .
##  Z  . . . . . . . . 1 1 1 1

## can also be computed via sparse.model.matrix():
f30 <- gl(3,0    )
f12 <- gl(3,0, 12)
stopifnot(
  all.equal(t( fac2sparse(ff) ),
    sparse.model.matrix(~ 0+ff),
    tolerance = 0, check.attributes=FALSE),
  is(M <- fac2sparse(f30, drop= TRUE),"CsparseMatrix"), dim(M) == c(0, 0),
  is(M <- fac2sparse(f30, drop=FALSE),"CsparseMatrix"), dim(M) == c(3, 0),
  is(M <- fac2sparse(f12, drop= TRUE),"CsparseMatrix"), dim(M) == c(0,12),
  is(M <- fac2sparse(f12, drop=FALSE),"CsparseMatrix"), dim(M) == c(3,12)
 )
```

`sparseLU-class` *Sparse LU Factorizations*

Description

`sparseLU` is the class of sparse, row- and column-pivoted LU factorizations of $n \times n$ real matrices A, having the general form

$$P_1 A P_2 = LU$$

or (equivalently)

$$A = P_1' L U P_2'$$

where P_1 and P_2 are permutation matrices, L is a unit lower triangular matrix, and U is an upper triangular matrix.

Slots

`Dim`, `Dimnames` inherited from virtual class `MatrixFactorization`.

`L` an object of class `dtCMatrix`, the unit lower triangular L factor.

`U` an object of class `dtCMatrix`, the upper triangular U factor.

`p`, `q` 0-based integer vectors of length `Dim[1]`, specifying the permutations applied to the rows and columns of the factorized matrix. `q` of length 0 is valid and equivalent to the identity permutation, implying no column pivoting. Using R syntax, the matrix P_1AP_2 is precisely `A[p+1, q+1]` (`A[p+1, ]` when `q` has length 0).

Extends

Class `LU`, directly. Class `MatrixFactorization`, by class `LU`, distance 2.

Instantiation

Objects can be generated directly by calls of the form `new("sparseLU", ...)`, but they are more typically obtained as the value of `lu(x)` for `x` inheriting from `sparseMatrix` (often `dgCMatrix`).

Methods

`determinant signature(from = "sparseLU", logarithm = "logical")`: computes the determinant of the factorized matrix A or its logarithm.

`expand signature(x = "sparseLU")`: see `expand-methods`.

`expand1 signature(x = "sparseLU")`: see `expand1-methods`.

`expand2 signature(x = "sparseLU")`: see `expand2-methods`.

`solve signature(a = "sparseLU", b = .)`: see `solve-methods`.

References

Davis, T. A. (2006). *Direct methods for sparse linear systems*. Society for Industrial and Applied Mathematics. doi:10.1137/1.9780898718881

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class `denseLU` for dense LU factorizations.

Class `dgCMatrix`.

Generic functions `lu`, `expand1` and `expand2`.

Examples

```
showClass("sparseLU")
set.seed(2)

A <- as(readMM(system.file("external", "pores_1.mtx", package = "Matrix")),
        "CsparseMatrix")
(n <- A@Dim[1L])

## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- list(paste0("r", seq_len(n)),
                          paste0("c", seq_len(n)))

(lu.A <- lu(A))
str(e.lu.A <- expand2(lu.A), max.level = 2L)

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ P1' L U P2' in floating point
stopifnot(exprs = {
    identical(names(e.lu.A), c("P1.", "L", "U", "P2."))
    identical(e.lu.A[["P1."]],
              new("pMatrix", Dim = c(n, n), Dimnames = c(dn[1L], list(NULL)),
                  margin = 1L, perm = invertPerm(lu.A@p, 0L, 1L)))
    identical(e.lu.A[["P2."]],
              new("pMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
                  margin = 2L, perm = invertPerm(lu.A@q, 0L, 1L)))
    identical(e.lu.A[["L"]], lu.A@L)
    identical(e.lu.A[["U"]], lu.A@U)
    ae1(A, with(e.lu.A, P1. %*% L %*% U %*% P2.))
    ae2(A[lu.A@p + 1L, lu.A@q + 1L], with(e.lu.A, L %*% U))
})

## Factorization handled as factorized matrix
b <- rnorm(n)
stopifnot(identical(det(A), det(lu.A)),
          identical(solve(A, b), solve(lu.A, b)))
```

`sparseMatrix` *General Sparse Matrix Construction from Nonzero Entries*

Description

User-friendly construction of sparse matrices (inheriting from virtual `class` `CsparseMatrix`, `RsparseMatrix`, or `TsparseMatrix`) from the positions and values of their nonzero entries.

This interface is recommended over direct construction via calls such as `new("..[CRT]Matrix", ...)`.

Usage

```
sparseMatrix(i, j, p, x, dims, dimnames,
             symmetric = FALSE, triangular = FALSE, index1 = TRUE,
             repr = c("C", "R", "T"), giveCsparse,
             check = TRUE, use.last.ij = FALSE)
```

Arguments

i, j	integer vectors of equal length specifying the positions (row and column indices) of the nonzero (or non-TRUE) entries of the matrix. Note that, when x is non-missing, the x_k corresponding to *repeated* pairs (i_k, j_k) are *added*, for consistency with the definition of class TsparseMatrix, unless use.last.ij is TRUE, in which case only the *last* such x_k is used.
p	integer vector of pointers, one for each column (or row), to the initial (zero-based) index of elements in the column (or row). Exactly one of i, j, and p must be missing.
x	optional, typically nonzero values for the matrix entries. If specified, then the length must equal that of i (or j) or equal 1, in which case x is recycled as necessary. If missing, then the result is a **n**onzero pattern matrix, i.e., inheriting from class nsparseMatrix.
dims	optional length-2 integer vector of matrix dimensions. If missing, then !index1+c(max(i),max(j)) is used.
dimnames	optional list of dimnames; if missing, then NULL ones are used.
symmetric	logical indicating if the resulting matrix should be symmetric. In that case, (i, j, p) should specify only one triangle (upper or lower).
triangular	logical indicating if the resulting matrix should be triangular. In that case, (i, j, p) should specify only one triangle (upper or lower).
index1	logical. If TRUE (the default), then i and j are interpreted as 1-based indices, following the R convention. That is, counting of rows and columns starts at 1. If FALSE, then they are interpreted as 0-based indices.
repr	character string, one of "C", "R", and "T", specifying the **repr**esentation of the sparse matrix result, i.e., specifying one of the virtual classes CsparseMatrix, RsparseMatrix, and TsparseMatrix.
giveCsparse	(**deprecated**, replaced by repr) logical indicating if the result should inherit from CsparseMatrix or TsparseMatrix. Note that operations involving CsparseMatrix are very often (but not always) more efficient.
check	logical indicating whether to check that the result is formally valid before returning. Do not set to FALSE unless you know what you are doing!
use.last.ij	logical indicating if, in the case of repeated (duplicated) pairs (i_k, j_k), only the last pair should be used. FALSE (the default) is consistent with the definiton of class TsparseMatrix.

Details

Exactly one of the arguments i, j and p must be missing.

In typical usage, p is missing, i and j are vectors of positive integers and x is a numeric vector. These three vectors, which must have the same length, form the triplet representation of the sparse matrix.

If i or j is missing then p must be a non-decreasing integer vector whose first element is zero. It provides the compressed, or "pointer" representation of the row or column indices, whichever is missing. The expanded form of p, `rep(seq_along(dp),dp)` where `dp <- diff(p)`, is used as the (1-based) row or column indices.

You cannot set both `singular` and `triangular` to true; rather use `Diagonal()` (or its alternatives, see there).

The values of i, j, p and `index1` are used to create 1-based index vectors i and j from which a `TsparseMatrix` is constructed, with numerical values given by x, if non-missing. Note that in that case, when some pairs (i_k, j_k) are repeated (aka "duplicated"), the corresponding x_k are *added*, in consistency with the definition of the `TsparseMatrix` class, unless `use.last.ij` is set to true.

By default, when `repr = "C"`, the `CsparseMatrix` derived from this triplet form is returned, where `repr = "R"` now allows to directly get an `RsparseMatrix` and `repr = "T"` leaves the result as `TsparseMatrix`.

The reason for returning a `CsparseMatrix` object instead of the triplet format by default is that the compressed column form is easier to work with when performing matrix operations. In particular, if there are no zeros in x then a `CsparseMatrix` is a unique representation of the sparse matrix.

Value

A sparse matrix, by default in compressed sparse column format and (formally) without symmetric or triangular structure, i.e., by default inheriting from both `CsparseMatrix` and `generalMatrix`.

Note

You *do* need to use `index1 = FALSE` (or add `+ 1` to i and j) if you want use the 0-based i (and j) slots from existing sparse matrices.

See Also

`Matrix(*, sparse=TRUE)` for the constructor of such matrices from a *dense* matrix. That is easier in small sample, but much less efficient (or impossible) for large matrices, where something like `sparseMatrix()` is needed. Further `bdiag` and `Diagonal` for (block-)diagonal and `bandSparse` for banded sparse matrix constructors.

Random sparse matrices via `rsparsematrix()`.

The standard R `xtabs(*, sparse=TRUE)`, for sparse tables and `sparse.model.matrix()` for building sparse model matrices.

Consider `CsparseMatrix` and similar class definition help files.

Examples

```
## simple example
i <- c(1,3:8); j <- c(2,9,6:10); x <- 7 * (1:7)
(A <- sparseMatrix(i, j, x = x))                    ##  8 x 10 "dgCMatrix"
summary(A)
```

```
str(A) # note that *internally* 0-based row indices are used

(sA <- sparseMatrix(i, j, x = x, symmetric = TRUE)) ## 10 x 10 "dsCMatrix"
(tA <- sparseMatrix(i, j, x = x, triangular= TRUE)) ## 10 x 10 "dtCMatrix"
stopifnot( all(sA == tA + t(tA)) ,
           identical(sA, as(tA + t(tA), "symmetricMatrix")))

## dims can be larger than the maximum row or column indices
(AA <- sparseMatrix(c(1,3:8), c(2,9,6:10), x = 7 * (1:7), dims = c(10,20)))
summary(AA)

## i, j and x can be in an arbitrary order, as long as they are consistent
set.seed(1); (perm <- sample(1:7))
(A1 <- sparseMatrix(i[perm], j[perm], x = x[perm]))
stopifnot(identical(A, A1))

## The slots are 0-index based, so
try( sparseMatrix(i=A@i, p=A@p, x= seq_along(A@x)) )
## fails and you should say so: 1-indexing is FALSE:
     sparseMatrix(i=A@i, p=A@p, x= seq_along(A@x), index1 = FALSE)

## the (i,j) pairs can be repeated, in which case the x's are summed
(args <- data.frame(i = c(i, 1), j = c(j, 2), x = c(x, 2)))
(Aa <- do.call(sparseMatrix, args))
## explicitly ask for elimination of such duplicates, so
## that the last one is used:
(A. <- do.call(sparseMatrix, c(args, list(use.last.ij = TRUE))))
stopifnot(Aa[1,2] == 9, # 2+7 == 9
          A.[1,2] == 2) # 2 was *after* 7

## for a pattern matrix, of course there is no "summing":
(nA <- do.call(sparseMatrix, args[c("i","j")]))

dn <- list(LETTERS[1:3], letters[1:5])
## pointer vectors can be used, and the (i,x) slots are sorted if necessary:
m <- sparseMatrix(i = c(3,1, 3:2, 2:1), p= c(0:2, 4,4,6), x = 1:6, dimnames = dn)
m
str(m)
stopifnot(identical(dimnames(m), dn))

sparseMatrix(x = 2.72, i=1:3, j=2:4) # recycling x
sparseMatrix(x = TRUE, i=1:3, j=2:4) # recycling x, |--> "lgCMatrix"

## no 'x' --> patter*n* matrix:
(n <- sparseMatrix(i=1:6, j=rev(2:7)))# -> ngCMatrix

## an empty sparse matrix:
(e <- sparseMatrix(dims = c(4,6), i={}, j={}))

## a symmetric one:
(sy <- sparseMatrix(i= c(2,4,3:5), j= c(4,7:5,5), x = 1:5,
                    dims = c(7,7), symmetric=TRUE))
stopifnot(isSymmetric(sy),
```

```
            identical(sy, ## switch i <-> j {and transpose }
        t( sparseMatrix(j= c(2,4,3:5), i= c(4,7:5,5), x = 1:5,
                        dims = c(7,7), symmetric=TRUE))))

## rsparsematrix() calls sparseMatrix() :
M1 <- rsparsematrix(1000, 20, nnz = 200)
summary(M1)

## pointers example in converting from other sparse matrix representations.
if(requireNamespace("SparseM") &&
   packageVersion("SparseM") >= "0.87" &&
   nzchar(dfil <- system.file("extdata", "rua_32_ax.rua", package = "SparseM"))) {
  X <- SparseM::model.matrix(SparseM::read.matrix.hb(dfil))
  XX <- sparseMatrix(j = X@ja, p = X@ia - 1L, x = X@ra, dims = X@dimension)
  validObject(XX)

  ## Alternatively, and even more user friendly :
  X. <- as(X, "Matrix")  # or also
  X2 <- as(X, "sparseMatrix")
  stopifnot(identical(XX, X.), identical(X., X2))
}
```

`sparseMatrix-class` *Virtual Class "sparseMatrix" — Mother of Sparse Matrices*

Description

Virtual Mother Class of All Sparse Matrices

Slots

`Dim`**:** Object of class `"integer"` - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

`Dimnames`**:** a list of length two - inherited from class `Matrix`, see `Matrix`.

Extends

Class `"Matrix"`, directly.

Methods

show `(object = "sparseMatrix")`: The `show` method for sparse matrices prints *"structural"* zeroes as `"."` using `printSpMatrix()` which allows further customization.

print `signature(x = "sparseMatrix")`, ...
The `print` method for sparse matrices by default is the same as `show()` but can be called with extra optional arguments, see `printSpMatrix()`.

format `signature(x = "sparseMatrix")`, ...
The `format` method for sparse matrices, see `formatSpMatrix()` for details such as the extra optional arguments.

summary `(object = "sparseMatrix", uniqT=FALSE)`: Returns an object of S3 class `"sparseSummary"` which is basically a `data.frame` with columns `(i,j,x)` (or just `(i,j)` for `nsparseMatrix` class objects) with the stored (typically non-zero) entries. The `print` method resembles Matlab's way of printing sparse matrices, and also the MatrixMarket format, see `writeMM`.

cbind2 `(x = *, y = *)`: several methods for binding matrices together, column-wise, see the basic `cbind` and `rbind` functions.
Note that the result will typically be sparse, even when one argument is dense and larger than the sparse one.

rbind2 `(x = *, y = *)`: binding matrices together row-wise, see `cbind2` above.

determinant `(x = "sparseMatrix", logarithm=TRUE)`: `determinant()` methods for sparse matrices typically work via `Cholesky` or `lu` decompositions.

diag `(x = "sparseMatrix")`: extracts the diagonal of a sparse matrix.

dim<- `signature(x = "sparseMatrix", value = "ANY")`: allows to *reshape* a sparse matrix to a sparse matrix with the same entries but different dimensions. `value` must be of length two and fulfill `prod(value) == prod(dim(x))`.

coerce `signature(from = "factor", to = "sparseMatrix")`: Coercion of a factor to `"sparseMatrix"` produces the matrix of indicator **rows** stored as an object of class `"dgCMatrix"`. To obtain columns representing the interaction of the factor and a numeric covariate, replace the `"x"` slot of the result by the numeric covariate then take the transpose. Missing values (`NA`) from the factor are translated to columns of all `0`s.

See also `colSums`, `norm`, ... for methods with separate help pages.

Note

In method selection for multiplication operations (i.e. `%*%` and the two-argument form of `crossprod`) the sparseMatrix class takes precedence in the sense that if one operand is a sparse matrix and the other is any type of dense matrix then the dense matrix is coerced to a `dgeMatrix` and the appropriate sparse matrix method is used.

See Also

`sparseMatrix`, and its references, such as `xtabs(*, sparse=TRUE)`, or `sparse.model.matrix()`, for constructing sparse matrices.

`T2graph` for conversion of `"graph"` objects (package **graph**) to and from sparse matrices.

Examples

```
showClass("sparseMatrix") ## and look at the help() of its subclasses
M <- Matrix(0, 10000, 100)
M[1,1] <- M[2,3] <- 3.14
M  ## show(.) method suppresses printing of the majority of rows

data(CAex, package = "Matrix")
dim(CAex) # 72 x 72 matrix
determinant(CAex) # works via sparse lu(.)

## factor -> t( <sparse design matrix> ) :
(fact <- gl(5, 3, 30, labels = LETTERS[1:5]))
```

```
(Xt <- as(fact, "sparseMatrix"))  # indicator rows

## missing values --> all-0 columns:
f.mis <- fact
i.mis <- c(3:5, 17)
is.na(f.mis) <- i.mis
Xt != (X. <- as(f.mis, "sparseMatrix")) # differ only in columns 3:5,17
stopifnot(all(X.[,i.mis] == 0), all(Xt[,-i.mis] == X.[,-i.mis]))
```

---

sparseQR-class *Sparse QR Factorizations*

Description

sparseQR is the class of sparse, row- and column-pivoted QR factorizations of $m \times n$ ($m \geq n$) real matrices, having the general form

$$P_1 A P_2 = QR = \begin{bmatrix} Q_1 & Q_2 \end{bmatrix} \begin{bmatrix} R_1 \\ 0 \end{bmatrix} = Q_1 R_1$$

or (equivalently)

$$A = P_1' Q R P_2' = P_1' \begin{bmatrix} Q_1 & Q_2 \end{bmatrix} \begin{bmatrix} R_1 \\ 0 \end{bmatrix} P_2' = P_1' Q_1 R_1 P_2'$$

where P_1 and P_2 are permutation matrices, $Q = \prod_{j=1}^{n} H_j$ is an $m \times m$ orthogonal matrix (Q_1 contains the first n column vectors) equal to the product of n Householder matrices H_j, and R is an $m \times n$ upper trapezoidal matrix (R_1 contains the first n row vectors and is upper *triangular*).

Usage

```
qrR(qr, complete = FALSE, backPermute = TRUE, row.names = TRUE)
```

Arguments

qr	an object of class sparseQR, almost always the result of a call to generic function qr with sparse x.
complete	a logical indicating if R should be returned instead of R_1.
backPermute	a logical indicating if R or R_1 should be multiplied on the right by P_2'.
row.names	a logical indicating if dimnames(qr)[1] should be propagated unpermuted to the result. If complete = FALSE, then only the first n names are kept.

Details

The method for `qr.Q` does not return Q but rather the (also orthogonal) product $P_1'Q$. This behaviour is algebraically consistent with the **base** implementation (see `qr`), which can be seen by noting that `qr.default` in **base** does not pivot rows, constraining P_1 to be an identity matrix. It follows that `qr.Q(qr.default(x))` also returns $P_1'Q$.

Similarly, the methods for `qr.qy` and `qr.qty` multiply on the left by $P_1'Q$ and $Q'P_1$ rather than Q and Q'.

It is wrong to expect the values of `qr.Q` (or `qr.R`, `qr.qy`, `qr.qty`) computed from "equivalent" sparse and dense factorizations (say, `qr(x)` and `qr(as(x, "matrix"))` for `x` of class `dgCMatrix`) to compare equal. The underlying factorization algorithms are quite different, notably as they employ different pivoting strategies, and in general the factorization is not unique even for fixed P_1 and P_2.

On the other hand, the values of `qr.X`, `qr.coef`, `qr.fitted`, and `qr.resid` are well-defined, and in those cases the sparse and dense computations *should* compare equal (within some tolerance).

The method for `qr.R` is a simple wrapper around `qrR`, but not back-permuting by default and never giving row names. It did not support `backPermute = TRUE` until **Matrix** `1.6-0`, hence code needing the back-permuted result should call `qrR` if **Matrix** `>= 1.6-0` is not known.

Slots

`Dim`, `Dimnames` inherited from virtual class `MatrixFactorization`.

`beta` a numeric vector of length `Dim[2]`, used to construct Householder matrices; see `V` below.

`V` an object of class `dgCMatrix` with `Dim[2]` columns. The number of rows `nrow(V)` is at least `Dim[1]` and at most `Dim[1]+Dim[2]`. `V` is lower trapezoidal, and its column vectors generate the Householder matrices H_j that compose the orthogonal Q factor. Specifically, H_j is constructed as `diag(Dim[1]) - beta[j] * tcrossprod(V[, j])`.

`R` an object of class `dgCMatrix` with `nrow(V)` rows and `Dim[2]` columns. `R` is the upper trapezoidal R factor.

`p`, `q` 0-based integer vectors of length `nrow(V)` and `Dim[2]`, respectively, specifying the permutations applied to the rows and columns of the factorized matrix. `q` of length 0 is valid and equivalent to the identity permutation, implying no column pivoting. Using R syntax, the matrix P_1AP_2 is precisely `A[p+1, q+1]` (`A[p+1, ]` when `q` has length 0).

Extends

Class `QR`, directly. Class `MatrixFactorization`, by class `QR`, distance 2.

Instantiation

Objects can be generated directly by calls of the form `new("sparseQR", ...)`, but they are more typically obtained as the value of `qr(x)` for `x` inheriting from `sparseMatrix` (often `dgCMatrix`).

Methods

`determinant signature(from = "sparseQR", logarithm = "logical")`: computes the determinant of the factorized matrix A or its logarithm.

`expand1 signature(x = "sparseQR")`: see `expand1-methods`.

`expand2 signature(x = "sparseQR")`: see `expand2-methods`.

`qr.Q signature(qr = "sparseQR")`: returns as a `dgeMatrix` either $P_1'Q$ or $P_1'Q_1$, depending on optional argument `complete`. The default is `FALSE`, indicating $P_1'Q_1$.

`qr.R signature(qr = "sparseQR")`: `qrR` returns R, R_1, $RP2'$, or R_1P2', depending on optional arguments `complete` and `backPermute`. The default in both cases is `FALSE`, indicating R_1, for compatibility with **base**. The class of the result in that case is `dtCMatrix`. In the other three cases, it is `dgCMatrix`.

`qr.X signature(qr = "sparseQR")`: returns A as a `dgeMatrix`, by default. If $m > n$ and optional argument `ncol` is greater than n, then the result is augmented with $P_1'QJ$, where J is composed of columns $(n+1)$ through `ncol` of the $m \times m$ identity matrix.

`qr.coef signature(qr = "sparseQR", y = .)`: returns as a `dgeMatrix` or vector the result of multiplying `y` on the left by $P_2R_1^{-1}Q_1'P_1$.

`qr.fitted signature(qr = "sparseQR", y = .)`: returns as a `dgeMatrix` or vector the result of multiplying `y` on the left by $P_1'Q_1Q_1'P_1$.

`qr.resid signature(qr = "sparseQR", y = .)`: returns as a `dgeMatrix` or vector the result of multiplying `y` on the left by $P_1'Q_2Q_2'P_1$.

`qr.qty signature(qr = "sparseQR", y = .)`: returns as a `dgeMatrix` or vector the result of multiplying `y` on the left by $Q'P_1$.

`qr.qy signature(qr = "sparseQR", y = .)`: returns as a `dgeMatrix` or vector the result of multiplying `y` on the left by $P_1'Q$.

`solve signature(a = "sparseQR", b = .)`: see `solve-methods`.

References

Davis, T. A. (2006). *Direct methods for sparse linear systems*. Society for Industrial and Applied Mathematics. doi:10.1137/1.9780898718881

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). Johns Hopkins University Press. doi:10.56021/9781421407944

See Also

Class `dgCMatrix`.

Generic function `qr` from **base**, whose default method `qr.default` "defines" the S3 class `qr` of dense QR factorizations.

`qr-methods` for methods defined in **Matrix**.

Generic functions `expand1` and `expand2`.

The many auxiliary functions for QR factorizations: `qr.Q`, `qr.R`, `qr.X`, `qr.coef`, `qr.fitted`, `qr.resid`, `qr.qty`, `qr.qy`, and `qr.solve`.

Examples

```
showClass("sparseQR")
set.seed(2)

m <- 300L
```

```
n <- 60L
A <- rsparsematrix(m, n, 0.05)

## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- list(paste0("r", seq_len(m)),
                          paste0("c", seq_len(n)))

(qr.A <- qr(A))
str(e.qr.A <- expand2(qr.A, complete = FALSE), max.level = 2L)
str(E.qr.A <- expand2(qr.A, complete =  TRUE), max.level = 2L)

t(sapply(e.qr.A, dim))
t(sapply(E.qr.A, dim))

## Horribly inefficient, but instructive :
slowQ <- function(V, beta) {
    d <- dim(V)
    Q <- diag(d[1L])
    if(d[2L] > 0L) {
        for(j in d[2L]:1L) {
            cat(j, "\n", sep = "")
            Q <- Q - (beta[j] * tcrossprod(V[, j])) %*% Q
        }
    }
    Q
}

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ P1' Q R P2' ~ P1' Q1 R1 P2' in floating point
stopifnot(exprs = {
    identical(names(e.qr.A), c("P1.", "Q1", "R1", "P2."))
    identical(names(E.qr.A), c("P1.", "Q" , "R" , "P2."))
    identical(e.qr.A[["P1."]],
              new("pMatrix", Dim = c(m, m), Dimnames = c(dn[1L], list(NULL)),
                  margin = 1L, perm = invertPerm(qr.A@p, 0L, 1L)))
    identical(e.qr.A[["P2."]],
              new("pMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
                  margin = 2L, perm = invertPerm(qr.A@q, 0L, 1L)))
    identical(e.qr.A[["R1"]], triu(E.qr.A[["R"]][seq_len(n), ]))
    identical(e.qr.A[["Q1"]],      E.qr.A[["Q"]][, seq_len(n)] )
    identical(E.qr.A[["R"]], qr.A@R)
 ## ae1(E.qr.A[["Q"]], slowQ(qr.A@V, qr.A@beta))
    ae1(crossprod(E.qr.A[["Q"]]), diag(m))
    ae1(A, with(e.qr.A, P1. %*% Q1 %*% R1 %*% P2.))
    ae1(A, with(E.qr.A, P1. %*% Q  %*% R  %*% P2.))
    ae2(A.perm <- A[qr.A@p + 1L, qr.A@q + 1L], with(e.qr.A, Q1 %*% R1))
    ae2(A.perm                                , with(E.qr.A, Q  %*% R ))
})

## More identities
b <- rnorm(m)
```

```
stopifnot(exprs = {
    ae1(qrX <- qr.X     (qr.A   ), A)
    ae2(qrQ <- qr.Q     (qr.A   ), with(e.qr.A, P1. %*% Q1))
    ae2(       qr.R     (qr.A   ), with(e.qr.A, R1))
    ae2(qrc <- qr.coef  (qr.A, b), with(e.qr.A, solve(R1 %*% P2., t(qrQ)) %*% b))
    ae2(qrf <- qr.fitted(qr.A, b), with(e.qr.A, tcrossprod(qrQ) %*% b))
    ae2(qrr <- qr.resid (qr.A, b), b - qrf)
    ae2(qrq <- qr.qy    (qr.A, b), with(E.qr.A, P1. %*% Q %*% b))
    ae2(qr.qty(qr.A, qrq), b)
})

## Sparse and dense computations should agree here
qr.Am <- qr(as(A, "matrix")) # <=> qr.default(A)
stopifnot(exprs = {
    ae2(qrX, qr.X     (qr.Am   ))
    ae2(qrc, qr.coef  (qr.Am, b))
    ae2(qrf, qr.fitted(qr.Am, b))
    ae2(qrr, qr.resid (qr.Am, b))
})
```

`sparseVector` *Sparse Vector Construction from Nonzero Entries*

Description

User friendly construction of sparse vectors, i.e., objects inheriting from `class sparseVector`, from indices and values of its non-zero entries.

Usage

```
sparseVector(x, i, length)
```

Arguments

`x`	vector of the non zero entries; may be missing in which case a `"nsparseVector"` will be returned.
`i`	integer vector (of the same length as `x`) specifying the indices of the non-zero (or non-`TRUE`) entries of the sparse vector.
`length`	length of the sparse vector.

Details

zero entries in `x` are dropped automatically, analogously as `drop0()` acts on sparse matrices.

Value

a sparse vector, i.e., inheriting from `class sparseVector`.

Author(s)

Martin Maechler

See Also

`sparseMatrix()` constructor for sparse matrices; the class `sparseVector`.

Examples

```
str(sv <- sparseVector(x = 1:10, i = sample(999, 10), length=1000))

sx <- c(0,0,3, 3.2, 0,0,0,-3:1,0,0,2,0,0,5,0,0)
ss <- as(sx, "sparseVector")
stopifnot(identical(ss,
   sparseVector(x = c(2, -1, -2, 3, 1, -3, 5, 3.2),
                i = c(15L, 10:9, 3L,12L,8L,18L, 4L), length = 20L)))

(ns <- sparseVector(i= c(7, 3, 2), length = 10))
stopifnot(identical(ns,
      new("nsparseVector", length = 10, i = c(2, 3, 7))))
```

`sparseVector-class` *Sparse Vector Classes*

Description

Sparse Vector Classes: The virtual mother class `"sparseVector"` has the five actual daughter classes `"dsparseVector"`, `"isparseVector"`, `"lsparseVector"`, `"nsparseVector"`, and `"zsparseVector"`, where we've mainly implemented methods for the `d*`, `l*` and `n*` ones.

Slots

`length`**:** class `"numeric"` - the `length` of the sparse vector. Note that `"numeric"` can be considerably larger than the maximal `"integer"`, `.Machine$integer.max`, on purpose.

`i`**:** class `"numeric"` - the (1-based) indices of the non-zero entries. Must *not* be `NA` and strictly sorted increasingly.

Note that `"integer"` is "part of" `"numeric"`, and can (and often will) be used for non-huge sparseVectors.

`x`**:** (for all but `"nsparseVector"`): the non-zero entries. This is of class `"numeric"` for class `"dsparseVector"`, `"logical"` for class `"lsparseVector"`, etc.

Methods

length `signature(x = "sparseVector")`: simply extracts the `length` slot.

show `signature(object = "sparseVector")`: The `show` method for sparse vectors prints *"structural"* zeroes as `"."` using the non-exported `prSpVector` function which allows further customization such as replacing `"."` by `" "` (blank).

Note that `options(max.print)` will influence how many entries of large sparse vectors are printed at all.

as.vector `signature(x = "sparseVector", mode = "character")` coerces sparse vectors to "regular", i.e., atomic vectors. This is the same as `as(x, "vector")`.

as ..: see `coerce` below

coerce `signature(from = "sparseVector", to = "sparseMatrix")`, and

coerce `signature(from = "sparseMatrix", to = "sparseVector")`, etc: coercions to and from sparse matrices (`sparseMatrix`) are provided and work analogously as in standard R, i.e., a vector is coerced to a 1-column matrix.

dim<- `signature(x = "sparseVector", value = "integer")` coerces a sparse vector to a sparse Matrix, i.e., an object inheriting from `sparseMatrix`, of the appropriate dimension.

head `signature(x = "sparseVector")`: as with R's (package **util**) `head`, `head(x,n)` (for $n >= 1$) is equivalent to `x[1:n]`, but here can be much more efficient, see the example.

tail `signature(x = "sparseVector")`: analogous to `head`, see above.

toeplitz `signature(x = "sparseVector")`: as `toeplitz(x)`, produce the $n \times n$ Toeplitz matrix from `x`, where `n = length(x)`.

rep `signature(x = "sparseVector")` repeat `x`, with the same argument list `(x, times, length.out, each, ...)` as the default method for rep().

which `signature(x = "nsparseVector")` and

which `signature(x = "lsparseVector")` return the indices of the non-zero entries (which is trivial for sparse vectors).

Ops `signature(e1 = "sparseVector", e2 = "*")`: define arithmetic, compare and logic operations, (see `Ops`).

Summary `signature(x = "sparseVector")`: define all the `Summary` methods.

is.na, is.finite, is.infinite `(x = "sparseVector")`, and

is.na, is.finite, is.infinite `(x = "nsparseVector")`: return `logical` or `"nsparseVector"` of the same length as `x`, indicating if/where `x` is `NA` (or `NaN`), finite or infinite, entirely analogously to the corresponding base R functions.

zapsmall `signature(x = "sparseVectors")`: typically used for numeric sparse vector: `round()` entries such that (relatively) very small entries become zero exactly.

`c.sparseVector()` is an S3 method for all `"sparseVector"`s, but automatic dispatch only happens for the first argument, so it is useful also as regular R function, see the examples.

See Also

`sparseVector()` for friendly construction of sparse vectors (apart from `as(*, "sparseVector")`).

Examples

```
getClass("sparseVector")
getClass("dsparseVector")

sx <- c(0,0,3, 3.2, 0,0,0,-3:1,0,0,2,0,0,5,0,0)
(ss <- as(sx, "sparseVector"))

ix <- as.integer(round(sx))
(is <- as(ix, "sparseVector")) ## an "isparseVector" (!)
(ns <- sparseVector(i= c(7, 3, 2), length = 10)) # "nsparseVector"
## rep() works too:
(ri <- rep(is, length.out= 25))

## Using `dim<-`  as in base R :
r <- ss
dim(r) <- c(4,5) # becomes a sparse Matrix:
r
## or coercion (as as.matrix() in base R):
as(ss, "Matrix")
stopifnot(all(ss == print(as(ss, "CsparseMatrix"))))

## currently has "non-structural" FALSE -- printing as ":"
(lis <- is & FALSE)
(nn <- is[is == 0]) # all "structural" FALSE

## NA-case
sN <- sx; sN[4] <- NA
(svN <- as(sN, "sparseVector"))

v <- as(c(0,0,3, 3.2, rep(0,9),-3,0,-1, rep(0,20),5,0),
        "sparseVector")
v <- rep(rep(v, 50), 5000)
set.seed(1); v[sample(v@i, 1e6)] <- 0
str(v)
system.time(for(i in 1:4) hv <- head(v, 1e6))
##   user  system elapsed
##  0.033   0.000   0.032
system.time(for(i in 1:4) h2 <- v[1:1e6])
##   user  system elapsed
##  1.317   0.000   1.319

stopifnot(identical(hv, h2),
          identical(is | FALSE, is != 0),
          validObject(svN), validObject(lis), as.logical(is.na(svN[4])),
          identical(is^2 > 0, is & TRUE),
          all(!lis), !any(lis), length(nn@i) == 0, !any(nn), all(!nn),
          sum(lis) == 0, !prod(lis), range(lis) == c(0,0))

## create and use the t(.) method:
t(x20 <- sparseVector(c(9,3:1), i=c(1:2,4,7), length=20))
(T20 <- toeplitz(x20))
stopifnot(is(T20, "symmetricMatrix"), is(T20, "sparseMatrix"),
```

```
          identical(unname(as.matrix(T20)),
                    toeplitz(as.vector(x20))))

## c() method for "sparseVector" - also available as regular function
(c1 <- c(x20, 0,0,0, -10*x20))
(c2 <- c(ns, is, FALSE))
(c3 <- c(ns, !ns, TRUE, NA, FALSE))
(c4 <- c(ns, rev(ns)))
## here, c() would produce a list {not dispatching to c.sparseVector()}
(c5 <- c.sparseVector(0,0, x20))

## checking (consistency)
.v <- as.vector
.s <- function(v) as(v, "sparseVector")
stopifnot(exprs = {
    all.equal(c1, .s(c(.v(x20), 0,0,0, -10*.v(x20))),      tol = 0)
    all.equal(c2, .s(c(.v(ns), .v(is), FALSE)),            tol = 0)
    all.equal(c3, .s(c(.v(ns), !.v(ns), TRUE, NA, FALSE)), tol = 0)
    all.equal(c4, .s(c(.v(ns), rev(.v(ns)))),              tol = 0,
              check.class = FALSE)
    all.equal(c5, .s(c(0,0, .v(x20))),                     tol = 0)
})
```

---

spMatrix *Sparse Matrix Constructor From Triplet*

Description

User friendly construction of a sparse matrix (inheriting from class TsparseMatrix) from the triplet representation.

This is much less flexible than sparseMatrix() and hence somewhat *deprecated*.

Usage

```
spMatrix(nrow, ncol, i = integer(0L), j = integer(0L), x = double(0L))
```

Arguments

nrow, ncol	integers specifying the desired number of rows and columns.
i, j	integer vectors of the same length specifying the locations of the non-zero (or non-TRUE) entries of the matrix.
x	atomic vector of the same length as i and j, specifying the values of the non-zero entries.

Value

A sparse matrix in triplet form, as an R object inheriting from both TsparseMatrix and generalMatrix.

The matrix M will have M[i[k], j[k]] == x[k], for $k = 1, 2, \ldots, n$, where n = length(i) and M[i', j'] == 0 for all other pairs (i', j').

See Also

Matrix(*, sparse=TRUE) for the more usual constructor of such matrices. Then, sparseMatrix is more general and flexible than spMatrix() and by default returns a CsparseMatrix which is often slightly more desirable. Further, bdiag and Diagonal for (block-)diagonal matrix constructors.

Consider TsparseMatrix and similar class definition help files.

Examples

```
## simple example
A <- spMatrix(10,20, i = c(1,3:8),
                     j = c(2,9,6:10),
                     x = 7 * (1:7))
A # a "dgTMatrix"
summary(A)
str(A) # note that *internally* 0-based indices (i,j) are used

L <- spMatrix(9, 30, i = rep(1:9, 3), 1:27,
              (1:27) %% 4 != 1)
L # an "lgTMatrix"


## A simplified predecessor of  Matrix'  rsparsematrix() function :

 rSpMatrix <- function(nrow, ncol, nnz,
                       rand.x = function(n) round(rnorm(nnz), 2))
 {
     ## Purpose: random sparse matrix
     ## ----------------------------------------------------------------
     ## Arguments: (nrow,ncol): dimension
     ##          nnz  :  number of non-zero entries
     ##         rand.x:  random number generator for 'x' slot
     ## ----------------------------------------------------------------
     ## Author: Martin Maechler, Date: 14.-16. May 2007
     stopifnot((nnz <- as.integer(nnz)) >= 0,
               nrow >= 0, ncol >= 0, nnz <= nrow * ncol)
     spMatrix(nrow, ncol,
              i = sample(nrow, nnz, replace = TRUE),
              j = sample(ncol, nnz, replace = TRUE),
              x = rand.x(nnz))
 }

 M1 <- rSpMatrix(100000, 20, nnz = 200)
 summary(M1)
```

---

subassign-methods *Methods for "[<-" - Assigning to Subsets for 'Matrix'*

Description

Methods for "[<-", i.e., extraction or subsetting mostly of matrices, in package **Matrix**.

Note: Contrary to standard matrix assignment in base R, in x[..] <- val it is typically an **error** (see stop) when the type or class of val would require the class of x to be changed, e.g., when x is logical, say "lsparseMatrix", and val is numeric. In other cases, e.g., when x is a "nsparseMatrix" and val is not TRUE or FALSE, a warning is signalled, and val is "interpreted" as logical, and (logical) NA is interpreted as TRUE.

Methods

There are *many many* more than these:

x = "Matrix", i = "missing", j = "missing", value= "ANY" is currently a simple fallback method implementation which ensures "readable" error messages.

x = "Matrix", i = "ANY", j = "ANY", value= "ANY" currently gives an error

x = "denseMatrix", i = "index", j = "missing", value= "numeric" ...

x = "denseMatrix", i = "index", j = "index", value= "numeric" ...

x = "denseMatrix", i = "missing", j = "index", value= "numeric" ...

See Also

[-methods for subsetting "Matrix" objects; the index class; Extract about the standard subset assignment (and extraction).

Examples

```
set.seed(101)
(a <- m <- Matrix(round(rnorm(7*4),2), nrow = 7))

a[] <- 2.2 # <<- replaces **every** entry
a
## as do these:
a[,] <- 3 ; a[TRUE,] <- 4

m[2, 3]  <- 3.14 # simple number
m[3, 3:4]<- 3:4  # simple numeric of length 2

## sub matrix assignment:
m[-(4:7), 3:4] <- cbind(1,2:4) #-> upper right corner of 'm'
m[3:5, 2:3] <- 0
m[6:7, 1:2] <- Diagonal(2)
m

## rows or columns only:
m[1,] <- 10
m[,2] <- 1:7
m[-(1:6), ] <- 3:0 # not the first 6 rows, i.e. only the 7th
as(m, "sparseMatrix")
```

subscript-methods *Methods for "[": Extraction or Subsetting in Package 'Matrix'*

Description

Methods for `"["`, i.e., extraction or subsetting mostly of matrices, in package **Matrix**.

Methods

There are more than these:

x = "Matrix", i = "missing", j = "missing", drop= "ANY" ...

x = "Matrix", i = "numeric", j = "missing", drop= "missing" ...

x = "Matrix", i = "missing", j = "numeric", drop= "missing" ...

x = "dsparseMatrix", i = "missing", j = "numeric", drop= "logical" ...

x = "dsparseMatrix", i = "numeric", j = "missing", drop= "logical" ...

x = "dsparseMatrix", i = "numeric", j = "numeric", drop= "logical" ...

See Also

`[<--methods` for sub*assign*ment to `"Matrix"` objects. `Extract` about the standard extraction.

Examples

```
str(m <- Matrix(round(rnorm(7*4),2), nrow = 7))
stopifnot(identical(m, m[]))
m[2, 3]   # simple number
m[2, 3:4] # simple numeric of length 2
m[2, 3:4, drop=FALSE] # sub matrix of class 'dgeMatrix'
## rows or columns only:
m[1,]     # first row, as simple numeric vector
m[,1:2]   # sub matrix of first two columns

showMethods("[", inherited = FALSE)
```

symmetricMatrix-class *Virtual Class of Symmetric Matrices in Package Matrix*

Description

The virtual class of symmetric matrices, `"symmetricMatrix"`, from the package **Matrix** contains numeric and logical, dense and sparse matrices, e.g., see the examples with the "actual" subclasses.

The main use is in methods (and C functions) that can deal with all symmetric matrices, and in `as(*, "symmetricMatrix")`.

Slots

`Dim`, `Dimnames` inherited from virtual class `Matrix`. See comments below about symmetry of `Dimnames`.

`factors` a list of `MatrixFactorization` objects caching factorizations of the matrix. Typically, it is initialized as an empty list and updated "automagically" whenever a factorization is computed.

`uplo` a character string, either `"U"` or `"L"` indicating that only entries in the upper or lower triangle are referenced.

Extends

Class `"Matrix"`, directly.

Methods

dimnames `signature(object = "symmetricMatrix")`: returns *symmetric* `dimnames`, even when the `Dimnames` slot only has row or column names. This allows to save storage for large (typically sparse) symmetric matrices.

isSymmetric `signature(object = "symmetricMatrix")`: returns `TRUE` trivially.

There's a C function `symmetricMatrix_validate()` called by the internal validity checking functions, and also from `getValidity(getClass("symmetricMatrix"))`.

Validity and `dimnames`

The validity checks do not require a symmetric `Dimnames` slot, so it can be `list(NULL, <character>)`, e.g., for efficiency. However, `dimnames()` and other functions and methods should behave as if the dimnames were symmetric, i.e., with both list components identical.

See Also

`isSymmetric` which has efficient methods (isSymmetric-methods) for the **Matrix** classes. Classes `triangularMatrix`, and, e.g., `dsyMatrix` for numeric *dense* matrices, or `lsCMatrix` for a logical *sparse* matrix class.

Examples

```
## An example about the symmetric Dimnames:
sy <- sparseMatrix(i= c(2,4,3:5), j= c(4,7:5,5), x = 1:5, dims = c(7,7),
                   symmetric=TRUE, dimnames = list(NULL, letters[1:7]))
sy # shows symmetrical dimnames
sy@Dimnames  # internally only one part is stored
dimnames(sy) # both parts - as sy *is* symmetrical

showClass("symmetricMatrix")

## The names of direct subclasses:
scl <- getClass("symmetricMatrix")@subclasses
directly <- sapply(lapply(scl, slot, "by"), length) == 0
names(scl)[directly]
```

```
## Methods -- applicaple to all subclasses above:
showMethods(classes = "symmetricMatrix")
```

---

symmpart-methods *Symmetric Part and Skew(symmetric) Part of a Matrix*

Description

symmpart(x) computes the symmetric part (x + t(x))/2 and skewpart(x) the skew symmetric part (x - t(x))/2 of a square matrix x, more efficiently for specific Matrix classes.

Note that x == symmpart(x) + skewpart(x) for all square matrices – apart from extraneous NA values in the RHS.

Usage

```
symmpart(x)
skewpart(x)
```

Arguments

x	a *square* matrix; either "traditional" of class "matrix", or typically, inheriting from the Matrix class.

Details

These are generic functions with several methods for different matrix classes, use e.g., showMethods(symmpart) to see them.

If the row and column names differ, the result will use the column names unless they are (partly) NULL where the row names are non-NULL (see also the examples).

Value

symmpart(x) returns a symmetric matrix, inheriting from symmetricMatrix or diagonalMatrix if x inherits from Matrix.

skewpart(x) returns a skew-symmetric matrix, inheriting from generalMatrix, symmetricMatrix or diagonalMatrix if x inherits from Matrix.

See Also

isSymmetric.

Examples

```
m <- Matrix(1:4, 2,2)
symmpart(m)
skewpart(m)

stopifnot(all(m == symmpart(m) + skewpart(m)))

dn <- dimnames(m) <- list(row = c("r1", "r2"), col = c("var.1", "var.2"))
stopifnot(all(m == symmpart(m) + skewpart(m)))
colnames(m) <- NULL
stopifnot(all(m == symmpart(m) + skewpart(m)))
dimnames(m) <- unname(dn)
stopifnot(all(m == symmpart(m) + skewpart(m)))


## investigate the current methods:
showMethods(skewpart, include = TRUE)
```

---

triangularMatrix-class

Virtual Class of Triangular Matrices in Package Matrix

Description

The virtual class of triangular matrices,"triangularMatrix", the package **Matrix** contains *square* (nrow == ncol) numeric and logical, dense and sparse matrices, e.g., see the examples. A main use of the virtual class is in methods (and C functions) that can deal with all triangular matrices.

Slots

uplo: String (of class "character"). Must be either "U", for upper triangular, and "L", for lower triangular.

diag: String (of class "character"). Must be either "U", for unit triangular (diagonal is all ones), or "N" for non-unit. The diagonal elements are not accessed internally when diag is "U". For denseMatrix classes, they need to be allocated though, such that the length of the x slot does not depend on diag.

Dim, Dimnames: The dimension (a length-2 "integer") and corresponding names (or NULL), inherited from the Matrix, see there.

Extends

Class "Matrix", directly.

Methods

There's a C function triangularMatrix_validity() called by the internal validity checking functions.

Currently, Schur, isSymmetric and as() (i.e. coerce) have methods with triangularMatrix in their signature.

See Also

isTriangular() for testing any matrix for triangularity; classes symmetricMatrix, and, e.g., dtrMatrix for numeric *dense* matrices, or ltCMatrix for a logical *sparse* matrix subclass of "triangularMatrix".

Examples

```
showClass("triangularMatrix")

## The names of direct subclasses:
scl <- getClass("triangularMatrix")@subclasses
directly <- sapply(lapply(scl, slot, "by"), length) == 0
names(scl)[directly]

(m <- matrix(c(5,1,0,3), 2))
as(m, "triangularMatrix")
```

TsparseMatrix-class *Class "TsparseMatrix" of Sparse Matrices in Triplet Form*

Description

The "TsparseMatrix" class is the virtual class of all sparse matrices coded in triplet form. Since it is a virtual class, no objects may be created from it. See showClass("TsparseMatrix") for its subclasses.

Slots

Dim, Dimnames: from the "Matrix" class,

i: Object of class "integer" - the row indices of non-zero entries *in 0-base*, i.e., must be in 0:(nrow(.)-1).

j: Object of class "integer" - the column indices of non-zero entries. Must be the same length as slot i and *0-based* as well, i.e., in 0:(ncol(.)-1). For numeric Tsparse matrices, (i,j) pairs can occur more than once, see dgTMatrix.

Extends

Class "sparseMatrix", directly. Class "Matrix", by class "sparseMatrix".

Methods

Extraction ("[") methods, see [-methods.

Note

Most operations with sparse matrices are performed using the compressed, column-oriented or CsparseMatrix representation. The triplet representation is convenient for creating a sparse matrix or for reading and writing such matrices. Once it is created, however, the matrix is generally coerced to a CsparseMatrix for further operations.

Note that all new(.), spMatrix and sparseMatrix(*, repr="T") constructors for "TsparseMatrix" classes implicitly add (i.e., "sum up") x_k's that belong to identical (i_k, j_k) pairs, see, the example below, or also "dgTMatrix".

For convenience, methods for some operations such as %*% and crossprod are defined for TsparseMatrix objects. These methods simply coerce the TsparseMatrix object to a CsparseMatrix object then perform the operation.

See Also

its superclass, sparseMatrix, and the dgTMatrix class, for the links to other classes.

Examples

```
showClass("TsparseMatrix")
## or just the subclasses' names
names(getClass("TsparseMatrix")@subclasses)

T3 <- spMatrix(3,4, i=c(1,3:1), j=c(2,4:2), x=1:4)
T3 # only 3 non-zero entries, 5 = 1+4 !
```

---

unpackedMatrix-class *Virtual Class* "unpackedMatrix" *of Unpacked Dense Matrices*

Description

Class "unpackedMatrix" is the *virtual* class of dense matrices in "unpacked" format, storing all m*n elements of an m-by-n matrix. It is used to define common methods for efficient subsetting, transposing, etc. of its *proper* subclasses: currently "[dln]geMatrix" (unpacked general), "[dln]syMatrix" (unpacked symmetric), "[dln]trMatrix" (unpacked triangular), and subclasses of these, such as "dpoMatrix".

Slots

Dim, Dimnames: as all Matrix objects.

Extends

Class "denseMatrix", directly. Class "Matrix", by class "denseMatrix", distance 2.

Methods

pack `signature(x = "unpackedMatrix")`: ...

unpack `signature(x = "unpackedMatrix")`: ...

isSymmetric `signature(object = "unpackedMatrix")`: ...

isTriangular `signature(object = "unpackedMatrix")`: ...

isDiagonal `signature(object = "unpackedMatrix")`: ...

t `signature(x = "unpackedMatrix")`: ...

diag `signature(x = "unpackedMatrix")`: ...

diag<- `signature(x = "unpackedMatrix")`: ...

Author(s)

Mikael Jagan

See Also

pack and unpack; its virtual "complement" "packedMatrix"; its proper subclasses "dsyMatrix", "ltrMatrix", etc.

Examples

```
showClass("unpackedMatrix")
showMethods(classes = "unpackedMatrix")
```

---

updown-methods *Updating and Downdating Sparse Cholesky Factorizations*

Description

Computes a rank-k update or downdate of a sparse Cholesky factorization

$$P_1 A P_1' = L_1 D L_1' = L L'$$

which for some k-column matrix C is the factorization

$$P_1 (A + sCC') P_1' = \tilde{L}_1 \tilde{D} \tilde{L}_1' = \tilde{L} \tilde{L}'$$

Here, $s = 1$ for an update and $s = -1$ for a downdate.

Usage

```
updown(update, C, L)
```

Arguments

update	a logical (TRUE or FALSE) or character ("+" or "-") indicating if L should be updated (or otherwise downdated).
C	a finite matrix or Matrix such that tcrossprod(C) has the dimensions of L.
L	an object of class dCHMsimpl or dCHMsuper specifying a sparse Cholesky factorization.

Value

A sparse Cholesky factorization with dimensions matching L, typically of class dCHMsimpl.

Author(s)

Initial implementation by Nicholas Nagle, University of Tennessee.

References

Davis, T. A., Hager, W. W. (2001). Multiple-rank modifications of a sparse Cholesky factorization. *SIAM Journal on Matrix Analysis and Applications*, *22*(4), 997-1013. doi:10.1137/S0895479899357346

See Also

Classes dCHMsimpl and dCHMsuper and their methods, notably for generic function update, which is *not* equivalent to updown(update = TRUE).

Generic function Cholesky.

Examples

```
m <- sparseMatrix(i = c(3, 1, 3:2, 2:1), p = c(0:2, 4, 4, 6), x = 1:6,
                  dimnames = list(LETTERS[1:3], letters[1:5]))
uc0 <- Cholesky(A <- crossprod(m) + Diagonal(5))
uc1 <- updown("+", Diagonal(5, 1), uc0)
uc2 <- updown("-", Diagonal(5, 1), uc1)
stopifnot(all.equal(uc0, uc2))
```

USCounties *Contiguity Matrix of U.S. Counties*

Description

This matrix gives the contiguities of 3111 U.S. counties, using the queen criterion of at least one shared vertex or edge.

Usage

```
data(USCounties)
```

Format

A 3111 × 3111 sparse, symmetric matrix of class dsCMatrix, with 9101 nonzero entries.

Source

GAL lattice file 'usc_q.GAL' (retrieved in 2008 from 'http://sal.uiuc.edu/weights/zips/usc.zip' with permission from Luc Anselin for use and distribution) was read into R using function read.gal from package **spdep**.

Neighbour lists were augmented with row-standardized (and then symmetrized) spatial weights, using functions nb2listw and similar.listw from packages **spdep** and **spatialreg**. The resulting listw object was coerced to class dsTMatrix using as_dsTMatrix_listw from **spatialreg**, and subsequently to class dsCMatrix.

References

Ord, J. K. (1975). Estimation methods for models of spatial interaction. *Journal of the American Statistical Association*, *70*(349), 120-126. doi:10.2307/2285387

Examples

```
data(UScounties, package = "Matrix")
(n <- ncol(UScounties))
I <- .symDiagonal(n)

set.seed(1)
r <- 50L
rho <- 1 / runif(r, 0, 0.5)

system.time(MJ0 <- sapply(rho, function(mult)
    determinant(UScounties + mult * I, logarithm = TRUE)$modulus))

## Can be done faster by updating the Cholesky factor:

C1 <- Cholesky(UScounties, Imult = 2)
system.time(MJ1 <- sapply(rho, function(mult)
    determinant(update(C1, UScounties, mult), sqrt = FALSE)$modulus))
stopifnot(all.equal(MJ0, MJ1))

C2 <- Cholesky(UScounties, super = TRUE, Imult = 2)
system.time(MJ2 <- sapply(rho, function(mult)
    determinant(update(C2, UScounties, mult), sqrt = FALSE)$modulus))
stopifnot(all.equal(MJ0, MJ2))
```

---

wrld_1deg *Contiguity Matrix of World One-Degree Grid Cells*

Description

This matrix gives the contiguities of 15260 one-degree grid cells of world land areas, using a criterion based on the great-circle distance between centers.

Usage

```
data(wrld_1deg)
```

Format

A 15260×15260 sparse, symmetric matrix of class `dsCMatrix`, with 55973 nonzero entries.

Source

Shoreline data were read into R from the GSHHS database using function `Rgshhs` from package **maptools**. Antarctica was excluded. An approximately one-degree grid was generated using function `Sobj_SpatialGrid`, also from **maptools**. Grid cells with centers on land were identified using the `over` method for classes `SpatialPolygons` and `SpatialGrid`, defined in package **sp**. Neighbours of these were identified by passing the resulting `SpatialPixels` object to function `dnearneigh` from package **spdep**, using as a cut-off a great-circle distance of `sqrt(2)` kilometers between centers.

Neighbour lists were augmented with row-standardized (and then symmetrized) spatial weights, using functions `nb2listw` and `similar.listw` from packages **spdep** and **spatialreg**. The resulting `listw` object was coerced to class `dsTMatrix` using `as_dsTMatrix_listw` from **spatialreg**, and subsequently to class `dsCMatrix`.

References

Ord, J. K. (1975). Estimation methods for models of spatial interaction. *Journal of the American Statistical Association*, *70*(349), 120-126. doi:10.2307/2285387

Examples

```
data(wrld_1deg, package = "Matrix")
(n <- ncol(wrld_1deg))
I <- .symDiagonal(n)

doExtras <- interactive() || nzchar(Sys.getenv("R_MATRIX_CHECK_EXTRA"))
set.seed(1)
r <- if(doExtras) 20L else 3L
rho <- 1 / runif(r, 0, 0.5)

system.time(MJ0 <- sapply(rho, function(mult)
    determinant(wrld_1deg + mult * I, logarithm = TRUE)$modulus))

## Can be done faster by updating the Cholesky factor:

C1 <- Cholesky(wrld_1deg, Imult = 2)
system.time(MJ1 <- sapply(rho, function(mult)
    determinant(update(C1, wrld_1deg, mult), sqrt = FALSE)$modulus))
```

```
stopifnot(all.equal(MJ0, MJ1))

C2 <- Cholesky(wrld_1deg, super = TRUE, Imult = 2)
system.time(MJ2 <- sapply(rho, function(mult)
    determinant(update(C2, wrld_1deg, mult), sqrt = FALSE)$modulus))
stopifnot(all.equal(MJ0, MJ2))
```

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