Package ‘gtools’

June 6, 2021

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').

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License  GPL-2

Depends  methods, stats, utils

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**Description**

Convert between characters and ASCII codes

**Usage**

```r
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@warne.net> from code posted on the 'Data Debrief' blog on 2011-03-09 at [https://datadebrief.blogspot.com/2011/03/ascii-code-table-in-r.html](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.
ask

Display a prompt and collect the user's response

Description

Display a prompt and collect the user's response

Usage

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

# 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

---

Defunct Functions in package gtools

Description

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

Usage

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

---
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

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]
```

---

**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

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 \( \min(\text{range}) \).
upper Upper limit of search range. Defaults to \( \max(\text{range}) \).
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 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 \( l_0 \) and \( h_1 \) to the extremes values of range. It then generates a new value center halfway between \( l_0 \) and \( h_1 \). If the value of \( \text{fun} \) at center exceeds target, it becomes the new value for \( l_0 \), otherwise it becomes the new value for \( h_1 \). This process is iterated until \( l_0 \) and \( h_1 \) are adjacent. If the function at one or the other equals the target, this value is returned, otherwise \( l_0 \), \( h_1 \), 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 if iterations was reached, the endpoints of the current subset of the range under consideration will be returned.
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

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

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

### Classical toy example

# 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

## 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  \hspace{1cm} \textit{Capitalize Words for Titles}

\textbf{Description}

This function capitalizes words for use in titles

\textbf{Usage}

\begin{verbatim}
capwords(
s,
strict = FALSE,
AP = TRUE,
onlyfirst = FALSE,
preserveMixed = FALSE,
sep = " ")
\end{verbatim}

\textbf{Arguments}

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

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 `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  

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 utilizes the internet to access the R project web site. If internet access is unavailable, the function will fail.

Author(s)

Gregory R. Warnes <gregory.warnes@rochester.edu>

See Also

R.Version
Examples

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

### combinations

Enumerate the Combinations or Permutations of the Elements of a Vector

**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 (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@warne.net>.

References


See Also

choose, options

Examples

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

Description

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 contain 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")
```
### dirichlet

Functions for the Dirichlet Distribution

**Description**

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

**Usage**

```r
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.

```r
plot.s("d", "v1", DOTS = "lwd=4") # use optional 'DOTS' argument

# Create a macro that defines new functions
plot.sf <- defmacro(
  type = "b", col = "black",
  title = deparse(substitute(x)), DOTS, expr =
  function(x, y) plot(x, y, type = type, col = col, main = title, ...)
)

plot.red <- plot.sf(col = "red", title = "Red is more Fun!")
plot.blue <- plot.sf(col = "blue", title = "Blue is Best!", lty = 2)

plot.red(1:100, rnorm(100))
plot.blue(1:100, rnorm(100))
```
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>
Examples

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

cbind(a, b, f)

getDependencies

Description

Get package dependencies

Usage

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.
gtools: Various R Programming Tools

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

```r
## A locally installed package
getDependencies("MASS", installed = TRUE, available = FALSE)
## Not run:
## A package on CRAN
getDependencies("gregmisc", installed = FALSE, available = TRUE)
## End(Not run)

## Show base and recommended dependencies
getDependencies("MASS", available = FALSE, base = TRUE, recommended = TRUE)
## Not run:
## 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)
```

Description
Functions to assist in R programming, including:

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, contains only NA and NULL values, or is a 'try-error' ‘invalid’
manipulate R’s .Last function ‘addLast’
define macros ‘defmacro’, ‘strmacro’
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’, ‘mixedorder’
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’, ‘fold-change2logratio’
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 ‘tcpNoDelay’
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’

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).

See Also

Deprecated
invalid

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

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)
  }
  plot(x, y)
}
keywords

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
keywords()

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

SearchPath Either the index of the package namespace in the current search path, or '-' if the package namespace is not in the search path. '1' corresponds to the top of the search path (the first namespace searched for values).

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

See Also

\texttt{loadedNamespaces, packageVersion, search, find.package}

Examples

\texttt{loadedPackages()}

\begin{verbatim}
logit
Generalized logit and inverse logit function
\end{verbatim}

Description

Compute generalized logit and generalized inverse logit functions.

Usage

\texttt{logit(x, min = 0, max = 1)}

\texttt{inv.logit(x, min = 0, max = 1)}

Arguments

\begin{itemize}
\item \texttt{x} value(s) to be transformed
\item \texttt{min} Lower end of logit interval
\item \texttt{max} Upper end of logit interval
\end{itemize}

Details

The generalized logit function takes values on $[\text{min}, \text{max}]$ and transforms them to span $[-\infty, \infty]$ it is defined as:

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

where

$$ p = \frac{(x - \text{min})}{(\text{max} - \text{min})} $$

\texttt{logit(x, min = 0, max = 1)}

\texttt{inv.logit(x, min = 0, max = 1)}
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

```r
x <- seq(0, 10, by = 0.25)
x <- logit(x, min = 0, max = 10)
cbind(x, xt)

y <- inv.logit(xt, min = 0, max = 10)
cbind(x, xt, y)
```

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".
mixedsort

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 decreasing=TRUE
  reverses the meanings of na.last and blanks.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 decreasing=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", "Asprin 10mg/day", "Asprin 50mg/day",
  "Asprin 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", "dclxxii", "cdxci",
  "dcxvii", "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.
Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

is.na, na.omit

Examples

```r
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

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

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@warnes.net>

See Also

sample

Examples

x <- 1:10
permute(x)
quantcut

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
```

---

**roman2int**

*Convert Roman Numerals to Integers*

**Description**

Convert roman numerals to integers

**Usage**

`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 roman. Character strings which are not valid roman numerals will be converted to NA.

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

as.roman

Examples

roman2int(c("I", "V", "X", "C", "L", "D", "M"))

# works regardless of case
roman2int("MMXVI")
roman2int("mmxvi")

# works beyond R's limit of 3899
val.3899 <- "MMMDCXXICIX"
val.3900 <- "MMMCM"
val.4000 <- "MMMCM"
as.numeric(as.roman(val.3899))
as.numeric(as.roman(val.3900))
as.numeric(as.roman(val.4000))

roman2int(val.3899)
roman2int(val.3900)
roman2int(val.4000)
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.
- **...** parameters to be passed to `fun`

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**

```r
scat(...) 
```

**Arguments**

`...` Arguments passed to `cat`

**Value**

NULL (invisibly)

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**See Also**

`cat`

**Examples**

```r
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.")
```
**script_file**

*Determine the directory or full path to the currently executing script*

Description

Determine the directory or full path to the currently executing script.

Usage

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

```r
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)


Examples

```r
getwd()
commandArgs(trailingOnly = FALSE)
```

```r
script_file("warning")
script_path("warning")
```
setTCPNoDelay

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

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
Examples

## Not run:
host <- "www.r-project.org"
socket <- make.socket(host, 80)
print(socket)
setTCPNoDelay(socket, TRUE)

write.socket(socket, "GET /\n\n")
write.socket(socket, "A")
write.socket(socket, "B\n")
while ((str <- read.socket(socket)) > "") {
    cat(str)
}
close.socket(socket)

## End(Not run)

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.
Description

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

Usage

```
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.
Generate significance stars from p-values

Stars

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

**Usage**

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

**Arguments**

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

**Details**

Mapping from p-value ranges to symbols:

<table>
<thead>
<tr>
<th>Range</th>
<th>Symbol</th>
</tr>
</thead>
<tbody>
<tr>
<td>0 - 0.001</td>
<td>***</td>
</tr>
<tr>
<td>0.001 - 0.01</td>
<td>**</td>
</tr>
<tr>
<td>0.01 - 0.05</td>
<td>*</td>
</tr>
<tr>
<td>0.05 - 0.1</td>
<td>+</td>
</tr>
<tr>
<td>0.1 - 1.0</td>
<td>(No symbol)</td>
</tr>
</tbody>
</table>

**Value**

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

**Author(s)**

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**See Also**

`symnum`

**Examples**

```r
p.val <- c(0.0004, 0.0015, 0.013, 0.044, 0.067, 0.24)
stars.pval(p.val)
```
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

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.

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)

Gregory R. Warnes <greg@warnes.net>

References

These functions were inspired as a work-around to R bug https://bugs.r-project.org/bugzilla/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
unByteCodeAssign(stats::plotNode)

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

# now the function does not crash
plot(dend)
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