Package ‘gtools’
November 20, 2023

Title Various R Programming Tools

Description Functions to assist in R programming, including:
- assist in developing, updating, and maintaining R and R packages ('ask', 'checkRVersion', 'getDependencies', 'keywords', 'scat'),
- calculate the logit and inverse logit transformations ('logit', 'inv.logit'),
- test if a value is missing, empty or contains only NA and NULL values ('invalid'),
- manipulate R's .Last function ('addLast'),
- define macros ('defmacro'),
- detect odd and even integers ('odd', 'even'),
- convert strings containing non-ASCII characters (like single quotes) to plain ASCII ('ASCIIfy'),
- perform a binary search ('binsearch'),
- sort strings containing both numeric and character components ('mixedsort'),
- create a factor variable from the quantiles of a continuous variable ('quantcut'),
- enumerate permutations and combinations ('combinations', 'permutation'),
- calculate and convert between fold-change and log-ratio ('foldchange', 'logratio2foldchange', 'foldchange2logratio'),
- calculate probabilities and generate random numbers from Dirichlet distributions ('rdirichlet', 'ddirichlet'),
- apply a function over adjacent subsets of a vector ('running'),
- modify the TCP_NODELAY ('de-Nagle') flag for socket objects,
- efficient 'rbind' of data frames, even if the column names don't match ('smartbind'),
- generate significance stars from p-values ('stars.pval'),
- convert characters to/from ASCII codes ('asc', 'chr'),
- convert character vector to ASCII representation ('ASCIIfy'),
- apply title capitalization rules to a character vector ('capwords').

Version 3.9.5
License GPL-2
Depends methods, stats, utils
URL https://github.com/r-gregmisc/gtools
BugReports https://github.com/r-gregmisc/gtools/issues
Language en-US
Suggests car, gplots, knitr, rstudioapi, SGP, taxize
RoxygenNote 7.2.3
**Encoding**  UTF-8

**NeedsCompilation**  yes

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**Repository**  CRAN

**Date/Publication**  2023-11-20 15:10:05 UTC

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**R topics documented:**

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Description

Convert between characters and ASCII codes

Usage

asc(char, simplify = TRUE)

chr(ascii)

Arguments

char vector of character strings
simplify logical indicating whether to attempt to convert the result into a vector or matrix object. See sapply for details.
ascii vector or list of vectors containing integer ASCII codes

Value

asc returns the integer ASCII values for each character in the elements of char. If simplify=FALSE the result will be a list containing one vector per element of char. If simplify=TRUE, the code will attempt to convert the result into a vector or matrix.
asc returns the characters corresponding to the provided ASCII values.

Functions

• asc(): return the characters corresponding to the specified ASCII codes
• chr(): return the ASCII codes for the specified characters.

Author(s)

Adapted by Gregory R. Warnes <greg@warnes.net> from code posted by Mark Davis on the 'Data Debrief' blog on 2011-03-09 at https://datadebrief.blogspot.com/2011/03/ascii-code-table-in-r.html.
See Also

strtoi, charToRaw, rawToChar, as.raw

Examples

```r
## ascii codes for lowercase letters
asc(letters)

## uppercase letters from ascii codes
chr(65:90)

## works on multi-character strings
(tmp <- asc("hello!"))
chr(tmp)

## Use 'simplify=FALSE' to return the result as a list
(tmp <- asc("hello!", simplify = FALSE))
chr(tmp)

## When simplify=FALSE the results can be...
asc(c("a", "e", "i", "o", "u", "y")) # a vector
asc(c("ae", "io", "uy")) # or a matrix

## When simplify=TRUE the results are always a list...
asc(c("a", "e", "i", "o", "u", "y"), simplify = FALSE)
asc(c("ae", "io", "uy"), simplify = FALSE)
```

### ASCIIify

**Convert Characters to ASCII**

**Description**

Convert character vector to ASCII, replacing non-ASCII characters with single-byte (\x00) or two-byte (\u0000) codes.

**Usage**

```r
ASCIIify(x, bytes = 2, fallback = "?")
```

**Arguments**

- **x**: a character vector, possibly containing non-ASCII characters.
- **bytes**: either 1 or 2, for single-byte (\x00) or two-byte (\u0000) codes.
- **fallback**: an output character to use, when input characters cannot be converted.
Value

A character vector like x, except non-ASCII characters have been replaced with `\x00` or `\u0000` codes.

Note

To render single backslashes, use these or similar techniques:

```r
write(ASCIIIfy(x), "file.txt")
cat(paste(ASCIIIfy(x), collapse="\n"), "\n", sep="")
```

The resulting strings are plain ASCII and can be used in R functions and datasets to improve package portability.

Author(s)

Arni Magnusson.

See Also

`showNonASCII` identifies non-ASCII characters in a character vector.

Examples

```r
cities <- c("S\u00e3o Paulo", "Reykjav\u00edk")
print(cities)
ASCIIIfy(cities, 1)
ASCIIIfy(cities, 2)

athens <- "\u0391\u03b8\u03ae\u03bd\u03b1"
print(athens)
ASCIIIfy(athens)
```

ask  
Display a prompt and collect the user's response

Description

Display a prompt and collect the user's response

Usage

```r
ask(msg = "Press <RETURN> to continue: ", con = stdin())
```

Arguments

`msg` Character vector providing the message to be displayed
`con` Character connection to query, defaults to stdin().
Details

The prompt message will be displayed, and then `readLines` is used to collect a single input value (possibly empty), which is then returned.

In most situations using the default `con=stdin()` should work properly. Under RStudio, it is necessary to specify `con=file("stdin")` for proper operation.

Value

A character scalar containing the input provided by the user.

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

`readLines`, `scan`

Examples

```r
# use default prompt
ask()

silly <- function() {
  age <- ask("How old are you? ")
  age <- as.numeric(age)
  cat("In 10 years you will be", age + 10, "years old!\n")
}
```

```
assert capture(expression, collapse = "\n") sprint(x, ...)```

---

**assert**

*Defunct Functions in package gtools*

Description

The functions or variables listed here are no longer part of package gtools.

Usage

```r
assert(...) capture(expression, collapse = "\n") sprint(x, ...)```
badDend

Arguments

expression, collapse, x, ...
ignored

Details

- `assert` is a defunct synonym for `stopifnot`.
- `addLast` has been replaced by `lastAdd`, which has the same purpose but applied using different syntax.
- `capture` and `capture.output` have been removed in favor of `capture.output` from the `utils` package.

See Also

`Defunct, stopifnot, lastAdd, capture.output`

---

**badDend**

*Dataset That Crashes Base:::Plot.Dendogram with 'Node Stack Overflow'*

**Description**

Base:::Plot.Dendogram() will generate a 'Node Stack Overflow' when run on a dendrogram appropriately constructed from this data set.

**Format**

The format is: num [1:2047, 1:12] 1 2 3 4 5 6 7 8 9 10 ... - attr(*, "dimnames")=List of 2 ..$ : NULL ..$. : chr [1:12] "X" "V1" "V2" "V3" ...

**Note**

See help page for `unByteCode` to see how to construct the 'bad' dendrogram from this data and how to work around the issue.

**Examples**

data(badDend)
baseOf

Transform an integer to an array of base-n digits

Description

Transform an integer to an array of base-n digits

Usage

baseOf(v, base = 10, len = 1)

Arguments

v A single integer value to be transformed.
base The base to which to transform to.
len The minimal length of the returned array.

Details

This function converts the elements of an integer vector as an array of its digits. The base of the numbering scheme may be changed away from 10, which defines our decimal system, to any other integer value. For base=2, the number is returned in the binary system. The least significant digit has the highest index in the array, i.e. it appears on the right. The highest exponent is at position 1, i.e. left.

To write decimal values in another base is very common in computer science. In particular at the basis 2 the then possible values 0 and 1 are often interpreted as logical false or true. And at the very interface to electrical engineering, it is indicated as an absence or presence of voltage. When several bit values are transported synchronously, then it is common to give every lane of such a data bus a unique 2^x value and interpret it as a number in the binary system. To distinguish 256 characters one once needed 8 bit (“byte”). It is the common unit in which larger non-printable data is presented. Because of the many non-printable characters and the difficulty for most humans to memorize an even longer alphabet, it is presented as two half bytes (“nibble”) of 4 bit in a hexadecimal presentation. Example code is shown below.

For statisticians, it is more likely to use bit representations for hashing. A bit set to 1 (TRUE) at e.g. position 2, 9 or 17 is interpreted as the presence of a particular feature combination of a sample. With baseOf, you can refer to the bit combination as a number, which is more easily and more efficiently dealt with than with an array of binary values. The example code presents a counter of combinations of features which may be interpreted as a Venn diagram.

Author(s)

Steffen Moeller <moeller@debian.org>
Examples

```r
# decimal representation
baseOf(123)

# binary representation
baseOf(123, base = 2)

# octal representation
baseOf(123, base = 8)

# hexadecimal representation
baseOf(123, base = 16)

# hexadecimal with more typical letter-notation
c(0:9, LETTERS)[baseOf(123, 16)]

# hexadecimal again, now showing a single string
paste(c(0:9, LETTERS)[baseOf(123, 16)], collapse = "")

# decimal representation but filling leading zeroes
baseOf(123, len = 5)

# and converting that back
sum(2^(4:0) * baseOf(123, len = 5))

# hashing and a tabular venn diagram derived from it
m <- matrix(sample(c(FALSE, TRUE), replace = TRUE, size = 300), ncol = 4)
colnames(m) <- c("strong", "colorful", "nice", "humorous")
names(dimnames(m)) <- c("samples", "features")
head(m)

m.val <- apply(m, 1, function(X) {
  return(sum(2^((ncol(m) - 1):0) * X))
})
m.val.rle <- rle(sort(m.val))
m.counts <- cbind(
  baseOf(m.val.rle$value, base = 2, len = ncol(m)),
  m.val.rle$lengths
)
colnames(m.counts) <- c(colnames(m), "num")
rownames(m.counts) <- apply(m.counts[, 1:ncol(m)], 1, paste, collapse = "")
m.counts[1 == m.counts[, "nice"] & 1 == m.counts[, "humorous"], , drop = FALSE]
m.counts[, "num", drop = TRUE]
```

---

**binsearch**

**Binary Search**
Description

Search within a specified range to locate an integer parameter which results in the specified monotonic function obtaining a given value.

Usage

```r
binsearch(
    fun,
    range,
    ...,
    target = 0,
    lower = ceiling(min(range)),
    upper = floor(max(range)),
    maxiter = 100,
    showiter = FALSE
)
```

Arguments

- `fun` Monotonic function over which the search will be performed.
- `range` 2-element vector giving the range for the search.
- `...` Additional parameters to the function `fun`.
- `target` Target value for `fun`. Defaults to 0.
- `lower` Lower limit of search range. Defaults to `min(range)`.
- `upper` Upper limit of search range. Defaults to `max(range)`.
- `maxiter` Maximum number of search iterations. Defaults to 100.
- `showiter` Boolean flag indicating whether the algorithm state should be printed at each iteration. Defaults to FALSE.

Details

This function implements an extension to the standard binary search algorithm for searching a sorted list. The algorithm has been extended to cope with cases where an exact match is not possible, to detect whether that the function may be monotonic increasing or decreasing and act appropriately, and to detect when the target value is outside the specified range.

The algorithm initializes two variable `lo` and `hi` to the extremes values of `range`. It then generates a new value `center` halfway between `lo` and `hi`. If the value of `fun` at center exceeds `target`, it becomes the new value for `lo`, otherwise it becomes the new value for `hi`. This process is iterated until `lo` and `hi` are adjacent. If the function at one or the other equals the target, this value is returned, otherwise `lo`, `hi`, and the function value at both are returned.

Note that when the specified target value falls between integers, the two closest values are returned. If the specified target falls outside of the specified range, the closest endpoint of the range will be returned, and an warning message will be generated. If the maximum number of iterations was reached, the endpoints of the current subset of the range under consideration will be returned.
binsearch

Value
A list containing:

- **call**: How the function was called.
- **numiter**: The number of iterations performed.
- **flag**: One of the strings, "Found", "Between Elements", "Maximum number of iterations reached", "Reached lower boundary", or "Reached upper boundary."
- **where**: One or two values indicating where the search terminated.
- **value**: Value of the function fun at the values of where.

Note
This function often returns two values for where and value. Be sure to check the flag parameter to see what these values mean.

Author(s)
Gregory R. Warnes <greg@warnes.net>

See Also
optim, optimize, uniroot

Examples

### Toy examples

```r
# search for x=10
binsearch(function(x) x - 10, range = c(0, 20))
```

```r
# search for x=10.1
binsearch(function(x) x - 10.1, range = c(0, 20))
```

### Classical toy example

```r
# binary search for the index of 'M' among the sorted letters
fun <- function(X) {
  ifelse(LETTERS[X] > "M", 1,
         ifelse(LETTERS[X] < "M", -1, 0)
  )
}
binsearch(fun, range = 1:26)
# returns $where=13
LETTERS[13]
```

### Substantive example, from genetics

```r
# Not run:
```
library(genetics)
# Determine the necessary sample size to detect all alleles with
# frequency 0.07 or greater with probability 0.95.
power.fun <- function(N) 1 - gregorius(N = N, freq = 0.07)$missprob

binsearch(power.fun, range = c(0, 100), target = 0.95)

# equivalent to
gregorius(freq = 0.07, missprob = 0.05)

## End(Not run)

capwords

Capitalize Words for Titles

Description

This function capitalizes words for use in titles

Usage

capwords(
  s,
  strict = FALSE,
  AP = TRUE,
  onlyfirst = FALSE,
  preserveMixed = FALSE,
  sep = " ",
)

Arguments

s character string to be processed
strict Logical, remove all additional capitalization.
AP Logical, apply the Associated Press (AP) rules for prepositions and conjunctions that should not be capitalized in titles.
onlyfirst Logical, only capitalize the first word.
preserveMixed Logical, preserve the capitalization mixed-case words containing an upper-case letter after a lower-case letter.
sep Character string, word separator
Details

This function separates the provided character string into separate words using sep as the word separator. If `firstonly==TRUE`, it then capitalizes the first letter the first word, otherwise (the default), it capitalizes the first letter of every word. If `AP==TRUE`, it then un-capitalizes words in the Associated Press's (AP) list of prepositions and conjunctions should not be capitalized in titles. Next, it capitalizes the first word. It then re-joins the words using the specified separator.

If `preserveMixed==TRUE`, words with an upper-case letter appearing after a lower-case letter will not be changed (e.g. "iDevice").

Value

A character scalar containing the capitalized words.

Author(s)

Gregory R. Warnes <greg@warnes.net> based on code from the `chartr` manual page, and Scott Chamberlain's `taxize_capwords` in the taxize package.

References


See Also

`chartr`, `taxize_capwords`, `capwords`

Examples

capwords("a function to capitalize words in a title")
capwords("a function to capitalize words in a title", AP = FALSE)

capwords("testing the iProduct for defects")
capwords("testing the iProduct for defects", strict = TRUE)
capwords("testing the iProduct for defects", onlyfirst = TRUE)
capwords("testing the iProduct for defects", preserveMixed = TRUE)

capwords("title_using_underscores_as_separators", sep = "_")
checkRVersion  

Check if a newer version of R is available

Description

Check if a newer version of R is available

Usage

checkRVersion(quiet = FALSE)

Arguments

quiet  Logical indicating whether printed output should be suppressed.

Details

This function accesses the R web site to discover the latest released version of R. It then compares this version to the running version. If the running version is the same as the latest version, it prints the message, "The latest version of R is installed:" followed by the version number, and returns NULL. If the running version is older than the current version, it displays the message, "A newer version of R is now available:" followed by the corresponding version number, and returns the version number.

If quiet=TRUE, no printing is performed.

Value

Either the version number of the latest version of R, if the running version is less than the latest version, or NULL.

Note

This function uses the internet to access the R project web site. If internet access is unavailable or the R project web site is down, the function will fail.

Author(s)

Gregory R. Warnes

See Also

R.Version
**combinations**

**Examples**

```r
try(
   ver <- checkRVersion()
)
print(ver)
```

---

<table>
<thead>
<tr>
<th>combinations</th>
<th>Enumerate the Combinations or Permutations of the Elements of a Vector</th>
</tr>
</thead>
</table>

**Description**

`combinations` enumerates the possible combinations of a specified size from the elements of a vector. `permutations` enumerates the possible permutations.

**Usage**

```r
combinations(n, r, v = 1:n, set = TRUE, repeats.allowed = FALSE)
permutations(n, r, v = 1:n, set = TRUE, repeats.allowed = FALSE)
```

**Arguments**

- `n` Size of the source vector
- `r` Size of the target vectors
- `v` Source vector. Defaults to `1:n`
- `set` Logical flag indicating whether duplicates should be removed from the source vector `v`. Defaults to `TRUE`.
- `repeats.allowed` Logical flag indicating whether the constructed vectors may include duplicated values. Defaults to `FALSE`.

**Details**

Caution: The number of combinations and permutations increases rapidly with `n` and `r`!.

To use values of `n` above about 45, you will need to increase R’s recursion limit. See the `expression` argument to the `options` command for details on how to do this.

Taken from an email by Brian D Ripley <ripley@stats.ox.ac.uk> to r-help dated Tue, 14 Dec 1999 11:14:04 +0000 (GMT) in response to Alex Ahgarin <datamanagement@email.com>. Original version was named "subsets" and was Written by Bill Venables.

**Value**

Returns a matrix where each row contains a vector of length `r`. 
Author(s)

Original versions by Bill Venables <Bill.Venables@cmis.csiro.au>. Extended to handle repeats.allowed by Gregory R. Warnes <greg@warnes.net>.

References


See Also

choose, options

Examples

```r
combinations(3,2,letters[1:3])
combinations(3,2,letters[1:3],repeats=TRUE)

permutations(3,2,letters[1:3])
permutations(3,2,letters[1:3],repeats=TRUE)

## Not run:
# To use large 'n', you need to change the default recursion limit
options(expressions=1e5)
cmat <- combinations(300,2)
dim(cmat) # 44850 by 2

## End(Not run)
```

defmacro Define a macro

defmacro define a macro that uses R expression replacement

Usage

defmacro(..., expr)

strmacro(..., expr, strexpr)

Arguments

.. macro argument list

expr R expression defining the macro body

strexpr character string defining the macro body
defmacro

Details

strmacro define a macro that uses string replacement
defmacro and strmacro create a macro from the expression given in expr, with formal arguments given by the other elements of the argument list.

A macro is similar to a function definition except for handling of formal arguments. In a function, formal arguments are simply variables that contains the result of evaluating the expressions provided to the function call. In contrast, macros actually modify the macro body by replacing each formal argument by the expression (defmacro) or string (strmacro) provided to the macro call.

For defmacro, the special argument name DOTS will be replaced by ... in the formal argument list of the macro so that ... in the body of the expression can be used to obtain any additional arguments passed to the macro. For strmacro you can mimic this behavior providing a DOTS="" argument. This is illustrated by the last example below.

Macros are often useful for creating new functions during code execution.

Value

A macro function.

Note

Note that because [the defmacro code] works on the parsed expression, not on a text string, defmacro avoids some of the problems of traditional string substitution macros such as strmacro and the C preprocessor macros. For example, in

mul <- defmacro(a, b, expr=(a*b))

a C programmer might expect mul(i, j + k) to expand (incorrectly) to i*j + k. In fact it expands correctly, to the equivalent of i*(j + k).

For a discussion of the differences between functions and macros, please Thomas Lumley’s R-News article (reference below).

Author(s)

Thomas Lumley wrote defmacro. Gregory R. Warnes <greg@warnes.net> enhanced it and created strmacro.

References

The original defmacro code was directly taken from:


See Also

function substitute, eval, parse, source, parse,
Examples

```r
###
# macro for replacing a specified missing value indicator with NA
# within a dataframe
###
setNA <- defmacro(df, var, values,
  expr = {
    df$var[df$var %in% values] <- NA
  }
)

# create example data using 999 as a missing value indicator
d <- data.frame(
  V1 = c(1, 2, 3, 4, 5, 6, 999, 8, 9, 10),
  V2 = c(1, 1, 1, 1, 1, 2, 999, 2, 999, 999),
  stringsAsFactors = TRUE
)

d
# Try it out
setNA(d, V1, 999)
setNA(d, V2, 999)

d
###
# Expression macro
###
plot.d <- defmacro(df, var, DOTS,
  col = "red", title = "", expr =
  plot(df$var ~ df$Grp, type = "b", col = col, main = title, ...)
)

plot.d(d, V1)
plot.d(d, V1, col = "blue")
plot.d(d, V1, lwd = 4) # use optional 'DOTS' argument

###
# String macro (note the quoted text in the calls below)
#
# This style of macro can be useful when you are reading
# function arguments from a text file
###
plot.s <- strmacro(DF, VAR,
  COL = "red", TITLE = "", DOTS = "", expr =
  plot(DF$VAR ~ DF$Grp, type = "b", col = COL, main = TITLE, DOTS)
)

plot.s("d", "V1")
plot.s(DF = "d", VAR = "V1", COL = "blue")
```
Functions for the Dirichlet Distribution

Description

Functions to compute the density of or generate random deviates from the Dirichlet distribution

Usage

ddirichlet(x, alpha)

rdirichlet(n, alpha)

Arguments

x A vector containing a single random deviate or matrix containing one random deviate per row.

alpha Vector or (for ddirichlet) matrix containing shape parameters.

n Number of random vectors to generate.

Details

The Dirichlet distribution is the multidimensional generalization of the beta distribution. It is the canonical Bayesian distribution for the parameter estimates of a multinomial distribution.

Value

ddirichlet returns a vector containing the Dirichlet density for the corresponding rows of x.

rdirichlet returns a matrix with n rows, each containing a single Dirichlet random deviate.
Functions

- `ddirichlet()`: Dirichlet distribution function.
- `rdirichlet()`: Generate dirichlet random deviates.

Author(s)

Code original posted by Ben Bolker to R-News on Fri Dec 15 2000. See https://stat.ethz.ch/pipermail/r-help/2000-December/009561.html. Ben attributed the code to Ian Wilson <i.wilson@maths.abdn.ac.uk>. Subsequent modifications by Gregory R. Warnes <greg@warnes.net>.

See Also

`dbeta`, `rbeta`

Examples

```r
x <- rdirichlet(20, c(1, 1, 1))
ddirichlet(x, c(1, 1, 1))
```

---

ELISA  
Data from an ELISA assay

Description

Observed signals and (for some observations) nominal concentrations for samples that were aliquoted to multiple assay plates, which were read multiple times on multiple days.

Format

a data frame with the following columns:

- PlateDay factor. Specifies one of four physically distinct 96 well plates
- Read factor. The signal was read 3 times for each plate.
- Description character. Indicates contents of sample.
- Concentration numeric. Nominal concentration of standards (NA for all other samples).
- Signal numeric. Assay signal. Specifically, optical density (a colorimetric assay).

Source

Anonymized data.
foldchange

Compute fold-change or convert between log-ratio and fold-change.

Description

foldchange computes the fold change for two sets of values. logratio2foldchange converts values from log-ratios to fold changes. foldchange2logratio does the reverse.

Usage

foldchange(num, denom)
logratio2foldchange(logratio, base = 2)
foldchange2logratio(foldchange, base = 2)

Arguments

num, denom vector/matrix of numeric values
logratio vector/matrix of log-ratio values
base Exponential base for the log-ratio.
foldchange vector/matrix of fold-change values

Details

Fold changes are commonly used in the biological sciences as a mechanism for comparing the relative size of two measurements. They are computed as: \( \frac{num}{denom} \) if \( num > denom \), and as \( -\frac{denom}{num} \) otherwise.

Fold-changes have the advantage of ease of interpretation and symmetry about \( num = denom \), but suffer from a discontinuity between -1 and 1, which can cause significant problems when performing data analysis. Consequently statisticians prefer to use log-ratios.

Value

A vector or matrix of the same dimensions as the input containing the converted values.

Functions

- foldchange(): Compute fold-change.
- logratio2foldchange(): Compute foldchange from log-ratio values.
- foldchange2logratio(): Compute log-ratio from fold-change values.

Author(s)

Gregory R. Warnes <greg@warnes.net>
getDependencies

Examples

```r
a <- 1:21
b <- 21:1
f <- foldchange(a, b)
cbind(a, b, f)
```

getDependencies  Get package dependencies

Description

Get package dependencies

Usage

```r
getDependencies(
  pkgs,
  dependencies = c("Depends", "Imports", "LinkingTo"),
  installed = TRUE,
  available = TRUE,
  base = FALSE,
  recommended = FALSE
)
```

Arguments

- `pkgs`: character vector of package names
- `dependencies`: character vector of dependency types to include. Choices are "Depends", "Imports", "LinkingTo", "Suggests", and "Enhances". Defaults to c("Depends", "Imports", "LinkingTo").
- `installed`: Logical indicating whether to pull dependency information from installed packages. Defaults to TRUE.
- `available`: Logical indicating whether to pull dependency information from available packages. Defaults to TRUE.
- `base`: Logical indicating whether to include dependencies on base packages that are included in the R installation. Defaults to FALSE.
- `recommended`: Logical indicating whether to include dependencies on recommended packages that are included in the R installation. Defaults to FALSE.

Details

This function recursively constructs the list of dependencies for the packages given by `pkgs`. By default, the dependency information is extracted from both installed and available packages. As a consequence, it works both for local and CRAN packages.
Value

A character vector of package names.

Note

If available=TRUE R will attempt to access the currently selected CRAN repository, prompting for one if necessary.

Author(s)

Gregory R. Warnes <greg@warnes.net> based on the non exported utils:::getDependencies and utils:::.clean_up_dependencies2.

See Also

installed.packages, available.packages

Examples

## Not run:
## A locally installed package
#' getDependencies("MASS", installed = TRUE, available = FALSE)

## A package on CRAN
getDependencies("gregmisc", installed = FALSE, available = TRUE)

## Show base and recommended dependencies
getDependencies("MASS", available = FALSE, base = TRUE, recommended = TRUE)

## Download the set of packages necessary to support a local package
deps <- getDependencies("MyLocalPackage", available = FALSE)
download.packages(deps, destdir = ".R_Packages")

## End(Not run)

gtools-deprecated  Deprecated Functions in the gtools package

Description

These functions are provided for compatibility with older versions of gtools, and may be defunct as soon as the next release.

Details

gtools currently contains no deprecated functions.
help("oldName-deprecated") (note the quotes).
Test if a value is missing, empty, contains only NA or NULL values, or is a try-error.

**Description**
Test if a value is missing, empty, contains only NA or NULL values, or is a try-error.

**Usage**
invalid(x)

**Arguments**
x  value to be tested

**Value**
Logical value.

**Author(s)**
Gregory R. Warnes <greg@warnes.net>

**See Also**
missing, is.na, is.null

**Examples**

```r
invalid(NA)
invalid()
invalid(c(NA, NA, NULL, NA))
invalid(list(a = 1, b = NULL))
x <- try(log("A"))
invalid(x)
```

# example use in a function
myplot <- function(x, y) {
  if (invalid(y)) {
    y <- x
    x <- 1:length(y)
  }
  # remaining code of the function
}``
keywords

} plot(x, y)
}
myplot(1:10)
myplot(1:10, NA)

---

list_valid_keywords_for_r_man_pages

Description

List valid keywords for R man pages

Usage

keywords(topic)

Arguments

topic : object or man page topic

Details

If topic is provided, return a list of the keywords associated with topic. Otherwise, display the list of valid R keywords from the R doc/KEYWORDS file.

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

help

Examples

## Show all valid R keywords
## Not run:
keywords()

## Show keywords associated with the 'merge' function
keywords(merge)
keywords("merge")

## End(Not run)
lastAdd

Non-destructively construct a .Last function to be executed when R exits.

Description

Non-destructively construct a .Last function to be executed when R exits.

Usage

lastAdd(fun)

Arguments

fun Function to be called.

Details

lastAdd constructs a new function which can be used to replace the existing definition of .Last, which will be executed when R terminates normally.

If a .Last function already exists in the global environment, the original definition is stored in a private environment, and the new function is defined to call the function fun and then to call the previous (stored) definition of .Last.

If no .Last function exists in the global environment, lastAdd simply returns the function fun.

Value

A new function to be used for .Last.

Note

This function replaces the (now defunct) addLast function.

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

.Last
Examples

```r
## Print a couple of cute messages when R exits.
helloWorld <- function() cat("\nHello World!\n")
byeWorld <- function() cat("\nGoodbye World!\n")

.Last <- lastAdd(byeWorld)
.Last <- lastAdd(helloWorld)

## Not run:
q("no")

## Should yield:
##
## Save workspace image? [y/n/c]: n
##
## Hello World!
##
## Goodbye World!
##
## Process R finished at Tue Nov 22 10:28:55 2005
##
## End(Not run)
```

---

**loadedPackages**  
*Provide Name, Version, and Path of Loaded Package Namespaces*

**Description**  
Provide name, version, and path of loaded package namespaces

**Usage**  
```r
loadedPackages(silent = FALSE)
```

**Arguments**  
- `silent` Logical indicating whether the results should be printed

**Value**  
Invisibly returns a data frame containing one row per loaded package namespace, with columns:
- `Package` Package name
- `Version` Version string
- `Path` Path to package files
Generalized logit and inverse logit function

Description

Compute generalized logit and generalized inverse logit functions.

Usage

logit(x, min = 0, max = 1)

inv.logit(x, min = 0, max = 1)

Arguments

x value(s) to be transformed
min Lower end of logit interval
max Upper end of logit interval

Details

The generalized logit function takes values on [min, max] and transforms them to span [-Inf,Inf] it is defined as:

\[ y = \log\left( \frac{p}{1 - p} \right) \]

where

\[ p = \frac{(x - \text{min})}{(\text{max} - \text{min})} \]
The generalized inverse logit function provides the inverse transformation:

\[ x = p'(max - min) + min \]

where

\[ p' = \frac{exp(y)}{1 + exp(y)} \]

Value

Transformed value(s).

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

logit

Examples

\[
\begin{align*}
x & \leftarrow \text{seq}(0, 10, \text{by} = 0.25) \\
x_t & \leftarrow \text{logit}(x, \text{min} = 0, \text{max} = 10) \\
\text{cbind}(x, x_t) \\
y & \leftarrow \text{inv.logit}(x_t, \text{min} = 0, \text{max} = 10) \\
\text{cbind}(x, x_t, y)
\end{align*}
\]

mixedsort

Order or Sort strings with embedded numbers so that the numbers are in the correct order

Description

These functions sort or order character strings containing embedded numbers so that the numbers are numerically sorted rather than sorted by character value. I.e. "Aspirin 50mg" will come before "Aspirin 100mg". In addition, case of character strings is ignored so that "a", will come before "B" and "C".
Usage

mixedsort(
  x,
  decreasing = FALSE,
  na.last = TRUE,
  blank.last = FALSE,
  numeric.type = c("decimal", "roman"),
  roman.case = c("upper", "lower", "both"),
  scientific = TRUE
)

mixedorder(
  x,
  decreasing = FALSE,
  na.last = TRUE,
  blank.last = FALSE,
  numeric.type = c("decimal", "roman"),
  roman.case = c("upper", "lower", "both"),
  scientific = TRUE
)

Arguments

x Vector to be sorted.
decreasing logical. Should the sort be increasing or decreasing? Note that descending=TRUE reverses the meanings of na.last and blank.last.
na.last for controlling the treatment of NA values. If TRUE, missing values in the data are put last; if FALSE, they are put first; if NA, they are removed.
blank.last for controlling the treatment of blank values. If TRUE, blank values in the data are put last; if FALSE, they are put first; if NA, they are removed.
numeric.type either "decimal" (default) or "roman". Are numeric values represented as decimal numbers (numeric.type="decimal") or as Roman numerals (numeric.type="roman")?
roman.case one of "upper", "lower", or "both". Are roman numerals represented using only capital letters ("IX") or lower-case letters ("ix") or both?
scientific logical. Should exponential notation be allowed for numeric values.

Details

I often have character vectors (e.g. factor labels), such as compound and dose, that contain both text and numeric data. This function is useful for sorting these character vectors into a logical order.

It does so by splitting each character vector into a sequence of character and numeric sections, and then sorting along these sections, with numbers being sorted by numeric value (e.g. "50" comes before "100"), followed by characters strings sorted by character value (e.g. "A" comes before "B") ignoring case (e.g. 'A' has the same sort order as 'a').

By default, sort order is ascending, empty strings are sorted to the front, and NA values to the end. Setting descending=TRUE changes the sort order to descending and reverses the meanings of na.last and blank.last.
Parsing looks for decimal numbers unless numeric.type="roman", in which parsing looks for roman numerals, with character case specified by roman.case.

Value

mixedorder returns a vector giving the sort order of the input elements. mixedsort returns the sorted vector.

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

sort, order

Examples

```r
## compound & dose labels
Treatment <- c("Control", "Aspirin 10mg/day", "Aspirin 50mg/day", "Aspirin 100mg/day", "Acetomycin 100mg/day", "Acetomycin 1000mg/day")

## ordinary sort puts the dosages in the wrong order
sort(Treatment)

## but mixedsort does the 'right' thing
mixedsort(Treatment)

## Here is a more complex example
x <- rev(c("AA 0.50 ml", "AA 1.5 ml", "AA 500 ml", "AA 1500 ml", "EXP 1", "AA 1e3 ml", "A A A", "1 2 3 A", "NA", NA, "1e2", ",", "-", "1A", "1 A", "100", "100A", "Inf")

mixedorder(x)

mixedsort(x) # Notice that plain numbers, including 'Inf' show up before strings, NAs at the end, and blanks at the beginning.

mixedsort(x, na.last = TRUE) # default
mixedsort(x, na.last = FALSE) # push NAs to the front

mixedsort(x, blank.last = FALSE) # default
mixedsort(x, blank.last = TRUE) # push blanks to the end
```
mixedsort(x, decreasing = FALSE) # default
mixedsort(x, decreasing = TRUE) # reverse sort order

## Roman numerals
chapters <- c(
    "V. Non Sequiturs", "II. More Nonsense",
    "I. Nonsense", "IV. Nonesensical Citations",
    "III. Utter Nonsense"
)
mixedsort(chapters, numeric.type = "roman")

## Lower-case Roman numerals
vals <- c(
    "xix", "xii", "mcv", "iii", "iv", "dcxxxii", "cdxii",
    "dcxii", "dci", "cci"
)
(ordered <- mixedsort(vals, numeric.type = "roman", roman.case = "lower"))
roman2int(ordered)

## Control scientific notation for number matching:
vals <- c("3E1", "2E3", "4E0")
mixedsort(vals) # With scientific notation
mixedsort(vals, scientific = FALSE) # Without scientific notation

---

**na.replace**  
*Replace Missing Values*

**Description**
Replace missing values

**Usage**

na.replace(x, replace, ...)

**Arguments**

- **x** vector possibly containing missing (NA) values
- **replace** either a scalar replacement value, or a function returning a scalar value
- **...** Optional arguments to be passed to replace

**Details**
This is a convenience function that is the same as x[is.na(x)] <- replace

**Value**
Vector with missing values (NA) replaced by the value of replace.
oddeven

Author(s)
Gregory R. Warnes <greg@warnes.net>

See Also
is.na, na.omit

Examples

x <- c(1, 2, 3, NA, 6, 7, 8, NA, NA)

# Replace with a specified value
na.replace(x, "999")

# Replace with the calculated median
na.replace(x, median, na.rm = TRUE)

oddeven

Detect odd/even integers

Description
detect odd/even integers

Usage

odd(x)

even(x)

Arguments

x vector of integers

Value

Vector of TRUE/FALSE values.

Author(s)
Gregory R. Warnes <greg@warnes.net>

See Also
round
Examples

```r
odd(4)
even(4)
odd(1:10)
even(1:10)
```

---

**permute**

*Randomly Permute the Elements of a Vector*

Description

Randomly Permute the elements of a vector

Usage

```r
permute(x)
```

Arguments

- `x` Vector of items to be permuted

Details

This is simply a wrapper function for `sample`.

Value

Vector with the original items reordered.

Author(s)

Gregory R. Warnes <greg@warner.net>

See Also

`sample`

Examples

```r
x <- 1:10
permute(x)
```
Create a Factor Variable Using the Quantiles of a Continuous Variable

Description

Create a factor variable using the quantiles of a continuous variable.

Usage

quantcut(x, q = 4, na.rm = TRUE, ...)

Arguments

x        Continuous variable.
q        Either a integer number of equally spaced quantile groups to create, or a vector
         of quantiles used for creating groups. Defaults to q=4 which is equivalent to
         q=seq(0, 1, by=0.25). See quantile for details.
na.rm    Boolean indicating whether missing values should be removed when computing
         quantiles. Defaults to TRUE.
...      Optional arguments passed to cut.

Details

This function uses quantile to obtain the specified quantiles of x, then calls cut to create a factor
variable using the intervals specified by these quantiles.

It properly handles cases where more than one quantile obtains the same value, as in the second
example below. Note that in this case, there will be fewer generated factor levels than the specified
number of quantile intervals.

Value

Factor variable with one level for each quantile interval.

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

cut, quantile
Examples

```r
## create example data
# testonly{
set.seed(1234)
# }
x <- rnorm(1000)

## cut into quartiles
quartiles <- quantcut(x)
table(quartiles)

## cut into deciles
deciles.1 <- quantcut(x, 10)
table(deciles.1)
# or equivalently
deciles.2 <- quantcut(x, seq(0, 1, by = 0.1))

# testonly{
stopifnot(identical(deciles.1, deciles.2))
# }

## show handling of 'tied' quantiles.
x <- round(x) # discretize to create ties
stem(x) # display the ties
deciles <- quantcut(x, 10)
table(deciles) # note that there are only 5 groups (not 10)
# due to duplicates
```

<table>
<thead>
<tr>
<th>roman2int</th>
<th>Convert Roman Numerals to Integers</th>
</tr>
</thead>
</table>

Description

Convert roman numerals to integers

Usage

```r
roman2int(roman)
```

Arguments

- `roman` character vector containing roman numerals

Details

This function will convert roman numerals to integers without the upper bound imposed by R (3899), ignoring case.
Value

A integer vector with the same length as \( \text{roman} \). Character strings which are not valid roman numerals will be converted to NA.

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

\( \text{as.roman} \)

Examples

\[
\begin{align*}
\text{roman2int(c("I", "V", "X", "C", "L", "D", "M"))} \\
# \text{works regardless of case} \\
\text{roman2int("MMXVI")} \\
\text{roman2int("mmxvi")} \\
# \text{works beyond R's limit of 3899} \\
\text{val.3899 <- "MMMMDCCCCCIX"} \\
\text{val.3900 <- "MMMMCM"} \\
\text{val.4000 <- "MMMMM"} \\
\text{as.numeric(as.roman(val.3899))} \\
\text{as.numeric(as.roman(val.3900))} \\
\text{as.numeric(as.roman(val.4000))} \\
\text{roman2int(val.3899)} \\
\text{roman2int(val.3900)} \\
\text{roman2int(val.4000)}
\end{align*}
\]

Description

Applies a function over subsets of the vector(s) formed by taking a fixed number of previous points.

Usage

\[
\text{running(} \\
\text{X,} \\
\text{Y = NULL,} \\
\text{fun = mean,} \\
\text{width = min(length(X), 20),} \\
\text{allow.fewer = FALSE,}
\text{)}
\]
running

```r
pad = FALSE,
align = c("right", "center", "left"),
simplify = TRUE,
by,
...
```

**Arguments**

- **X**: data vector
- **Y**: data vector (optional)
- **fun**: Function to apply. Default is `mean`
- **width**: Integer giving the number of vector elements to include in the subsets. Defaults to the lesser of the length of the data and 20 elements.
- **allow.fewer**: Boolean indicating whether the function should be computed for subsets with fewer than `width` points
- **pad**: Boolean indicating whether the returned results should be 'padded' with NAs corresponding to sets with less than `width` elements. This only applies when `allow.fewer` is FALSE.
- **align**: One of "right", "center", or "left". This controls the relative location of 'short' subsets with less than `width` elements: "right" allows short subsets only at the beginning of the sequence so that all of the complete subsets are at the end of the sequence (i.e. 'right aligned'), "left" allows short subsets only at the end of the data so that the complete subsets are 'left aligned', and "center" allows short subsets at both ends of the data so that complete subsets are 'centered'.
- **simplify**: Boolean. If FALSE the returned object will be a list containing one element per evaluation. If TRUE, the returned object will be coerced into a vector (if the computation returns a scalar) or a matrix (if the computation returns multiple values). Defaults to FALSE.
- **by**: Integer separation between groups. If `by=width` will give non-overlapping windows. Default is missing, in which case groups will start at each value in the X/Y range.

**Details**

`running` applies the specified function to a sequential windows on `X` and (optionally) `Y`. If `Y` is specified the function must be bivariate.

**Value**

List (if `simplify==TRUE`), vector, or matrix containing the results of applying the function `fun` to the subsets of `X` (running) or `X` and `Y`.

Note that this function will create a vector or matrix even for objects which are not simplified by `sapply`. 
Author(s)

Gregory R. Warnes <greg@warnes.net>, with contributions by Nitin Jain <nitin.jain@pfizer.com>.

See Also

wapply to apply a function over an x-y window centered at each x point, sapply, lapply

Examples

```r
# show effect of pad
running(1:20, width = 5)
running(1:20, width = 5, pad = TRUE)

# show effect of align
running(1:20, width = 5, align = "left", pad = TRUE)
running(1:20, width = 5, align = "center", pad = TRUE)
running(1:20, width = 5, align = "right", pad = TRUE)

# show effect of simplify
running(1:20, width = 5, fun = function(x) x) # matrix
running(1:20, width = 5, fun = function(x) x, simplify = FALSE) # list

# show effect of by
running(1:20, width = 5) # normal
running(1:20, width = 5, by = 5) # non-overlapping
running(1:20, width = 5, by = 2) # starting every 2nd

# Use 'pad' to ensure correct length of vector, also show the effect
# of allow.fewer.
par(mfrow = c(2, 1))
plot(1:20, running(1:20, width = 5, allow.fewer = FALSE, pad = TRUE), type = "b")
plot(1:20, running(1:20, width = 5, allow.fewer = TRUE, pad = TRUE), type = "b")
par(mfrow = c(1, 1))

# plot running mean and central 2 standard deviation range
# estimated by *last* 40 observations
dat <- rnorm(500, sd = 1 + (1:500) / 500)
plot(dat)
sdfun <- function(x, sign = 1) mean(x) + sign * sqrt(var(x))
lines(running(dat, width = 51, pad = TRUE, fun = mean), col = "blue")
lines(running(dat, width = 51, pad = TRUE, fun = sdfun, sign = -1), col = "red")
lines(running(dat, width = 51, pad = TRUE, fun = sdfun, sign = 1), col = "red")

# plot running correlation estimated by last 40 observations (red)
# against the true local correlation (blue)
sd.Y <- seq(0, 1, length = 500)
X <- rnorm(500, sd = 1)
```
Y <- rnorm(500, sd = sd.Y)

plot(running(X, X + Y, width = 20, fun = cor, pad = TRUE), col = "red", type = "s")

r <- 1 / sqrt(1 + sd.Y^2) # true cor of (X,X+Y)
lines(r, type = "l", col = "blue")

---

scat 

Display debugging text

Description

If `getOption('DEBUG')`==TRUE, write text to STDOUT and flush so that the text is immediately displayed. Otherwise, do nothing.

Usage

scat(...)

Arguments

... Arguments passed to `cat`

Value

NULL (invisibly)

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

cat

Examples

options(DEBUG = NULL) # make sure DEBUG isn't set
scat("Not displayed")

options(DEBUG = TRUE)
scat("This will be displayed immediately (even in R BATCH output \n")
scat("files), provided options()$DEBUG is TRUE.")
Determine the directory or full path to the currently executing script

**Description**

Determine the directory or full path to the currently executing script

**Usage**

script_file(fail = c("stop", "warning", "quiet"))

script_path(fail = c("stop", "warning", "quiet"))

**Arguments**

- **fail**: character, one of "stop", "warning", "quiet". specifying what should be done when the script path cannot be determined: "stop" causes an error to be generated, "warn" generates a warning message and returns NA, "quiet" silently returns NA.

  These function should work with Rscript, source(), Rmarkdown RStudio's "Run selection", and the RStudio Console.

**Value**

A character scalar containing the full path to the currently executing script file (script_file) or its directory (script_path). If unable to determine the script path, it generates a warning and returns "" (empty string).

**Functions**

- script_file(): Determine the full path of the currently executing script
- script_path(): Determine the directory of the currently executing script

**Author(s)**

Greg Warnes <greg@warnes.net> based on on a Stack Overflow post by jerry-t (https://stackoverflow.com/users/2292993/jerry-t) at https://stackoverflow.com/a/36777602/2744062.

**Examples**

getwd()
commandArgs(trailingOnly = FALSE)

script_file("warning")
script_path("warning")
Description

Modify the TCP_NODELAY ('de-Nagle') flag for socket objects

Usage

setTCPNoDelay(socket, value = TRUE)

Arguments

socket A socket connection object
value Logical indicating whether to set (TRUE) or unset (FALSE) the flag

Details

By default, TCP connections wait a small fixed interval before actually sending data, in order to permit small packets to be combined. This algorithm is named after its inventor, John Nagle, and is often referred to as 'Nagling'.

While this reduces network resource utilization in these situations, it imposes a delay on all outgoing message data, which can cause problems in client/server situations.

This function allows this feature to be disabled (de-Nagling, value=TRUE) or enabled (Nagling, value=FALSE) for the specified socket.

Value

The character string "SUCCESS" will be returned invisible if the operation was successful. On failure, an error will be generated.

Author(s)

Gregory R. Warnes <greg@warnes.net>

References

"Nagle's algorithm" [https://en.wikipedia.org/wiki/Nagle’s_algorithm],

See Also

make.socket, socketConnection
## smartbind

### Efficient rbind of data frames, even if the column names don’t match

#### Description

Efficient rbind of data frames, even if the column names don’t match

#### Usage

smartbind(..., list, fill = NA, sep = ":", verbose = FALSE)

#### Arguments

- ...: Data frames to combine
- list: List containing data frames to combine
- fill: Value to use when ‘filling’ missing columns. Defaults to NA.
- sep: Character string used to separate column names when pasting them together.
- verbose: Logical flag indicating whether to display processing messages. Defaults to FALSE.

#### Value

The returned data frame will contain:

- **columns**: all columns present in any provided data frame
- **rows**: a set of rows from each provided data frame, with values in columns not present in the given data frame filled with missing (NA) values.

The data type of columns will be preserved, as long as all data frames with a given column name agree on the data type of that column. If the data frames disagree, the column will be converted into a character strings. The user will need to coerce such character columns into an appropriate type.


**split_path**

**Description**

This function converts a character scalar containing a *valid* file path into a character vector of path components (e.g. directories).

**Usage**

```r
split_path(x, depth_first = TRUE)
```

**Arguments**

- `x`: character scalar. Path to be processed.
- `depth_first`: logical. Should path be returned depth first? Defaults to `TRUE`.

**Value**

Character vector of path components, depth first.

**Examples**

```r
df1 <- data.frame(A = 1:10, B = LETTERS[1:10], C = rnorm(10))
df2 <- data.frame(A = 11:20, D = rnorm(10), E = letters[1:10])

# rbind would fail
## Not run:
brbind(df1, df2)
# Error in match.names(clabs, names(xi)) : names do not match previous
# names:
# D, E

## End(Not run)
# but smartbind combines them, appropriately creating NA entries
smartbind(df1, df2)

# specify fill=0 to put 0 into the missing row entries
smartbind(df1, df2, fill = 0)
```
Generate significance stars from p-values

**Description**

Generate significance stars (e.g. '***', '**', '*', '.') from p-values using R’s standard definitions.

**Usage**

```
stars.pval(p.value)
```

**Arguments**

- `p.value`: numeric vector of p-values

**Details**

Mapping from p-value ranges to symbols:

- 0 - 0.001: '***'
- 0.001 - 0.01: '**'
- 0.01 - 0.05: '*'
- 0.05 - 0.1: '.'
- 0.1 - 1.0: '' (No symbol)

**Value**

A character vector containing the same number of elements as `p.value`, with an attribute "legend" providing the conversion pattern.

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**See Also**

- `symnum`

**Examples**

```r
p.val <- c(0.0004, 0.0015, 0.013, 0.044, 0.067, 0.24)
stars.pval(p.val)
```
stat_mode  Most frequently occurring value

Description

Most frequently occurring value

Usage

stat_mode(x, na.rm = TRUE, ties = c("all", "first", "last", "missing"), ...)

Arguments

  x   vector of values
  na.rm  logical. Should NA values be removed before processing?
  ties  character. Which value(s) should be returned in the case of ties?
  ...  optional additional parameters.

Value

vector of the same class as x

Author(s)

Genei Ryodan and Gregory R. Warnes <greg@warnes.net>.

Examples

  # Character vector
  chr_vec <- c("a", "d", "d", "h", "h", NA, NA)  # Multiple modes
  stat_mode(x = chr_vec)
  stat_mode(x = chr_vec, na.rm = FALSE)
  stat_mode(x = chr_vec, na.rm = FALSE, ties = "first")
  stat_mode(x = chr_vec, na.rm = FALSE, ties = "last")

  # - # Numeric vector
  # See that it keeps the original vector type
  num_vec <- c(2, 3, 3, 4, 4, NA, NA)
  stat_mode(x = num_vec)
  stat_mode(x = num_vec, na.rm = FALSE)
  stat_mode(x = num_vec, na.rm = FALSE, ties = "first")
  stat_mode(x = num_vec, na.rm = FALSE, ties = "last")

  # The default option is ties="all" but it is very easy for the user to control
  # the ties without changing this parameter.
  # Select always just one mode, being that the first mode
  stat_mode(x = num_vec)[1]
# Select the first and the second stat_mode
stat_mode(x = num_vec)[c(1, 2)]

# Logical Vectors
stat_mode(x = c(TRUE, TRUE))
stat_mode(x = c(FALSE, FALSE, TRUE, TRUE))

# - # Single element cases
stat_mode(x = c(NA_real_))
stat_mode(x = 2)
stat_mode(x = NA)
stat_mode(x = c("a"))

# Not allowing multiple stat_mode, returning NA if that happens
stat_mode(x = c(1, 1, 2, 2), multiple_modes = FALSE) # multiple stat_mode
stat_mode(x = c(1, 1), multiple_modes = FALSE) # single mode

# Empty vector cases
# The ties of any empty vector will be itself (an empty vector of the same type)
stat_mode(x = double())
stat_mode(x = complex())
stat_mode(x = vector("numeric"))
stat_mode(x = vector("character"))

unByteCode
Convert a byte-code function to an interpreted-code function

Description
The purpose of these functions is to allow a byte coded function to be converted back into a fully interpreted function as a temporary work around for issues in byte-code interpretation.

Usage
unByteCode(fun)
assignEdgewise(name, env, value)
unByteCodeAssign(fun)

Arguments
fun function to be modified
name object name
env namespace
value new function body
Details

unByteCode returns a copy of the function that is directly interpreted from text rather than from byte-code.

`assignEdgewise` makes an assignment into a locked environment.

`unByteCodeAssign` changes the specified function in its source environment to be directly interpreted from text rather than from byte-code.

The latter two functions no longer work out of the box because `assignEdgewise` (which `unByteCodeAssign` uses) makes use of an unsafe `unlockBinding` call, but running `assignEdgewise()` will...

Value

All three functions return a copy of the modified function or assigned value.

Note

These functions are not intended as a permanent solution to issues with byte-code compilation or interpretation. Any such issues should be promptly reported to the R maintainers via the R Bug Tracking System at https://bugs.r-project.org and via the R-devel mailing list https://stat.ethz.ch/mailman/listinfo/r-devel.

Author(s)

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References

These functions were inspired as a work-around to R bug https://bugs.r-project.org/show_bug.cgi?id=15215.

See Also

`disassemble`, `assign`

Examples

data(badDend)
dist2 <- function(x) as.dist(1 - cor(t(x), method = "pearson"))
hclust1 <- function(x) hclust(x, method = "single")

distance <- dist2(badDend)
cluster <- hclust1(distance)

dend <- as.dendrogram(cluster)
## Not run:
## In R 2.3.0 and earlier crashes with a node stack overflow error
plot(dend)
## Error in xy.coords(x, y, recycle = TRUE) : node stack overflow
## End(Not run)
## convert stats:::plotNode from byte-code to interpreted-code
## (no longer available unless assignEdgewise is defined by the user)
## unByteCodeAssign(stats:::plotNode)
## illustrated in https://stackoverflow.com/questions/16559250/error-in-heatmap-2-gplots

# increase recursion limit
options("expressions" = 5e4)

# now the function does not crash
plot(dend)
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