

Package ‘matrixStats’

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Title Functions that Apply to Rows and Columns of Matrices (and to Vectors)

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Description High-performing functions operating on rows and columns of matrices, e.g. col / rowMedians(), col / rowRanks(), and col / rowSds(). Functions optimized per data type and for subsetted calculations such that both memory usage and processing time is minimized. There are also optimized vector-based methods, e.g. binMeans(), madDiff() and weightedMedian().

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matrixStats-package *Package matrixStats*

Description

High-performing functions operating on rows and columns of matrices, e.g. `col / rowMedians()`, `col / rowRanks()`, and `col / rowSds()`. Functions optimized per data type and for subsetting calculations such that both memory usage and processing time is minimized. There are also optimized vector-based methods, e.g. `binMeans()`, `madDiff()` and `weightedMedian()`.

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Author(s)

Henrik Bengtsson, Hector Corrada Bravo, Robert Gentleman, Ola Hossjer, Harris Jaffee, Dongcan Jiang, Peter Langfelder

`anyMissing` *Checks if there are any missing values in an object or not*

Description

Checks if there are any missing values in an object or not. *Please use `base::anyNA()` instead of `anyMissing()`, `colAnyNAs()` instead of `colAnyMissings()`, and `rowAnyNAs()` instead of `rowAnyMissings()`.*

Usage

```
anyMissing(x, idxs = NULL, ...)
```

```
colAnyMissings(x, rows = NULL, cols = NULL, ..., useNames = NA)
```

```
rowAnyMissings(x, rows = NULL, cols = NULL, ..., useNames = NA)
```

```
colAnyNAs(x, rows = NULL, cols = NULL, ..., useNames = NA)
```

```
rowAnyNAs(x, rows = NULL, cols = NULL, ..., useNames = NA)
```

Arguments

x	A vector , a list , a matrix , a data.frame , or NULL .
idxs	A vector indicating subset of elements to operate over. If NULL , no subsetting is done.
...	Not used.
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.

Details

The implementation of this method is optimized for both speed and memory. The method will return [TRUE](#) as soon as a missing value is detected.

Value

Returns [TRUE](#) if a missing value was detected, otherwise [FALSE](#).

Author(s)

Henrik Bengtsson

See Also

Starting with R v3.1.0, there is `anyNA()` in the **base**, which provides the same functionality as `anyMissing()`.

Examples

```
x <- rnorm(n = 1000)
x[seq(300, length(x), by = 100)] <- NA
stopifnot(anyMissing(x) == any(is.na(x)))
```

`binCounts`*Fast element counting in non-overlapping bins*

Description

Counts the number of elements in non-overlapping bins

Usage

```
binCounts(x, idxs = NULL, bx, right = FALSE, ...)
```

Arguments

<code>x</code>	A numeric vector of K positions for to be binned and counted.
<code>idxs</code>	A vector indicating subset of elements to operate over. If <code>NULL</code> , no subsetting is done.
<code>bx</code>	A numeric vector of $B + 1$ ordered positions specifying the $B > 0$ bins $[bx[1], bx[2])$, $[bx[2], bx[3])$, ..., $[bx[B], bx[B + 1])$.
<code>right</code>	If <code>TRUE</code> , the bins are right-closed (left open), otherwise left-closed (right open).
<code>...</code>	Not used.

Details

`binCounts(x, bx, right = TRUE)` gives equivalent results as `rev(binCounts(-x, bx = rev(-bx), right = FALSE))`, but is faster and more memory efficient.

Value

Returns an [integer vector](#) of length B with non-negative integers.

Missing and non-finite values

Missing values in `x` are ignored/dropped. Missing values in `bx` are not allowed and gives an error.

Author(s)

Henrik Bengtsson

See Also

An alternative for counting occurrences within bins is [hist](#), e.g. `hist(x, breaks = bx, plot = FALSE)$counts`. That approach is ~30-60% slower than `binCounts(..., right = TRUE)`.

To count occurrences of indices `x` (positive [integers](#)) in $[1, B]$, use `tabulate(x, nbins = B)`, where `x` does *not* have to be sorted first. For details, see [tabulate\(\)](#).

To average values within bins, see [binMeans\(\)](#).

binMeans

*Fast mean calculations in non-overlapping bins***Description**

Computes the sample means in non-overlapping bins

Usage

```
binMeans(y, x, idxs = NULL, bx, na.rm = TRUE, count = TRUE, right = FALSE, ...)
```

Arguments

y	A numeric or logical vector of K values to calculate means on.
x	A numeric vector of K positions for to be binned.
idxs	A vector indicating subset of elements to operate over. If NULL , no subsetting is done.
bx	A numeric vector of B + 1 ordered positions specifying the B > 0 bins [bx[1],bx[2]], [bx[2],bx[3]), ..., [bx[B],bx[B + 1]].
na.rm	If TRUE , missing values in y are dropped before calculating the mean, otherwise not.
count	If TRUE , the number of data points in each bins is returned as attribute count, which is an integer vector of length B.
right	If TRUE , the bins are right-closed (left open), otherwise left-closed (right open).
...	Not used.

Details

binMeans(x,bx,right = TRUE) gives equivalent results as rev(binMeans(-x,bx = sort(-bx),right = FALSE)), but is faster.

Value

Returns a [numeric vector](#) of length B.

Missing and non-finite values

Data points where either of y and x is missing are dropped (and therefore are also not counted). Non-finite values in y are not allowed and gives an error. Missing values in bx are not allowed and gives an error.

Author(s)

Henrik Bengtsson with initial code contributions by Martin Morgan [1].

References

[1] R-devel thread *Fastest non-overlapping binning mean function out there?* on Oct 3, 2012

See Also

[binCounts\(\)](#), [aggregate](#) and [mean\(\)](#).

Examples

```
x <- 1:200
mu <- double(length(x))
mu[1:50] <- 5
mu[101:150] <- -5
y <- mu + rnorm(length(x))

# Binning
bx <- c(0, 50, 100, 150, 200) + 0.5
y_s <- binMeans(y, x = x, bx = bx)

plot(x, y)
for (kk in seq_along(y_s)) {
  lines(bx[c(kk, kk + 1)], y_s[c(kk, kk)], col = "blue", lwd = 2)
}
```

indexByRow

Translates matrix indices by rows into indices by columns

Description

Translates matrix indices by rows into indices by columns.

Usage

```
indexByRow(dim, idxs = NULL, ...)
```

Arguments

dim	A numeric vector of length two specifying the length of the "template" matrix.
idxs	A vector indicating subset of elements to operate over. If NULL , no subsetting is done.
...	Not used.

Value

Returns an [integer vector](#) of indices.

Known limitations

The current implementation does not support long-vector indices, because both input and output indices are of type integers. This means that the indices in argument `idxs` can only be in range $[1, 2^{31}-1]$. Using a greater value will be coerced to `NA_integer_`. Moreover, returned indices can only be in the same range $[1, 2^{31}-1]$.

Author(s)

Henrik Bengtsson

Examples

```
dim <- c(5, 4)
X <- matrix(NA_integer_, nrow = dim[1], ncol = dim[2])
Y <- t(X)
idxs <- seq_along(X)

# Assign by columns
X[idxs] <- idxs
print(X)

# Assign by rows
Y[indexByRow(dim(Y), idxs)] <- idxs
print(Y)

stopifnot(X == t(Y))
```

logSumExp

Accurately computes the logarithm of the sum of exponentials

Description

Accurately computes the logarithm of the sum of exponentials, that is, $\log(\text{sum}(\exp(lx)))$. If $lx = \log(x)$, then this is equivalently to calculating $\log(\text{sum}(x))$.

Usage

```
logSumExp(lx, idxs = NULL, na.rm = FALSE, ...)
```

Arguments

<code>lx</code>	A numeric vector . Typically <code>lx</code> are $\log(x)$ values.
<code>idxs</code>	A vector indicating subset of elements to operate over. If <code>NULL</code> , no subsetting is done.
<code>na.rm</code>	If <code>TRUE</code> , missing values are excluded.
<code>...</code>	Not used.

Details

This function, which avoid numerical underflow, is often used when computing the logarithm of the sum of small numbers ($|x| \ll 1$) such as probabilities.

This function is more accurate than $\log(\text{sum}(\exp(\mathbf{1x})))$ when the values of $x = \exp(\mathbf{1x})$ are $|x| \ll 1$. The implementation of this function is based on the observation that

$$\log(a + b) = [\mathbf{la} = \log(a), \mathbf{lb} = \log(b)] = \log(\exp(\mathbf{la}) + \exp(\mathbf{lb})) = \mathbf{la} + \log(1 + \exp(\mathbf{lb} - \mathbf{la}))$$

Assuming $\mathbf{la} > \mathbf{lb}$, then $|\mathbf{lb} - \mathbf{la}| < |\mathbf{lb}|$, and it is less likely that the computation of $1 + \exp(\mathbf{lb} - \mathbf{la})$ will not underflow/overflow numerically. Because of this, the overall result from this function should be more accurate. Analogously to this, the implementation of this function finds the maximum value of $\mathbf{1x}$ and subtracts it from the remaining values in $\mathbf{1x}$.

Value

Returns a `numeric` scalar.

Benchmarking

This method is optimized for correctness, that avoiding underflowing. It is implemented in native code that is optimized for speed and memory.

Author(s)

Henrik Bengtsson

References

- [1] R Core Team, *Writing R Extensions*, v3.0.0, April 2013.
- [2] Laurent El Ghaoui, *Hyper-Textbook: Optimization Models and Applications*, University of California at Berkeley, August 2012. (Chapter 'Log-Sum-Exp (LSE) Function and Properties')
- [3] R-help thread *logsumexp function in R*, 2011-02-17. <https://stat.ethz.ch/pipermail/r-help/2011-February/269205.html>

See Also

To compute this function on rows or columns of a matrix, see `rowLogSumExps()`.

For adding *two* double values in native code, R provides the C function `logspace_add()` [1]. For properties of the log-sum-exponential function, see [2].

Examples

```
## EXAMPLE #1
lx <- c(1000.01, 1000.02)
y0 <- log(sum(exp(lx)))
print(y0) ## Inf

y1 <- logSumExp(lx)
print(y1) ## 1000.708
```

```
## EXAMPLE #2
lx <- c(-1000.01, -1000.02)
y0 <- log(sum(exp(lx)))
print(y0) ## -Inf

y1 <- logSumExp(lx)
print(y1) ## -999.3218

## EXAMPLE #3
## R-help thread 'Beyond double-precision?' on May 9, 2009.

set.seed(1)
x <- runif(50)

## The logarithm of the harmonic mean
y0 <- log(1 / mean(1 / x))
print(y0) ## -1.600885

lx <- log(x)
y1 <- log(length(x)) - logSumExp(-lx)
print(y1) ## [1] -1.600885

# Sanity check
stopifnot(all.equal(y1, y0))
```

product

Calculates the product for each row (column) in a matrix

Description

Calculates the product for each row (column) in a matrix.

Usage

```
product(x, idxs = NULL, na.rm = FALSE, ...)

rowProds(x, rows = NULL, cols = NULL, na.rm = FALSE,
  method = c("direct", "expSumLog"), ..., useNames = NA)

colProds(x, rows = NULL, cols = NULL, na.rm = FALSE,
  method = c("direct", "expSumLog"), ..., useNames = NA)
```

Arguments

`x` An $N \times K$ [matrix](#) or, if `dim.` is specified, an $N * K$ [vector](#).

idxs	A vector indicating subset of elements to operate over. If NULL , no subsetting is done.
na.rm	If TRUE , missing values are excluded.
...	Not used.
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
method	A character string specifying how each product is calculated.
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.

Details

If `method = "expSumLog"`, then then [product\(\)](#) function is used, which calculates the product via the logarithmic transform (treating negative values specially). This improves the precision and lowers the risk for numeric overflow. If `method = "direct"`, the direct product is calculated via the [prod\(\)](#) function.

Value

Returns a [numeric vector](#) of length $N(K)$.

Missing values

Note, if `method = "expSumLog"`, `na.rm = FALSE`, and `x` contains missing values ([NA](#) or [NaN](#)), then the calculated value is also missing value. Note that it depends on platform whether [NaN](#) or [NA](#) is returned when an [NaN](#) exists, cf. [is.nan\(\)](#).

Author(s)

Henrik Bengtsson

rowAlls	<i>Checks if a value exists / does not exist in each row (column) of a matrix</i>
---------	---

Description

Checks if a value exists / does not exist in each row (column) of a matrix.

Usage

```
rowAlls(x, rows = NULL, cols = NULL, value = TRUE, na.rm = FALSE,
        dim. = dim(x), ..., useNames = NA)
```

```
colAlls(x, rows = NULL, cols = NULL, value = TRUE, na.rm = FALSE,
        dim. = dim(x), ..., useNames = NA)
```

```
allValue(x, idxs = NULL, value = TRUE, na.rm = FALSE, ...)
```

```
rowAnys(x, rows = NULL, cols = NULL, value = TRUE, na.rm = FALSE,
        dim. = dim(x), ..., useNames = NA)
```

```
colAnys(x, rows = NULL, cols = NULL, value = TRUE, na.rm = FALSE,
        dim. = dim(x), ..., useNames = NA)
```

```
anyValue(x, idxs = NULL, value = TRUE, na.rm = FALSE, ...)
```

Arguments

x	An NxK matrix or, if <code>dim.</code> is specified, an N * K vector .
rows	A vector indicating subset of rows to operate over. If <code>NULL</code> , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If <code>NULL</code> , no subsetting is done.
value	A value to search for.
na.rm	If <code>TRUE</code> , missing values are excluded.
dim.	An integer vector of length two specifying the dimension of x, also when not a matrix . <i>Comment:</i> The reason for this argument being named with a period at the end is purely technical (we get a run-time error if we try to name it <code>dim</code>).
...	Not used.
useNames	If <code>NA</code> , the default behavior of the function about naming support is remained. If <code>FALSE</code> , no naming support is done. Else if <code>TRUE</code> , names attributes of result are set.
idxs	A vector indicating subset of elements to operate over. If <code>NULL</code> , no subsetting is done.

Details

These functions takes either a matrix or a vector as input. If a vector, then argument `dim.` must be specified and fulfill `prod(dim.) == length(x)`. The result will be identical to the results obtained when passing `matrix(x, nrow = dim.[1L], ncol = dim.[2L])`, but avoids having to temporarily create/allocate a matrix, if only such is needed only for these calculations.

Value

`rowAlls()` (`colAlls()`) returns an [logical vector](#) of length N (K). Analogously for `rowAnys()` (`rowAlls()`).

Logical value

When value is logical, the result is as if the function is applied on `as.logical(x)`. More specifically, if `x` is numeric, then all zeros are treated as FALSE, non-zero values as TRUE, and all missing values as NA.

Author(s)

Henrik Bengtsson

See Also

rowCounts

Examples

```
x <- matrix(FALSE, nrow = 10, ncol = 5)
x[3:7, c(2, 4)] <- TRUE
x[2:4, ] <- TRUE
x[, 1] <- TRUE
x[5, ] <- FALSE
x[, 5] <- FALSE
print(x)

print(rowCounts(x))      # 1 4 4 4 0 3 3 1 1 1
print(colCounts(x))     # 9 5 3 5 0

print(rowAnys(x))
print(which(rowAnys(x))) # 1 2 3 4 6 7 8 9 10
print(colAnys(x))
print(which(colAnys(x))) # 1 2 3 4
```

rowCollapse

Extracts one cell per row (column) from a matrix

Description

Extracts one cell per row (column) from a matrix. The implementation is optimized for memory and speed.

Usage

```
rowCollapse(x, idxs, rows = NULL, dim. = dim(x), ..., useNames = NA)
```

```
colCollapse(x, idxs, cols = NULL, dim. = dim(x), ..., useNames = NA)
```

Arguments

x	An NxK matrix or, if dim. is specified, an N * K vector .
idxs	An index vector of (maximum) length N (K) specifying the columns (rows) to be extracted.
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
dim.	An integer vector of length two specifying the dimension of x, also when not a matrix . <i>Comment:</i> The reason for this argument being named with a period at the end is purely technical (we get a run-time error if we try to name it dim).
...	Not used.
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.

Value

Returns a **vector** of length N (K).

Author(s)

Henrik Bengtsson

See Also

Matrix indexing to index elements in matrices and arrays, cf. `[]()`.

Examples

```
x <- matrix(1:27, ncol = 3)

y <- rowCollapse(x, 1)
stopifnot(identical(y, x[, 1]))

y <- rowCollapse(x, 2)
stopifnot(identical(y, x[, 2]))

y <- rowCollapse(x, c(1, 1, 1, 1, 1, 3, 3, 3, 3))
stopifnot(identical(y, c(x[1:5, 1], x[6:9, 3])))

y <- rowCollapse(x, 1:3)
print(y)
y_truth <- c(x[1, 1], x[2, 2], x[3, 3], x[4, 1], x[5, 2],
             x[6, 3], x[7, 1], x[8, 2], x[9, 3])
stopifnot(identical(y, y_truth))
```

rowCounts	<i>Counts the number of occurrences of a specific value</i>
-----------	---

Description

The row- and column-wise functions take either a matrix or a vector as input. If a vector, then argument `dim.` must be specified and fulfill `prod(dim.) == length(x)`. The result will be identical to the results obtained when passing `matrix(x, nrow = dim.[1L], ncol = dim.[2L])`, but avoids having to temporarily create/allocate a matrix, if only such is needed only for these calculations.

Usage

```
rowCounts(x, rows = NULL, cols = NULL, value = TRUE, na.rm = FALSE,
          dim. = dim(x), ..., useNames = NA)
```

```
colCounts(x, rows = NULL, cols = NULL, value = TRUE, na.rm = FALSE,
          dim. = dim(x), ..., useNames = NA)
```

```
count(x, idxs = NULL, value = TRUE, na.rm = FALSE, ...)
```

Arguments

<code>x</code>	An <code>NxK matrix</code> or, if <code>dim.</code> is specified, an <code>N * K vector</code> .
<code>rows</code>	A <code>vector</code> indicating subset of rows to operate over. If <code>NULL</code> , no subsetting is done.
<code>cols</code>	A <code>vector</code> indicating subset of columns to operate over. If <code>NULL</code> , no subsetting is done.
<code>value</code>	A value to search for.
<code>na.rm</code>	If <code>TRUE</code> , missing values are excluded.
<code>dim.</code>	An <code>integer vector</code> of length two specifying the dimension of <code>x</code> , also when not a <code>matrix</code> . <i>Comment:</i> The reason for this argument being named with a period at the end is purely technical (we get a run-time error if we try to name it <code>dim</code>).
<code>...</code>	Not used.
<code>useNames</code>	If <code>NA</code> , the default behavior of the function about naming support is remained. If <code>FALSE</code> , no naming support is done. Else if <code>TRUE</code> , names attributes of result are set.
<code>idxs</code>	A <code>vector</code> indicating subset of elements to operate over. If <code>NULL</code> , no subsetting is done.

Value

`rowCounts()` (`colCounts()`) returns an `integer vector` of length `N` (`K`). `count()` returns a scalar of type `integer` if the count is less than $2^{31}-1$ (`= .Machine$integer.max`) otherwise a scalar of type `double`.

Author(s)

Henrik Bengtsson

See Also

rowAlls

Examples

```
x <- matrix(0:11, nrow = 4, ncol = 3)
x[2:3, 2:3] <- 2:5
x[3, 3] <- NA_integer_
print(x)

print(rowCounts(x, value = 2))
## [1] 0 1 NA 0
print(colCounts(x, value = 2))
## [1] 1 1 NA
print(colCounts(x, value = NA_integer_))
## [1] 0 0 1

print(rowCounts(x, value = 2, na.rm = TRUE))
## [1] 0 1 1 0
print(colCounts(x, value = 2, na.rm = TRUE))
## [1] 1 1 0

print(rowAnys(x, value = 2))
## [1] FALSE TRUE TRUE FALSE
print(rowAnys(x, value = NA_integer_))
## [1] FALSE FALSE TRUE FALSE

print(colAnys(x, value = 2))
## [1] TRUE TRUE NA
print(colAnys(x, value = 2, na.rm = TRUE))
## [1] TRUE TRUE FALSE

print(colAlls(x, value = 2))
## [1] FALSE FALSE FALSE
```

rowCumsums

Cumulative sums, products, minima and maxima for each row (column) in a matrix

Description

Cumulative sums, products, minima and maxima for each row (column) in a matrix.

Usage

```

rowCumsums(x, rows = NULL, cols = NULL, dim. = dim(x), ..., useNames = NA)
colCumsums(x, rows = NULL, cols = NULL, dim. = dim(x), ..., useNames = NA)
rowCumprods(x, rows = NULL, cols = NULL, dim. = dim(x), ..., useNames = NA)
colCumprods(x, rows = NULL, cols = NULL, dim. = dim(x), ..., useNames = NA)
rowCummins(x, rows = NULL, cols = NULL, dim. = dim(x), ..., useNames = NA)
colCummins(x, rows = NULL, cols = NULL, dim. = dim(x), ..., useNames = NA)
rowCummaxs(x, rows = NULL, cols = NULL, dim. = dim(x), ..., useNames = NA)
colCummaxs(x, rows = NULL, cols = NULL, dim. = dim(x), ..., useNames = NA)

```

Arguments

x	An NxK matrix or, if dim. is specified, an N * K vector .
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
dim.	An integer vector of length two specifying the dimension of x, also when not a matrix . <i>Comment:</i> The reason for this argument being named with a period at the end is purely technical (we get a run-time error if we try to name it dim).
...	Not used.
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.

Value

Returns a **numeric** NxK **matrix** of the same mode as x, except when x is of mode **logical**, then the return type is **integer**.

Author(s)

Henrik Bengtsson

See Also

See [cumsum\(\)](#), [cumprod\(\)](#), [cummin\(\)](#), and [cummax\(\)](#).

Examples

```

x <- matrix(1:12, nrow = 4, ncol = 3)
print(x)

yr <- rowCumsums(x)
print(yr)

yc <- colCumsums(x)
print(yc)

yr <- rowCumprods(x)
print(yr)

yc <- colCumprods(x)
print(yc)

yr <- rowCummaxs(x)
print(yr)

yc <- colCummaxs(x)
print(yc)

yr <- rowCummins(x)
print(yr)

yc <- colCummins(x)
print(yc)

```

rowDiffs

Calculates difference for each row (column) in a matrix

Description

Calculates difference for each row (column) in a matrix.

Usage

```

rowDiffs(x, rows = NULL, cols = NULL, lag = 1L, differences = 1L,
  dim. = dim(x), ..., useNames = NA)

colDiffs(x, rows = NULL, cols = NULL, lag = 1L, differences = 1L,
  dim. = dim(x), ..., useNames = NA)

```

Arguments

x An NxK [matrix](#) or, if `dim.` is specified, an N * K [vector](#).

rows A [vector](#) indicating subset of rows to operate over. If `NULL`, no subsetting is done.

cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
lag	An integer specifying the lag.
differences	An integer specifying the order of difference.
dim.	An integer vector of length two specifying the dimension of <code>x</code> , also when not a matrix . <i>Comment:</i> The reason for this argument being named with a period at the end is purely technical (we get a run-time error if we try to name it <code>dim</code>).
...	Not used.
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.

Value

Returns a [numeric](#) $N \times (K-1)$ or $(N-1) \times K$ [matrix](#).

Author(s)

Henrik Bengtsson

See Also

See also [diff2\(\)](#).

Examples

```
x <- matrix(1:27, ncol = 3)

d1 <- rowDiffs(x)
print(d1)

d2 <- t(colDiffs(t(x)))
stopifnot(all.equal(d2, d1))
```

rowIQRs

Estimates of the interquartile range for each row (column) in a matrix

Description

Estimates of the interquartile range for each row (column) in a matrix.

Usage

```
rowIQRs(x, rows = NULL, cols = NULL, na.rm = FALSE, ..., useNames = NA)

colIQRs(x, rows = NULL, cols = NULL, na.rm = FALSE, ..., useNames = NA)

iqr(x, idxs = NULL, na.rm = FALSE, ...)
```

Arguments

<code>x</code>	An <code>NxK matrix</code> or, if <code>dim.</code> is specified, an <code>N * K vector</code> .
<code>rows</code>	A <code>vector</code> indicating subset of rows to operate over. If <code>NULL</code> , no subsetting is done.
<code>cols</code>	A <code>vector</code> indicating subset of columns to operate over. If <code>NULL</code> , no subsetting is done.
<code>na.rm</code>	If <code>TRUE</code> , missing values are excluded.
<code>...</code>	Additional arguments passed to <code>rowQuantiles()</code> (<code>colQuantiles()</code>).
<code>useNames</code>	If <code>NA</code> , the default behavior of the function about naming support is remained. If <code>FALSE</code> , no naming support is done. Else if <code>TRUE</code> , names attributes of result are set.
<code>idxs</code>	A <code>vector</code> indicating subset of elements to operate over. If <code>NULL</code> , no subsetting is done.

Value

Returns a `numeric vector` of length `N (K)`.

Missing values

Contrary to `IQR`, which gives an error if there are missing values and `na.rm = FALSE`, `iqr()` and its corresponding row and column-specific functions return `NA_real_`.

Author(s)

Henrik Bengtsson

See Also

See `IQR`. See `rowSds()`.

Examples

```
set.seed(1)

x <- matrix(rnorm(50 * 40), nrow = 50, ncol = 40)
str(x)

# Row IQRs
q <- rowIQRs(x)
print(q)
q0 <- apply(x, MARGIN = 1, FUN = IQR)
stopifnot(all.equal(q0, q))

# Column IQRs
q <- colIQRs(x)
print(q)
q0 <- apply(x, MARGIN = 2, FUN = IQR)
stopifnot(all.equal(q0, q))
```

rowLogSumExps	<i>Accurately computes the logarithm of the sum of exponentials across rows or columns</i>
---------------	--

Description

Accurately computes the logarithm of the sum of exponentials across rows or columns.

Usage

```
rowLogSumExps(lx, rows = NULL, cols = NULL, na.rm = FALSE,
  dim. = dim(lx), ..., useNames = NA)
```

```
colLogSumExps(lx, rows = NULL, cols = NULL, na.rm = FALSE,
  dim. = dim(lx), ..., useNames = NA)
```

Arguments

lx	A numeric NxK matrix . Typically lx are $\log(x)$ values.
rows, cols	A vector indicating subset of rows (and/or columns) to operate over. If NULL , no subsetting is done.
na.rm	If TRUE , any missing values are ignored, otherwise not.
dim.	An integer vector of length two specifying the dimension of x, also when not a matrix .
...	Not used.
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.

Value

A **numeric vector** of length N (K).

Benchmarking

These methods are implemented in native code and have been optimized for speed and memory.

Author(s)

Native implementation by Henrik Bengtsson. Original R code by Nakayama ??? (Japan).

See Also

To calculate the same on vectors, [logSumExp\(\)](#).

rowMads

*Standard deviation estimates for each row (column) in a matrix***Description**

Standard deviation estimates for each row (column) in a matrix.

Usage

```
rowMads(x, rows = NULL, cols = NULL, center = NULL, constant = 1.4826,
        na.rm = FALSE, dim. = dim(x), ..., useNames = NA)
```

```
colMads(x, rows = NULL, cols = NULL, center = NULL, constant = 1.4826,
        na.rm = FALSE, dim. = dim(x), ..., useNames = NA)
```

```
rowSds(x, rows = NULL, cols = NULL, na.rm = FALSE, center = NULL,
        dim. = dim(x), ..., useNames = NA)
```

```
colSds(x, rows = NULL, cols = NULL, na.rm = FALSE, center = NULL,
        dim. = dim(x), ..., useNames = NA)
```

Arguments

x	An NxK matrix or, if dim. is specified, an N * K vector .
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
center	(optional) The center, defaults to the row means for the SD estimators and row medians for the MAD estimators.
constant	A scale factor. See mad for details.
na.rm	If TRUE , missing values are excluded.
dim.	An integer vector of length two specifying the dimension of x, also when not a matrix . <i>Comment:</i> The reason for this argument being named with a period at the end is purely technical (we get a run-time error if we try to name it dim).
...	Additional arguments passed to rowMeans() and rowSums().
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.

Value

Returns a **numeric vector** of length N (K).

Author(s)

Henrik Bengtsson

See Also[sd](#), [mad](#) and [var](#). [rowIQRs\(\)](#).

`rowMeans2`*Calculates the mean for each row (column) in a matrix*

Description

Calculates the mean for each row (column) in a matrix.

Usage

```
rowMeans2(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x),
  ..., useNames = NA)
```

```
colMeans2(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x),
  ..., useNames = NA)
```

Arguments

<code>x</code>	An <code>NxK</code> matrix or, if <code>dim.</code> is specified, an <code>N * K</code> vector .
<code>rows</code>	A vector indicating subset of rows to operate over. If <code>NULL</code> , no subsetting is done.
<code>cols</code>	A vector indicating subset of columns to operate over. If <code>NULL</code> , no subsetting is done.
<code>na.rm</code>	If <code>TRUE</code> , missing values are excluded.
<code>dim.</code>	An integer vector of length two specifying the dimension of <code>x</code> , also when not a matrix . <i>Comment:</i> The reason for this argument being named with a period at the end is purely technical (we get a run-time error if we try to name it <code>dim</code>).
<code>...</code>	Not used.
<code>useNames</code>	If <code>NA</code> , the default behavior of the function about naming support is remained. If <code>FALSE</code> , no naming support is done. Else if <code>TRUE</code> , names attributes of result are set.

DetailsThe implementation of `rowMeans2()` and `colMeans2()` is optimized for both speed and memory.**Value**Returns a [numeric vector](#) of length `N (K)`.

Author(s)

Henrik Bengtsson

rowMedians

*Calculates the median for each row (column) in a matrix***Description**

Calculates the median for each row (column) in a matrix.

Usage

```
rowMedians(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x),
  ..., useNames = NA)
```

```
colMedians(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x),
  ..., useNames = NA)
```

Arguments

x	An NxK matrix or, if dim. is specified, an N * K vector .
rows, cols	A vector indicating subset of rows (and/or columns) to operate over. If NULL , no subsetting is done.
na.rm	If TRUE , NAs are excluded first, otherwise not.
dim.	An integer vector of length two specifying the dimension of x, also when not a matrix .
...	Not used.
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.

Details

The implementation of rowMedians() and colMedians() is optimized for both speed and memory. To avoid coercing to **doubles** (and hence memory allocation), there is a special implementation for **integer** matrices. That is, if x is an **integer matrix**, then rowMedians(as.double(x)) (rowMedians(as.double(x))) would require three times the memory of rowMedians(x) (colMedians(x)), but all this is avoided.

ValueReturns a **numeric vector** of length N (K).**Author(s)**

Henrik Bengtsson, Harris Jaffee

See Also

See [rowWeightedMedians\(\)](#) and [colWeightedMedians\(\)](#) for weighted medians. For mean estimates, see [rowMeans2\(\)](#) and [rowMeans\(\)](#).

rowOrderStats	<i>Gets an order statistic for each row (column) in a matrix</i>
---------------	--

Description

Gets an order statistic for each row (column) in a matrix.

Usage

```
rowOrderStats(x, rows = NULL, cols = NULL, which, dim. = dim(x), ...,
              useNames = NA)
```

```
colOrderStats(x, rows = NULL, cols = NULL, which, dim. = dim(x), ...,
              useNames = NA)
```

Arguments

x	An $N \times K$ matrix or, if <code>dim.</code> is specified, an $N * K$ vector .
rows	A vector indicating subset of rows to operate over. If <code>NULL</code> , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If <code>NULL</code> , no subsetting is done.
which	An integer index in $[1, K]$ ($[1, N]$) indicating which order statistic to be returned.
dim.	An integer vector of length two specifying the dimension of <code>x</code> , also when not a matrix . <i>Comment:</i> The reason for this argument being named with a period at the end is purely technical (we get a run-time error if we try to name it <code>dim</code>).
...	Not used.
useNames	If <code>NA</code> , the default behavior of the function about naming support is remained. If <code>FALSE</code> , no naming support is done. Else if <code>TRUE</code> , names attributes of result are set.

Details

The implementation of `rowOrderStats()` is optimized for both speed and memory. To avoid coercing to [doubles](#) (and hence memory allocation), there is a unique implementation for [integer](#) matrices.

Value

Returns a [numeric vector](#) of length N (K).

Missing values

This method does *not* handle missing values, that is, the result corresponds to having `na.rm = FALSE` (if such an argument would be available).

Author(s)

The native implementation of `rowOrderStats()` was adopted by Henrik Bengtsson from Robert Gentleman's `rowQ()` in the **Biobase** package.

See Also

See `rowMeans()` in `colSums()`.

rowQuantiles	<i>Estimates quantiles for each row (column) in a matrix</i>
--------------	--

Description

Estimates quantiles for each row (column) in a matrix.

Usage

```
rowQuantiles(x, rows = NULL, cols = NULL, probs = seq(from = 0, to = 1,
  by = 0.25), na.rm = FALSE, type = 7L, ..., useNames = NA,
  drop = TRUE)
```

```
colQuantiles(x, rows = NULL, cols = NULL, probs = seq(from = 0, to = 1,
  by = 0.25), na.rm = FALSE, type = 7L, ..., useNames = NA,
  drop = TRUE)
```

Arguments

x	An integer , numeric or logical NxK matrix with $N \geq 0$.
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
probs	A numeric vector of J probabilities in [0, 1].
na.rm	If TRUE , missing values are excluded.
type	An integer specify the type of estimator. See quantile for more details.
...	Additional arguments passed to quantile .
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.
drop	If TRUE , singleton dimensions in the result are dropped, otherwise not.

Value

Returns a $N \times J$ ($K \times J$) *matrix*, where N (K) is the number of rows (columns) for which the J quantiles are calculated. The return type is either integer or numeric depending on type.

Author(s)

Henrik Bengtsson

See Also

[quantile](#).

Examples

```
set.seed(1)

x <- matrix(rnorm(50 * 40), nrow = 50, ncol = 40)
str(x)

probs <- c(0.25, 0.5, 0.75)

# Row quantiles
q <- rowQuantiles(x, probs = probs)
print(q)
q_0 <- apply(x, MARGIN = 1, FUN = quantile, probs = probs)
stopifnot(all.equal(q_0, t(q)))

# Column IQRs
q <- colQuantiles(x, probs = probs)
print(q)
q_0 <- apply(x, MARGIN = 2, FUN = quantile, probs = probs)
stopifnot(all.equal(q_0, t(q)))
```

rowRanges

Gets the range of values in each row (column) of a matrix

Description

Gets the range of values in each row (column) of a matrix.

Usage

```
rowRanges(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x),
  ..., useNames = NA)

rowMins(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x), ...,
  useNames = NA)
```

```
rowMaxs(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x), ...,
        useNames = NA)
```

```
colRanges(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x),
          ..., useNames = NA)
```

```
colMins(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x), ...,
        useNames = NA)
```

```
colMaxs(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x), ...,
        useNames = NA)
```

Arguments

x	An NxK matrix or, if dim. is specified, an N * K vector .
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
na.rm	If TRUE , missing values are excluded.
dim.	An integer vector of length two specifying the dimension of x, also when not a matrix . <i>Comment:</i> The reason for this argument being named with a period at the end is purely technical (we get a run-time error if we try to name it dim).
...	Not used.
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.

Value

rowRanges() (colRanges()) returns a [numeric](#) Nx2 (Kx2) [matrix](#), where N (K) is the number of rows (columns) for which the ranges are calculated.

rowMins()/rowMaxs() (colMins()/colMaxs()) returns a [numeric vector](#) of length N (K).

Author(s)

Henrik Bengtsson

See Also

[rowOrderStats\(\)](#) and [pmin.int\(\)](#).

rowRanks	<i>Gets the rank of the elements in each row (column) of a matrix</i>
----------	---

Description

Gets the rank of the elements in each row (column) of a matrix.

Usage

```
rowRanks(x, rows = NULL, cols = NULL, ties.method = c("max", "average",
  "first", "last", "random", "max", "min", "dense"), dim. = dim(x), ...,
  useNames = NA)
```

```
colRanks(x, rows = NULL, cols = NULL, ties.method = c("max", "average",
  "first", "last", "random", "max", "min", "dense"), dim. = dim(x),
  preserveShape = FALSE, ..., useNames = NA)
```

Arguments

x	An NxK matrix or, if dim. is specified, an N * K vector .
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
ties.method	A character string specifying how ties are treated. For details, see below.
dim.	An integer vector of length two specifying the dimension of x, also when not a matrix . <i>Comment:</i> The reason for this argument being named with a period at the end is purely technical (we get a run-time error if we try to name it dim).
...	Not used.
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.
preserveShape	A logical specifying whether the matrix returned should preserve the input shape of x, or not.

Details

These functions rank values and treats missing values the same way as `rank()`. For equal values ("ties"), argument `ties.method` determines how these are ranked among each other. More precisely, for the following values of `ties.method`, each index set of ties consists of:

- "first" - increasing values that are all unique
- "last" - decreasing values that are all unique
- "min" - identical values equaling the minimum of their original ranks

- "max" - identical values equaling the maximum of their original ranks
- "average" - identical values that equal the sample mean of their original ranks. Because the average is calculated, the returned ranks may be non-integer values
- "random" - randomly shuffled values of their original ranks.
- "dense" - increasing values that are all unique and, contrary to "first", never contain any gaps

For more information on `ties.method = "dense"`, see `frank()` of the **data.table** package. For more information on the other alternatives, see `rank()`.

Note that, due to different randomization strategies, the shuffling order produced by these functions when using `ties.method = "random"` does not reproduce that of `rank()`.

WARNING: For backward-compatibility reasons, the default is `ties.method = "max"`, which differs from `rank()` which uses `ties.method = "average"` by default. Since we plan to change the default behavior in a future version, we recommend to explicitly specify the intended value of argument `ties.method`.

Value

A `matrix` of type `integer` is returned, unless `ties.method = "average"` when it is of type `numeric`.

The `rowRanks()` function always returns an `NxK matrix`, where `N` (`K`) is the number of rows (columns) whose ranks are calculated.

The `colRanks()` function returns an `NxK matrix`, if `preserveShape = TRUE`, otherwise a `KxN matrix`.

Any `names` of `x` are ignored and absent in the result.

Missing values

Missing values are ranked as `NA_integer_`, as with `na.last = "keep"` in the `rank()` function.

Performance

The implementation is optimized for both speed and memory. To avoid coercing to `doubles` (and hence memory allocation), there is a unique implementation for `integer` matrices. Furthermore, it is more memory efficient to do `colRanks(x, preserveShape = TRUE)` than `t(colRanks(x, preserveShape = FALSE))`.

Author(s)

Hector Corrada Bravo and Harris Jaffee. Peter Langfelder for adding 'ties.method' support. Brian Montgomery for adding more 'ties.method's. Henrik Bengtsson adapted the original native implementation of `rowRanks()` from Robert Gentleman's `rowQ()` in the **Biobase** package.

See Also

For developers, see also Section 'Utility functions' in 'Writing R Extensions manual', particularly the native functions `R_qsort_I()` and `R_qsort_int_I()`.

rowSums2	<i>Calculates the sum for each row (column) in a matrix</i>
----------	---

Description

Calculates the sum for each row (column) in a matrix.

Usage

```
rowSums2(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x),  
        ..., useNames = NA)
```

```
colSums2(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x),  
        ..., useNames = NA)
```

Arguments

x	An NxK matrix or, if dim. is specified, an N * K vector .
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
na.rm	If TRUE , missing values are excluded.
dim.	An integer vector of length two specifying the dimension of x, also when not a matrix . <i>Comment:</i> The reason for this argument being named with a period at the end is purely technical (we get a run-time error if we try to name it dim).
...	Not used.
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.

Details

The implementation of rowSums2() and colSums2() is optimized for both speed and memory.

Value

Returns a **numeric vector** of length N (K).

Author(s)

Henrik Bengtsson

rowTabulates	<i>Tabulates the values in a matrix by row (column).</i>
--------------	--

Description

Tabulates the values in a matrix by row (column).

Usage

```
rowTabulates(x, rows = NULL, cols = NULL, values = NULL, ..., useNames = NA)
```

```
colTabulates(x, rows = NULL, cols = NULL, values = NULL, ..., useNames = NA)
```

Arguments

x	An integer , a logical , or a raw NxK matrix .
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
values	An vector of J values of count. If NULL , all (unique) values are counted.
...	Not used.
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.

Details

An alternative to these functions, is to use `table(x,row(x))` and `table(x,col(x))`, with the exception that the latter do not support the [raw](#) data type. When there are no missing values in `x`, we have that `all(rowTabulates(x) == t(table(x,row(x))))` and `all(colTabulates(x) == t(table(x,col(x))))`. When there are missing values, we have that `all(rowTabulates(x) == t(table(x,row(x),useNA = "always")[,seq_len(nrow(x))]))` and `all(colTabulates(x) == t(table(x,col(x),useNA = "always")[,seq_len(ncol(x))]))`.

Value

Returns a NxJ (KxJ) [matrix](#) where N (K) is the number of row (column) [vectors](#) tabulated and J is the number of values counted.

Author(s)

Henrik Bengtsson

Examples

```
x <- matrix(1:5, nrow = 10, ncol = 5)
print(x)
print(rowTabulates(x))
print(colTabulates(x))
# Count only certain values
print(rowTabulates(x, values = 1:3))

y <- as.raw(x)
dim(y) <- dim(x)
print(y)
print(rowTabulates(y))
print(colTabulates(y))
```

rowVars

*Variance estimates for each row (column) in a matrix***Description**

Variance estimates for each row (column) in a matrix.

Usage

```
rowVars(x, rows = NULL, cols = NULL, na.rm = FALSE, center = NULL,
        dim. = dim(x), ..., useNames = NA)
```

```
colVars(x, rows = NULL, cols = NULL, na.rm = FALSE, center = NULL,
        dim. = dim(x), ..., useNames = NA)
```

Arguments

x	An NxK matrix or, if dim. is specified, an N * K vector .
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
na.rm	If TRUE , missing values are excluded.
center	(optional; a vector or length N (K)) If the row (column) means are already estimated, they can be pre-specified using this argument. This avoid re-estimating them again. (*Warning: If biased estimated are given, the estimate of the spread will also be biased.*) If NULL (default), the row/column means are estimated internally.
dim.	An integer vector of length two specifying the dimension of x, also when not a matrix . <i>Comment:</i> The reason for this argument being named with a period at the end is purely technical (we get a run-time error if we try to name it dim).

... Additional arguments passed to `rowMeans()` and `rowSums()`.

`useNames` If `NA`, the default behavior of the function about naming support is remained. If `FALSE`, no naming support is done. Else if `TRUE`, names attributes of result are set.

Value

Returns a [numeric vector](#) of length N (K).

Author(s)

Henrik Bengtsson

See Also

See `rowMeans()` and `rowSums()` in `colSums()`.

Examples

```
set.seed(1)

x <- matrix(rnorm(20), nrow = 5, ncol = 4)
print(x)

# Row averages
print(rowMeans(x))
print(rowMedians(x))

# Column averages
print(colMeans(x))
print(colMedians(x))

# Row variabilities
print(rowVars(x))
print(rowSds(x))
print(rowMads(x))
print(rowIQRs(x))

# Column variabilities
print(colVars(x))
print(colSds(x))
print(colMads(x))
print(colIQRs(x))

# Row ranges
print(rowRanges(x))
print(cbind(rowMins(x), rowMaxs(x)))
print(cbind(rowOrderStats(x, which = 1), rowOrderStats(x, which = ncol(x))))

# Column ranges
print(colRanges(x))
```

```

print(cbind(colMins(x), colMaxs(x)))
print(cbind(colOrderStats(x, which = 1), colOrderStats(x, which = nrow(x))))

x <- matrix(rnorm(2000), nrow = 50, ncol = 40)

# Row standard deviations
d <- rowDiffs(x)
s1 <- rowSds(d) / sqrt(2)
s2 <- rowSds(x)
print(summary(s1 - s2))

# Column standard deviations
d <- colDiffs(x)
s1 <- colSds(d) / sqrt(2)
s2 <- colSds(x)
print(summary(s1 - s2))

```

rowWeightedMeans	<i>Calculates the weighted means for each row (column) in a matrix</i>
------------------	--

Description

Calculates the weighted means for each row (column) in a matrix.

Usage

```

rowWeightedMeans(x, w = NULL, rows = NULL, cols = NULL, na.rm = FALSE,
  ..., useNames = NA)

colWeightedMeans(x, w = NULL, rows = NULL, cols = NULL, na.rm = FALSE,
  ..., useNames = NA)

```

Arguments

x	An NxK matrix or, if dim. is specified, an N * K vector .
w	A numeric vector of length K (N).
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
na.rm	If TRUE , missing values are excluded.
...	Not used.
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.

Details

The implementations of these methods are optimized for both speed and memory. If no weights are given, the corresponding `rowMeans()`/`colMeans()` is used.

Value

Returns a [numeric vector](#) of length N (K).

Author(s)

Henrik Bengtsson

See Also

See `rowMeans()` and `colMeans()` in `colSums()` for non-weighted means. See also [weighted.mean](#).

Examples

```
x <- matrix(rnorm(20), nrow = 5, ncol = 4)
print(x)

# Non-weighted row averages
mu_0 <- rowMeans(x)
mu <- rowWeightedMeans(x)
stopifnot(all.equal(mu, mu_0))

# Weighted row averages (uniform weights)
w <- rep(2.5, times = ncol(x))
mu <- rowWeightedMeans(x, w = w)
stopifnot(all.equal(mu, mu_0))

# Weighted row averages (excluding some columns)
w <- c(1, 1, 0, 1)
mu_0 <- rowMeans(x[, (w == 1), drop = FALSE])
mu <- rowWeightedMeans(x, w = w)
stopifnot(all.equal(mu, mu_0))

# Weighted row averages (excluding some columns)
w <- c(0, 1, 0, 0)
mu_0 <- rowMeans(x[, (w == 1), drop = FALSE])
mu <- rowWeightedMeans(x, w = w)
stopifnot(all.equal(mu, mu_0))

# Weighted averages by rows and columns
w <- 1:4
mu_1 <- rowWeightedMeans(x, w = w)
mu_2 <- colWeightedMeans(t(x), w = w)
stopifnot(all.equal(mu_2, mu_1))
```

rowWeightedMedians *Calculates the weighted medians for each row (column) in a matrix*

Description

Calculates the weighted medians for each row (column) in a matrix.

Usage

```
rowWeightedMedians(x, w = NULL, rows = NULL, cols = NULL,  
  na.rm = FALSE, ..., useNames = NA)
```

```
colWeightedMedians(x, w = NULL, rows = NULL, cols = NULL,  
  na.rm = FALSE, ..., useNames = NA)
```

Arguments

x	An NxK matrix or, if dim. is specified, an N * K vector .
w	A numeric vector of length K (N).
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
na.rm	If TRUE , missing values are excluded.
...	Additional arguments passed to weightedMedian() .
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.

Details

The implementations of these methods are optimized for both speed and memory. If no weights are given, the corresponding [rowMedians\(\)/colMedians\(\)](#) is used.

Value

Returns a [numeric vector](#) of length N (K).

Author(s)

Henrik Bengtsson

See Also

Internally, [weightedMedian\(\)](#) is used. See [rowMedians\(\)](#) and [colMedians\(\)](#) for non-weighted medians.

Examples

```
x <- matrix(rnorm(20), nrow = 5, ncol = 4)
print(x)

# Non-weighted row averages
mu_0 <- rowMedians(x)
mu <- rowWeightedMedians(x)
stopifnot(all.equal(mu, mu_0))

# Weighted row averages (uniform weights)
w <- rep(2.5, times = ncol(x))
mu <- rowWeightedMedians(x, w = w)
stopifnot(all.equal(mu, mu_0))

# Weighted row averages (excluding some columns)
w <- c(1, 1, 0, 1)
mu_0 <- rowMedians(x[, (w == 1), drop = FALSE])
mu <- rowWeightedMedians(x, w = w)
stopifnot(all.equal(mu, mu_0))

# Weighted row averages (excluding some columns)
w <- c(0, 1, 0, 0)
mu_0 <- rowMedians(x[, (w == 1), drop = FALSE])
mu <- rowWeightedMedians(x, w = w)
stopifnot(all.equal(mu, mu_0))

# Weighted averages by rows and columns
w <- 1:4
mu_1 <- rowWeightedMedians(x, w = w)
mu_2 <- colWeightedMedians(t(x), w = w)
stopifnot(all.equal(mu_2, mu_1))
```

varDiff

Estimation of scale based on sequential-order differences

Description

Estimation of scale based on sequential-order differences, corresponding to the scale estimates provided by [var](#), [sd](#), [mad](#) and [IQR](#).

Usage

```
varDiff(x, idxs = NULL, na.rm = FALSE, diff = 1L, trim = 0, ...)

sdDiff(x, idxs = NULL, na.rm = FALSE, diff = 1L, trim = 0, ...)

madDiff(x, idxs = NULL, na.rm = FALSE, diff = 1L, trim = 0,
        constant = 1.4826, ...)
```

```

iqrDiff(x, idxs = NULL, na.rm = FALSE, diff = 1L, trim = 0, ...)

rowVarDiffs(x, rows = NULL, cols = NULL, na.rm = FALSE, diff = 1L,
  trim = 0, ..., useNames = NA)

colVarDiffs(x, rows = NULL, cols = NULL, na.rm = FALSE, diff = 1L,
  trim = 0, ..., useNames = NA)

rowSdDiffs(x, rows = NULL, cols = NULL, na.rm = FALSE, diff = 1L,
  trim = 0, ..., useNames = NA)

colSdDiffs(x, rows = NULL, cols = NULL, na.rm = FALSE, diff = 1L,
  trim = 0, ..., useNames = NA)

rowMadDiffs(x, rows = NULL, cols = NULL, na.rm = FALSE, diff = 1L,
  trim = 0, ..., useNames = NA)

colMadDiffs(x, rows = NULL, cols = NULL, na.rm = FALSE, diff = 1L,
  trim = 0, ..., useNames = NA)

rowIQRDiffs(x, rows = NULL, cols = NULL, na.rm = FALSE, diff = 1L,
  trim = 0, ..., useNames = NA)

colIQRDiffs(x, rows = NULL, cols = NULL, na.rm = FALSE, diff = 1L,
  trim = 0, ..., useNames = NA)

```

Arguments

x	A numeric vector of length N or a numeric NxK matrix .
idxs	A vector indicating subset of elements to operate over. If NULL , no subsetting is done.
na.rm	If TRUE , missing values are excluded.
diff	The positional distance of elements for which the difference should be calculated.
trim	A double in [0,1/2] specifying the fraction of observations to be trimmed from each end of (sorted) x before estimation.
...	Not used.
constant	A scale factor adjusting for asymptotically normal consistency.
rows	A vector indicating subset of rows to operate over. If NULL , no subsetting is done.
cols	A vector indicating subset of columns to operate over. If NULL , no subsetting is done.
useNames	If NA , the default behavior of the function about naming support is remained. If FALSE , no naming support is done. Else if TRUE , names attributes of result are set.

Details

Note that n-order difference MAD estimates, just like the ordinary MAD estimate by `mad`, apply a correction factor such that the estimates are consistent with the standard deviation under Gaussian distributions.

The interquartile range (IQR) estimates does *not* apply such a correction factor. If asymptotically normal consistency is wanted, the correction factor for IQR estimate is $1 / (2 * qnorm(3/4))$, which is half of that used for MAD estimates, which is $1 / qnorm(3/4)$. This correction factor needs to be applied manually, i.e. there is no constant argument for the IQR functions.

Value

Returns a [numeric vector](#) of length 1, length N, or length K.

Author(s)

Henrik Bengtsson

References

[1] J. von Neumann et al., *The mean square successive difference*. *Annals of Mathematical Statistics*, 1941, 12, 153-162.

See Also

For the corresponding non-differentiated estimates, see `var`, `sd`, `mad` and `IQR`. Internally, `diff2()` is used which is a faster version of `diff()`.

 weightedMad

Weighted Median Absolute Deviation (MAD)

Description

Computes a weighted MAD of a numeric vector.

Usage

```
weightedMad(x, w = NULL, idxs = NULL, na.rm = FALSE, constant = 1.4826,
  center = NULL, ...)
```

```
rowWeightedMads(x, w = NULL, rows = NULL, cols = NULL, na.rm = FALSE,
  constant = 1.4826, center = NULL, ..., useNames = NA)
```

```
colWeightedMads(x, w = NULL, rows = NULL, cols = NULL, na.rm = FALSE,
  constant = 1.4826, center = NULL, ..., useNames = NA)
```


Arguments

x	vector of type <code>integer</code> , <code>numeric</code> , or <code>logical</code> .
w	a vector of weights the same length as x giving the weights to use for each element of x. Negative weights are treated as zero weights. Default value is equal weight to all values.
idxs	A <code>vector</code> indicating subset of elements to operate over. If <code>NULL</code> , no subsetting is done.
na.rm	If <code>TRUE</code> , missing values are excluded.
constant	A <code>numeric</code> scale factor, cf. <code>mad</code> .
center	Optional <code>numeric</code> scalar specifying the center location of the data. If <code>NULL</code> , it is estimated from data.
...	Not used.
rows	A <code>vector</code> indicating subset of rows to operate over. If <code>NULL</code> , no subsetting is done.
cols	A <code>vector</code> indicating subset of columns to operate over. If <code>NULL</code> , no subsetting is done.
useNames	If <code>NA</code> , the default behavior of the function about naming support is remained. If <code>FALSE</code> , no naming support is done. Else if <code>TRUE</code> , names attributes of result are set.

Value

Returns a `numeric` scalar.

Missing values

Missing values are dropped at the very beginning, if argument `na.rm` is `TRUE`, otherwise not.

Author(s)

Henrik Bengtsson

See Also

For the non-weighted MAD, see `mad`. Internally `weightedMedian()` is used to calculate the weighted median.

Examples

```
x <- 1:10
n <- length(x)

m1 <- mad(x)
m2 <- weightedMad(x)
stopifnot(identical(m1, m2))

w <- rep(1, times = n)
```

```

m1 <- weightedMad(x, w)
stopifnot(identical(m1, m2))

# All weight on the first value
w[1] <- Inf
m <- weightedMad(x, w)
stopifnot(m == 0)

# All weight on the first two values
w[1:2] <- Inf
m1 <- mad(x[1:2])
m2 <- weightedMad(x, w)
stopifnot(identical(m1, m2))

# All weights set to zero
w <- rep(0, times = n)
m <- weightedMad(x, w)
stopifnot(is.na(m))

```

weightedMean

Weighted Arithmetic Mean

Description

Computes the weighted sample mean of a numeric vector.

Usage

```
weightedMean(x, w = NULL, idxs = NULL, na.rm = FALSE, refine = FALSE, ...)
```

Arguments

<code>x</code>	An <code>NxK matrix</code> or, if <code>dim.</code> is specified, an <code>N * K vector</code> .
<code>w</code>	a vector of weights the same length as <code>x</code> giving the weights to use for each element of <code>x</code> . Negative weights are treated as zero weights. Default value is equal weight to all values. If a missing-value weight exists, the result is always a missing value.
<code>idxs</code>	A <code>vector</code> indicating subset of elements to operate over. If <code>NULL</code> , no subsetting is done.
<code>na.rm</code>	If <code>TRUE</code> , missing values are excluded.
<code>refine</code>	If <code>TRUE</code> and <code>x</code> is <code>numeric</code> , then extra effort is used to calculate the average with greater numerical precision, otherwise not.
<code>...</code>	Not used.

Value

Returns a `numeric` scalar. If `x` is of zero length, then `NaN` is returned, which is consistent with `mean()`.

Missing values

This function handles missing values consistently with `weighted.mean`. More precisely, if `na.rm = FALSE`, then any missing values in either `x` or `w` will give result `NA_real_`. If `na.rm = TRUE`, then all `(x, w)` data points for which `x` is missing are skipped. Note that if both `x` and `w` are missing for a data point, then it is also skipped (by the same rule). However, if only `w` is missing, then the final results will always be `NA_real_` regardless of `na.rm`.

Author(s)

Henrik Bengtsson

See Also

`mean()` and `weighted.mean`.

Examples

```
x <- 1:10
n <- length(x)

w <- rep(1, times = n)
m0 <- weighted.mean(x, w)
m1 <- weightedMean(x, w)
stopifnot(identical(m1, m0))

# Pull the mean towards zero
w[1] <- 5
m0 <- weighted.mean(x, w)
m1 <- weightedMean(x, w)
stopifnot(identical(m1, m0))

# Put even more weight on the zero
w[1] <- 8.5
m0 <- weighted.mean(x, w)
m1 <- weightedMean(x, w)
stopifnot(identical(m1, m0))

# All weight on the first value
w[1] <- Inf
m0 <- weighted.mean(x, w)
m1 <- weightedMean(x, w)
stopifnot(identical(m1, m0))

# All weight on the last value
w[1] <- 1
w[n] <- Inf
m0 <- weighted.mean(x, w)
m1 <- weightedMean(x, w)
stopifnot(identical(m1, m0))

# All weights set to zero
```

```
w <- rep(0, times = n)
m0 <- weighted.mean(x, w)
m1 <- weightedMean(x, w)
stopifnot(identical(m1, m0))
```

weightedMedian	<i>Weighted Median Value</i>
----------------	------------------------------

Description

Computes a weighted median of a numeric vector.

Usage

```
weightedMedian(x, w = NULL, idxs = NULL, na.rm = FALSE,
  interpolate = is.null(ties), ties = NULL, ...)
```

Arguments

<code>x</code>	vector of type <code>integer</code> , <code>numeric</code> , or <code>logical</code> .
<code>w</code>	a vector of weights the same length as <code>x</code> giving the weights to use for each element of <code>x</code> . Negative weights are treated as zero weights. Default value is equal weight to all values.
<code>idxs</code>	A <code>vector</code> indicating subset of elements to operate over. If <code>NULL</code> , no subsetting is done.
<code>na.rm</code>	a logical value indicating whether <code>NA</code> values in <code>x</code> should be stripped before the computation proceeds, or not. If <code>NA</code> , no check at all for <code>NAs</code> is done.
<code>interpolate</code>	If <code>TRUE</code> , linear interpolation is used to get a consistent estimate of the weighted median.
<code>ties</code>	If <code>interpolate == FALSE</code> , a character string specifying how to solve ties between two <code>x</code> 's that are satisfying the weighted median criteria. Note that at most two values can satisfy the criteria. When <code>ties</code> is "min" ("lower weighted median"), the smaller value of the two is returned and when it is "max" ("upper weighted median"), the larger value is returned. If <code>ties</code> is "mean", the mean of the two values is returned. Finally, if <code>ties</code> is "weighted" (or <code>NULL</code>) a weighted average of the two are returned, where the weights are weights of all values <code>x[i] <= x[k]</code> and <code>x[i] >= x[k]</code> , respectively.
<code>...</code>	Not used.

Value

Returns a `numeric` scalar.

For the n elements $x = c(x[1], x[2], \dots, x[n])$ with positive weights $w = c(w[1], w[2], \dots, w[n])$ such that $\text{sum}(w) = S$, the *weighted median* is defined as the element $x[k]$ for which the total weight of all elements $x[i] < x[k]$ is less or equal to $S/2$ and for which the total weight of all elements $x[i] > x[k]$ is less or equal to $S/2$ (c.f. [1]).

When using linear interpolation, the weighted mean of $x[k-1]$ and $x[k]$ with weights $S[k-1]$ and $S[k]$ corresponding to the cumulative weights of those two elements is used as an estimate.

If w is missing then all elements of x are given the same positive weight. If all weights are zero, `NA_real_` is returned.

If one or more weights are `Inf`, it is the same as these weights have the same weight and the others have zero. This makes things easier for cases where the weights are result of a division with zero.

If there are missing values in w that are part of the calculation (after subsetting and dropping missing values in x), then the final result is always `NA` of the same type as x .

The weighted median solves the following optimization problem:

$$\alpha^* = \arg_{\alpha} \min \sum_{i=1}^n w_i |x_i - \alpha|$$

where $x = (x_1, x_2, \dots, x_n)$ are scalars and $w = (w_1, w_2, \dots, w_n)$ are the corresponding "weights" for each individual x value.

Author(s)

Henrik Bengtsson and Ola Hossjer, Centre for Mathematical Sciences, Lund University. Thanks to Roger Koenker, Econometrics, University of Illinois, for the initial ideas.

References

[1] T.H. Cormen, C.E. Leiserson, R.L. Rivest, Introduction to Algorithms, The MIT Press, Massachusetts Institute of Technology, 1989.

See Also

`median`, `mean()` and `weightedMean()`.

Examples

```
x <- 1:10
n <- length(x)

m1 <- median(x) # 5.5
m2 <- weightedMedian(x) # 5.5
stopifnot(identical(m1, m2))

w <- rep(1, times = n)
m1 <- weightedMedian(x, w) # 5.5 (default)
m2 <- weightedMedian(x, ties = "weighted") # 5.5 (default)
m3 <- weightedMedian(x, ties = "min") # 5
m4 <- weightedMedian(x, ties = "max") # 6
stopifnot(identical(m1, m2))

# Pull the median towards zero
w[1] <- 5
m1 <- weightedMedian(x, w) # 3.5
```

```

y <- c(rep(0, times = w[1]), x[-1])      # Only possible for integer weights
m2 <- median(y)                          # 3.5
stopifnot(identical(m1, m2))

# Put even more weight on the zero
w[1] <- 8.5
weightedMedian(x, w)                     # 2

# All weight on the first value
w[1] <- Inf
weightedMedian(x, w)                     # 1

# All weight on the last value
w[1] <- 1
w[n] <- Inf
weightedMedian(x, w)                     # 10

# All weights set to zero
w <- rep(0, times = n)
weightedMedian(x, w)                     # NA

# Simple benchmarking
bench <- function(N = 1e5, K = 10) {
  x <- rnorm(N)
  gc()
  t <- c()
  t[1] <- system.time(for (k in 1:K) median(x))[3]
  t[2] <- system.time(for (k in 1:K) weightedMedian(x))[3]
  t <- t / t[1]
  names(t) <- c("median", "weightedMedian")
  t
}

print(bench(N = 5, K = 100))
print(bench(N = 50, K = 100))
print(bench(N = 200, K = 100))
print(bench(N = 1000, K = 100))
print(bench(N = 10e3, K = 20))
print(bench(N = 100e3, K = 20))

```

 weightedVar

Weighted variance and weighted standard deviation

Description

Computes a weighted variance / standard deviation of a numeric vector or across rows or columns of a matrix.

Usage

```
weightedVar(x, w = NULL, idxs = NULL, na.rm = FALSE, center = NULL, ...)
```

```
weightedSd(...)
```

```
rowWeightedVars(x, w = NULL, rows = NULL, cols = NULL, na.rm = FALSE,
  ..., useNames = NA)
```

```
colWeightedVars(x, w = NULL, rows = NULL, cols = NULL, na.rm = FALSE,
  ..., useNames = NA)
```

```
rowWeightedSds(x, w = NULL, rows = NULL, cols = NULL, na.rm = FALSE,
  ..., useNames = NA)
```

```
colWeightedSds(x, w = NULL, rows = NULL, cols = NULL, na.rm = FALSE,
  ..., useNames = NA)
```

Arguments

x	vector of type <code>integer</code> , <code>numeric</code> , or <code>logical</code> .
w	a vector of weights the same length as x giving the weights to use for each element of x. Negative weights are treated as zero weights. Default value is equal weight to all values.
idxs	A <code>vector</code> indicating subset of elements to operate over. If <code>NULL</code> , no subsetting is done.
na.rm	If <code>TRUE</code> , missing values are excluded.
center	Optional <code>numeric</code> scalar specifying the center location of the data. If <code>NULL</code> , it is estimated from data.
...	Not used.
rows	A <code>vector</code> indicating subset of rows to operate over. If <code>NULL</code> , no subsetting is done.
cols	A <code>vector</code> indicating subset of columns to operate over. If <code>NULL</code> , no subsetting is done.
useNames	If <code>NA</code> , the default behavior of the function about naming support is remained. If <code>FALSE</code> , no naming support is done. Else if <code>TRUE</code> , names attributes of result are set.

Details

The estimator used here is the same as the one used by the "unbiased" estimator of the **Hmisc** package. More specifically, `weightedVar(x, w = w) == Hmisc::wtd.var(x, weights = w)`,

Value

Returns a `numeric` scalar.

Missing values

This function handles missing values consistently with [weightedMean\(\)](#). More precisely, if `na.rm = FALSE`, then any missing values in either `x` or `w` will give result `NA_real_`. If `na.rm = TRUE`, then all (x, w) data points for which `x` is missing are skipped. Note that if both `x` and `w` are missing for a data points, then it is also skipped (by the same rule). However, if only `w` is missing, then the final results will always be `NA_real_` regardless of `na.rm`.

Author(s)

Henrik Bengtsson

See Also

For the non-weighted variance, see [var](#).

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