

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 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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Author(s)

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

anyMissing	<i>Checks if there are any missing values in an object or not</i>
------------	---

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, ...)  
rowAnyMissings(x, rows = NULL, cols = NULL, ...)  
colAnyNAs(x, rows = NULL, cols = NULL, ...)  
rowAnyNAs(x, rows = NULL, cols = NULL, ...)
```

Arguments

<code>x</code>	A vector , a list , a matrix , a data.frame , or <code>NULL</code> .
<code>idxs, rows, cols</code>	A vector indicating subset of elements (or rows and/or columns) to operate over. If <code>NULL</code> , no subsetting is done.
<code>...</code>	Not used.

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

<code>y</code>	A numeric or logical vector of <code>K</code> values to calculate means on.
<code>x</code>	A numeric vector of <code>K</code> positions for to be binned.
<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 <code>B + 1</code> ordered positions specifying the <code>B > 0</code> bins <code>[bx[1], bx[2]), [bx[2], bx[3]), ..., [bx[B], bx[B + 1])</code> .
<code>na.rm</code>	If <code>TRUE</code> , missing values in <code>y</code> are dropped before calculating the mean, otherwise not.
<code>count</code>	If <code>TRUE</code> , the number of data points in each bins is returned as attribute count, which is an integer vector of length <code>B</code> .
<code>right</code>	If <code>TRUE</code> , the bins are right-closed (left open), otherwise left-closed (right open).
<code>...</code>	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](#) of indices. If `NULL`, all indices are returned.
... Not use.

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> , any missing values are ignored, otherwise not.
<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 is function is more accurate than $\log(\text{sum}(\exp(\text{lx})))$ when the values of $x = \exp(\text{lx})$ are $|x| \ll 1$. The implementation of this function is based on the observation that

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

Assuming $\text{la} > \text{lb}$, then $|\text{lb} - \text{la}| < |\text{lb}|$, and it is less likely that the computation of $1 + \exp(\text{lb} - \text{la})$ 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 `lx` and subtracts it from the remaining values in `lx`.

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"), ...)
```

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

Arguments

`x` A [numeric NxK matrix](#).

`idxs, rows, cols` A [vector](#) indicating subset of elements (or rows and/or columns) to operate over. If `NULL`, no subsetting is done.

`na.rm` If `TRUE`, missing values are ignored, otherwise not.

`...` Not used.

`method` A [character](#) string specifying how each product is calculated.

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

<code>rowAlls</code>	<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), ...)
```

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

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

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

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

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

Arguments

<code>x</code>	An <code>NxK matrix</code> or an <code>N * K vector</code> .
<code>value</code>	A value to search for.
<code>na.rm</code>	If <code>TRUE</code> , <code>NA</code> s are excluded first, otherwise not.
<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> .
<code>...</code>	Not used.
<code>idxs, rows, cols</code>	A <code>vector</code> indicating subset of elements (or rows and/or columns) 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()` (`colAnys()`).

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), ...)
```

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

Arguments

x	An NxK matrix .
idxs	An index vector of (maximum) length N (K) specifying the columns (rows) to be extracted.
rows, cols	A vector indicating subset of rows (and/or 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 .
...	Not used.

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

Counts the number of occurrences of a specific value

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), ...)
```

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

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

Arguments

<code>x</code>	An <code>NxK matrix</code> or an <code>N * K vector</code> .
<code>value</code>	A value to search for.
<code>na.rm</code>	If <code>TRUE</code> , <code>NA</code> s are excluded first, otherwise not.
<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> .
<code>...</code>	Not used.
<code>idxs, rows, cols</code>	A <code>vector</code> indicating subset of elements (or rows and/or columns) 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	<i>Cumulative sums, products, minima and maxima for each row (column) in a matrix</i>
------------	---

Description

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

Usage

```

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

```

Arguments

x	An NxK matrix .
rows, cols	A vector indicating subset of elements (or rows and/or 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 .
...	Not used.

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), ...)
```

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


Arguments

<code>x</code>	A numeric NxK matrix .
<code>rows, cols</code>	A vector indicating subset of rows (and/or columns) to operate over. If <code>NULL</code> , no subsetting is done.
<code>lag</code>	An integer specifying the lag.
<code>differences</code>	An integer specifying the order of difference.
<code>dim.</code>	An integer vector of length two specifying the dimension of <code>x</code> , also when not a matrix .
<code>...</code>	Not used.

Value

Returns a [numeric](#) Nx(K-1) or (N-1)xK [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, ...)

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

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

Arguments

`x` A **numeric** $N \times K$ **matrix**.

`na.rm` If **TRUE**, missing values are dropped first, otherwise not.

`...` Additional arguments passed to `rowQuantiles()` (`colQuantiles()`).

`idxs, rows, cols` A **vector** indicating subset of elements (or rows and/or columns) to operate over. If **NULL**, 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), ...)
```

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

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.

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), ...)
```

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

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

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

Arguments

x	A numeric NxK matrix .
rows, cols	A vector indicating subset of rows (and/or 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 , NAs are excluded first, otherwise not.
dim.	An integer vector of length two specifying the dimension of x, also when not a matrix .
...	Additional arguments passed to rowMeans() and rowSums() .

Value

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

Author(s)

Henrik Bengtsson

See Also

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

rowMeans2	<i>Calculates the mean for each row (column) in a matrix</i>
-----------	--

Description

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

Usage

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

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

Arguments

x	A numeric or a logical NxK matrix .
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.

Details

The 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), ...)
```

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

Arguments

<code>x</code>	A numeric NxK matrix .
<code>rows, cols</code>	A vector indicating subset of rows (and/or columns) to operate over. If <code>NULL</code> , no subsetting is done.
<code>na.rm</code>	If <code>TRUE</code> , <code>NAs</code> are excluded first, otherwise not.
<code>dim.</code>	An integer vector of length two specifying the dimension of <code>x</code> , also when not a matrix .
<code>...</code>	Not used.

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.

Value

Returns 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), ...)
```

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

Arguments

x	A numeric NxK matrix .
rows, cols	A vector indicating subset of rows (and/or columns) to operate over. If NULL , 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 x, also when not a matrix .
...	Not used.

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

*Estimates quantiles for each row (column) in a matrix***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, ..., drop = TRUE)
```

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

Arguments

<code>x</code>	An integer , numeric or logical <code>NxK</code> matrix with $N \geq 0$.
<code>rows, cols</code>	A vector indicating subset of rows (and/or columns) to operate over. If <code>NULL</code> , no subsetting is done.
<code>probs</code>	A numeric vector of <code>J</code> probabilities in <code>[0, 1]</code> .
<code>na.rm</code>	If <code>TRUE</code> , <code>NA</code> s are excluded first, otherwise not.
<code>type</code>	An integer specify the type of estimator. See quantile for more details.
<code>...</code>	Additional arguments passed to quantile .
<code>drop</code>	If <code>TRUE</code> , singleton dimensions in the result are dropped, otherwise not.

Value

Returns a `NxJ` (`KxJ`) [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	<i>Gets the range of values in each row (column) of a matrix</i>
-----------	--

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), ...)
rowMins(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x), ...)
rowMaxs(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x), ...)
colRanges(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x), ...)
colMins(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x), ...)
colMaxs(x, rows = NULL, cols = NULL, na.rm = FALSE, dim. = dim(x), ...)

```

Arguments

x	A numeric NxK matrix .
rows, cols	A vector indicating subset of rows (and/or columns) to operate over. If <code>NULL</code> , no subsetting is done.
na.rm	If <code>TRUE</code> , <code>NA</code> s are excluded first, otherwise not.
dim.	An integer vector of length two specifying the dimension of x, also when not a matrix .
...	Not used.

Value

rowRanges() (colRanges()) returns a **numeric** $N \times 2$ ($K \times 2$) **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), ...)
```

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

Arguments

x	A numeric or integer $N \times K$ matrix .
rows, cols	A vector indicating subset of rows (and/or 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 .
...	Not used.
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), ...)
```

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

Arguments

x	A numeric or a logical NxK matrix .
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.

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, ...)
```

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

Arguments

x	An <i>integer</i> , a <i>logical</i> , or a <i>raw</i> NxK <i>matrix</i> .
rows, cols	A <i>vector</i> indicating subset of rows (and/or columns) to operate over. If <i>NULL</i> , no subsetting is done.
values	An <i>vector</i> of J values of count. If <i>NULL</i> , all (unique) values are counted.
...	Not used.

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), ...)
```

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

Arguments

x	A numeric NxK matrix .
rows, cols	A vector indicating subset of rows (and/or columns) to operate over. If NULL , no subsetting is done.
na.rm	If TRUE , missing values are excluded first, otherwise not.
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 .
...	Additional arguments passed to rowMeans() and rowSums().

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(rowVars(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(2400), 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, ...)
colWeightedMeans(x, w = NULL, rows = NULL, cols = NULL, na.rm = FALSE, ...)
```

Arguments

<code>x</code>	A numeric NxK matrix .
<code>w</code>	A numeric vector of length <code>K</code> (<code>N</code>).
<code>rows, cols</code>	A vector indicating subset of rows (and/or columns) to operate over. If <code>NULL</code> , no subsetting is done.
<code>na.rm</code>	If <code>TRUE</code> , missing values are excluded from the calculation, otherwise not.
<code>...</code>	Not used.

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

Arguments

x A numeric NxK matrix.
w A numeric vector of length K (N).

rows, cols	A vector indicating subset of rows (and/or columns) to operate over. If <code>NULL</code> , no subsetting is done.
na.rm	If <code>TRUE</code> , missing values are excluded from the calculation, otherwise not.
...	Additional arguments passed to weightedMedian() .

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, ...)
```

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

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

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

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

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

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

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

Arguments

<code>x</code>	A numeric vector of length N or a numeric NxK matrix .
<code>idxs, rows, cols</code>	A vector indicating subset of elements (or rows and/or columns) to operate over. If <code>NULL</code> , no subsetting is done.
<code>na.rm</code>	If <code>TRUE</code> , NAs are excluded, otherwise not.
<code>diff</code>	The positional distance of elements for which the difference should be calculated.
<code>trim</code>	A double in <code>[0,1/2]</code> specifying the fraction of observations to be trimmed from each end of (sorted) <code>x</code> before estimation.
<code>...</code>	Not used.
<code>constant</code>	A scale factor adjusting for asymptotically normal consistency.

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	<i>Weighted Median Absolute Deviation (MAD)</i>
-------------	---

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, ...)
```

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

Arguments

x	a numeric vector containing the values whose weighted MAD is to be computed.
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, rows, cols	A vector indicating subset of elements (or rows and/or columns) to operate over. If <code>NULL</code> , no subsetting is done.
na.rm	a logical value indicating whether <code>NA</code> values in x should be stripped before the computation proceeds, or not. If <code>NA</code> , no check at all for <code>NAs</code> is done. Default value is <code>NA</code> (for efficiency).
constant	A numeric scale factor, cf. mad .
center	Optional numeric scalar specifying the center location of the data. If <code>NULL</code> , it is estimated from data.
...	Not used.

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

x a [numeric](#) or [logical vector](#) containing the values whose weighted mean is to be computed.

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. If a missing-value weight exists, the result is always a missing value.
idxs	A vector indicating subset of elements to operate over. If <code>NULL</code> , no subsetting is done.
na.rm	a logical value indicating whether <code>NA</code> values in x should be stripped before the computation proceeds, or not. If <code>NA</code> , no check at all for <code>NAs</code> is done. Default value is <code>NA</code> (for efficiency).
refine	If <code>TRUE</code> and x is <code>numeric</code> , then extra effort is used to calculate the average with greater numerical precision, otherwise not.
...	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 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

[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

Weighted Median Value

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

x	a numeric or logical vector containing the values whose weighted median is to be computed.
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 vector indicating subset of elements to operate over. If NULL , no subsetting is done.
na.rm	a logical value indicating whether NA values in x should be stripped before the computation proceeds, or not. If NA , no check at all for NAs is done. Default value is NA (for efficiency).

interpolate	If <code>TRUE</code> , linear interpolation is used to get a consistent estimate of the weighted median.
ties	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.
...	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, ...)

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

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

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

```

Arguments

x	a numeric vector containing the values whose weighted variance is to be computed.
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, rows, cols	A vector indicating subset of elements (or rows and/or columns) to operate over. If NULL , no subsetting is done.
na.rm	a logical value indicating whether NA values in x should be stripped before the computation proceeds, or not. If NA , no check at all for NAs is done. Default value is NA (for efficiency).
center	Optional numeric scalar specifying the center location of the data. If NULL , it is estimated from data.
...	Not used.

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 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

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

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