

Package: Ecfun (via r-universe)

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Title Functions for 'Ecdat'

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VignetteBuilder knitr

Imports fda, tis, jpeg, MASS, stringi, methods, xml2, BMA, mvtnorm, rvest, readr, rworldmap

Description Functions and vignettes to update data sets in 'Ecdat' and to create, manipulate, plot, and analyze those and similar data sets.

License GPL (>= 2)

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Arrows	<i>Draw arrows between pairs of points.</i>
--------	---

Description

Generalizes `graphics::arrows` to allow all arguments to be vectors. (As of R 3.1.0, only the first component of the length argument is used by `graphics::arrows`; others are ignored without a warning.)

Usage

```
Arrows(x0, y0, x1 = x0, y1 = y0, length = 0.25, angle = 30,
       code = 2, col = par("fg"), lty = par("lty"),
       lwd = par("lwd"), warnZeroLength=FALSE, ...)
```

Arguments

`x0`, `y0`, `x1`, `y1`, `length`, `angle`, `code`, `col`, `lty`, `lwd`, ...
as for [arrows](#).

`warnZeroLength` Issue a warning for zero length arrow? [arrow](#) does; skip if FALSE.

Details

1. Put all arguments in a `data.frame` to force them to shared length.
2. Call [arrows](#) once for each row.

Author(s)

Spencer Graves

See Also

[arrows](#)

Examples

```
##  
## 1. Simple example:  
##   3 arrows, the first with length 0 is suppressed  
##  
plot(1:3, type='n')  
Arrows(1, 1, c(1, 2, 2), c(1, 2:3), col=1:3, length=c(1, .2, .6))  
  
##  
## 2. with an NA  
##  
plot(1:3, type='n')  
Arrows(1, 1, c(1, 2, 2), c(1, 2, NA), col=1:3, length=c(1, .2, .6))
```

as.Date1970

Date from a number of days since the start of 1970.

Description

as.Date.numeric requires origin to be specified. The present function assumes that this origin is January 1, 1970.

Usage

```
as.Date1970(x, ...)
```

Arguments

x a numeric vector of dates in days since the start of 1970.
... optional arguments to pass to as.Date.

Value

Returns a vector of Dates

Author(s)

Spencer Graves

See Also

[as.Date](#) [as.POSIXct1970](#)

Examples

```

days <- c(0, 1, 365)
Dates <- as.Date1970(days)

all.equal(c('1970-01-01', '1970-01-02', '1971-01-01'),
          as.character(Dates))

all.equal(days, as.numeric(Dates))

```

asNumericDF

Coerce to numeric dropping commas and info after a blank

Description

For `asNumericChar`, delete leading blanks and a leading dollar sign plus commas (thousand separators) and drop information after a blank (other than leading blanks), then coerce to numeric or to factors, Dates, or POSIXct as desired.

For a `data.frame`, apply `asNumericChar` to all columns and drop columns except those in `keep`, `ignore`, factors, Dates, POSIX and MSdates.

Then order the rows by the `orderBy` column. Some Excel imports include commas as thousand separators; this replaces any commas with `char(0)`, `"`, before trying to convert to numeric.

Similarly, if `"%"` is found as the last character in any field, drop the percent sign and divide the resulting numeric conversion by 100 to convert to proportion.

Also, some character data includes footnote references following the year.

For example Table F-1 from the US Census Bureau needs all three of these numeric conversion features: It needs `orderBy`, because the most recent year appears first, just the opposite of most other data sets where the most recent year appears last. It has footnote references following a character string indicating the year. And it includes commas as thousand separators.

Usage

```

asNumericChar(x, leadingChar='^\\$',
              suppressChar=',', pctChar='%$',
              class=NULL, format=NULL)
asNumericDF(x, keep=
            function(x)any(!is.na(x)),
            orderBy=NA, ignore=NULL, factors=NULL,
            Dates=NULL, POSIX=NULL, MSdates=NULL,
            format=NULL, leadingChar='^\\$',
            suppressChar=',', pctChar='%$')

```

Arguments

x	For asNumericChar, this is a character vector to be converted to numeric after <code>gsub(',', '', x)</code> . For asNumericDF, this is a data.frame with all character columns to be converted to numerics.
keep	something to indicate which columns to keep, in addition to columns specified in ignore, factors, Dates, and POSIX.
orderBy	Which columns to order the rows of <code>x[, keep]</code> by. Default is to keep the input order.
ignore	vector identifying columns of x to ignore, i.e., to keep and not attempt to convert to another data type.
factors	vector indicating columns of x to convert to <code>factor</code>
Dates	vector indicating columns of x to convert using <code>as.Date(, format)</code> .
POSIX	vector indicating columns of x to convert using <code>as.POSIXct(, format)</code> .
class.	Desired class of output. Default is <code>numeric</code> .
format.	Character vector of length 1 to pass as argument format to <code>as.Date</code> and / or <code>as.POSIXct</code> for conversion from <code>character</code> . For Dates, <code>as.Date</code> is first tried with format = <code>'%Y-%m-%d'</code> , then with <code>'%Y/%m/%d'</code> , <code>'%m-%d-%Y'</code> , and <code>'%m/%d/%Y'</code> . The conversion with the fewest NAs is kept. If two match for numbers of NAs, the one with the minimum absolute deviations from <code>as.Date1970(0)</code> is used.
MSdates	The names or numbers identifying columns of x identifying dates as integer numbers of days since 1899-12-31. In Microsoft Excel, dates are stored in that format.
leadingChar	A regular expression passed to <code>grep</code> and <code>sub</code> to replace something like an initial dollar sign with character <code>(0)</code> .
suppressChar	a regular expression passed to <code>gsub</code> to replace all occurrences of something like <code>","</code> (a thousands separator in the U.S.) with character <code>(0)</code> .
pctChar	A regular expression passed to <code>grep</code> to identify percent columns. <code>pctChar</code> is then passed to <code>sub</code> to replace <code>pctChar</code> with character <code>(0)</code> , and the converted numbers are then divided by 100 to convert them to proportions.

Details

For asNumericChar:

1. Replace commas by nothing
2. `strsplit` on `' '` and take only the first part, thereby eliminating the footnote references.
3. Replace any blanks with NAs
4. `as.numeric`

for asNumericDF:

1. Copy x to X.

2. Confirm that ignore, factors, Dates, and POSIX all refer to columns of x and do not overlap. [*** NOTE: as of 2016-07-21, these checks have only been implemented for ignore.]
3. Convert factors, Dates, and POSIX.
4. Apply asNumericChar to all columns not in ignore, factors, Dates, or POSIX.
5. Keep columns specified by keep.
6. return the result.

Value

a `data.frame`

Author(s)

Spencer Graves

References

"Add (sum) or subtract dates; Applies To: Excel 2013". Microsoft. (accessed 2016-08-11)

See Also

`scan` `gsub` `Quotes` `stripBlanks` `as.numeric`, `factor`, `as.Date`, `as.POSIXct` `read.xlsx`

Examples

```
##
## 1. an example
##
(xDate <- as.Date('1970-01-01')+c(0, 365))
(xPOSIX <- as.POSIXct(xDate)+c(1, 99))
xMSdate <- as.Date(1,
  as.Date('1899-12-31'))+1:2
(fakeF1 <- data.frame(yr=c('1948',
  '1947 (1)'),
  q1=c(' 1,234 ', ''), duh=rep(NA, 2),
  dol=c('$1,234', ''),
  pct=c('1%', '2%'),
  xDate=format(xDate, '%Y-%m-%d'),
  xPOSIX=format(xPOSIX, '%Y-%m-%d %H:%M:%S'),
  xMSdate=2:3, junk=c('this is',
  'junk'))))

# This converts the last 3 columns to NAs and drops them:

str(nF1.1 <- asNumericChar(fakeF1$yr))
str(nF1.2 <- asNumericChar(fakeF1$q1))
str(nF1.3 <- asNumericChar(fakeF1$duh))
(nF1.4 <- asNumericChar('1969-12-31 18:00:01',
  class.='POSIXct'))
```

```

(nF1 <- asNumericDF(fakeF1))
(nF2 <- asNumericDF(fakeF1, Dates=6,
  MSdate='xMSdate',
  ignore=c('junk', 'xPOSIX'),
  format.='%Y-%m-%d'))
# check
nF1. <- data.frame(yr=
  asNumericChar(fakeF1$yr),
  q1=asNumericChar(fakeF1$q1),
  dol=asNumericChar(fakeF1$dol),
  pct=c(.01, .02), xMSdate=2:3)

nF1c <- data.frame(yr=1948:1947,
  q1=c(1234, NA), dol=c(1234, NA),
  pct=c(.01, .02), xMSdate=2:3)

all.equal(nF1, nF1.)

all.equal(nF1., nF1c)

##
## 2. as.Date default example
##
xD <- asNumericChar(
  as.character(xDate), class.='Date')

all.equal(xDate, xD)

##
## 3. as.POSIXct default example
##
xPOSIX
(xPOSIXch <- as.character(xPOSIX))
(xP <- asNumericChar(xPOSIXch, class.='POSIXct'))
attr(xPOSIX, 'tzone')
attr(xP, 'tzone')
# R-Devel after 4.2.1 breaks earlier code; fix
if(is.null(attr(xPOSIX, 'tzone'))
  attr(xPOSIX, 'tzone') <- attr(xP, 'tzone'))
(dP <- difftime(xPOSIX, xP, units='secs'))
(madP <- max(abs(as.numeric(dP))))

{
#all.equal(xPOSIX, xP)
# As of 2022-10-06 I don't know how to write code
# that will get a consistent answer with
# different version R-devel with differences
# less than an hour
if(madP>(6*60*60)){

```



```

    madPmsg <- paste('Discrepancy betw fn and manual comp ',
                    'too large; is ', madP, 'seconds')
    stop(madPmsg)
  }
  TRUE
}

##
## 4.  orderBy=1:2
##
nF. <- asNumericDF(fakeF1, orderBy=1:2)

all.equal(nF., nF1c[2:1,])

##
## 5.  Will it work for a tibble?
##
if(require(tibble)){
  nF1t <- asNumericDF(as_tibble(fakeF1))

  all.equal(nF1, nF1t)
}

```

BoxCox

Box-Cox power transformation and its inverse

Description

Box and Cox (1964) considered the following family of transformations indexed by λ :

$$w = (y^\lambda - 1) / \lambda$$

$$= \expm1(\lambda \log(y)) / \lambda,$$

with the $\lambda=0$ case defined as $\log(y)$ to make w continuous in λ for constant y .

They estimate λ assuming w follows a normal distribution. This raises a theoretical problem in that y must be positive, which means that w must follow a truncated normal distribution conditioned on $\lambda w > (-1)$.

Bickel and Doksum (1981) removed the restriction to positive y , i.e., to $w > (-1/\lambda)$ by modifying the transformation as follows:

$$w =$$

$$(\text{sgn}(y) * \text{abs}(y)^\lambda - 1) / \lambda \text{ if } \lambda \neq 0 \text{ and}$$

$$\text{sgn}(y) * \log(\text{abs}(y)) \text{ if } \lambda = 0,$$

where $\text{sgn}(y) = 1$ if $y \geq 0$ and -1 otherwise.

NOTE: $\text{sgn}(y)$ is different from $\text{sign}(y)$, which is 0 for $y = 0$. A two-argument update to the sign function in the base package has been added to this Ecfun package, so $\text{sign}(y, 1) = \text{sgn}(y)$.

If $(y < 0)$, this transformation is discontinuous at $\lambda = 0$. To see this, we rewrite this as

$$w = (\text{sgn}(y) * \expm1(\lambda * \log(\text{abs}(y)))) + (\text{sgn}(y) - 1) / \lambda$$

$$= \text{sgn}(y) * (\log(\text{abs}(y)) + O(\lambda)) + (\text{sgn}(y) - 1) / \lambda,$$

where $O(\lambda)$ indicates a term that is dominated by a constant times λ .

If $y < 0$, this latter term $(\text{sgn}(y) - 1) / \lambda = (-2) / \lambda$ and becomes Inf as $\lambda \rightarrow 0$.

In practice, we assume that $y > 0$, so this distinction has little practical value. However, the BoxCox function computes the Bickel-Doksum version.

Box and Cox further noted that proper estimation of λ should include the Jacobian of the transformation in the $\log(\text{likelihood})$. Doing this can be achieved by rescaling the transformation with the n th root of the Jacobian, which can be written as follows:

$$j(y, \lambda) = J(y, \lambda)^{(1/n)} = \text{GeometricMean}(y)^{(\lambda - 1)}.$$

With this the rescaled power transformation is as follows:

$$z = (y^{\lambda - 1}) / (\lambda * j(y, \lambda)) \text{ if } \lambda \neq 0 \text{ or } \text{GeometricMean}(y) * \log(y) \text{ if } \lambda == 0.$$

In addition to facilitating estimation of λ , rescaling has the advantage that the units of z are the same as the units of y .

The output has class `BoxCox`, which has attributes that allow the input to be recovered using `invBoxCox`. The default values of the arguments of `invBoxCox` are provided by the corresponding `attributes` of z .

Usage

```
BoxCox(y, lambda, rescale=TRUE, na.rm=rescale)
invBoxCox(z, lambda, sign.y, GeometricMean, rescale)
```

Arguments

<code>y</code>	a numeric vector for which the power transform is desired
<code>lambda</code>	A numeric vector of length 1 or 2. The first component is the power. If the second component is provided, y is replaced by $y + \lambda[2]$.
<code>rescale</code>	logical or numeric. If logical: For <code>BoxCox</code> , this is <code>TRUE</code> to return the power transform with <code>rescale</code> , z , above, and <code>FALSE</code> to return the power transform without the n th root of the Jacobian, w , above. This defaults to <code>TRUE</code> , because this will give z the same units as y . For <code>invBoxCox</code> , this is <code>TRUE</code> if the input argument z is assumed to have been rescaled by the n th root of the Jacobian of the transformation. This defaults to a <code>rescale</code> attribute of z if present or to <code>TRUE</code> if absent. If numeric, it is assumed to be the geometric mean of another set of y values to use with new y 's.
<code>na.rm</code>	logical: <code>TRUE</code> to remove NAs from y before computing the geometric mean. <code>FALSE</code> to compute NA for the geometric mean if <code>any(is.na(y))</code> . NOTE: If <code>na.rm = FALSE</code> , the output will be all NA if <code>rescale = TRUE</code> . This could produce non usable answers in most cases. To avoid that, the default for

	na.rm is TRUE whenever rescale = TRUE. Conversely, applications using na.rm = FALSE will likely also want rescale = FALSE to avoid returning a non-answer in these cases. This explains the default na.rm = rescale.
z	a numeric vector or an object of class BoxCox for which the inverse Box-Cox transform is desired.
sign.y	an optional logical vector giving sign(y-lambda[2]) of the data values that presumably generated z. Defaults to a sign.y attribute of z or to rep(1, length(z)) if no such attribute is present.
GeometricMean	an optional numeric scalar giving the geometric mean of the data values that presumably generated z. Defaults to a GeometricMean attribute of z or to 1 if no such attribute is present.

Details

Box and Cox (1964) discussed

$$w(y, \lambda) = (y^\lambda - 1) / \lambda.$$

They noted that w is continuous in λ with $w(y, \lambda) = \log(y)$ if $\lambda = 0$ (by l'Hopital's rule).

They also discussed

$$z(y, \lambda) = (y^\lambda - 1) / (\lambda * g^{(\lambda-1)}),$$

where g = the geometric mean of y .

They noted that proper estimation of λ should include the Jacobian of $w(y, \lambda)$ with the likelihood. They further showed that a naive normal likelihood using $z(y, \lambda)$ as the response without a Jacobian is equivalent to the normal likelihood using $w(y, \lambda)$ adjusted appropriately using the Jacobian. See Box and Cox (1964) or [the Wikipedia article on "Power transform"](#).

Bickel and Doksum (1981) suggested adding $\text{sign}(y)$ to the transformation, as discussed above.

NUMERICAL ANALYSIS:

Consider the Bickel and Doksum version described above:

$$w \leftarrow (\text{sign}(y) * \text{abs}(y)^{\lambda-1}) / \lambda$$

if (any(y==0)), GeometricMean(y) = 0. This creates a problem with the above math.

Let $ly = \log(\text{abs}(y))$. Then with $la = \lambda$,

$$w = (\text{sign}(y) * \exp(la * ly) - 1) / la$$

$$= \text{sign}(y) * ly * (1 + (la * ly / 2) * (1 + (la * ly / 3) * (1 + (la * ly / 4) * (1 + 0(la * ly)))))) + (\text{sign}(y) - 1) / la$$

For $y > 0$, the last term is zero. `boxcox` ignores cases with $y \leq 0$ and uses this formula (ignoring the final $0(la * ly)$) whenever $\text{abs}(la) \leq \text{eps} = 1/50$. That form is used here also.

For `invBoxCox` a complementary analysis is as follows:

$$\text{abs}(y + \lambda[2]) = \text{abs}(1 + la * w)^{(1/la)}$$

$$= \exp(\log1p(la * w) / la) \text{ for } \text{abs}(la * w) < 1$$

$$= w * (1 - la * w * ((1/2) - la * w * ((1/3) - la * w * (1/4 - \dots))))$$

Value

BoxCox returns an object of class BoxCox, being a numeric vector of the same length as `y` with the following optional attributes:

`lambda` the value of `lambda` used in the transformation

`sign.y` `sign(y)` (or `sign(y-lambda[2])` if `lambda[2]` is provided and if any of these quantities are negative. Otherwise, this is omitted and all are assumed to be positive.

`rescale` logical: TRUE if `z(y, lambda)` is returned rescaled by $g^{(\lambda-1)}$ with g = the geometric mean of `y` and FALSE if `z(y, lambda)` is not so rescaled.

`GeometricMean` If `rescale` is numeric, `attr(, 'GeometricMean') <- rescale`.

Otherwise, `attr(, 'GeometricMean')` is the Geometric mean of `abs(y) = exp(mean(log(abs(y))))` or of `abs(y+lambda[2])` if `(length(lambda)>1)`.

`invBoxCox` returns a numeric vector, reconstructing `y` from `BoxCox(y, ...)`.

Source

Bickel, Peter J., and Doksum, Kjell A. (1981) "An analysis of transformation revisited", *Journal of the American Statistical Association*, 76 (374): 296-311

Box, George E. P.; Cox, D. R. (1964). "An analysis of transformations", *Journal of the Royal Statistical Society, Series B* 26 (2): 211-252.

Box, George E. P.; Cox, D. R. (1982). "An analysis of transformations revisited, rebutted", *Journal of the American Statistical Association*, 77(377): 209-210.

References

[Wikipedia, "Power transform"](#)

See Also

[boxcox](#) in the MASS package

[quine](#) in the MASS package for data used in an example below.

[boxcox](#) and [boxcoxCensored](#) in the EnvStats package.

[boxcox.drc](#) in the drc package.

[boxCox](#) in the car package.

These other uses all wrap the Box-Cox transformation in something larger and do not give the transformation itself directly.

Examples

```
##
## 1. A simple example to check the two algorithms
##
Days <- 0:9
bc1 <- BoxCox(Days, c(0.01, 1))
```

```

# Taylor expansion used for obs 1:7; expm1 for 8:10

# check
GM <- exp(mean(log(abs(Days+1))))

bc0 <- (((Days+1)^0.01)-1)/0.01
bc1. <- (bc0 / (GM^(0.01-1)))
# log(Days+1) ranges from 0 to 4.4
# lambda = 0.01 will invoke both the obvious
# algorithm and the alternative assumed to be
# more accurate for (lambda(log(y)) < 0.02).
attr(bc1., 'lambda') <- c(0.01, 1)
attr(bc1., 'rescale') <- TRUE
attr(bc1., 'GeometricMean') <- GM
class(bc1.) <- 'BoxCox'

all.equal(bc1, bc1.)

##
## 2. another simple example with lambda=0
##
bc0.4 <- BoxCox(1:5, 0)
GM5 <- prod(1:5)^.2
bc0.4. <- log(1:5)*GM5
attr(bc0.4., 'lambda') <- 0
attr(bc0.4., 'rescale') <- TRUE
attr(bc0.4., 'GeometricMean') <- GM5
class(bc0.4.) <- 'BoxCox'

all.equal(bc0.4, bc0.4.)

bc0.4e9 <- BoxCox(1:5, .Machine$double.eps)
bc0.4ex <- log(1:5)*exp(mean(log(1:5)))

all.equal(bc0.4ex, as.numeric(bc0.4e9))

# now invert:

bc0.4i <- invBoxCox(bc0.4.)

all.equal(1:5, bc0.4i)

all.equal(1:5, invBoxCox(bc0.4e9))

##

```

```

## 3. The "boxcox" function in the MASS package
##   computes a maximum likelihood estimate with
##   BoxCox(Days+1, lambda=0.21)
##   with a 95 percent confidence interval of
##   approximately (0.08, 0.35)
##
bcDays1 <- BoxCox(MASS::quine$Days, c(0.21, 1))

# check
GeoMean <- exp(mean(log(abs(MASS::quine$Days+1))))

bcDays1. <- (((MASS::quine$Days+1)^0.21)-1) /
            (0.21*GeoMean^(0.21-1))
# log(Days+1) ranges from 0 to 4.4
attr(bcDays1., 'lambda') <- c(0.21, 1)
attr(bcDays1., 'rescale') <- TRUE
attr(bcDays1., 'GeometricMean') <- GeoMean
class(bcDays1.) <- 'BoxCox'

all.equal(bcDays1, bcDays1.)

iDays <- invBoxCox(bcDays1)

all.equal(iDays, MASS::quine$Days)

##
## 4. Easily computed example
##
bc2 <- BoxCox(c(1, 4), 2)

# check
bc2. <- (c(1, 4)^2-1)/4
attr(bc2., 'lambda') <- 2
attr(bc2., 'rescale') <- TRUE
attr(bc2., 'GeometricMean') <- 2
class(bc2.) <- 'BoxCox'

all.equal(bc2, bc2.)

all.equal(invBoxCox(bc2), c(1, 4))

##
## 5. plot(BoxCox())
##
y0 <- seq(-2, 2, .1)
z2 <- BoxCox(y0, 2, rescale=FALSE)

```

```

plot(y0, z2)

# check
z2. <- (sign(y0)*y0^2-1)/2

attr(z2., 'lambda') <- 2
attr(z2., 'sign.y') <- sign(y0, 1)
attr(z2., 'rescale') <- FALSE
attr(z2., 'GeometricMean') <- 0
class(z2.) <- 'BoxCox'

all.equal(z2, z2.)

all.equal(invBoxCox(z2), y0)

```

camelParse	<i>Split a character string where a capital letter follows a lowercase letter</i>
------------	---

Description

Split a character string where a capital letter follows a lowercase letter.

Usage

```
camelParse(x, except=c('De', 'Mc', 'Mac'))
```

Arguments

x	a character vector
except	character vector giving exceptions: If any of these are found, ignore and look for the next one

Details

Find all places where a lowercase letter is followed by a capital.
Split on those points

Value

list of character vectors

Author(s)

Spencer Graves

See Also[strsplit](#)**Examples**

```
tst <- c('Smith, JohnJohn Smith',
        'EducationNational DefenseOther Committee',
        'McCain, JohnJohn McCain')
tst. <- camelParse(tst)

all.equal(tst., list(c('Smith, John', 'John Smith'),
                    c('Education', 'National Defense', 'Other Committee'),
                    c('McCain, John', 'John McCain') ) )
```

`canbeNumeric`*Can a variable reasonably be coerced to numeric?*

Description

Can [seq](#) be reasonably applied to `x`? Returns TRUE if yes and FALSE otherwise.

We'd like to use this with, for example, date-time objects in [as.Date](#) and [as.POSIXct](#) formats. However, [as.numeric](#) of such objects is FALSE. Moreover, [as.numeric](#) of [factors](#) is TRUE.

The current algorithm (which may change in the future) returns TRUE if `(mode(x) == 'numeric') & (!('levels' %in% names(attributes(x))))`.

Usage

```
canbeNumeric(x)
```

Arguments

`x` an R object

Value

A [logical](#) as described above.

Author(s)

Spencer Graves

See Also[mode](#)

Examples

```
##
## Examples adapted from "mode"
##
cex4 <- c('letters[1:4]', "as.Date('2014-01-02')",
  'factor(letters[1:4])', "NULL", "1", "1:1", "1i",
  "list(1)", "data.frame(x = 1)", "pairlist(pi)",
  "c", "lm", "formals(lm)[[1]]", "formals(lm)[[2]]",
  "y ~ x", "expression((1))[[1]]", "(y ~ x)[[1]]",
  "expression(x <- pi)[[1]][[1]]")
lex4 <- sapply(cex4, function(x) eval(parse(text = x)))
mex4 <- t(sapply(lex4, function(x)
  c(typeof(x), storage.mode(x), mode(x), canbeNumeric(x))))
dimnames(mex4) <- list(cex4,
  c("typeof(.)", "storage.mode(.)", "mode(.)", 'canbeNumeric(x)'))
mex4

# check
mex. <- as.character(as.logical(c(0, 1, 0, 0, 1, 1, rep(0, 12))))
names(mex.) <- cex4

all.equal(mex4[,4], mex.)
```

checkNames

Check and return names

Description

Check and return [names](#). If names are not provided or are not unique, write a message and return [make.names](#) consistent with [warn](#) and [unique](#).

Usage

```
checkNames(x, warn=0, unique=TRUE,
  avoid=character(0),
  message0=head(deparse(substitute(x)), 25), 2), ...)
```

Arguments

x	an R object suitable for names
warn	Numeric code for how to treat problems, consistent with the argument warn in options : Negative to ignore, 0 to save and print later, 1 to print as they occur, 2 or greater to convert to errors.
unique	logical: TRUE to check that <code>names(x)</code> are unique. Fix any duplicates with make.names .

`avoid` a vector of regular expressions to avoid adding in the output of `make.names` with a companion replacement when found.
Thus, `length(avoid)` must be a nonnegative even integer, with `avoid[2*j-1]` providing the pattern for `regexpr` and `sub`, and `avoid[2*j]` providing the replacement. See the second example.

`message0` Base to prepend to any message

... optional arguments for `make.names`

Details

1. `namex <- names(x)`
2. Check per `warn` and `unique`
3. Return an appropriate version of `namex`

Value

a character vector of the same length as `x`. If any problem is found, this character vector will have an attribute `message` describing the problem found. Message checking considers `unique` but ignores `warn`.

Author(s)

Spencer Graves

See Also

[names](#) [make.names](#) [options](#) for `warn`

Examples

```
##
## 1. standard operation with no names
##
tst1 <- checkNames(1:2)

# check
tst1. <- make.names(character(2), unique=TRUE)
attr(tst1., 'message') <- paste(
  "1:2: names = NULL; returning",
  "make.names(character(length(x))), TRUE)")

all.equal(tst1, tst1.)

##
## 2. avoid=c('\\.0$', '\\.1$')
##
tst2 <- checkNames(1:2,
  avoid=c('\\.0$', '.2',
    '\\.1$', '.3') )
```

```
# check
tst2. <-c('X', 'X.3')
attr(tst2., 'message') <- paste(
  "1:2: names = NULL; returning",
  "make.names(character(length(x))), TRUE)")

all.equal(tst2, tst2.)
```

classIndex

Convert class to an integer 1-8 and vice versa

Description

classIndex converts the class of x to an integer:

1. NULL
2. logical
3. integer
4. numeric
5. complex
6. raw
7. character
8. other

index2class converts an integer back to the corresponding class.

Usage

```
classIndex(x)
index2class(i, otherCharacter=TRUE)
```

Arguments

x an object whose class index is desired.

i an integer to be converted to the name of the corresponding class

otherCharacter logical: TRUE to convert 8 to "character"; FALSE to convert 8 to "other".

Details

The [Writing R Extensions](#) lists six different kinds of "atomic vectors": logical, integer, numeric, complex, character, and raw: See also [Wickham \(2013, section on "Atomic vectors" in the chapter on "Data structures"\)](#). These form a standard hierarchy, except for "raw", in that standard operations combining objects with different atomic classes will create an object of the higher class. For example, `TRUE + 2 + pi` returns a numeric object ((approximately 6.141593). Similarly, `paste(1, 'a')` returns the character string "1 a".

For "interpolation", we might expect users interpolating between objects of class "raw" (i.e., bytes) might most likely prefer "Numeric" to "Character" interpolation, coerced back to type "raw".

The index numbers for the classes run from 1 to 8 to make it easy to convert them back from integers to character strings.

Value

`classIndex` returns an integer between 1 and 7 depending on `class(x)`.

`index2class` returns a character string for the inverse transformation.

Author(s)

Spencer Graves

References

Wickham, Hadley (2014) *Advanced R*, especially [Wickham \(2013, section on "Atomic vectors" in the chapter on "Data structures"\)](#).

See Also

[interpChar](#)

Examples

```
##
## 1. classIndex
##
x1 <- classIndex(NULL)
x2 <- classIndex(logical(0))
x3 <- classIndex(integer(1))
x4 <- classIndex(numeric(2))
x5 <- classIndex(complex(3))
x6 <- classIndex(raw(4))
x7 <- classIndex(character(5))
x8 <- classIndex(list())

# check

all.equal(c(x1, x2, x3, x4, x5, x6, x7, x8), 1:8)

##
```

```
## 2. index2class
##
c1 <- index2class(1)
c2 <- index2class(2)
c3 <- index2class(3)
c4 <- index2class(4)
c5 <- index2class(5)
c6 <- index2class(6)
c7 <- index2class(7)
c8 <- index2class(8)
c8o <- index2class(8, FALSE)

# check

all.equal(c(c1, c2, c3, c4, c5, c6, c7, c8, c8o),
          c('NULL', 'logical', 'integer', 'numeric',
            'complex', 'raw', 'character', 'character',
            'other'))
```

compareLengths

Compare the lengths of two objects

Description

Issue a warning or error if the lengths of two objects are not compatible.

Usage

```
compareLengths(x, y,
               name.x=deparse(substitute(x), width.cutoff,
                               nlines=1, ...),
               name.y=deparse(substitute(y), width.cutoff,
                               nlines=1, ...),
               message0='', compFun=c('NROW', 'length'),
               action=c(compatible='', incompatible='warning'),
               length0=c('compatible', 'incompatible', 'stop'),
               width.cutoff=20, ...)
```

Arguments

<code>x, y</code>	objects whose lengths are to be compared
<code>name.x, name.y</code>	names of <code>x</code> and <code>y</code> to use in a message. Default = <code>deparse(substitute(.), width.cutoff, nlines=1)</code> .
<code>message0</code>	character string to be included with <code>name.x</code> and <code>name.y</code> in a message.
<code>compFun</code>	function to use in the comparison.

action	A character vector of length 2 giving the names of functions to call if the lengths are not equal but are either 'compatible' or 'incompatible'; "" means no action.
length0	If length(x) or length(y) = 0 (but not both), treat this case as specified by length0.
width.cutoff	width.cutoff argument to pass to deparse . This gives the maximum number of characters to use in a name in error and warning messages.
...	optional arguments for deparse

Details

1. If `nchar(name.x) = 0 = nchar(name.y)`, set `name.x <- 'x'`, `name.y <- 'y'`, and append 'in compareLengths:' to `message0` for more informative messaging.
2. `lenx <- do.call(compFun, list(x)); leny <- do.call(compFun, list(y))`
3. `if(lenx==leny)return(c('equal', ''))`
4. Compatible?
5. Compose the message.
6. "action", as indicated

Value

A character vector of length 2. The first element is either 'equal', 'compatible' or 'incompatible'. The second element is the message composed.

Author(s)

Spencer Graves with help from Duncan Murdoch

See Also

[interpChar](#)

Examples

```
##
## 1. equal
##

all.equal(compareLengths(1:3, 4:6), c("equal", ''))

##
## 2. compatible
##
a <- 1:2
b <- letters[1:6]
comp.ab <- compareLengths(a, b, message0='Chk:')
comp.ba <- compareLengths(b, a, message0='Chk:')
# check
```

```

chk.ab <- c('compatible',
           'Chk: length(b) = 6 is 3 times length(a) = 2')

all.equal(comp.ab, chk.ab)

all.equal(comp.ba, chk.ab)

##
## 3. incompatible
##
Z <- LETTERS[1:3]
comp.aZ <- compareLengths(a, Z)
# check
chk.aZ <- c('incompatible',
           ' length(Z) = 3 is not a multiple of length(a) = 2')

all.equal(comp.aZ, chk.aZ)

##
## 4. problems with name.x and name.y
##
comp.ab2 <- compareLengths(a, b, '', '')
# check
chk.ab2 <- c('compatible',
           'in compareLengths: length(y) = 6 is 3 times length(x) = 2')

all.equal(comp.ab2, chk.ab2)

##
## 5. zeroLength
##
zeroLen <- compareLengths(logical(0), 1)
# check
zeroL <- c('compatible', ' length(logical(0)) = 0')

all.equal(zeroLen, zeroL)

```

compareOverlap

Compare y between newDat and refDat for shared values of x

Description

Compute $dy <- (y - yRef)$ for all cases where $x == xRef$, where x and y are columns of `newDat` and `xRef` and `yRef` are columns of `refDat`.

Also compute $dyRef <- dy / yRef$.

Return silently a data.frame with columns `x`, `y`, `yRef`, `dy`, and `dyRef`.

Also if $\min(yRef) * \max(yRef) > 0$ plot(`dyRef`) else plot(`dy`).

Usage

```
compareOverlap(y=2, yRef=y, x=1,
              xRef=x, newDat, refDat,
              ignoreCase=TRUE, ...)
```

Arguments

y, yRef	columns of newDat, refDat, respectively, to compare, ignoring case in the names unless ignoreCase is FALSE.
x, xRef	columns of newDat, refDat, respectively, to match when comparing y with yRef. As with y and yRef, ignore case in name matching unless ignoreCase is FALSE.
newDat, refDat	data.frames of new and reference data in which to search for overlap, i.e., common values of newD[, x] and refDat[, xRef], and for those observations to compare newDat[, y] to refDat[, yRef].
ignoreCase	logical: If TRUE, ignore case when searching for columns of newDat and refDat to match y, yRef, x, and xRef.
...	optional arguments to pass to plot

Details

This function is particularly useful for updating datasets that are obtained from sources like the [Bureau of Justice Statistics](#), which publish many series with each update including the most recent 11 years. This function can be used to evaluate the extent of equivalence between, e.g., historical data in refDat with the latest data in newDat.

Value

Invisibly return a `data.frame` with columns `x`, `paste0(y, 'New')`, `paste0(yRef, 'Ref')`, `dy`, and `dyRef` of the data compared.

Author(s)

Spencer Graves

Examples

```
nDat <- data.frame(yr=2000:2015,
                  Y=0:15)
rDat <- data.frame(Yr=2018:2011,
                  y=c(17:13, 13:11))
nrDat <- compareOverlap(
  newDat=nDat, refDat=rDat)

# Correct answer
NRdat <- data.frame(yr=2011:2015,
                  YNew=11:15, yRef=c(11:13, 13:14),
                  dy=c(0,0,0, 1, 1),
                  dyRef=c(0,0,0, 1,1) /
```



```
c(11:13, 13:14))
```

```
all.equal(nrDat, NRdat)
```

confint.var

Confidence interval for sample variance or standard deviation

Description

Computes the standard normal (i.e., chi-square) confidence intervals for a sample variance or standard deviation.

Usage

```
## S3 method for class 'var'
confint(object, parm, level=0.95, ...)
## S3 method for class 'sd'
confint(object, parm, level=0.95, ...)
```

Arguments

object	a numeric vector possibly with a <code>df</code> or <code>df.residuals</code> attribute assumed to represent a sample variance, possibly computed as root mean square of residuals from a model.
parm	degrees of freedom in the estimated variance or standard deviation.
level	the confidence level required
...	optional arguments not used.

Details

1. If `object` is not numeric, throw an error.
2. If `parm` is missing, look for an attribute of `object` starting with `df`. If present, use that for `parm`. If `parm` is absent or not numeric, throw an error.
3. replicate `object`, `parm`, and `level` to the same length. Issue a warning if the longest is not a multiple of the others.
4. `alph2 <- (1-level)/2`
5. `Qntls <- cbind(lower=qchisq(alph2, parm, lower=FALSE), upper=qchisq(alph2, parm))`
6. `CI <- (object*parm/Qntls)`
7. `attr(CI, 'level') <- Level`
7. `return(CI)`

Value

a matrix with columns "lower" and "upper", nrow = the longest of the lengths of object, parm, and level, and an attribute "level".

Author(s)

Spencer Graves

References

[Wikipedia, "Standard deviation"](#), accessed 2016-07-06.

See Also

[cor.test](#), [VarCI](#)

Examples

```
##
## 1. simple examples
##
(CI.v <- confint.var(c(1,1,4), c(1, 9, 9)))
(CI.s <- confint.sd(c(1,1,2), c(1, 9, 9)))

# Compare with the examples on Wikipedia

all.equal(CI.s, sqrt(CI.v))

WikipEx <- t(matrix(c(0.45, 31.9, 0.69, 1.83, 1.38, 3.66),
                  nrow=2))
colnames(WikipEx) <- c('lower', 'upper')

(dCI <- (CI.s-WikipEx))
#Confirm within 2-digit roundoff

max(abs(dCI))<0.0102

##
## 2. test df attributes
##
v <- c(1,1,4)
attr(v, 'df.') <- c(1, 9, 9)
class(v) <- 'var'
vCI <- confint(v)

# check

all.equal(vCI, CI.v)
```

```
s <- sqrt(v)
class(s) <- 'sd'
sCI <- confint(s)

# check

all.equal(sCI, CI.s)
```

countByYear

Allocate a total by year

Description

Allocate total to countByYear for a constant count per day between start and end.

Usage

```
countByYear(start, end, total=1)
```

Arguments

start, end	objects of class "Date" specifying the start, end, respectively, of the event
total	A number to be allocated by year in proportion to the number of days in the event each year.

Value

a numeric vector whose `sum` is total with names for all the years between start and end

Author(s)

Spencer Graves

Examples

```
##
## 1. All in one year
##
start73 <- as.Date('1973-01-22')
tst1 <- countByYear(start73, start73+99, 123)

# check
tst1. <- 123
names(tst1.) <- 1973

all.equal(tst1, tst1.)
```

```
##
## 2. Two years
##
tst2 <- countByYear(start73, start73+365, 123)

# check
dur <- 366
days1 <- (365-21)
days2 <- 22
tst2. <- 123 * c(days1, days2)/dur
names(tst2.) <- 1973:1974

all.equal(tst2, tst2.)

##
## 3. Ten years
##
tst10 <- countByYear(start73, start73+10*365.2, 123)

# check
days <- (c(rep(c(rep(365, 3), 366), length=10), 0)
          + c(-21, rep(0, 9), 22) )
tst10. <- 123 * days/(10*365.2+1)
names(tst10.) <- 1973:1983

all.equal(tst10, tst10.)
```

countsByYear

Allocate totals by year

Description

Allocate total to countByYear for a constant count per day between start and end for multiple events.

Usage

```
countsByYear(data, start="Start1", end='End1',
             total='BatDeath', event='WarName',
             endNA=max(data[, c(start,end)]))
```

Arguments

data a [data.frame](#) with columns start, end, and total

start, end	columns of data of class Date with start <= end during which total is to be allocated
total	A quantity to be allocated by year giving a constant rate per day.
event	name of the event whose total is to be allocated.
endNA	Date to use if is.na(data[, end]).

Value

a numeric `matrix` whose `colSums` match `total` with names for all the years between `start` and `end`. The number of columns of the output matrix match the number of rows of data. The `colSums` match `total`.

Author(s)

Spencer Graves

Examples

```
##
## 1. data.frame(WarName, Start1, End1, BatDeath)
##
start73 <- as.Date('1973-01-22')
tstWars <- data.frame(WarName=c('short', '2yr', '10yr'),
  Start1=c(start73, start73+365, start73-365),
  End1=start73+c(99, 2*365, NA),
  BatDeath=c(100, 123, 456))
##
## 2. do
##
deathsByYr <- countsByYear(tstWars,
  endNA=start73+9*365.2)

# check
Counts <- matrix(0, 11, 3,
  dimnames=list(c(1972:1982), tstWars$WarName) )
Counts['1973', 1] <- 100
Counts[as.character(1974:1975), 2] <- with(tstWars,
  countByYear(Start1[2], End1[2], BatDeath[2]) )
Counts[as.character(1972:1982), 3] <- with(tstWars,
  countByYear(Start1[3], start73+9*365.2, BatDeath[3]) )

all.equal(deathsByYr, Counts)
```

createMessage	<i>Compose a message as a single substring from a character vector</i>
---------------	--

Description

This is a utility function to make it easier to automatically compose informative error and warning messages without using too many characters.

Usage

```
createMessage(x, width.cutoff=45, default='x',
             collapse='; ', endchars='...')
```

Arguments

x	input for paste
width.cutoff	maximum number of characters from x to return in a single string. This differs from the width.cutoff argument in deparse in that the output included here considers endchars, not part of deparse .
default	character string to return if nchar(x) = 0.
collapse	collapse argument for paste
endchars	a character string to indicate that part of the input string(s) was truncated.

Details

```
x. <- paste(..., collapse='; ') nchx <- nchar(x.) maxch <- (maxchar-nchar(endchars)) if(nchx>maxch){
x2 <- substring(x., 1, maxch) x. <- paste0(x2, endchar) }
```

Value

a character string with at most width.cutoff characters.

Author(s)

Spencer Graves

See Also

[paste](#) [substr](#) [nchar](#)

Examples

```
##
## 1. typical use
##
tstVec <- c('Now', 'is', 'the', 'time')
msg <- createMessage(tstVec, 9, collapse=':',
                    endchars='//')

all.equal(msg, 'Now:is://')

##
## 2. in a function
##
tstFn <- function(cl)createMessage(deparse(cl), 9)
Cl <- quote(plot(1:3, y=4:6, col='red', main='Title'))
msg0 <- tstFn(Cl)
# check
msg. <- 'plot(1...)'

all.equal(msg0, msg.)

##
## 3. default
##
y <- createMessage(character(3), default='y')

all.equal(y, 'y')
```

createX2matchY

Create X to match Y

Description

Return a default object of class `index2class(max(classIndex(x), classIndex(y)))` and `length = length(y)`.

For example, suppose `class(x) == 'numeric'`, for which `classIndex = 4`. If `class(y) = 'integer'`, then an object of class `'numeric'` is returned. However, if `class(y) = 'character'`, then an object of class `'character'` is returned.

Usage

```
createX2matchY(x, y)
```

Arguments

`x, y` objects of possibly different classes and lengths.

Value

A vector of the same length as `y` whose class is `index2class(max(classIndex(x), classIndex(y)))`.

Author(s)

Spencer Graves

See Also

[interpPairs](#)

Examples

```
##
## 1. NULL
## -
null <- createX2matchY(NULL, NULL)
# check

all.equal(null, NULL)

##
## 2. logical
##
lgcl3 <- createX2matchY(NULL,
                        c(FALSE, TRUE, FALSE))

# check

all.equal(lgcl3, logical(3))

##
## 3. integer
##
int3 <- createX2matchY(integer(0),
                       c(FALSE, TRUE, FALSE))
# check

all.equal(int3, integer(3))

##
## 4. list -> character
##
ch3 <- createX2matchY(integer(0),
                      list(a=1, b=2, c=3))
# check

all.equal(ch3, character(3))
```

Date3to1	<i>Convert three YMD vectors to a Date</i>
----------	--

Description

Given a `data.frame` with 3 columns, assume they represent Year, Month and Day and return a vector of class `Date`.

Usage

```
Date3to1(data, default='Start')
```

Arguments

`data` a `data.frame` with 3 columns assumed to represent Year, Month and Day.

`default` A character string to indicate how missing months and days should be treated. If the first letter is "S" or "s", the default month will be 1 and the default day will be 1. Otherwise, "End" is assumed, for which the default month will be 12 and the default day will be the last day of the month.

NOTE: Any number outside the range of 1 to the last day of the month is considered missing and its subscript is noted in the optional attribute "missing".

Details

The data sets from the [Correlates of War](#) project include dates coded in triples of columns with names like

```
c("StartMonth1", "StartDay1", "StartYear1", "EndMonth1", ..., "EndYear2").
```

This function will accept one triple and translate it into a vector of class `Date`.

Value

Returns an object of class `Date` with an optional attribute `missing` giving the indices of any elements with missing months or days, for which a default month or day was supplied.

Author(s)

Spencer Graves

See Also

[dateCols](#)

Examples

```

date.frame <- data.frame(Year=c(NA, -1, 1971:1979),
  Month=c(1:2, -1, NA, 13, 2, 12, 6:9),
  Day=c(0, 0:6, NA, -1, 32) )

DateVecS <- Date3to1(date.frame)
DateVecE <- Date3to1(date.frame, "End")

# check
na <- c(1:5, 9:11)
DateVs <- as.Date(c(NA, NA,
  '1971-01-01', '1972-01-01', '1973-01-01',
  '1974-02-04', '1975-12-05', '1976-06-06',
  '1977-07-01', '1978-08-01', '1979-09-01') )
DateVe <- as.Date(c(NA, NA,
  '1971-12-31', '1972-12-31', '1973-12-31',
  '1974-02-04', '1975-12-05', '1976-06-06',
  '1977-07-31', '1978-08-31', '1979-09-30') )

attr(DateVs, 'missing') <- na
attr(DateVe, 'missing') <- na

all.equal(DateVecS, DateVs)

all.equal(DateVecE, DateVe)

```

dateCols	<i>Identify YMD names in a character vector</i>
----------	---

Description

`grep` for YMD (year, month, day) in `col.names`. Return a named list of integer vectors of length 3 for each triple found.

Usage

```
dateCols(col.names, YMD=c('Year', 'Month', 'Day'))
```

Arguments

<code>col.names</code>	either a character vector in which to search for names matching YMD or an object with non-null <code>colnames</code>
<code>YMD</code>	a character vector of patterns to use in <code>grep</code> to identify triples of columns coding YMD in <code>col.names</code>

Details

The data sets from the [Correlates of War](#) project include dates coded in triples of columns with names like `c("StartMonth1", "StartDay1", "StartYear1", "EndMonth1", ..., "EndYear2")`. This function will find all relevant date triples in a character vector of column names and return a list of integer vectors of length 3 with names like "Start1", "End1", ..., "End2" giving the positions in `col.names` of the desired date components.

Algorithm:

1. `if(!is.null(colnames(YMD)))YMD <- colnames(YMD)`
2. `ymd <- grep` for YMD (Year, Month, Day) in `col.names`.
3. `groupNames <- sub` pattern with " in `ymd`
4. Throw a [warning](#) for any `groupNames` character string that does not appear with all three of Year, Month, and Day.
5. Return a list of integer vectors of length 3 for each triple found.

Value

Returns a named list of integer vectors of length 3 identifying the positions in `col.names` of the desired date components.

Author(s)

Spencer Graves

See Also

[Date3to1](#)

Examples

```
##
## 1. character vector
##
colNames <- c('war', 'StartMonth1',
              'StartDay1', 'StartYear1',
              'EndMonth1', 'EndMonth2',
              'EndDay2', 'EndYear2', 'Initiator')

colNums <- dateCols(colNames)
# Should issue a warning:
# Warning message:
# In dateCols(colNames) :
#   number of matches for Year = 2
#   != number of matches for Month = 3

# check
colN <- list(Start1=c(Year=4, Month=2, Day=3),
            End2=c(Year=8, Month=6, Day=7) )

all.equal(colNums, colN)
```

```
##
## 2. array
##
A <- matrix(ncol=length(colNames),
            dimnames=list(NULL, colNames))

Anums <- dateCols(A)

# check

all.equal(Anums, colN)
```

Dates3to1

Convert 3-column dates in data to class Date

Description

Return a [data.frame](#) with columns of class "Date" replacing all 3-column dates.

Usage

```
Dates3to1(data, YMD=c('Year', 'Month', 'Day'))
```

Arguments

data	a data.frame assumed to include dates coded in three column sets with names matching YMD.
YMD	a character vector of length 3 of patterns to use in grep to identify triples of columns coding YMD in <code>col.names(data)</code> .

Details

The data sets from the [Correlates of War](#) project include dates coded in triples of columns with names like `c("StartMonth1", "StartDay1", "StartYear1", "EndMonth1", ..., "EndYear2")`. This function will accept a [data.frame](#) obtained via [read.csv](#) of such a file and replace each such triple with a single column of class 'Date' combining the triple appropriately.

Value

Return a [data.frame](#) containing the information in data reformatted as described above.

Author(s)

Spencer Graves

See Also

[dateCols Date3to1](#)

Examples

```

cow0 <- data.frame(rec=1:3, startMonth=4:6, startDay=7:9,
  startYear=1971:1973, endMonth1=10:12, endDay1=13:15,
  endYear1=1974:1976, txt=letters[1:3])

cow0. <- Dates3to1(cow0)

# check
cow0x <- data.frame(rec=1:3, txt=letters[1:3],
  start=as.Date(c('1971-04-07', '1972-05-08', '1973-06-09')),
  end1=as.Date(c('1974-10-13', '1975-11-14', '1976-12-15')) )

all.equal(cow0., cow0x)

```

deletedFunctions

Functions deleted from the Ecfun package

Description

Several functions were deleted from Ecfun 0.2-5, because they no longer worked, and it was not clear if there was demand for them.

If you need them, you can get the documentation and code for them from CRAN > Packages > Archive (near the bottom center) > Ecfun > Ecfun_0.2-0.tar.gz. I don't expect the code to work. However, I might be willing to collaborate in restoring the functionality to Ecfun.

readFinancialCrisisFiles was a companion to a book. This function required the gdata package, which was scheduled to be removed from CRAN.

USsenateClass called by default readUSsenate. UShouse.senate and mergeUShouse.senate called by default both readUSsenate and readUShouse. The latter two and the remaining functions deleted did web scraping, and the web sites from which they scraped information changed, and it did not seem worth the work required to continue to maintain them.

findCountry

Find a 3-letter country code in rworldmap::countrySynonyms

Description

Search for a specific country name on 8 different columns of alternative names in [countrySynonyms](#). Return either a 3-character code or a longer character string saying, e.g., "No match found for country" followed by the name of the country not found.

NOTE: This code will be offered to the maintainer of the rworldmap package. If they like it, it may not stay in Ecfun.

Usage

```
findCountry(string, referenceTable =
            rworldmap::countrySynonyms)
```

Arguments

`string` Character vector of strings to look for matches in `rworldmap::countrySynonyms[, 3:10]`.

`referenceTable` [data.frame](#) with the second column containing reference codes to be returned if found. `referenceTable[-(1:2)]` are forced [toupper](#) then presented in sequence in [grep](#) until a match for `pattern = toupper(string[i])` is found.

Details

1. Force `string` and `rworldmap::countrySynonyms[, 3:10]` [toupper](#).
2. [grep](#) for `string[i]` in `rworldmap::countrySynonyms[, 3:10]` and return the element of `rworldmap::countrySynonyms$ISO3` that corresponds to anything found if it's 3 characters and an appropriate message otherwise.

Value

A character of 3-character codes or longer not-found messages with `names = string`.

Author(s)

Spencer Graves

See Also

[grep](#), [toupper](#), [countrySynonyms](#)

Examples

```
tstCodes <- findCountry(
  c('Iran', 'Christmas Island', 'eSwatini'))

answer <- c(Iran='IRN',
  'Christmas Island'="referenceTable[53, 2] = ''",
  'eSwatini'="No match found for country eSwatini")

all.equal(tstCodes, answer)
```

getElement2	<i>Extract a named element from an object with a default</i>
-------------	--

Description

Get element name of object. If object does not have an element name, return default.

If the name element of object is NULL the result depends on warn.NULL: If TRUE, issue a warning and return default. Otherwise, return NULL

Usage

```
getElement2(object, name=1, default=NA,
            warn.NULL=TRUE, envir=list(), returnName)
```

Arguments

object	object from which to extract component name.
name	Name or index of the element to extract
default	default value if name is not part of object.
warn.NULL	logical to decide how to treat cases where object has a component name: If TRUE, return default with a warning. Otherwise, return NULL.
envir	Supplemental list beyond object in which to look for names in case object[[name]] is a language object that must be evaluated.
returnName	logical: TRUE to return <code>as.character</code> of any <code>name</code> found as an element of object. FALSE to <code>eval</code> any <code>name</code> found in the environment of object. Default = TRUE if name == 1 or a character string matching the name of the first element of object.

Details

1. If `is.numeric(name)` `In <- (1 <= name <= length(object))`
2. else `In <- if(name %in% names(object))`
3. `E1 <- if(In) object[[name]] else default`
4. `warn.NULL?`
5. `if(returnName) return(as.character(E1)) else return(eval(E1, envir=object))`

Value

an object of the form of `object[[name]]`; if object does not have an element or slot name, return default.

Author(s)

Spencer Graves with help from Marc Schwartz and Hadley Wickham

See Also

[getElement](#), which also can return slots from S4 objects.

Examples

```
##
## 1. name in object, return
##
e1 <- getElement2(list(ab=1), 'ab', 2) # 1
# check

all.equal(e1, 1)

##
## 2. name not in object, return default
##
eNA <- getElement2(list(), 'ab') # default default = NA
# check

all.equal(eNA, NA)

e0 <- getElement2(list(), 'ab', 2) # name not in object

all.equal(e0, 2)

e2 <- getElement2(list(ab=1), 'a', 2) # partial matching not used

all.equal(e2, 2)

##
## 3. name NULL in object, return default
##
ed <- getElement2(list(a=NULL), 'a', 2) # 2 with a warning

all.equal(ed, 2)

e. <- getElement2(list(a=NULL), 'a', 2, warn.NULL=FALSE) # NULL

all.equal(e., NULL)

eNULL <- getElement2(list(a=NULL), 'a', NULL) # NULL

all.equal(eNULL, NULL)

##
```



```
## 4. Language: find, eval, return
##
Qte <- quote(plot(1:4, y=x, col=c2))
if(require(pryr)){
  Qt <- pryr::standardise_call(Qte) # add the name 'x'
  fn <- getElement2(Qt)
  eQuote <- getElement2(Qt, 'y')
  Col2 <- getElement2(Qt, 'col', envir=list(c2=2))
# check

  all.equal(fn, 'plot')

  all.equal(eQuote, 1:4)

  all.equal(Col2, 2)
}
```

```
grepNonStandardCharacters
```

```
grep for nonstandard characters
```

Description

Return the indices of elements of `x` containing characters that are not in `standardCharacters`.

Usage

```
grepNonStandardCharacters(x, value=FALSE,
  standardCharacters=c(letters, LETTERS, ' ',
    '.', ',', '0:9', '\\", "\\'", '- ', '_ ', '( ',
    ')', '[', ']', '\\n'),
  ... )
```

Arguments

<code>x</code>	character vector in which it is desired to identify elements containing characters not in <code>standardCharacters</code> .
<code>value</code>	logical: TRUE to return the values found in <code>x</code> , FALSE to return their indices.
<code>standardCharacters</code>	Characters to overlook in <code>x</code> to identify anything not in <code>standardCharacters</code> .
<code>...</code>	optional arguments for regexpr

Details

1. `x.<- strsplit(x, '')`: convert the input character vector to a list of vectors of character vectors with `nchar(x.[i]) == 1` for `i` in `1:length(x)`.
2. `sapply(x., ...)` to identify all elements for which any element of `x[[i]]` is not in `standardCharacters`.

Value

an integer vector identifying all elements of `x` containing a character not in `standardCharacters`.

Author(s)

Spencer Graves

See Also

[stringi-package](#) [grep](#), [regexpr](#), [subNonStandardCharacters](#), [showNonASCII](#)

Examples

```
Names <- c('Raul', 'Ra`l', 'Torres,Raul', 'Torres, Raul')
# confusion in character sets can create
# names like Names[2]
```

```
chk <- grepNonStandardCharacters(Names)
```

```
all.equal(chk, 2)
```

```
chkv <- grepNonStandardCharacters(Names, TRUE)
```

```
all.equal(chkv, Names[2])
```

Interp

Interpolate between numbers or numbers of characters

Description

Numeric interpolation is defined in the usual way:

```
xOut <- x*(1-proportion) + y*proportion
```

Character interpolation does linear interpolation on the number of characters of `x` and `y`. If `length(proportion) == 1`, interpolation is done on `cumsum(nchar(.))`. If `length(proportion) > 1`, interpolation is based on `nchar`. In either case, the interpolant is rounded to an integer number of characters. `Interp` then returns `substring(y, ...)` unless `nchar(x) > nchar(y)`, when it returns `substring(x, ...)`.

Character interpolation is used in two cases: (1) At least one of `x` and `y` is character. (2) At least one of `x` and `y` is neither logical, integer, numeric, complex nor raw, and `class(unclass(.))` is either integer or character.

In all other cases, numeric interpolation is used.

NOTE: This seems to provide a relatively simple default for what most people would want from the six classes of atomic vectors (logical, integer, numeric, complex, raw, and character) and most other classes. For example, `class(unclass(factor))` is integer. The second rule would apply to this converting it to character. The `coredata` of an object of class `zoo` could be most anything, but this relatively simple rule would deliver what most people want in most case. An exception would be an object with integer `coredata`. To handle this as numeric, a `Interp.zoo` function would have to be written.

Usage

```
Interp(x, ...)
## Default S3 method:
Interp(x, y, proportion,
       argnames=character(3),
       message0=character(0), ...)
InterpChkArgs(x, y, proportion,
              argnames=character(3),
              message0=character(0), ...)
InterpChar(argsChk, ...)
InterpNum(argsChk, ...)
```

Arguments

<code>x, y</code>	two vectors of the same class or to be coerced to the same class.
<code>proportion</code>	A number or numeric vector assumed to be between 0 and 1.
<code>argnames</code>	a character vector of length 3 giving arguments <code>name.x</code> , <code>name.y</code> , and <code>proportion</code> to pass to <code>compareLengths</code> to improve the value of any diagnostic message in case lengths are not compatible.
<code>message0</code>	A character string to be passed with <code>argnames</code> to <code>compareLengths</code> to improve the value of any diagnostic message in case lengths are not compatible.
<code>argsChk</code>	a list as returned by <code>interpChkArgs</code>
<code>...</code>	optional arguments for <code>compareLengths</code>

Details

`Interp` is an S3 generic function to allow users to easily modify the behavior to interpolate between special classes of objects.

`Interp` has two basic algorithms for "Numeric" and "Character" interpolation.

The computations begin by calling `InterpChkArgs` to dispose quickly of simple cases (e.g. `x` or `y` `missing` or `length 0` or if `proportion` is `<= 0` or `>= 1` or `missing`). It returns a list.

If the list contains a component named `xout`, `Interp` returns that value with no further computations.

Otherwise, the list returned by `InterpChkArgs` includes components "algorithm", "x", "y", "proportion", `pLength1` (defined below), "raw", and "outclass". The "algorithm" component must be either "Numeric" or "Character". That algorithm is then performed as discussed below using arguments "x", "y", and "proportion"; all three will have the same length. The class of "x" and "y" will match the algorithm. The list component "raw" is logical: TRUE if the output will be raw or such that `class(unclass(.))` of the output will be raw. In that case, a "Numeric" interpolation will be transformed back into "raw". "outclass" will either be a list of attributes to apply to the output or NA. If a list, `xout` will be added as component ".Data" to the list "outclass" and then then processed as `do.call('structure', outclass)` to produce the desired output.

These two basic algorithms ("Numeric" and "Character") are the same if `proportion` is missing or not numeric: In that case `Interp` throws an error.

We now consider "Character" first, because it's domain of applicability is easier to describe. The "Numeric" algorithm is used in all other cases

1. "CHARACTER"

* 1.1. The "CHARACTER" algorithm is used when at least one of `x` and `y` is neither logical, integer, numeric, complex nor raw and satisfies one of the following two additional conditions:

** 1.1.1. Either `x` or `y` is character.

** 1.1.2. `class(unclass(.))` for at least one of `x` and `y` is either character or integer.

NOTE: The strengths and weaknesses of 1.1.2 can be seen in considering factors and integer vectors of class `zoo`: For both, `class(unclass(.))` is integer. For factors, we want to use `as.character(.)`. For `zoo` objects with `coredata` of class integer, we would want to use numeric interpolation. This is not allowed with the current code but could be easily implemented by writing `Interp.zoo`.

* 1.2. If either `x` or `y` is missing or has `length 0`, the one that is provided is returned unchanged.

* 1.3. Next determine the class of the output. This depends on whether neither, one or both of `x` and `y` have one of the six classes of atomic vectors (logical, integer, numeric, complex, raw, character):

** 1.3.1. If both `x` and `y` have one of the six atomic classes and one is character, return a character object.

** 1.3.2. If only one of `x` and `y` have an atomic class, return an object of the class of the other.

** 1.3.3. If neither of `x` nor `y` have a basic class, return an object with the class of `y`.

* 1.4. Set `pLength1 <- (length(proportion) == 1)`:

** 1.4.1. If `pLength1` do the linear interpolation on `cumsum(nchar(.))`.

** 1.4.2. Else do the linear interpolation on `nchar`.

* 1.5. Next check `x`, `y` and `proportion` for comparable lengths: If all have `length 0`, return an object of the appropriate class. Otherwise, call `compareLengths(x, proportion)`, `compareLengths(y, proportion)`, and `compareLengths(x, y)`.

* 1.6. Extend `x`, `y`, and `proportion` to the length of the longest using `rep`.

* 1.7. `nchOut <-` the number of characters to output using numeric interpolation and rounding the result to integer.

* 1.8. Return `substring(y, 1, nchOut)` except when the number of characters from `x` exceed those from `y`, in which case return `substring(x, 1, nchOut)`. [NOTE: This meets the naive end conditions that the number of characters matches that of `x` when `proportion` is 0 and matches that of `y` when `proportion` is 1. This can be used to "erase" characters moving from one frame to the next in a video. See the examples.

2. "NUMERIC"

- * 2.1. Confirm that this does NOT satisfy the condition for the "Character" algorithm.
- * 2.2. If either x or y is missing or has `length 0`, return the one provided.
- * 2.3. Next determine the class of the output. As for "Character" described in section 1.3, this depends on whether neither, one or both of x and y have a basic class other than character (logical, integer, numeric, complex, raw):
 - ** 2.3.1. If `proportion <= 0`, return x unchanged. If `proportion >= 1`, return y unchanged.
 - ** 2.3.2. If neither x nor y has a basic class, return an object of class equal that of y.
 - ** 2.3.3. If exactly one of x and y does not have a basic class, return an object of class determined by `class(unclass(.))` of the non-basic argument.
 - ** 2.3.4. When interpolating between two objects of class raw, convert the interpolant back to class raw. Do this even when 2.3.2 or 2.3.3 applies and `class(unclass(.))` of both x and y are of class raw.
- * 2.4. Next check x, y and `proportion` for comparable lengths: If all have length 0, return an object of the appropriate class. Otherwise, call `compareLengths(x, proportion)`, `compareLengths(y, proportion)`, and `compareLengths(x, y)`.
- * 2.5. Compute the desired interpolation and convert it to the required class per step 2.3 above.

Value

Interp returns a vector whose class is described in "* 1.3" and "* 2.3" in "Details" above.

InterpChkArgs returns a list or throws an error as described in "Details" above.

Author(s)

Spencer Graves

References

The *Writing R Extensions* manual (available via `help.start()`) lists six different classes of atomic vectors: `logical`, `integer`, `numeric`, `complex`, `raw` and `character`. See also Wickham, Hadley (2014) *Advanced R*, especially Wickham (2013, section on "Atomic vectors" in the chapter on "Data structures").

See Also

[classIndex](#) [interpPairs](#)

Many other packages have functions with names like `interp`, `interp1`, and `interpolate`. Some do one-dimensional interpolation. Others do two-dimensional interpolation. Some offer different kinds of interpolation beyond linear. At least one is a wrapper for [approx](#).

Examples

```

##
## 1. numerics
##
# 1.1. standard
xNum <- interpChar(1:3, 4:5, (0:3)/4)
# answer
xN. <- c(1, 2.75, 3.5, 4)

all.equal(xNum, xN.)

# 1.2. with x but not y:
# return that vector with a warning

xN1 <- Interp(1:4, p=.5)
# answer
xN1. <- 1:4

all.equal(xN1, xN1.)

##
## 2. Single character vector
##

i.5 <- Interp(c('a', 'bc', 'def'), character(0), p=0.3)
# with y = NULL or character(0),
# Interp returns x

all.equal(i.5, c('a', 'bc', 'def'))

i.5b <- Interp('', c('a', 'bc', 'def'), p=0.3)
# Cumulative characters (length(proportion)=1):
# 0.3*(total 6 characters) = 1.2 characters
i.5. <- c('a', 'b', '')

all.equal(i.5b, i.5.)

##
## 3. Reverse character example
##
i.5c <- Interp(c('a', 'bc', 'def'), '', 0.3)
# check: 0.7*(total 6 characers) = 4.2 characters
i.5c. <- c('a', 'bc', 'd')

all.equal(i.5c, i.5c.)

```

```

##
## 4. More complicated example
##
xCh <- Interp('', c('Do it', 'with R.'),
              c(0, .5, .9))
# answer
xCh. <- c('', 'with', 'Do i')

all.equal(xCh, xCh.)

##
## 5. Still more complicated
##
xC2 <- Interp(c('a', 'fabulous', 'bug'),
              c('bigger or', 'just', 'big'),
              c(.3, .3, 1) )
x.y.longer <- c('bigger or', 'fabulous', 'big')
# use y with ties
# nch smaller      1      4      3
# nch larger       9      8      3
# d.char           8,     4,     0
# prop            .3,     .7,     1
# prop*d.char     2.4,   2.8,     0
# smaller+p*d     3,     7,     3
xC2. <- c('big', 'fabulou', 'big')

all.equal(xC2, xC2.)

##
## 6. with one NULL
##
null1 <- Interp(NULL, 1, .3)

all.equal(null1, 1)

null2 <- Interp('abc', NULL, .3)

all.equal(null2, 'abc')

##
## 7. length=0
##
log0 <- interpChar(logical(0), 2, .6)

all.equal(log0, 1.2)

##
## 8. Date
##
(Jan1.1980 <- as.Date('1980-01-01'))

```

```

Jan1.1972i <- Interp(0, Jan1.1980, .2)
# check
Jan1.1972 <- as.Date('1972-01-01')

all.equal(Jan1.1972, round(Jan1.1972i))

##
## 9. POSIXct
##
(Jan1.1980c <- as.POSIXct(Jan1.1980))

(Jan1.1972ci <- Interp(0, Jan1.1980c, .2))
# check
(Jan1.1972ct <- as.POSIXct(Jan1.1972))

abs(difftime(Jan1.1972ct, Jan1.1972ci,
             units="days"))<0.5

```

interpChar

Interpolate between numbers or numbers of characters

Description

For x and y logical, integer, numeric, Date or POSIX:

```
xOut <- x*(1-.proportion) + y*.proportion
```

Otherwise, coerce to character and return a [substring](#) of x or y with number of characters interpolating linearly between nchar(x) and nchar(y); see details.

*** NOTE: This function is currently in flux. The results may not match the documentation and may change in the future.

The current version does character interpolation on the cumulative number of characters with defaults with only one argument that may not be easy to understand and use. Proposed:

old: interpolate on number of characters in each string with the default for a missing argument being character(length(x)) [or character(length(y)) or numeric(length(x)) or ...]

2014-08-08: default with either x or y missing should be to set the other to the one we have, so interpChar becomes a no op – except that values with .proportion outside (validProportion = [0, 1] by default) should be dropped.

Usage

```

interpChar(x, ...)
## S3 method for class 'list'
interpChar(x, .proportion,

```



```

        argnames=character(3),
        message0=character(0), ...)
## Default S3 method:
interpChar(x, y, .proportion,
           argnames=character(3),
           message0=character(0), ...)

```

Arguments

x	either a vector or a list. If a list, pass the first two elements as the first two arguments of <code>interpChar.default</code> .
y	a vector
.proportion	A number or numeric vector assumed to be between 0 and 1.
argnames	a character vector of length 3 giving arguments <code>name.x</code> , <code>name.y</code> , and <code>.proportion</code> to pass to <code>compareLengths</code> to improve the value of any diagnostic message in case lengths are not compatible.
message0	A character string to be passed with <code>argnames</code> to <code>compareLengths</code> to improve the value of any diagnostic message in case lengths are not compatible.
...	optional arguments for <code>compareLengths</code>

Details

1. `x`, `y` and `.proportion` are first compared for compatible lengths using `compareLengths`. A warning is issued if the lengths are not compatible. They are then all extended to the same length using `rep`.
2. If `x` and `y` are both numeric, `interpChar` returns the standard linear interpolation (described above).
3. If `x`, `y`, and `.proportion` are all provided with at least one of `x` and `y` not being numeric or logical, the algorithm does linear interpolation on the difference in the number of characters between `x` and `y`. It returns characters from `y` except when `nchar(x) > nchar(y)`, in which case it returns characters from `x`. This meets the end conditions that the number of characters matches that of `x` when `.proportion` is 0 and matches that of `y` when `.proportion` is 1. This can be used to "erase" characters moving from one frame to the next in a video. See the examples.
4. If either `x` or `y` is missing, it is replaced by a default vector of the same type and length; for example, if `y` is missing and `x` is numeric, `y = numeric(length(x))`. (If the one supplied is not numeric or logical, it is coerced to character.)

Value

A vector: Numeric if `x` and `y` are both numeric and character otherwise. The length = max length of `x`, `y`, and `.proportion`.

Author(s)

Spencer Graves

See Also

[interpPairs](#), which calls interpChar

[classIndex](#), which is called by interpChar to help decide the class of the interpolant.

Examples

```
##
## 1. numerics
##
# 1.1. standard
xNum <- interpChar(1:3, 4:5, (0:3)/4)
# answer
xN. <- c(1, 2.75, 3.5, 4)

all.equal(xNum, xN.)

# 1.2. list of length 1 with a numeric vector:
#       return that vector with a warning
xN1 <- interpChar(list(a.0=1:4), .5)
# answer
xN1. <- 1:4

all.equal(xN1, xN1.)

##
## 2. Single character vector
##
i.5 <- interpChar(list(c('a', 'bc', 'def')), .p=0.3)
# If cumulative characters:
#       0.3*(total 6 characters) = 1.8 characters
#
# However, the current code does something different,
# returning "a", "bc", "d" <- like using 1-.p?
# This is a problem with the defaults with a single
# argument; ignore this issue for now.
# 2014-06-04
i.5. <- c('a', 'b', '')
#all.equal(i.5, i.5.)

##
## 3. Reverse character example
##
i.5c <- interpChar(c('a', 'bc', 'def'), '', 0.3)
# check: 0.7*(total 6 characers) = 4.2 characters
i.5c. <- c('a', 'bc', 'd')

all.equal(i.5c, i.5c.)

# The same thing specified in a list
```

```

i.5d <- interpChar(list(c('a', 'bc', 'def'), ''), 0.3)

all.equal(i.5d, i.5c.)

##
## 4. More complicated example
##
xCh <- interpChar(list(c('Do it', 'with R.')),
                  c(0, .5, .9))
# answer
xCh. <- c('', 'with', 'Do ')
# With only one input, it's assumed to be y.
# It is replicated to length(.proportion),
# With nchar = 5, 7, 5, cum = 5, 12, 17.

all.equal(xCh, xCh.)

##
## 5. Still more complicated
##
xC2 <- interpChar(c('a', 'fabulous', 'bug'),
                  c('bigger or', 'just', 'big'),
                  c(.3, .3, 1) )
# answer
x.y.longer <- c('bigger or', 'fabulous', 'big')
# use y with ties
# nch smaller      1      4      3
# nch larger       9      8      3
# d.char           8,     4,     0
# cum characters   8,    12,    12
# prop            .3,    .7,     1
# prop*12         3.6,   8.4,    12
# cum.sm          1,     5,     8
# cum.sm+prop*12  5,    13,    20
# -cum(larger[-1]) 5,     4,     3
xC2. <- c('bigge', 'fabu', 'big')

all.equal(xC2, xC2.)

##
## 6. with one NULL
##
null1 <- interpChar(NULL, 1, 1)

all.equal(null1, 1)

null2 <- interpChar('abc', NULL, .3)

all.equal(null2, 'ab')

```

```
##
## 7. length=0
##
log0 <- interpChar(logical(0), 2, .6)

all.equal(log0, 1.2)

##
## 8. Date
##

##
## 9. POSIXct
##
```

 interpPairs

interpolate between pairs of vectors in a list

Description

This does two things:

1. Computes a `.proportion` interpolation between pairs by passing each pair with `.proportion` to `interpChar`. `interpChar` does standard linear interpolation with numerics and interpolates based on the number of characters with non-numerics.
2. Discards rows of interpolants for which `.proportion` is outside `validProportion`. If object is a list, corresponding rows of other vectors of the same length are also discarded.

NOTE: There are currently discrepancies between the documentation and the code over defaults when one but not both elements of a pair are provided. The code returns an answer. If that's not acceptable, provide the other half of the pair. After some experience is gathered, the question of defaults will be revisited and the code or the documentation will change.

Usage

```
interpPairs(object, ...)
## S3 method for class 'call'
interpPairs(object,
  nFrames=1, iFrame=nFrames,
  endFrames=round(0.2*nFrames),
  envir = parent.frame(),
  pairs=c('1'='\\0$', '2'='\\.1$',
    replace0='', replace1='.2',
    replace2='.3'),
  validProportion=0:1, message0=character(0), ...)
```

```
## S3 method for class 'function'
interpPairs(object,
  nFrames=1, iFrame=nFrames,
  endFrames=round(0.2*nFrames),
  envir = parent.frame(),
  pairs=c('1'='\\.0$', '2'='\\.1$',
  replace0='', replace1='.2', replace2='.3'),
  validProportion=0:1, message0=character(0), ...)
## S3 method for class 'list'
interpPairs(object,
  .proportion, envir=list(),
  pairs=c('1'='\\.0$', '2'='\\.1$',
  replace0='', replace1='.2',
  replace2='.3'), validProportion=0:1,
  message0=character(0), ...)
```

Arguments

object	<p>A call, function, list or <code>data.frame</code> with names possibly matching <code>pairs[1:2]</code>. When names matching both of <code>pairs[1:2]</code>, they are converted to potentially common names using <code>sub(pairs[i], pairs[3], ...)</code>. When matches are found among the potentially common names, they are passed with <code>.proportion</code> to interpChar to compute an interpolation. The matches are removed and replaced with the interpolant, shortened by excluding any rows for which <code>.proportion</code> is outside <code>validProportion</code>.</p> <p>Elements with "common names" that do not have a match are replaced by elements with the common names that have been shortened by omitting rows with <code>.proportion</code> outside <code>validProportion</code>. Thus, if <code>x.0</code> is found without <code>x.1</code>, <code>x.0</code> is removed and replaced by <code>x</code>.</p>
nFrames	number of distinct plots to create.
iFrame	integer giving the index of the single frame to create. Default = <code>nFrames</code> . An error is thrown if both <code>iFrame</code> and <code>.proportion</code> are not <code>NULL</code> .
endFrames	Number of frames to hold constant at the end.
.proportion	<p>a numeric vector assumed to lie between 0 and 1 specifying how far to go from <code>suffixes[1]</code> to <code>suffixes[2]</code>. For example, if <code>x.0</code> and <code>x.1</code> are found and are numeric, $x = x.0 + .proportion * (x.1 - x.0)$. Rows of <code>x</code> and any other element of <code>object</code> of the same length are dropped for any <code>.proportion</code> outside <code>validProportion</code>.</p> <p>An error is thrown if both <code>iFrame</code> and <code>.proportion</code> are not <code>NULL</code>.</p>
envir	environment / list to use with <code>object</code> , which can optionally provide other variables to compute what gets plotted; see the example below using this argument.
pairs	<p>a character vector of two regular expressions to identify elements of <code>object</code> between which to interpolate and three replacements.</p> <p>(1) The first of the three replacements is used in sub to convert each <code>pairs[1:2]</code> name found to the desired name of the interpolate. Common names found are then passed with <code>.proportion</code> to interpChar, which does the actual interpolation.</p>

(2, 3) interpPairs also calls checkNames(object, avoid = pairs[c(1, 3, 2, 5)]). This confirms that object has names, and all such names are unique. If object does not have names or has some duplicate names, the make.names is called to fix that problem, and any new names that match pairs[1:2] are modified using sub to avoid creating a new match. If the modification still matches pairs[1:2], it generates an error.

validProportion	Range of values of .proportion to retain, as noted with the discussion of the object argument.
message0	a character string passed to interpChar to improve the value of diagnostic messages
...	optional arguments for sub

Details

*** FUNCTION ***

First interpPairs.function looks for arguments firstFrame, lastFrame, and Keep. If any of these are found, they are stored locally and removed from the function. If iFrame is provided, it is used with with these arguments plus nFrames and endFrames to compute .proportion.

If .proportion is outside validProportion, interpPairs does nothing, returning enquote(NULL).

If any(.proportion) is inside validProportion, interpPairs.function next uses grep to look for arguments with names matching pairs[1:2]. If any are found, they are passed with .proportion to interpChar. The result is stored in the modified object with the common name obtained from sub(pairs[i], pairs[3], ...), i = 1, 2.

The result is then evaluated and then returned.

*** LIST ***

1. ALL.OUT: if(none(0<=.proportion<=1))return 'no.op' = list(fun='return', value=NULL)
2. FIND PAIRS: Find names matching pairs[1:2] using grep. For example, names like x.0 match the default pairs[1], and names like x.1 match the default pairs[1].
3. MATCH PAIRS: Use sub(pairs[i], pairs[3], ...) for i = 1:2, to translate each name matching pairs[1:2] into something else for matching. For example, the default pairs thus translates, e.g., x.0 and x.1 both into x. In the output, x.0 and x.1 are dropped, replaced by x = interpChar(x.0, x.1, .proportion, ...). Rows with .proportion outside validProportion are dropped in x. Drop similar rows of any numeric or character vector or data.frame with the same number of rows as x or .proportion.
4. Add component .proportion to envir to make it available to eval any language component of object in the next step.
5. Loop over all elements of object to create outList, evaluating any expressions and computing the desired interpolation using interpChar. Computing xleft in this way allows xright to be specified later as quote(xleft + xinch(0.6)), for example. This can be used with a call to rasterImageAdj.
6. Let N = the maximum number of rows of elements of outList created by interpolation in the previous step. If .proportion is longer, set N = length(.proportion). Find all vectors and data.frames in outList with N rows and delete any rows for which .proportion is outside validProportion.

7. Delete the raw pairs found in steps 1-3, retaining the element with the target name computed in steps 4 and 5 above. For other elements of object modified in the previous step, retain the shortened form. Otherwise, retain the original, unevaluated element.

Value

a list with elements containing the interpolation results.

Author(s)

Spencer Graves

See Also

[interpChar](#) for details on interpolation. [compareLengths](#) for how lengths are checked and messages composed and written. [enquote](#)

Examples

```
###
###
### 1. interpPairs.function
###
###

##
## 1.1. simple
##
plot0 <- quote(plot(0))
plot0. <- interpPairs(plot0)
# check

all.equal(plot0, plot0.)

##
## 1.2. no op
##
noop <- interpPairs(plot0, iFrame=-1)
# check

all.equal(noop, enquote(NULL))

##
## 1.3. a more typical example
## example function for interpPairs
tstPlot <- function(){
  plot(1:2, 1:2, type='n')
  lines(firstFrame=1:3,
        lastFrame=4,
        x.1=seq(1, 2, .5),
```

```

        y.1=x,
        z.0=0, z.1=1,
        txt.1=c('CRAN is', 'good', '...'),
        col='red')
}
tstbo <- body(tstPlot)
iPlot <- interpPairs(tstbo[[2]])
# check
iP <- quote(plot(1:2, 1:2, type='n'))

all.equal(iPlot, iP)

iLines <- interpPairs(tstbo[[3]], nFrames=5, iFrame=2)
# check:
# .proportion = (iFrame-firstFrame)/(lastFrame-firstFrame)
# = c(1/3, 0, -1/3)
# if x.0 = 0 and y.0 = 0 by default:
iL <- quote(linex(x=c(1/3, 0), y=c(1/9, 0), z=c(1/3, 0),
                tst=c('CR', '')))
##
##### This example seems to give the wrong answer
##### 2014-06-03: Ignore for the moment
##
#all.equal(iLines, iL)

##
## 1.4. Don't throw a cryptic error with NULL
##
ip0 <- interpPairs(quote(text(labels.1=NULL)))

###
###
### 2. interpPairs.list
###
###

##
## 2.1. (x.0, y.0, x.1, y.1) -> (x,y)
##
tstList <- list(x.0=1:5, y.0=5:9, y.1=9:5, x.1=9,
               ignore=letters, col=1:5)
xy <- interpPairs(tstList, 0.1)
# check
xy. <- list(ignore=letters, col=1:5,
            x=1:5 + 0.1*(9-1:5),
            y=5:9 + 0.1*(9:5-5:9) )
# New columns, 'x' and 'y', come after
# columns 'col' and 'ignore' already in tstList

all.equal(xy, xy.)

```



```
##
## 2.2. Select the middle 2:
##     x=(1-(0,1))*3+4+0:1*0=(3,0)
##
xy0 <- interpPairs(tstList[-4], c(-Inf, -1, 0, 1, 2) )
# check
xy0. <- list(ignore=letters, col=3:4, x=c(3,0), y=7:6)

all.equal(xy0, xy0.)

##
## 2.3. Null interpolation because of absence of y.1 and x.0
##
xy02 <- interpPairs(tstList[c(2, 4)], 0.1)
# check
#### NOT the current default answer; revisit later.
xy02. <- list(y=5:9, x=9)

# NOTE: length(x) = 1 = length(x.1) in testList
#all.equal(xy02, xy02.)

##
## 2.4. Select an empty list (make sure this works)
##
x0 <- interpPairs(list(), 0:1)
# check
x0. <- list()
names(x0.) <- character(0)

all.equal(x0, x0.)

##
## 2.5. subset one vector only
##
xyz <- interpPairs(list(x=1:4), c(-1, 0, 1, 2))
# check
xyz. <- list(x=2:3)

all.equal(xyz, xyz.)

##
## 2.6. with elements of class call
##
xc <- interpPairs(list(x=1:3, y=quote(x+sin(pi*x/6))), 0:1)
# check
xc. <- list(x=1:3, y=quote(x+sin(pi*x/6)))

all.equal(xc, xc.)
```

```

##
## 2.7. text
##
# 2 arguments
j.5 <- interpPairs(list(x.0='', x.1=c('a', 'bc', 'def')), 0.5)
# check
j.5. <- list(x=c('a', 'bc', ''))

all.equal(j.5, j.5.)

##
## 2.8. text, 1 argument as a list
##
j.50 <- interpPairs(list(x.1=c('a', 'bc', 'def')), 0.5)
# check

all.equal(j.50, j.5.)

##
## 2.9. A more complicated example with elements to eval
##
logo.jpg <- paste(R.home(), "doc", "html", "logo.jpg",
                 sep = .Platform$file.sep)
if(require(jpeg)){
  Rlogo <- try(readJPEG(logo.jpg))
  if(!inherits(Rlogo, 'try-error')){
# argument list for a call to rasterImage or rasterImageAdj
  RlogoLoc <- list(image=Rlogo,
    xleft.0 = c(NZ=176.5,CH=172,US=171,
               CN=177,RU= 9.5,UK= 8),
    xleft.1 = c(NZ=176.5,CH= 9,US=-73.5,
               CN=125,RU= 37, UK= 2),
    ybottom.0=c(NZ=-37, CH=-34,US=-34,
                CN=-33,RU= 48, UK=47),
    ybottom.1=c(NZ=-37, CH= 47,US= 46,
                CN= 32,RU=55.6,UK=55),
    xright=quote(xleft+xinch(0.6)),
    ytop = quote(ybottom+yinch(0.6)),
    angle.0 =0,
    angle.1 =c(NZ=0,CH=3*360,US=5*360,
               CN=2*360,RU=360,UK=360)
  )

  RlogoInterp <- interpPairs(RlogoLoc,
    .proportion=rep(c(0, -1), c(2, 4)) )
# check

all.equal(names(RlogoInterp),
  c('image', 'xright', 'ytop',
    'xleft', 'ybottom', 'angle'))

```

```

# NOTE: 'xleft', and 'ybottom' were created in interpPairs,
# and therefore come after 'xright' and 'ytop', which were
# already there.

##
## 2.10. using envir
##
RlogoDiag <- list(x0=quote(Rlogo.$xleft),
                 y0=quote(Rlogo.$ybottom),
                 x1=quote(Rlogo.$xright),
                 y1=quote(Rlogo.$ytop) )

RlogoD <- interpPairs(RlogoDiag, .p=1,
                     envir=list(Rlogo.=RlogoInterp) )

all.equal(RlogoD, RlogoDiag)

}
}
##
## 2.11. assign; no interp but should work
##
tstAsgn <- as.list(quote(op <- (1:3)^2))
intAsgn <- interpPairs(tstAsgn, 1)

# check
intA. <- tstAsgn
names(intA.) <- c('X', 'X.3', 'X.2')

all.equal(intAsgn, intA.)

# op <- par(...)
tstP <- quote(op <- par(mar=c(5, 4, 2, 2)+0.1))
tstPar <- as.list(tstP)
intPar <- interpPairs(tstPar, 1)

# check
intP. <- list(quote(`<-`), quote(op),
             quote(par(mar=c(5, 4, 2, 2)+0.1)) )
names(intP.) <- c("X", 'X.3', 'X.2')

all.equal(intPar, intP.)

intP. <- interpPairs(tstP)

all.equal(intP., tstP)

##

```

```
## NULL
##
all.equal(interpPairs(NULL), quote(NULL))
```

logVarCor

Log-diagonal representation of a variance matrix

Description

Translate a square symmetric matrix with positive diagonal elements into a vector of the logarithms of the diagonal elements with the correlations as an attribute, and vice versa.

Usage

```
logVarCor(x, corr, ...)
```

Arguments

x	If a matrix, translate into a vector with a "corr" attribute. If a vector, translate into a matrix.
corr	optional vector of correlations for the <code>lower.tri</code> portion of a covariance matrix whose diagonal is <code>exp(x)</code> . Use a "corr" attribute of x only if this argument is <code>missing</code> .
...	(not currently used)

Value

if(`length(dim(x))==2`) return `log(diag(x))` with an attribute "corr" equal to the `lower.tri` of `cov2cor(x)`.

Otherwise, return a covariance matrix from x as described above.

Author(s)

Spencer Graves

See Also

`log diag cov2cor lower.tri pdLogChol` converts a k-dimensional covariance matrix into a vector of length `choose(k+1, 2)`. By contrast, `logVarCor` returns a vector of length k with a "corr" attribute of length `choose(k, 2)`.

Examples

```
##
## 1. Trivial 1 x 1 matrix
##
# 1.1. convert vector to "matrix"
mat1 <- logVarCor(1)
# check

all.equal(mat1, matrix(exp(1), 1))

# 1.2. Convert 1 x 1 matrix to vector
lVCd1 <- logVarCor(diag(1))
# check
lVCd1. <- 0
attr(lVCd1., 'corr') <- numeric(0)

all.equal(lVCd1, lVCd1.)

##
## 2. simple 2 x 2 matrix
##
# 2.1. convert 1:2 into a matrix
lVC2 <- logVarCor(1:2)
# check
lVC2. <- diag(exp(1:2))

all.equal(lVC2, lVC2.)

# 2.2. Convert a matrix into a vector
lVC2d <- logVarCor(diag(1:2))
# check
lVC2d. <- log(1:2)
attr(lVC2d., 'corr') <- 0

all.equal(lVC2d, lVC2d.)

##
## 3. 3-d covariance matrix with nonzero correlations
##
# 3.1. Create matrix
(ex3 <- tcrossprod(matrix(c(rep(1,3), 0:2), 3)))
dimnames(ex3) <- list(letters[1:3], letters[1:3])

# 3.2. Convert to vector
(Ex3 <- logVarCor(ex3))

# check
Ex3. <- log(c(1, 2, 5))
```

```

names(Ex3.) <- letters[1:3]
attr(Ex3., 'corr') <- c(1/sqrt(2), 1/sqrt(5), 3/sqrt(10))

all.equal(Ex3, Ex3.)

# 3.3. Convert back to a matrix
Ex3.2 <- logVarCor(Ex3)
# check

all.equal(ex3, Ex3.2)

```

match.data.frame	<i>Identify the row of y best matching each row of x</i>
------------------	--

Description

For each row of `x[, by.x]`, find the best matching row of `y[, by.y]`, with the best match defined by `grep.` and `split.`

`grep.` and `split.` must either be `missing` or have the same length as `by.x` and `by.y`. If `grep.[i]` and `split[i]` are NA, do a complete match of `x[, by.x[i]]` and `y[, by.y[i]]`. Otherwise, for each row `j`, look for a match for `strsplit(x[j, by.x[i]], split[i])[[1]][1]` among `strsplit(y[, by.y[i]], split[i])`. See details.

Usage

```

match.data.frame(x, y, by, by.x=by, by.y=by,
  grep., split, sep='')

```

Arguments

<code>x, y</code>	<code>data.frames</code>
<code>by, by.x, by.y</code>	names of columns of <code>x</code> and <code>y</code> to match.
<code>grep.</code>	a character vector of the type of match for each element of <code>by.x</code> and <code>by.y</code> . If NA, require a perfect match. Alternatives are <code>grep</code> and <code>agrep</code> to find a match for the first segment in <code>strsplit(x, split=split[i])</code> among any of the segments of <code>strsplit(y, split=split[i])</code> . Use <code>fixed=TRUE</code> with the calls to these functions. NOTE: These alternatives are not examined if a unique match is found between <code>x[, by.x[is.na(grep.) & is.na(split)]]</code> and the corresponding columns of <code>y</code> .
<code>split</code>	A character vector of split characters to pass to <code>strsplit</code> ; <code>strsplit</code> is not called if <code>is.na(split)</code> .
<code>sep</code>	a <code>sep</code> argument to use with <code>paste</code> to produce a matching key for the columns of <code>x</code> and <code>y</code> for which perfect matches are required. If <code>(missing(sep) && not(missing(grep.)))</code> <code>sep <- ' '</code> except where <code>grep. = NAs</code> .

Details

1. Check `by.x`, `by.y`, `grep`. and `split`. `If((missing(by.x) | missing(by.y)) && missing(by))`
`by <- names(x)`
2. `fullMatch <- (is.na(grep.) & is.na(split))`. Create `keyfx` and `keyfy` by pasting columns of `x[, by.x[fullMatch]]` and `y[, by.y[fullMatch]]`. Also create `x.` and `y.` = `strsplit` of `x[, by.x[!fullMatch]]`.
3. Iterate over rows of `x` looking for the best match. This includes an inner loop over columns of `x[, by.x[!fullMatch]]`, stopping on the first unique match. Return (-1) if no unique match is found.

Value

an integer vector of length `nrow(x)` containing the index of the best matching row of `y` or NA if no adequate match was found.

Author(s)

Spencer Graves

See Also

[strsplit](#), [is.na](#) [grep](#), [agrep](#) [match](#), [row.match](#), [join](#), [match_df](#) [classify](#)

Examples

```
newdata <- data.frame(state=c("AL", "MI", "NY"),
                     surname=c("Rogers", "Rogers", "Smith"),
                     givenName=c("Mike R.", "Mike K.", "Al"),
                     stringsAsFactors=FALSE)
reference <- data.frame(state=c("NY", "NY", "MI", "AL", "NY", "MI"),
                      surname=c("Smith", "Rogers", "Rogers (MI)",
                                "Rogers (AL)", "Smith", 'Jones'),
                      givenName=c("John", "Mike", "Mike", "Mike",
                                  "T. Albert", 'Al Thomas'),
                      stringsAsFactors=FALSE)
newInRef <- match.data.frame(newdata, reference,
                             grep.=c(NA, 'agrep', 'agrep'))

all.equal(newInRef, c(4, 3, 5))
```

matchName	<i>Match surname and givenName in a table</i>
-----------	---

Description

Use `parseName` to split a name into surname and givenName, the look for matches in table.

Usage

```
matchName(x, data, Names=1:2,
          nicknames=matrix(character(0), 0, 2),
          namesNotFound="attr.replacement", ...)
matchName1(x1, data, name=data[, 1],
           nicknames=matrix(character(0), 0, 2), ...)
```

Arguments

x	One of the following: <ul style="list-style-type: none"> • A character matrix or <code>data.frame</code> with the same number of rows as <code>data</code>. The best partial match is sought in <code>Names</code>. The algorithm stops when a unique match is found; any remaining columns of <code>x</code> are then ignored. Any nicknames are ignored for the first column but not for subsequent columns. • A character vector whose length matches the number of rows of <code>data</code>. This will be replaced by <code>parseName(x)</code>.
data	a character matrix or a <code>data.frame</code> . If surname and givenName are character vectors of names, their length must match the number of rows of <code>data</code> .
Names	One of the following in which matches for <code>x</code> will be sought: <ul style="list-style-type: none"> • A character vector or matrix or a <code>data.frame</code> for which <code>NROW(Names) == nrow(data)</code>. • Something to select columns of <code>data</code> to produce a character vector or matrix or <code>data.frame</code> via <code>data[, Names]</code>. In this case, accents will be stripped using <code>subNonStandardNames</code>.
nicknames	a character matrix with two columns, each row giving a pair of names like "Pete" and "Peter" that should be regarded as equivalent if no exact match(es) is(are) found.
...	optional arguments passed to <code>subNonStandardNames</code>
x1	a character vector of names to match <code>name</code> . NOTE: <code>matchName</code> calls <code>subNonStandardNames</code> , but <code>matchName1</code> does not. Thus, <code>x1</code> is assumed to NOT to contain characters not in standard English.
name	A character vector or matrix for which <code>NROW(name) == nrow(data)</code> . NOTE: <code>matchName</code> calls <code>subNonStandardNames</code> , but <code>matchName1</code> does not. Thus, <code>name</code> is assumed to NOT to contain characters not in standard English.
namesNotFound	character vector passed to <code>subNonStandardNames</code> and used to compute any <code>namesNotFound</code> attribute of the object returned by <code>parseName</code> .

Details

```

*** 1. matchName(x, data, Names, nicknames, ...):
1.1. if(length(dim(x)<2))x <- parseName(x, ...)
1.2. x1 <- matchName1(x[, 1], cata, Names[1], ...)
1.3. For any component i of x1 with multiple rows, let x1i <- matchName1(x[i, 2], x1[[i]],
Name[-1], nicknames=nicknames, ...). If nrow(x1i)>0, x1[[i]] <- x1i; else leave unchanged.
1.4. return x1.

=====

*** 2. matchName1(x1, data, name, nicknames, ...):
2.1. If name indicates a column of data, replace with data[, name].
2.2. xsplit <- strsplit(x1, ' ').
2.3. nx <- length(x1); xlist <- vector(nx, mode='list')
2.4. for(j in 1:nx):
2.5. xj <- xsplit[[j]]
2.6. let jd = the subset of names that match xj or subNonStandardNames(xj) or nicknames of xj;
xlist[j] <- jd.
2.7. return xlist

```

Value

matchName returns a list of the same length as x, each of whose components is an object obtained as a subset of rows of data or NULL if no acceptable matches are found. The list may have an attribute namesNotFound as determined per the argument of that name.

matchNames1 returns a list of vectors of integers for subsets of data matching x1.

Author(s)

Spencer Graves

See Also

[parseName](#) [subNonStandardNames](#)

Examples

```

##
## 1. Names to match exercising many possible combinations
## of surname with 0, 1, >1 matches possibly after
## replacing with subNonStandardNames
## combined with possibly multiple givenName combinations
## with 0, 1, >1 matches possibly requiring replacing with
## subNonStandardNames or nicknames
##
# NOTE: "-" could also be "e" with an accent;
# not included with this documentation, because

```

```

# non-English characters generate warnings in standard tests.
Names2mtch <- c("Andr_ Bruce C_rdenas", "Dolores Ella Feinstein",
               "George Homer", "Inez Jane Kappa", "Luke Michael Noel",
               "Oscar Papa", "Quincy Ra_l Stevens",
               "Thomas U. Vel_zquez", "William X. Young",
               "Zebra")

##
## 2. Data = matrix(..., byrow=TRUE) to exercise the combinations
## the combinations from 1
##
Data1 <- matrix(c("Feld", "Don", "789",
                 "C_rdenas", "Don", "456",
                 "C_rdenas", "Andre B.", "123",
                 "Smith", "George", "aaa",
                 "Young", "Bill", "369"),
               ncol=3, byrow=TRUE)
Data1. <- subNonStandardNames(Data1)
##
## 3. matchName1
##
parceNm1 <- parseName(Names2mtch)
match1.1 <- matchName1(parceNm1[, 'surname'], Data1.)

# check
match1.1s <- vector('list', 10)
match1.1s[[1]] <- 2:3
match1.1s[[9]] <- 5
names(match1.1s) <- parceNm1[, 'surname']

all.equal(match1.1, match1.1s)

##
## 4. matchName1 with name = multiple columns
##
match1.2 <- matchName1(c('Cardenas', 'Don'), Data1.,
                      name=Data1.[, 1:2])

# check
match1.2a <- list(Cardenas=2:3, Don=1:2)

all.equal(match1.2, match1.2a)

##
## 5. matchName
##
nickNames <- matrix(c("William", "Bill"), 1, byrow=TRUE)

match1 <- matchName(Names2mtch, Data1, nicknames=nickNames)

# check
match1a <- list("Cardenas, Andre Bruce"=Data1[3,, drop=FALSE ],

```

```

    "Feinstein, Dolores Ella"=NULL,
    "Homer, George"=NULL, "Kappa, Inez Jane"=NULL,
    "Noel, Luke Michael"=NULL, "Papa, Oscar"=NULL,
    "Stevens, Quincy Raul"=NULL,
    "Velazquez, Thomas U."=NULL,
    "Young, William X."=Data1[5,, drop=FALSE],
    "Zebra"=NULL)

all.equal(match1, match1a)

##
## 6. namesNotFound
##
tstNotFound <- matchName('xx_x', Data1)

# check
tstNF <- list('xx_x'=NULL)
attr(tstNF, 'namesNotFound') <- 'xx_x'

all.equal(tstNotFound, tstNF)

##
## 7. matchName(NULL) to simplify use
##
mtchNULL <- matchName(NULL, Data1)

all.equal(mtchNULL, NULL)

```

matchQuote

Match isolated quotes across records

Description

Look for unmatched quotes in a character vector. If found, look for a matching quote starting the next character string in the vector, possibly after a blank line. If found, merge the two strings and return the resulting shortened character vector.

Usage

```

matchQuote(x, Quote='"', sep=' ',
           maxChars2append=2, ...)

```

Arguments

x a character vector to scan for unmatched Quotes.
Quote the Quote character that should appear in pairs

sep sep argument passed to [paste](#) to combine pairs of successive lines with unmatched quotes.

maxChars2append maximum number of characters in the following string to concatenate two adjacent strings (possibly separated by a blank line) with unmatched Quotes.

... optional arguments for [gsub](#)

Details

This function was written to help parse data from the US Department of Health and Human Services on [cyber-security breaches affecting 500 or more individuals](#). As of 2014-06-03 the csv version of these data included commas in quotes that are not sep characters, quotes that are not matched, lines with zero characters, followed by lines with 3 characters being a quote and a comma. This function was written to drop the blank lines and append the quote-comma line to the preceding line so it contained matching quotes.

Value

The input character vector possibly shortened with the following attributes explaining what was found:

indices of the input x with an unmatched

unmatchedQuotes Quote.

blankLinesDropped indices of the input x that were dropped because they (1) followed an unmatched Quote and (2) contained no non-blank characters.

quoteLinesAppended indices of the input x that were concatenated with a preceding line because the two lines contained unmatched Quote characters, and concatenating them produced a line with all Quotes matched.

ncharsAppended an integer vector of the same length as quoteLinesConcatenated giving the number of characters in the second line concatenated onto the previous line.

Author(s)

Spencer Graves

See Also

[strsplit1](#) [delimMatch](#)

Examples

```
chvec <- c('abc', 'de"f', ' ', '"', 'g"h',
          'matched"quotes"', '')
ch. <- matchQuote(chvec)

# check
chv. <- c('abc', 'de"f "', 'g"h',
         'matched"quotes"', '')
attr(chv., 'unmatchedQuotes') <- c(2, 4, 5)
```

```

attr(chv., 'blankLinesDropped') <- 3
attr(chv., 'quoteLinesAppended') <- 4
attr(chv., 'ncharsAppended') <- 2

all.equal(ch., chv.)

```

mergeVote

Merge Roll Call Vote

Description

Merge roll call vote record with a `data.frame` containing other information. The vote records are typically incomplete, so match first on `houseSenate` and `surname`. If this match is incomplete, try using `givenName`. If that fails, try `state` and `district`, which may not always be present in `vote`.

Usage

```

mergeVote(x, vote, Office="House", vote.x,
          check.x=TRUE)

```

Arguments

<code>x</code>	a <code>data.frame</code> whose columns include <code>Office</code> , <code>surname</code> , and <code>givenName</code> .
<code>vote</code>	a <code>data.frame</code> with column names which when forced <code>tolower</code> would match <code>surname</code> , <code>givenname</code> , and <code>vote</code> . However, the <code>givenname</code> may not be complete, so use it only if the <code>surname</code> is not sufficient.
<code>Office</code>	Either "House" or "Senate"; ignored if <code>vote</code> includes a column <code>Office</code> .
<code>vote.x</code>	name of a column of <code>x</code> containing a vote to be updated with the <code>vote</code> column of the <code>vote data.frame</code> . If <code>missing</code> and <code>x</code> has a column with a name matching "vote", then <code>vote.x</code> is that column. If <code>missing</code> but <code>x</code> has no such column, then append a column to <code>x</code> with the name of the <code>vote</code> column of the <code>vote data.frame</code> .
<code>check.x</code>	logical: If <code>TRUE</code> , check for rows of <code>x[, vote.x]</code> that are NOT in <code>vote</code> and throw an error if found.

Details

1. Parse `vote.x` to get the name of the column of `x` into which to write the `vote` column of the `vote data.frame`.
2. If the `vote data.frame` contains a column `Office`, ignore the `Office` argument. Otherwise, add the argument `houseSenate` as a column of `vote`.
3. Create `keyx <- with(x, paste(Office, surname, sep=":"))`, `keyx2 <- paste(keyx, givenName, sep=":"))`, `keyx <- paste(houseSenate, state, district, sep=":"))`, and similarly `keyv`, `levv2`, and `keyv` from `vote`.

4. Look for keyv in keyx. When a unique match is found, transfer the vote the vote column of x. When no match is found, try for keyv2 in keyx2 or keyv. in keyx. If those fail, print an error message with the information from vote on all failures and ask the user to add state and district information.
5. if(check.x), check for rows in x[, vote.x] that are NOT notEligible but are also not in vote: Throw an error if any are found.

Value

a `data.frame` with the same columns as x with its vote column modified per the vote argument.

Author(s)

Spencer Graves

See Also

[mergeUSHouse.senate](#)

Examples

```
##
## 1. Test good cases
##
votetst <- data.frame(
  surName=c('Smith', 'Jones', 'Graves', 'Jsn', 'Jsn', 'Gay'),
  givenName=c("Sam", "", "", "John", "John", ''),
  votex=factor(c('Y', 'N', 'abstain', 'Y', 'Y', 'Y')),
  State=factor(rep(c("CA", "", "SC", "NY"), c(1, 2, 1, 2))),
  district=rep(c("13", "1", "2", "1"), c(1, 2, 2, 1)),
  stringsAsFactors=FALSE )

x1 <- data.frame(
  Office=factor(rep(c("House", "Senate"), e=8)),
  state=rep(c("NY", "SC", "SD", "CA", "AK", "AR", "NY", "NJ"), 2),
  District=rep(c("2", "2", "At Large", "13", "1", "9", "1", "3"), 2),
  surname=rep(c('Jsn', 'Jsn', 'Smith', 'Smith', 'Jones',
    'Graves', 'Rx', 'Agnew'), 2),
  givenName=rep(c("John D.", "John J.",
    "Samual", "Samual", "Mary", "Mary", "Susan", 'Spiro'), 2),
  don=1:16, stringsAsFactors=FALSE)

x1. <- mergeVote(x1, votetst)

x2 <- cbind(x1, votex=factor( rep(
  c('Y', 'notEligible', 'Y', 'N', 'abstain', 'Y', 'notEligible'),
  c(2,1,1,1,1,1,9) ) ) )

all.equal(x1., x2)
```

```
##  
## 2. Test a case with a vote error in x  
##  
x1a <- cbind(x1, voterr=rep(  
  c('notEligible', 'Y', 'notEligible'), c(7, 1, 8)))  
  
x1a. <- try(mergeVote(x1a, votetst))  
  
class(x1a.)=='try-error'
```

missing0

Missing or length 0

Description

TRUE if x is missing or if length(x) is 0.

Usage

```
missing0(x)
```

Arguments

x a formal argument as for [missing](#)

Details

Only makes sense called from within another function

Value

logical: TRUE if x is [missing](#) or if length(x) is 0.

Author(s)

Spencer Graves

See Also

[missing](#)

Examples

```
tstFn <- function(x)missing0(x)
# missing

all.equal(tstFn(), TRUE)

# length 0
all.equal(tstFn(logical()), TRUE)

# supplied
all.equal(tstFn(1), FALSE)
```

nchar0

Zero characters or NULL

Description

Returns TRUE if $(\text{is.null}(x) \mid\mid (\text{length}(x) == 0) \mid\mid (\text{max}(\text{nchar}(x)) == 0))$.

Usage

```
nchar0(x, ...)
```

Arguments

x a character vector or something that can be coerced to mode character
... optional arguments to be passed to [nchar](#)

Value

TRUE if x is either NULL or $\text{max}(\text{nchar}(x)) == 0$. FALSE otherwise.

Author(s)

Spencer Graves

See Also

[nchar](#)

Examples

```
all.equal(nchar0(NULL), TRUE)
```

```
all.equal(nchar0(character(0)), TRUE)
```

```
all.equal(nchar0(character(3)), TRUE)
```

```
all.equal(nchar0(c('a', 'c')), FALSE)
```

Newdata

Create a new data.frame for predict

Description

Generate a new [data.frame](#) or [matrix](#) from another with column(s) selected by `x` adopting `n` values in `range(data[,x])` and all other columns constant.

If `canbeNumeric(x)` is TRUE, the output has `x` adopting `n` values in the `range(x)` and all other numeric variables at their `median` and other variables at their most common values.

If `canbeNumeric(x)` is FALSE, the output has `x` adopting all possible values of `x` with all other variables at the same constant values as when `canbeNumeric(x)` is TRUE (and `n` is ignored). If `x` has a `levels` attribute, the possible values are defined by that `levels` attribute. Otherwise, it is defined by `unique(x)`.

This is designed to create a new [data.frame](#) to be used as `newdata` for `predict`.

Usage

```
Newdata(data, x, n, na.rm=TRUE)
```

Arguments

<code>data</code>	a data.frame or matrix.
<code>x</code>	name of a column of data. If NA or NULL, select all columns of data.
<code>n</code>	an integer vector indicating the number of levels of <code>data[, x]</code> if <code>canbeNumeric(data[, x])</code> . If <code>canbeNumeric(data[, x])</code> is FALSE, take at most <code>n</code> of the most popular levels. Default is 2 if <code>length(x) > 1</code> or if <code>x</code> is either NA or NULL. If <code>n = 1</code> , use the median for <code>canbeNumeric</code> and the most popular level otherwise. If <code>n < 1</code> , drop that variable.
<code>na.rm</code>	logical passed to <code>range(x)</code>

Details

1. Check data, x.
2. If `canbeNumeric(x)` is TRUE, let xNew be n values spanning `range(x)`. Else, let `xNew <- levels(x)`.
3. If `is.null(xNew)`, set it to `sort(unique(x))`.
4. let `newDat <- data[rep(1, n),]`, and replace x by xNew.
5. `otherVars <- colnames(data) != x`
6. for(`x2` in `otherVars`) replace `newDat[, x2]`: If `canbeNumeric(x2)` is TRUE, use `median(x2)`. Otherwise, use its (first) most common value.

Value

A `data.frame` with n rows and columns matching those of data, as described above.

Author(s)

Spencer Graves

See Also

[predict.lm](#)

Examples

```
##
## 1. A reasonable test with numerics, dates,
##    an ordered factor and character variables
##
xDate <- as.Date('2001-02-03')+1:4
tstDF <- data.frame(x1=1:4, xDate=xDate,
  xD2=as.POSIXct(xDate),
  sex=ordered(c('M', 'F', 'M', 'F'))),
  huh=letters[c(1:3, 3)], stringsAsFactors=FALSE)

newDat <- Newdata(tstDF, 'xDate', n=5)

# check
newD <- data.frame(x1=2.5,
  xDate=xDate[1]+seq(0, 3, length=5),
  xD2=as.POSIXct(xDate[2]+0.5),
  sex=ordered(c('M', 'F', 'M', 'F'))[2],
  huh=letters[3], stringsAsFactors=FALSE)
attr(newD, 'out.attrs') <- attr(newDat, 'out.attrs')

all.equal(newDat, newD)

##
## 2. Test with only one column
##
```

```
newDat1 <- Newdata(tstDF[, 2, drop=FALSE], 'xDate', n=5)

# check
newDat1. <- newD[, 2, drop=FALSE]
attr(newDat1., 'out.attrs') <- attr(newDat1, 'out.attrs')

all.equal(newDat1, newDat1.)

##
## 3. Test with a factor
##
newSex <- Newdata(tstDF, 'sex')

# check
newS <- with(tstDF, data.frame(
  x1=2.5, xDate=xDate[1]+1.5,
  xD2=as.POSIXct(xDate[1]+1.5),
  sex=ordered(c('M', 'F'))[2:1],
  huh=letters[3], stringsAsFactors=FALSE) )
attr(newS, 'out.attrs') <- attr(newSex, 'out.attrs')

all.equal(newSex, newS)

##
## 4. Test with an integer column number
##
newDat2 <- Newdata(tstDF, 2, n=5)

# check

all.equal(newDat2, newD)

##
## 5. Test with all
##
NewAll <- Newdata(tstDF)

# check
tstLvls <- as.list(tstDF[c(1, 4), ])
tstLvls$sex <- tstDF$sex[2:1]
tstLvls$huh <- letters[c(3, 1)]
tstLvls$stringsAsFactors <- FALSE

NewA. <- do.call(expand.grid, tstLvls)
attr(NewA., 'out.attrs') <- attr(NewAll, 'out.attrs')

all.equal(NewAll, NewA.)
```

 parseCommas

Convert character string with Dollar signs and commas to numerics

Description

as.numeric of character strings after suppressing commas and dollar signs. This is a generalization of [parseDollars](#).

Usage

```

parseCommas(x, pattern='\\$|,',
            replacement='', acceptableErrorRate=0, ...)
## Default S3 method:
parseCommas(x,
            pattern='\\$|,', replacement='',
            acceptableErrorRate=0, ...)
## S3 method for class 'data.frame'
parseCommas(x,
            pattern='\\$|,', replacement='',
            acceptableErrorRate=0, ...)

```

Arguments

x	vector of character strings to be converted to numerics
pattern	regular expression to be replaced by replacement
replacement	Character string to substitute for each occurrence of pattern
acceptableErrorRate	number indicating the proportion of new NAs to that can be introduced and still assume it's numeric
...	optional arguments to pass to gsub

Details

```
as.numeric(gsub(x, ...))
```

The `data.frame` method outputs another `data.frame` with character or factor columns converted to numerics using `parseDollars` whenever that can be done without creating NAs.

Value

Numeric vector converted from the character strings in `x` or a `data.frame` with columns that are obviously numbers in character format converted to numerics.

Author(s)

Spencer Graves

See Also

[gsub as.numeric parseDollars](#)

Examples

```
##
## 1. a character vector
##
X2 <- c('-2,500', '$5,000.50')
x2 <- parseDollars(X2)

all.equal(x2, c(-2500, 5000.5))

##
## A data.frame
##
chDF <- data.frame(let=letters[1:2], Dol=X2, dol=x2)
numDF <- parseCommas(chDF)

chkDF <- chDF
chkDF$Dol <- x2

all.equal(numDF, chkDF)
```

parseDollars

Convert character string with Dollar signs and commas to numerics

Description

as.numeric of character strings after suppressing commas and dollar signs. This is a special case of [parseCommas](#).

Usage

```
parseDollars(x, pattern='\\$|',
             replacement='', ...)
```

Arguments

x	vector of character strings to be converted to numerics
pattern	regular expression to be replaced by replacement
replacement	Character string to substitute for each occurrence of pattern
...	optional arguments to pass to gsub

Details

as.numeric(gsub(x, ...)). See also [parseCommas](#).

Value

Numeric vector converted from x.

Author(s)

Spencer Graves

See Also

[gsub](#) [as.numeric](#) [parseCommas](#)

Examples

```
##
## 1. a character vector
##
X2 <- c('-$2,500', '$5,000.50')
x2 <- parseDollars(X2)

all.equal(x2, c(-2500, 5000.5))

##
## A data.frame
##
chDF <- data.frame(let=letters[1:2], Dol=X2, dol=x2)
numDF <- parseCommas(chDF)

chkDF <- chDF
chkDF$Dol <- x2

all.equal(numDF, chkDF)
```

parseName

Parse surname and given name

Description

Identify the presumed surname in a character string assumed to represent a name and return the result in a character matrix with surname followed by givenName. If only one name is provided (without punctuation), it is assumed to be the givenName; see Wikipedia, "[Given name](#)" and "[Surname](#)".

Usage

```
parseName(x,
  surnameFirst=(median(regexpr(',', x))>0),
  suffix=c('Jr.', 'I', 'II', 'III', 'IV',
           'Sr.', 'Dr.', 'Jr', 'Sr'),
  fixNonStandard=subNonStandardNames,
  removeSecondLine=TRUE,
  namesNotFound="attr.replacement", ...)
```

Arguments

x	a character vector
surnameFirst	logical: If TRUE, the surname comes first followed by a comma (","), then the given name. If FALSE, parse the surname from a standard Western "John Smith, Jr." format. If missing(surnameFirst), use TRUE if half of the elements of x contain a comma.
suffix	character vector of strings that are NOT a surname but might appear at the end without a comma that would otherwise identify it as a suffix.
fixNonStandard	function to look for and repair nonstandard names such as names containing characters with accent marks that are sometimes mangled by different software. Use identity if this is not desired.
removeSecondLine	logical: If TRUE, delete anything following "\n" and return it as an attribute secondLine.
namesNotFound	character vector passed to subNonStandardNames and used to compute any namesNotFound attribute of the object returned by parseName.
...	optional arguments passed to fixNonStandard

Details

If surnameFirst is FALSE:

1. If the last character is ")" and the matching "(" is 3 characters earlier, drop all that stuff. Thus, "John Smith (AL)" becomes "John Smith".
2. Look for commas to identify a suffix like Jr. or III; remove and call the rest x2.
3. `split <- strsplit(x2, " ")`
4. Take the last as the surname.
5. If the "surname" found per 3 is in suffix, save to append it to the givenName and recurse to get the actual surname.

NOTE: This gives the wrong answer with double surnames written without a hyphen in the Spanish tradition, in which, e.g., "Anastasio Somoza Debayle", "Somoza Debayle" give the (first) surnames of Anastasio's father and mother, respectively: The current algorithm would return "Debayle" as the surname, which is incorrect.

6. Recompose the rest with any suffix as the givenName.

Value

a character matrix with two columns: surname and givenName.

This matrix also has a namesNotFound attribute if one is returned by subNonStandardNames.

Author(s)

Spencer Graves

See Also

[strsplit](#) [identity](#) [subNonStandardNames](#)

Examples

```
##
## 1. Parse standard first-last name format
##
tstParse <- c('Joe Smith (AL)', 'Teresa Angelica Sanchez de Gomez',
             'John Brown, Jr.', 'John Brown Jr.',
             'John W. Brown III', 'John Q. Brown, I',
             'Linda Rosa Smith-Johnson', 'Anastasio Somoza Debayle',
             'Ra_l Vel_zquez', 'Sting', 'Colette, ')
parsed <- parseName(tstParse)

tstParse2 <- matrix(c('Smith', 'Joe', 'Gomez', 'Teresa Angelica Sanchez de',
                    'Brown', 'John, Jr.', 'Brown', 'John, Jr.',
                    'Brown', 'John W., III', 'Brown', 'John Q., I',
                    'Smith-Johnson', 'Linda Rosa', 'Debayle', 'Anastasio Somoza',
                    'Velazquez', 'Raul', '', 'Sting', 'Colette', ''),
                  ncol=2, byrow=TRUE)
# NOTE: The 'Anastasio Somoza Debayle' is in the Spanish tradition
# and is handled incorrectly by the current algorithm.
# The correct answer should be "Somoza Debayle", "Anastasio".
# However, fixing that would complicate the algorithm excessively for now.
colnames(tstParse2) <- c("surname", "givenName")

all.equal(parsed, tstParse2)

##
## 2. Parse "surname, given name" format
##
tst3 <- c('Smith (AL),Joe', 'Sanchez de Gomez, Teresa Angelica',
         'Brown, John, Jr.', 'Brown, John W., III', 'Brown, John Q., I',
         'Smith-Johnson, Linda Rosa', 'Somoza Debayle, Anastasio',
         'Vel_zquez, Ra_l', '', 'Sting', 'Colette,')
tst4 <- parseName(tst3)

tst5 <- matrix(c('Smith', 'Joe', 'Sanchez de Gomez', 'Teresa Angelica',
                'Brown', 'John, Jr.', 'Brown', 'John W., III', 'Brown', 'John Q., I',
```



```

'Smith-Johnson', 'Linda Rosa', 'Somoza Debayle', 'Anastasio',
'Velazquez', 'Raul', '', 'Sting', 'Colette', ''),
ncol=2, byrow=TRUE)
colnames(tst5) <- c("surname", 'givenName')

all.equal(tst4, tst5)

##
## 3. secondLine
##
L2 <- parseName(c('Adam\n2nd line', 'Ed \n --Vacancy', 'Frank'))

# check
L2. <- matrix(c('', 'Adam', '', 'Ed', '', 'Frank'),
              ncol=2, byrow=TRUE)
colnames(L2.) <- c('surname', 'givenName')
attr(L2., 'secondLine') <- c('2nd line', ' --Vacancy', NA)

all.equal(L2, L2.)

##
## 4. Force surnameFirst when in a minority
##
snf <- c('Sting', 'Madonna', 'Smith, Al')
SNF <- parseName(snf, surnameFirst=TRUE)

# check
SNF2 <- matrix(c('', 'Sting', '', 'Madonna', 'Smith', 'Al'),
               ncol=2, byrow=TRUE)
colnames(SNF2) <- c('surname', 'givenName')

all.equal(SNF, SNF2)

##
## 5. nameNotFound
##
noSub <- parseName('xx_x')

# check
noSub. <- matrix(c('', 'xx_x'), 1)
colnames(noSub.) <- c('surname', 'givenName')
attr(noSub., 'namesNotFound') <- 'xx_x'

all.equal(noSub, noSub.)

```

Description

***NOTE: THIS IS A PRELIMINARY VERSION OF THIS FUNCTION; ***NOTE: IT MAY BE CHANGED OR REMOVED IN A FUTURE RELEASE.

ping a Uniform resource locator (URL) or Internet Protocol (IP) address.

NOTE: Some Internet Service Providers (ISPs) play games with "ping". That makes the results of Ping unreliable.

Usage

```
Ping(url, pingArgs='', warn=NA,
      show.output.on.console=FALSE)
```

Arguments

url	a character string of a URL or IP address to ping. If url is a vector of length greater than 1, only the first component is used.
pingArgs	arguments to pass to the ping command of typical operating systems via <code>pingResult <- system(paste('ping', pingArgs, url), intern=TRUE, ...)</code>
warn	value for options('warn') during the call to <code>system</code> . NA to not change options('warn') during this call.
show.output.on.console	argument for <code>system</code> .

Details

1. `urlSplit0 <- strsplit(url, '://')[[1]]`
2. `urlS0 <- urlSplit0[$\min(2, \text{length}(\text{urlSplit0}))$]`
3. `host <- strsplit(urlS0, '/')[[1]][1]`
4. `pingCmd <- paste('ping', pingArgs, host)`
5. `system(pingCmd, intern=TRUE, ...)`

Value

list with the following components:

rawResults	character vector of the raw results from the ping command
rawNumbers	numeric vector of the times measured
counts	numeric vector of numbers of packets sent, received, and lost
p.lost	proportion lost = lost / sent
stats	numeric vector of min, avg (mean), max, and mdev (standard deviation) of the measured round trip times

Author(s)

Spencer Graves

See Also[system, options](#)**Examples**

```
##
## Some ISPs play games with ping.
## Therefore, the results are not reliable.
##
## Not run:
##
## good
##
(google <- Ping('https://google.com/ping works on host not pages'))

\dontshow{stopifnot()}
with(google, (counts[1]>0) && (counts[3]<1))
\dontshow{}}

##
## ping oops <<-- at one time, this failed.
##     However, with some ISPs, it works, so don't test it.
##

##
(couldnotfindhost <- Ping('oops'))

\dontshow{stopifnot()}
with(couldnotfindhost,
     length(grep('could not find host', rawResults))>0)
\dontshow{}}

##
## impossible, but not so obvious
##
(requesttimedout <- Ping('requesttimedout.com'))

\dontshow{stopifnot()}
with(requesttimedout, (counts[1]>0) && (counts[2]<1) &&
                    (counts[3]>0))
\dontshow{}}

## End(Not run)
```

Description

pmatch2 returns a list of the positions of matches or partial matches of x in table.

This does sloppy matching to find "Peter" to match "Pete" only if "Pete" is not in table, and we want "John Peter" if neither "Pete" nor "Peter" are in table.

Usage

```
pmatch2(x, table)
```

Arguments

x	the values to be matched
table	the values to be matched against

Details

```
1. nx <- length(x); out <- vector(nx, "list"); names(out) <- x
2. for(ix in seq(length=nx)): 3. xi <- which(x[ix] %in% table)
4. if(length(xi)<1) xi <- grep(paste0('^', x[ix]), table).
5. if(length(xi)<1)xi <- grep(x[ix], table).
6. out[[ix]] <- xi
```

Value

A list of integer vectors indicating the positions in table matching each element of x

Author(s)

Spencer Graves

See Also

[match](#) [pmatch](#) [grep](#) [matchName](#)

Examples

```
##
## 1. common examples
##
x2match <- c('Pete', 'Peter', 'Ma', 'Mo', 'Paul',
            'Cardenas')

tbl <- c('Peter', 'Mary', 'Martha', 'John Paul', 'Peter',
        'Cardenas', 'Cardenas')

x2mtchd <- pmatch2(x2match, tbl)

# answer
x2mtchd. <- list(Pete=c(1, 5), Peter=c(1, 5), Ma=2:3,
```

```

    Mo=integer(0), Paul=4, Cardenas=6:7)

all.equal(x2mtchd, x2mtchd.)

##
## 2. strange cases that caused errors and are now warnings
##
huh <- pmatch2("7", tbl)

# answer
huh. <- list("7"=integer(0))

all.equal(huh, huh.)

```

pmatchIC

pmatch ignoring case

Description

pmatch with an additional ignoreCase argument, returning a name not an index like [pmatch](#) (and returning a name if supplied a number, unlike [pmatch](#), which coerces the input to numeric).

Usage

```

pmatchIC(x, table, nomatch = NA_integer_,
         duplicates.ok = FALSE,
         ignoreCase=TRUE)

```

Arguments

x	the values to be matched. If <code>is.numeric(x)</code> , <code>pmatch2</code> returns <code>table[x]</code> . This is different from pmatch , which matches <code>as.character(x)</code> . Otherwise, if <code>ignoreCase</code> is <code>TRUE</code> , <code>pmatchIC</code> returns <code>pmatch(tolower(x), tolower(table))</code> .
table	the values to be matched against: converted to a character vector, per pmatch .
nomatch	the value to be returned at non-matching or multiply partially matching positions.
duplicates.ok	should elements be in table be used more than once? (See pmatch for an example.)
ignoreCase	logical: if <code>TRUE</code> and <code>x</code> is character, <code>pmatchIC</code> returns <code>pmatch(tolower(x), tolower(table))</code> .

Value

A character vector of matches.

Author(s)

Spencer Graves

See Also[pmatch](#)**Examples**

```

yr <- pmatchIC('Yr', c('y1', 'yr', 'y2'))

all.equal('yr', yr)

# integer
m2 <- pmatchIC(2, table=letters)

all.equal(m2, 'b')
```

qqnorm2

*Normal Probability Plot with Multiple Symbols***Description**

Create a normal probability plot with one line and different symbols for the values of another variable, *z*.

qqnorm2 produces an object of class qqnorm2, whose plot method produces the plot.

To create a normal normal probability plots with multiple lines, see [qqnorm2t](#) or [qqnorm2s](#): *x*.

- [qqnorm2s](#) produces a plot with multiple lines specified either by different names in a character vector *y* or by different [data.frames](#) in a list *data.*, with different points labeled according to the different levels of *z*.
- [qqnorm2t](#) produces a plot with multiple lines with *y* split on different levels of *x*, optionally with different points labeled according to different levels of *z*.

Usage

```

qqnorm2(y, z, plot.it=TRUE, datax=TRUE, pch=NULL,
        ...)
## S3 method for class 'qqnorm2'
plot(x, y, ...)
## S3 method for class 'qqnorm2'
lines(x, ...)
## S3 method for class 'qqnorm2'
points(x, ...)
```

Arguments

y	For qqnorm2, y is a numeric vector for which a normal probability plot is desired. For plot.qqnorm2, y is ignored; it is included, because the generic <code>plot</code> function requires it.
z	A variable to indicate different plotting symbols. NOTE: <code>is.logical(z)</code> is replaced by <code>z <- as.character(z)</code> . Otherwise, <code>pch[z]</code> would delete symbols in <code>pch</code> for which <code>z</code> is FALSE and would recycle the remaining symbols. That would rarely be what we want.
plot.it	logical: Should the result be plotted?
datax	The datax argument of <code>qqnorm</code> : If TRUE, the data are displayed on the horizontal rather than the vertical axis. (The default value for datax is the opposite of that for <code>qqnorm</code> .)
x	an object of class qqnorm2.
pch	a named vector of the plotting symbols to be used with names corresponding to the levels of z. If pch is provided, it must either have names corresponding to levels of z, or z must be integers between 1 and <code>length(pch)</code> . Otherwise, if z takes levels FALSE and TRUE (or 0 and 1), <code>pch=c(4, 1)</code> to plot an "x" for FALSE and "o" for TRUE. Or if z assumes integer values between 0 and 255, by default, the symbols are chosen as described with <code>points</code> . NOTE: <code>points.qqnorm2</code> may not work properly for z being integer between 0 and 255. <code>lines.qqnorm2</code> is more likely to work in such cases. <code>*** No time to fix this as of 2018-01-20.</code> Otherwise, by default, z is coerced to <code>character</code> , and the result is plotted.
...	Optional arguments. For <code>plot.qqnorm2</code> , they are passed to <code>plot</code> . For <code>qqnorm2</code> , they are passed to <code>qqnorm</code> and to <code>plot.qqnorm2</code> .

Details

For qqnorm2:

```
qq1. q2 <- qqnorm(y, datax=datax, ...)
```

```
qq2. q2[["z"]] <- z
```

```
qq3. q2[["pch"]] gets whatever pch decodes to.
```

```
qq4. Silently return(list(x, y, z, pch, ...)), where x and y are as returned by qqnorm in step 1 above. If pch is not provided and z is not logical or positive integers, then z itself will be plotted and pch will not be in the returned list.
```

For plot.qqnorm2:

```
plot1. plot(x\$x, x\$y, type="n", ...) with ... taking precedence over x, where the same plot argument appears in both.
```

```
plot2. if(type %in% c('l', 'b', 'c', 'o')) lines(x\$x, x\$y, ...)
```

```
plot3. if(type %in% c('p', 'b', 'o')): if(is.null(x\$z))points(x\$x, x\$y, ...) else if(is.logical(x\$z)) points(x\$x, x\$y, pch=x\$pch[x\$z], ...) else if(is.numeric(x\$z))
```

```

&& (min(z0 <- round(x$z))>0) && (max(abs(x$z-z0))<10*.Machine$double.eps)) points(x$x,
x$y, pch=x$pch[x$z], ...) else text(x$x, x$y, x$z, ...)
For lines.qqnorm2 lines1. if(type != 'p')lines(x$x, x$y, ...);
lines2. if(type %in% c('p', 'b', 'o')) if(is.null(pch))text(x$x, x$y, x$z, ...) else
if(is.character(pch)) text(x$x, x$y, x$pch[x$z], ...) else points(x$x, x$y, pch=x$pch[x$z],
...)
For points.qqnorm2 points1. if(type %in% c('p', 'b', 'o')) if(is.null(pch))text(x$x,
x$y, x$z, ...) else if(is.character(pch)) text(x$x, x$y, x$pch[x$z], ...) else
points(x$x, x$y, pch=x$pch[x$z], ...)
points2. if(!(type %in% c('p', 'n')))) lines(x$x, x$y, ...)

```

Value

qqnorm2 returns a list with components, x, y, z, and pch.

Author(s)

Spencer Graves

See Also

[qqnorm](#), [qqnorm2s](#), [qqnorm2t](#) [plot](#) [points](#) [lines](#)

Examples

```

##
## a simple test data.frame to illustrate the plot
## but too small to illustrate qqnorm concepts
##
tstDF <- data.frame(y=1:3, z1=1:3, z2=c(TRUE, TRUE, FALSE),
                   z3=c('tell', 'me', 'why'), z4=c(1, 2.4, 3.69) )
# plotting symbols circle, triangle, and "+"
qn1 <- with(tstDF, qqnorm2(y, z1))

# plotting symbols "x" and "o"
qn2 <- with(tstDF, qqnorm2(y, z2))

# plotting with "-" and "+"
qn. <- with(tstDF, qqnorm2(y, z2, pch=c('FALSE'='-', 'TRUE'='+')))

# plotting with "tell", "me", "why"
qn3 <- with(tstDF, qqnorm2(y, z3))

# plotting with the numeric values
qn4 <- with(tstDF, qqnorm2(y, z4))

##
## test plot, lines, points
##
plot(qn4, type='n') # establish the scales

```



```
lines(qn4)          # add a line
points(qn4)         # add points

##
## Check the objects created above
##
# check qn1
qn1. <- qqnorm(1:3, datax=TRUE, plot.it=FALSE)
qn1.$xlab <- 'y'
qn1.$ylab <- 'Normal scores'
qn1.$z <- tstDF$z1
qn1.$pch <- 1:3
names(qn1.$pch) <- 1:3
qn11 <- qn1.[c(3:4, 1:2, 5:6)]
class(qn11) <- 'qqnorm2'

all.equal(qn1, qn11)

# check qn2
qn2. <- qqnorm(1:3, datax=TRUE, plot.it=FALSE)
qn2.$xlab <- 'y'
qn2.$ylab <- 'Normal scores'
qn2.$z <- tstDF$z2
qn2.$pch <- c('FALSE'=4, 'TRUE'=1)
qn22 <- qn2.[c(3:4, 1:2, 5:6)]
class(qn22) <- 'qqnorm2'

all.equal(qn2, qn22)

# check qn.
qn.. <- qqnorm(1:3, datax=TRUE, plot.it=FALSE)
qn..$xlab <- 'y'
qn..$ylab <- 'Normal scores'
qn..$z <- tstDF$z2
qn..$pch <- c('FALSE'='-', 'TRUE'='+')
qn.2 <- qn..[c(3:4, 1:2, 5:6)]
class(qn.2) <- 'qqnorm2'

all.equal(qn., qn.2)

# check qn3
qn3. <- qqnorm(1:3, datax=TRUE, plot.it=FALSE)
qn3.$xlab <- 'y'
qn3.$ylab <- 'Normal scores'
qn3.$z <- as.character(tstDF$z3)
qn3.$pch <- as.character(tstDF$z3)
names(qn3.$pch) <- qn3.$pch
qn33 <- qn3.[c(3:4, 1:2, 5:6)]
class(qn33) <- 'qqnorm2'
```

```

all.equal(qn3, qn33)

# check qn4
qn4. <- qqnorm(1:3, datax=TRUE, plot.it=FALSE)
qn4.$xlab <- 'y'
qn4.$ylab <- 'Normal scores'
qn4.$z <- tstDF$z4
qn44 <- qn4.[c(3:4, 1:2, 5)]
qn44$pch <- NULL
class(qn44) <- 'qqnorm2'

all.equal(qn4, qn44)

##
## Test lines(qn4) without z
##
# just as a test, so this code can be used
# in other contexts
qn4. <- qn4
qn4.$z <- NULL
plot(qn4.)

```

qqnorm2s

Normal Probability Plot with Multiple Lines and Multiple Symbols

Description

Create a normal probability plot with one line for each y variable or each `data.frame` in a list `data.` with different plotting symbols for the values of `z`.

To create a normal probability plot with one y variable split on a `link{factor}` or `character` variable `x`, see [qqnorm2t](#).

`qqnorm2s` produces an object of class `qqnorm2s`, whose `plot` method produces the plot.

Usage

```

qqnorm2s(y, z=NULL, data., plot.it=TRUE,
         datax=TRUE, outnames=NULL, pch=NULL,
         col=c(1:4, 6), legend.=NULL, ...)
## S3 method for class 'qqnorm2s'
plot(x, y, ...)

```

Arguments

<code>y</code>	<p>a character vector of names of columns of <code>data.</code> for which normal probability plots are desired. <code>data.</code> is either a data.frame or a list of data.frames of the same length as <code>y</code>, with <code>y[i]</code> being the name of a column of the data.frame <code>data.[[i]]</code>. <code>z</code> is a similar character vector of names of columns of <code>data.</code>, which identify symbols for plotting different points in a normal probability plot. The lengths of <code>y</code>, and <code>z</code> must match the number of data.frames in <code>data.</code>; if not, the lengths of the shorter are replicated to the length of the longest before computations begin.</p> <p>For <code>plot.qqnorm2s</code>, <code>y</code> is ignored; it is included, because the generic plot function requires it.</p>
<code>z</code>	<p>A character vector giving the names of columns of <code>data.</code> to indicate different plotting symbols. <code>z</code> should be the same length as <code>y</code> and must equal the number of data.frames in the list <code>data.</code> of data.frames. If not, the shorter are replicated to the length of the longer.</p>
<code>data.</code>	a data.frame or a list of data.frames with columns named in <code>y</code> and <code>z</code> .
<code>plot.it</code>	logical: Should the result be plotted?
<code>datax</code>	The <code>datax</code> argument of qqnorm : If TRUE, the data are displayed on the horizontal rather than the vertical axis. (The default value for <code>datax</code> is the opposite of that for qqnorm .)
<code>outnames</code>	Names for the components of the <code>qqnorm2s</code> object returned by the <code>qqnorm2s</code> function.
<code>pch</code>	<p>a named vector of the plotting symbols to be used with names corresponding to the levels of <code>z</code>.</p> <p>By default, if <code>z</code> takes levels FALSE and TRUE (or 0 and 1), <code>pch=c(4, 1)</code> to plot a "x" for FALSE and "o" for TRUE.</p> <p>If <code>z</code> assumes integer values between 0 and 255, by default, the symbols are chosen as described with points.</p> <p>Otherwise, by default, <code>z</code> is coerced to character, and the result is plotted.</p> <p>If <code>pch</code> is provided, it must either have names corresponding to levels of <code>z</code>, or <code>z</code> must be integers between 1 and <code>length(pch)</code>.</p>
<code>col</code>	A vector indicating the colors corresponding to each element of <code>y</code> . Defaults to <code>rep(c(1:4, 6), length=length(y))</code> , with 1:4 and 6 being black, red, green, blue, and pink.
<code>x</code>	an object of class <code>qqnorm2</code> .
<code>legend.</code>	<p>A list with components <code>pch</code> and <code>col</code> providing information for legend to identify the plotting symbols (<code>pch</code>) and colors (<code>col</code>).</p> <p>By default, <code>pch = list(x='right', legend=names(qq2s[[1]][['pch']]), pch=qq2s[[1]][['pch']])</code>, where <code>qq2s</code> is described below in details.</p> <p>Similarly, by default, <code>lines = list(x='bottomright', legend=y, lty=1, pch=NA, col=qq2s[[1]][['col']])</code>.</p>
<code>...</code>	<p>Optional arguments.</p> <p>For <code>plot.qqnorm2s</code>, they are passed to <code>plot</code>.</p> <p>For <code>qqnorm2s</code>, they are passed to qqnorm2 and to <code>plot.qqnorm2s</code>.</p>

Details

For qqnorm2s:

1. Create qq2s = a list of objects of class qqnorm2
2. Add legend. to qq2s.
3. class(qq2s) <- 'qqnorm2s'
4. if(plot.it)plot(qq2s, ...)
5. Silently return(qq2s).

For plot.qqnorm2s, create a plot with one line for each variable named in y.

Value

qqnorm2s returns a named list with components of class qqnorm2 with names = y with each component having an additional component col plus one called "legend."

Author(s)

Spencer Graves

See Also

[qqnorm2 plot](#)

Examples

```
##
## One data.frame
##
tstDF2 <- data.frame(y=1:3, y2=3:5,
  z2=c(TRUE, TRUE, FALSE),
  z3=c('tell', 'me', 'why'),
  z4=c(1, 2.4, 3.69) )
# produce the object and plot it
Qn2 <- qqnorm2s(c('y', 'y2'), 'z2', tstDF2)

# plot the object previously created
plot(Qn2)

# Check the object
qy <- with(tstDF2, qqnorm2(y, z2, type='b'))
qy$col <- 1
qy2 <- with(tstDF2, qqnorm2(y2, z2, type='b'))
qy2$col <- 2
legend. <- list(
  pch=list(x='right',
    legend=c('FALSE', 'TRUE'),
    pch=c('FALSE'=4, 'TRUE'= 1)),
  col=list(x='bottomright',
    legend=c('y', 'y2'), lty=1, col=1:2))
Qn2. <- list(y=qy, y2=qy2, legend.=legend.)
```

```

class(Qn2.) <- 'qqnorm2s'

all.equal(Qn2, Qn2.)

##
## Two data.frames
##
tstDF2b <- tstDF2
tstDF2b$y <- c(0.1, 0.1, 9)
Qn2b <- qqnorm2s('y', 'z2',
  list(tstDF2, tstDF2b),
  outnames=c('ok', 'oops'), log='x' )
##
## Split one data.frame
##
tstDF2. <- rbind(cbind(tstDF2, z1=1),
  cbind(tstDF2b, z1=2) )
Qn2. <- qqnorm2s('y', 'z1', tstDF2.)
# Plot has only one line, because only 1 y variable.
##
## Two data.frames without z
##
Qn2.0 <- qqnorm2s('y',
  data.=list(tstDF2, tstDF2b),
  outnames=c('ok', 'oops'), log='x' )

```

qqnorm2t

Normal Probability Plot with Multiple Lines and Multiple Symbols

Description

Create a normal probability plot of *y* with one line for each level of a [factor](#) or [character](#) variable *x* and (optionally) different symbols for the different levels of a variable *z*.

To create a normal probability plot with one line for each of multiple *y* variables, see [qqnorm2s](#).

To create a normal probability plot with one line and different symbols for each level of a variable *z*, see [qqnorm2](#).

Usage

```

qqnorm2t(y, x, z=NULL, data., plot.it=TRUE,
  datax=TRUE, outnames=NULL, pch=NULL,
  col=c(1:4, 6), legend.=NULL, ...)

```

Arguments

y a [character](#) vector of length 1 with the name of a column of data. for which normal probability plots are desired, with one line for each level of *x*.

<code>x</code>	a factor or character vector indicating how to split <code>y</code> for plotting.
<code>z</code>	A character vector giving the name of a column of data. to indicate different plotting symbols.
<code>data.</code>	a data.frame with columns named in <code>y</code> , <code>x</code> , and <code>z</code> .
<code>plot.it</code>	logical: Should the result be plotted?
<code>datax</code>	The <code>datax</code> argument of qqnorm : If TRUE, the data are displayed on the horizontal rather than the vertical axis. (The default value for <code>datax</code> is the opposite of that for qqnorm .)
<code>outnames</code>	Names for the components of the <code>qqnorm2s</code> object returned by the <code>qqnorm2s</code> function. Equal to the levels of <code>x</code> by default.
<code>pch</code>	a named vector of the plotting symbols to be used with names corresponding to the levels of <code>z</code> . By default, if <code>z</code> takes levels FALSE and TRUE (or 0 and 1), <code>pch=c(4, 1)</code> to plot a "x" for FALSE and "o" for TRUE. If <code>z</code> assumes integer values between 0 and 255, by default, the symbols are chosen as described with points . Otherwise, by default, <code>z</code> is coerced to character , and the result is plotted. If <code>pch</code> is provided, it must either have names corresponding to levels of <code>z</code> , or <code>z</code> must be integers between 1 and <code>length(pch)</code> .
<code>col</code>	A vector indicating the colors corresponding to each element of <code>x</code> . Defaults to <code>rep(c(1:4, 6), length=length(x))</code> , with 1:4 and 6 being black, red, green, blue, and pink.
<code>legend.</code>	A list with components <code>pch</code> and <code>col</code> providing information for legend to identify the plotting symbols (<code>pch</code>) and colors (<code>col</code>). By default, <code>pch = list(x='right', legend=names(qq2s[[1]][['pch']]), pch=qq2s[[1]][['pch']])</code> , where <code>qq2s</code> is described below in details. Similarly, by default, <code>lines = list(x='bottomright', legend=y, lty=1, pch=NA, col=qq2s[[1]][['col']])</code> .
<code>...</code>	Optional arguments. For <code>plot.qqnorm2s</code> , they are passed to <code>plot</code> . For <code>qqnorm2s</code> , they are passed to qqnorm2 and to <code>plot.qqnorm2s</code> .

Details

`data.` is split by `x` and the result is passed to `qqnorm2s`

Value

Returns an object of class [qqnorm2s](#).

Author(s)

Spencer Graves

See Also

[qqnorm2](#), [qqnorm2s](#), [plot](#)

Examples

```
##
## One data.frame
##
tstDF2 <- data.frame(y=1:6, x=c('a','b'),
  z2=c(TRUE, TRUE, FALSE),
  z3=c('tell', 'me', 'why') )
# produce the object and plot it
Qnt <- qqnorm2t('y', 'x', 'z2', tstDF2)

# plot the object previously created
plot(Qnt)

Qnt0 <- qqnorm2t('y', 'x', data.=tstDF2)
# without z
qqnorm2t('y', 'x', data.=tstDF2)
```

rasterImageAdj

rasterImage adjusting to zero distortion

Description

Call `rasterImage` to plot image from $(x_{\text{left}}, y_{\text{bottom}})$ to either x_{right} or y_{top} , shrinking one toward the center to avoid distortion.

`angle` specifies a rotation around the midpoint $((x_{\text{left}}+x_{\text{right}})/2, (y_{\text{bottom}}+y_{\text{top}})/2)$. This is different from `rasterImage`, which rotates around $(x_{\text{left}}, y_{\text{bottom}})$.

NOTE: The code may change in the future. The visual image with rotation looks a little off in the examples below, but the code seems correct. If you find an example where this is obviously off, please report to the maintainer – especially if you find a fix for this.

Usage

```
rasterImageAdj(image, xleft=par('usr')[1],
  ybottom=par('usr')[3], xright=par('usr')[2],
  ytop=par('usr')[4], angle = 0, interpolate = TRUE,
  xsub=NULL, ysub=NULL, ...)
```

Arguments

<code>image</code>	a raster object, or an object that can be coerced to one by as.raster .
<code>xleft</code>	a vector (or scalar) of left x positions.
<code>ybottom</code>	a vector (or scalar) of bottom y positions.
<code>xright</code>	a vector (or scalar) of right x positions.

ytop	a vector (or scalar) of top y positions.
angle	angle of rotation in degrees, anti-clockwise about the centroid of image. NOTE: <code>rasterImage</code> rotates around (xleft, ybottom). <code>rasterImage</code> rotates around the center $((xleft+xright)/2, (ybottom+ytop)/2)$. See the examples.
interpolate	a logical vector (or scalar) indicating whether to apply linear interpolation to the image when drawing.
xsub, ysub	subscripts to subset image
...	graphical parameters (see <code>par</code>).

Details

1. `imagePixels` = number of (x, y) pixels in image. Do this using `dim(as.raster(image))[2:1]`, because the first dimension of `image` can be either x or y depending on `class(image)`. For example `link[EBImage]{Image}` returns `dim` with x first then y and an optional third dimension for color. A simple 3-dimensional array is assumed by `rasterImage` to have the y dimension first. `as.raster` puts all these in a standard format with y first, then x.
2. `imageUnits` <- c(x=xright-xleft, ytop-ybottom)
3. `xyinches` = (x, y) units per inch in the current plot, obtained from `xyinch`.
4. Compute pixel density (pixels per inch) in both x and y dimension: `pixelsPerInch` <- `imagePixels` * `xyinches` / `imageUnits`.
5. Compute `imageUnitsAdj` solving 4 for `imageUnits` and replacing `pixelsPerInch` by the max pixel density: `imageUnitsAdj` <- `imagePixels` * `xyinches` / `max(pixelsPerInch)`.
6. `(dX, dY)` = `imageUnitsAdj/2` = half of the (width, height) in plotting units.
7. `cntr` = (xleft, ybottom) + (dX, dY).
`xleft0` = `cntr[1]+sin((angle-90)*pi/180)*dX*sqrt(2)`;
`ybottom0` = `cntr[2]-cos((angle-90)*pi/180)*dY*sqrt(2)`;
`(xright0, ytop0)` = (upper right without rotation about lower left)
`xright0` = `xleft0+imageUnitsAdj[2]`
`ytop0` = `ybottom0+imageUnitsAdj[2]`
8. `rasterImage(image, xleft0, ybottom0, xright0, ytop0, angle, interpolate, ...)`

Value

a named vector giving the values of `xleft`, `ybottom`, `xright`, and `ytop` passed to `rasterImage`. (`rasterImage` returns NULL, at least for some inputs.) This shows the adjustment, shrinking toward the center and rotating as desired.

Author(s)

Spencer Graves

See Also

`rasterImage`

Examples

```

# something to plot
logo.jpg <- file.path(R.home('doc'), 'html', 'logo.jpg')
if(require(jpeg)){
##
## 1. Shrink as required
##
  Rlogo <- try(readJPEG(logo.jpg))
  if(inherits(Rlogo, 'array')){

    all.equal(dim(Rlogo), c(76, 100, 3))

    plot(1:2)
# default
    rasterImageAdj(Rlogo)

    plot(1:2, type='n', asp=0.75)
# Tall and thin
    rasterImage(Rlogo, 1, 1, 1.2, 2)
# Fix
    rasterImageAdj(Rlogo, 1.2, 1, 1.4, 2)

# short and wide
    rasterImage(Rlogo, 1.4, 1, 2, 1.2)
# Fix
    rasterImage(Rlogo, 1.4, 1.2, 2, 1.4)
##
## 2. rotate
##
# 2.1. angle=90: rasterImage left of rasterImageAdj
  plot(0:1, 0:1, type='n', asp=1)
  rasterImageAdj(Rlogo, .5, .5, 1, 1, 90)
  rasterImage(Rlogo, .5, .5, 1, 1, 90)
# 2.2. angle=180: rasterImage left and below
  plot(0:1, 0:1, type='n', asp=1)
  rasterImageAdj(Rlogo, .5, .5, 1, 1, 180)
  rasterImage(Rlogo, .5, .5, 1, 1, 180)
# 2.3. angle=270: rasterImage below
  plot(0:1, 0:1, type='n', asp=1)
  rasterImageAdj(Rlogo, .5, .5, 1, 1, 270)
  rasterImage(Rlogo, .5, .5, 1, 1, 270)
##
## 3. subset
##
  dim(Rlogo)
# 76 100 3
  Rraster <- as.raster(Rlogo)
  dim(Rraster)
# 76 100:
# x=1:100, left to right
# y=1:76, top to bottom

```

```

    rasterImageAdj(Rlogo, 0, 0, .5, .5, xsub=40:94)
  }
}

```

read.transpose *Read a data table in transpose form*

Description

Read a text (e.g., csv) file, find rows with more than 3 sep characters. Parse the initial contiguous block of those into a matrix. Add attributes headers, footers, and a summary.

The initial application for this function is to read "Table 6.16. Income and employment by industry" in the National Income and Product Account (NIPA) tables published by the Bureau of Economic Analysis (BEA) of the United States Department of Commerce.

Usage

```
read.transpose(file, header=TRUE, sep=',',
              na.strings='---', ...)
```

Arguments

file	the name of a file from which the data are to be read.
header	Logical: Is the second column of the identified data matrix to be interpreted as variable names?
sep	The field space separator character.
na.strings	character string(s) that translate into NA
...	optional arguments for strsplit

Details

1. txt <- readLines(file)
2. Split into fields.
3. Identify headers, Data, footers.
4. Recombine the second component of each Data row if necessary so all have the same number of fields.
5. Extract variable names
6. Numbers?
7. return the transpose

Value

A matrix of the transpose of the rows with the max number of fields with attributes headers, footers, other, and summary. If this matrix can be coerced to numeric with no NAs, it will be. Otherwise, it will be left as character.

Author(s)

Spencer Graves

References

Table 6.16. Income and employment by industry in the National Income and Product Account (NIPA) tables published by the Bureau of Economic Analysis (BEA) of the United States Department of Commerce. As of February 2013, there were 4 such tables available: Table 6.16A, 6.16B, 6.16C and 6.16D. Each of the last three are available in annual and quarterly summaries. The USFinanceIndustry data combined the first 4 rows of the 4 annual summary tables.

NOTE: The structure of the BEA web site seems to have changes between 2013 and 2022. As of 2022-07-01 it does not seem easy to find these tables at the BEA website.

Line 5 in the sample tables saved in 2013 contained "a non-breaking space in Latin-1", which was not a valid code in UTF-8 and was rejected by a development version of R. Since it wasn't easy to update those tables, the "non-breaking spaces" were replaced with " ".

See Also

[read.table](#) [readLines](#) [strsplit](#)

Examples

```
# Find demoFiles/*.csv
demoDir <- system.file('demoFiles', package='Ecdat')
(demoCsv <- dir(demoDir, pattern='csv$', full.names=TRUE))

# Use the fourth example
# to ensure the code will handle commas in a name
# and NAs
nipa6.16D <- read.transpose(demoCsv[4])
str(nipa6.16D)
```

readDates3to1

read.csv with Dates in 3 columns

Description

[read.csv](#), converting 3-column dates into vectors of class Date.

Usage

```
readDates3to1(file, YMD=c('Year', 'Month', 'Day'),
              ...)
```

Arguments

file	the name of a file from which the data are to be read.
YMD	Character vector of length 3 passed to dateCols
...	optional arguments for read.csv

Details

Some files (e.g., from the [Correlates of War](#) project) have dates specified in three separate columns with names like startMonth1, startDay1, startYear1, endMonth1, ..., endYear2. This function looks for such triples and replaces each found with a single column with a name like, start1, end1, ..., end2.

ALGORITHM

1. `dat <- read.csv(file, ...)`
2. `Dates3to1(dat, YMD)`

Value

a [data.frame](#) with 3-column dates replace by single-column vectors of class `Date`.

Author(s)

Spencer Graves

See Also

[read.csv](#) [Dates3to1](#) [dateCols](#)

Examples

```
##
## 1. Write a file to be read
##
cow0 <- data.frame(rec=1:3, startMonth=4:6,
  startDay=7:9, startYear=1971:1973,
  endMonth1=10:12, endDay1=13:15,
  endYear1=1974:1976, txt=letters[1:3])

cowFile <- tempfile('cow0')
write.csv(cow0, cowFile, row.names=FALSE)
##
## 2. Read it
##
cow0. <- readDates3to1(cowFile)

# check
cow0x <- data.frame(rec=1:3, txt=letters[1:3],
  start=as.Date(c('1971-04-07', '1972-05-08', '1973-06-09')),
  end1=as.Date(c('1974-10-13', '1975-11-14', '1976-12-15')) )
```

```
all.equal(cow0., cow0x)
```

readDW_NOMINATE	<i>Read the DW-NOMINATE data from their website.</i>
-----------------	--

Description

Read **the DW-NOMINATE data** from their website using `read_csv`, adding a `Year = 2*congress+1787`, which is the first year of each 2-year congress.

Usage

```
readDW_NOMINATE(file=
  "https://voteview.com/static/data/out/members/HSall_members.csv",
  ...)
```

Arguments

<code>file</code>	file argument passed to <code>read_csv</code> .
<code>...</code>	optional arguments for <code>read_csv</code> .

Details

This is written to make it easy for users to download the DW-NOMINATE data from their website, assuming it should be easier to remember `readDW_NOMINATE` than

```
readr::read_csv("https://voteview.com/static/data/out/members/HSall_members.csv").
```

Value

a `tibble` with columns

<code>congress</code>	number of the Congress starting with 1 in 1789.
<code>chamber</code>	character 'House', 'Senate' or 'President'
<code>icpsr</code>	number icpsr (number assigned by the Inter-university Consortium for Political and Social Research (ICPSR)).
<code>state_icpsr</code>	number for the state used by ICPSR.
<code>district_code</code>	number between 0 and 99 indicating the district number within the state. This is 0 when (<code>chamber %in% c('President', 'Senate')</code>) and occasionally when (<code>chamber == 'House'</code>). "At-large" members of the US House are coded 98 or 99. There were some before 1970. However, as of 2024-10-01, but there have been none since 1970.
<code>state_abbrev</code>	Either 'USA' or a 2-letter abbreviation for this state in the US.

party_code	positive numeric. As of 2024-09-30, over 80 percent of the members of Congress since 1857 have been either 100 (Democrats) or 200 (Republicans), and since 1943, less than 1 percent of the US Congress has not been either 100 or 200.
occupancy, last_means	numeric = 0:7 or 'NA' with all 'NA's prior to 2017.
bioname	character name of politician, starting with "WASHINGTON, George".
bioguide_id	character The ID code used by the Biographical directory of the United States Congress , being the first character of the last name of the person followed by a 6-digit number or 'NA' for US Presidents who were never members of Congress.
born, died	numeric 4-digit birth year or 'NA'
nominate_dim1, nominate_dim2	numeric between -1 or 1 or 'NA' described in Poole (2005).
nominate_log_likelihood	numeric negative number or 'NA'
nominate_goe_mean_probabilty	numeric number between 0 and 1 or 'NA'
nominate_number_of_votes	numeric positive number or 'NA'
nominate_number_of_errors	numeric nonnegative number or 'NA'
conditional	logical or 'NA'
nokken_poole_dim1, nokken_poole_dim2	numeric between -1 or 1 or 'NA' described by Nokken and Poole (2004).
Year	numeric First year of each 2-year computed from congress as (2*congress+1787).

Author(s)

Spencer Graves

Source

Embedded in an [R Markdown vignette](#) by [UCLA political science professor Jeff Lewis](#) in the [voteview](#) project on 'GitHub'.

References

[Voteview.com website.](#)

Timothy P. Nokken and Keith T. Poole (2004) "Congressional Party Defection in American History." *Legislative Studies Quarterly*, 29:545-568,.

Keith T. Poole (2005) *Spatial models of parliamentary voting* (Cambridge U. Pr.).

See Also

[read_csv](#)

Examples

```
# Wrap in try(...) so it won't throw an error
# if the Voteview website is not available.

Nominate <- try(readDW_NOMINATE())
```

readNIPA	<i>Read a National Income and Product Accounts data table</i>
----------	---

Description

Read multiple files with data in rows using `read.transpose` and combine the initial columns.

Usage

```
readNIPA(files, sep.footnote='/', ...)
```

Arguments

<code>files</code>	A character vector of names of files from which the data are to be read using <code>read.transpose</code> .
<code>sep.footnote</code>	a single character to identify footnote references in the variable names in some but not all of files.
<code>...</code>	optional arguments for <code>read.transpose</code>

Details

This is written first and foremost to facilitate updating `USFinanceIndustry` from Table 6.16: Income and employment by industry in the National Income and Product Account tables published by the Bureau of Economic Analysis of the United States Department of Commerce. As of February 2013, this table can be obtained from <https://www.bea.gov>: Under "U.S. Economic Accounts", first select "Corporate Profits" under "National". Then next to "Interactive Tables", select, "National Income and Product Accounts Tables". From there, select "Begin using the data...". Under "Section 6 - income and employment by industry", select each of the tables starting "Table 6.16". As of February 2013, there were 4 such tables available: Table 6.16A, 6.16B, 6.16C and 6.16D. Each of the last three are available in annual and quarterly summaries. The `USFinanceIndustry` data combined the first 4 rows of the 4 annual summary tables.

This is available in 4 separate files, which must be downloaded and combined using `readNIPA`. The first three of these are historical data and are rarely revised. For convenience and for testing, they are provided in the `demoFiles` subdirectory of this `Ecdat` package.

It has not been tested on other data but should work for annual data with a sufficiently similar structure.

The algorithm proceeds as follows:

1. `Data <- lapply(files, read.transpose)`
2. Is `Data` a list of numeric matrices? If no, print an error.

3. `cbind` common initial variables, averaging overlapping years, reporting percent difference
4. attributes: stats from files and overlap. Stats include the first and last year and the last revision date for each file, plus the number of years overlap with the previous file and the relative change in the common files kept between those two files.

Value

a `matrix` of the common variables

Author(s)

Spencer Graves

References

United States Department of Commerce Bureau of Economic Analysis National Income and Product Account tables

See Also

`read.table` `readLines` `strsplit`

Examples

```
# Find demoFiles/*.csv
demoDir <- system.file('demoFiles', package='Ecdat')
(demoCsv <- dir(demoDir, pattern='csv$', full.names=TRUE))

nipa6.16 <- readNIPA(demoCsv)
str(nipa6.16)
```

recode2

bivariate recode

Description

Recode `x1` and `x2` per the lexical codes table.

Usage

```
recode2(x1, x2, codes)
```

Arguments

`x1`, `x2` vectors of the same length assuming a discrete number of levels

`codes` a 2-dimensional matrix indexed by the levels of `x1` and `x2`. If `dimnames(codes)` are not provided, they are assumed to be `unique(x1)` (or `unique(x2)`).

Details

1. If `length(x1) != length(x2)`, complain.
2. `if(is.logical(x1)) l1 <- c(FALSE, TRUE) else l1 <- unique(x1)`; ditto for `x2`.
3. `If(missing(codes)) codes <- outer(unique(x1), unique(x2))`
4. `if(is.null(dim(codes))) dim(codes) <- c(length(unique(x1)), length(unique(x2)))`
5. If `is.null(rownames(codes))`, set as follows: If `nrow(codes) == length(unique(x1))`, `rownames(codes) <- unique(x1)`. Else, if `nrow(codes) = max(x1)`, set `rownames(codes) <- seq(1, max(x1))`. Else throw an error. Ditto for `colnames`, `ncol`, and `x2`.
6. `codes[x1, x2]`

Value

a vector of the same length as `x1` and `x2`.

Author(s)

Spencer Graves

See Also

[dim rownames link{colnames}](#)

Examples

```
contrib <- c(-1, 0, 0, 1)
contrib0 <- c(FALSE, FALSE, TRUE, FALSE)

contribCodes <- recode2(contrib>0, contrib0,
  c('returned', 'received', '0', 'ERR') )

cC <- c('returned', 'returned', '0', 'received')

all.equal(contribCodes, cC)
```

 rgrep

Reverse grep

Description

Find which pattern matches `x`.

Usage

```
rgrep(pattern, x, ignore.case = FALSE,
  perl = FALSE, value = FALSE, fixed = FALSE,
  useBytes = FALSE, invert = FALSE)
```

Arguments

pattern a [character](#) vector of regular expressions to be matched to x
 x a [character](#) string or vector for which a matching regular expression is desired.
 ignore.case, perl, value, fixed, useBytes, invert
 as for [grep](#)

Details

```
1. np <- length(pattern)
2. g. <- rep(NA, np)
3. for(i in seq(length=np)){ g.[i] <- (length(grep(pattern[i], x))>0) }
4. return(which(g.))
```

Value

an [integer](#) vector of indices of elements of pattern with a match in x.

Author(s)

Spencer Graves

See Also

[grep](#), [pmatch](#)

Examples

```
##
## 1. return index
##
dd <- data.frame(a = gl(3,4), b = gl(4,1,12)) # balanced 2-way
mm <- model.matrix(~ a + b, dd)

b. <- rgrep(names(dd), colnames(mm)[5])
# check

all.equal(b., 2)

##
## 2. return value
##
bv <- rgrep(names(dd), colnames(mm)[5], value=TRUE)
# check

all.equal(bv, 'b')
```

sign	<i>Sign function with zero option</i>
------	---------------------------------------

Description

sign returns a vector with the signs of the corresponding elements of *x*, being 1, zero, or -1 if the number is positive, zero or negative, respectively.

This generalizes the [sign](#) function in the base package to allow something other than 0 as the the "sign" of 0.

Usage

```
sign(x, zero=0L)
```

Arguments

<i>x</i>	a numeric vector for which signs are desired
<i>zero</i>	an integer value to be assigned for <i>x</i> ==0.

Value

an [integer](#) vector of the same length as *x* assuming values 1, zero and -1, as discussed above.

See Also

[sign](#)

Examples

```
##  
## 1. default  
##  
sx <- sign((-2):2)  
  
# check  
  
all.equal(sx, base::sign((-2):2))  
  
##  
## 2. with zero = 1  
##  
s1 <- sign((-2):2, 1)  
  
# check  
  
all.equal(s1, rep(c(-1, 1), c(2,3)))
```

simulate.bic.glm A "simulate" method for a BMA::bic.glm object

Description

Simulate predictions for newdata for a model of class `bic.glm`.

NOTES: The `stats` package has a `simulate` method for "lm" objects which is used for `lm` and `glm` objects. This `simulate.bic.glm` function differs from the `stats::simulate` function in the same two fundamental and important ways as the `simulate.glm` function:

1. `stats::simulate` returns simulated data consistent with the model fit assuming the estimated model parameters are true and exact, i.e., ignoring the uncertainty in parameter estimation. Thus, if `family = poisson`, `stats::simulate` returns nonnegative integers. By contrast the `simulate.bic.glm` function documented here returns optionally simulated `coef` (coefficients) plus simulated values for the link and / or response but currently *NOT* pseudo-random numbers on the scale of the response.
2. The `simulate.bic.glm` function documented here also accepts an optional `newdata` argument, not accepted by `stats::simulate`. The `stats::simulate` function only returns simulated values for the cases in the training set with no possibilities for use for different sets of conditions.

Usage

```
## S3 method for class 'bic.glm'
simulate(object, nsim = 1,
         seed = NULL, newdata=NULL,
         type = c("coef", "link", "response"), ...)
```

Arguments

<code>object</code>	an object representing a fitted model of class <code>bic.glm</code> .
<code>nsim</code>	number of response vectors to simulate. Defaults to 1.
<code>seed</code>	Argument passed as the first argument to <code>set.seed</code> if not NULL.
<code>newdata</code>	optionally, a <code>data.frame</code> in which to look for variables with which to predict. If omitted, predictors used in fitting are used.
<code>type</code>	the type of simulations required. <ul style="list-style-type: none"> • <code>coef</code>: <code>type = "coef"</code> returns pseudo-random numbers generated by <code>rmvnorm::rmvnorm</code> with <code>mean = coef</code> and <code>sigma = vcov</code> for the component of the BMA mixture randomly selected for each simulation. (Obviously, this does not use <code>newdata</code>.) • <code>link</code>: <code>type='link'</code> returns simulations on the scale of the linear predictors using <code>rmvnorm</code> applied to randomly selected components of the mixture with <code>mean = coef</code> and <code>sigma = vcov</code> for that component. For a default binomial model, these are of log-odds (probabilities on logit scale).

- response: object[['linkinv']] of type = 'link'. For a binomial model, these are predicted probabilities.
- ... further arguments passed to or from other methods.

Details

1. Save current seed and optionally set it using code copied from `stats::simulate.lm`.
2. `postprob <- object[['postprob']]`; `x <- object[['x']]`; `y <- object[['y']]`; `mle <- object[['mle']]`; `linkinv <- object[['linkinv']]`.
3. `cl <- as.list(object[['call']])`; `wt <- cl[['wt']]`; `fam <- cl[['glm.family']]`
4. `if(is.null(newdata))newdata <- x` else ensure that all levels of factors of `newdata` match `x`.
5. `xMat <- model.matrix(~., x)`; `newMat <- model.matrix(~., newdata)`
6. `nComponents <- length(postprob)`; `nobs <- NROW(newdata)`
7. `sims <- matrix(NA, nobs, nsim)`
8. `rmdl <- sample(1:nComponents, nsims, TRUE, postprob)`
9. `for(Comp in 1:nComponents) nsimComp <- sum(rmdl==Comp)`; `refitComp <- glm.fit(xMat[, mle[Comp,]!=0], y, wt, mle[Comp, mle[Comp,]!=0], family=fam)`; `simCoef <- mvtnorm::rmvnorm(nsimComp, coef(refitComp), vcov(refitComp))`; `sims[rmdl==Comp,] <- tcrossprod(newMat[, mle[Comp,]!=0], simCoef)`
10. If `length(type) == 1`: return a [data.frame](#) with one column for each desired simulation, consistent with the behavior of the generic [simulate](#) applied to objects of class `lm` or `glm`. Otherwise, return a list of [data.frames](#) of the desired types.

Value

Returns either a [data.frame](#) or a list of [data.frames](#) depending on 'type':

- | | |
|-----------------------------------|--|
| <code>coef</code> | a data.frame with <code>nsim</code> columns and one row for each variable in the max model. Values are non-zero for variables in the model in the BMA mixture selected for that simulation. The non-zero values are generated using <code>mvtnorm::rmvnorm</code> with mean = <code>coef</code> and covariance matrix = <code>vcov</code> of the model fit to the subset of variables in that component model. |
| <code>link</code> | a data.frame with <code>nsim</code> columns of <code>nobs</code> values each giving the simulations on the link scale for each row in <code>newdata</code> (or the training set if <code>newdata</code> is not provided). |
| <code>response</code> | a data.frame with <code>nsim</code> columns of <code>nobs</code> values each giving the simulations on the response scale, being <code>linkinv</code> of the simulations on the link scale. |
| <code>if length(type)>1</code> | a list with simulations on the desired scales. |

The value also has an attribute "seed". If argument `seed` is `NULL`, the attribute is the value of [.Random.seed](#) before the simulation started. Otherwise it is the value of the argument with a "kind" attribute with value `as.list(RNGkind())`.

NOTE: This function currently may not work with a model fit that involves a multivariate link or response.

Author(s)

Spencer Graves

See Also[simulate](#) [simulate.glm](#) [bic.glm](#) [predict.bic.glm](#) [set.seed](#) [rmvnorm](#)**Examples**

```

library(BMA)
library(mvtnorm)
##
## 1. a factor and a numeric
##
PoisReg2 <- data.frame(
  x=factor(rep(0:2, 2)), x1=rep(1:2, e=3))
bicGLM2 <- bic.glm(PoisReg2, y=1:6, poisson)

newDat2 <- data.frame(
  x=factor(rep(c(0, 2), 2), levels=0:2),
  x1=3:6)
# NOTE: Force newDat2['x'] to have the same levels
# as PoisReg2['x']

bicGLMsim2n <- simulate(bicGLM2, nsim=5, seed=2,
  newdata=newDat2[1:3,])

##
## 2. One variable: BMA returns
## a mixture of constant & linear models
##
PoisRegDat <- data.frame(x=1:2, y=c(5, 10))
bicGLMex <- bic.glm(PoisRegDat['x'],
  PoisRegDat[, 'y'], poisson)
(postprob <- bicGLMex[['postprob']])
bicGLMex['mle']

# Simulate for the model data
bicGLMsim <- simulate(bicGLMex, nsim=2, seed=1)

# Simulate for new data
newDat <- data.frame(x=3:4,
  row.names=paste0('f', 3:4))
bicGLMsin <- simulate(bicGLMex, nsim=3, seed=2,
  newdata=newDat)

# Refit with bic.glm.matrix and confirm
# that simulate returns the same answers

bicGLMat <- bic.glm(as.matrix(PoisRegDat['x']),
  PoisRegDat[, 'y'], poisson)
bicGLMatsim <- simulate(bicGLMat, nsim=3, seed=2,

```

```

                                newdata=newDat)

all.equal(bicGLMsin, bicGLMatsim)

# The same problem using bic.glm.formula
bicGLMfmla <- bic.glm(y ~ x, PoisRegDat, poisson)
bicGLMfm1sim <- simulate(bicGLMfmla, nsim=3, seed=2,
                        newdata=newDat)

all.equal(bicGLMsin, bicGLMfm1sim)

##
## 2a. Compute the correct answers manually
##
GLMex1 <- glm(y~x, poisson, PoisRegDat)
GLMex0 <- glm(y~1, poisson, PoisRegDat)

postProb <- bicGLMfmla$postprob
nComp <- length(postProb)
newMat <- model.matrix(~., newDat)
set.seed(2)
(rmdl <- sample(1:nComp, 3, TRUE,
               postprob))
GLMsim. <- matrix(NA, 2, 3)
dimnames(GLMsim.) <- list(
  rownames(newMat),
  paste0('sim_', 1:3) )

sim1 <- mvtnorm::rmvnorm(2, coef(GLMex1),
                       vcov(GLMex1))
sim0 <- mvtnorm::rmvnorm(1, coef(GLMex0),
                       vcov(GLMex0))
GLMsim.[, rmdl==1] <- tcrossprod(newMat, sim1)
GLMsim.[, rmdl==2] <- tcrossprod(
  newMat[, 1, drop=FALSE], sim0)

all.equal(bicGLMsin[[2]], data.frame(GLMsim.),
          tolerance=4*sqrt(.Machine$double.eps))
# tcrossprod numeric precision is mediocre
# for the constant model in this example.

```

Description

Simulate predictions for newdata for a model of class `glm` with mean `coef(object)` and variance `vcov(object)`.

NOTES: The `stats` package has a `simulate` method for "lm" objects which is used for `lm` and `glm` objects. It differs from the current `simulate.glm` function in two fundamental and important ways:

1. `stats::simulate` returns simulated data consistent with the model fit assuming the estimated model parameters are true and exact, i.e., ignoring the uncertainty in parameter estimation. Thus, if `family = poisson`, `stats::simulate` returns nonnegative integers.
By contrast the `simulate.glm` function documented here returns optionally simulated `coef` (coefficients) plus simulated values for the `link` and / or response but currently *NOT* pseudo-random numbers on the scale of the response.
2. The `simulate.glm` function documented here also accepts an optional `newdata` argument, not accepted by `stats::simulate`. The `stats::simulate` function only returns simulated values for the cases in the training set with no possibilities for use for different sets of conditions.

Usage

```
## S3 method for class 'glm'
simulate(object, nsim = 1,
         seed = NULL, newdata=NULL,
         type = c("coef", "link", "response"), ...)
```

Arguments

<code>object</code>	an object representing a fitted model of class <code>glm</code> .
<code>nsim</code>	number of response vectors to simulate. Defaults to 1.
<code>seed</code>	Argument passed as the first argument to <code>set.seed</code> if not NULL.
<code>newdata</code>	optionally, a <code>data.frame</code> in which to look for variables with which to predict. If omitted, predictors used in fitting are used.
<code>type</code>	the type of simulations required. <ul style="list-style-type: none"> • <code>coef</code>: Simulated coefficients using <code>rmvnorm::rmvnorm(nsim, coef(object), vcov(object))</code>. • <code>link</code>: The default <code>type='link'</code> is on the scale of the linear predictors using <code>rmvnorm</code> applied to randomly selected components of the mixture with <code>mean = coef</code> and <code>sigma = vcov</code> for that component. For a default binomial model, these are of log-odds (probabilities on logit scale). • <code>response</code>: <code>object[['linkinv']]</code> of <code>type = 'link'</code>. For a binomial model, these are predicted probabilities.
<code>...</code>	further arguments passed to or from other methods.

Details

1. Save current seed and optionally set it using code copied from `stats:::simulate.lm`.
2. `if(is.null(newdata))newdata` gets the data used in the call to `glm`.
3. `newMat <- model.matrix(~., newdata)`
4. `simCoef <- mvtnorm::rmvnorm(nsim, coef(object), vcov(object))`
5. `sims <- tcrossprod(newMat, simCoef)`
6. If `length(type) == 1`: return a `data.frame` with one column for each desired simulation, consistent with the behavior of the generic `simulate` applied to objects of class `lm` or `glm`. Otherwise, return a list of `data.frames` of the desired types.

Value

Returns either a `data.frame` or a list of `data.frames` depending on 'type':

<code>coef</code>	a <code>data.frame</code> with <code>nsim</code> columns giving simulated parameters generated using <code>mvtnorm::rmvnorm(nsim, coef(object), vcov(object))</code> .
<code>link</code>	a <code>data.frame</code> with <code>nsim</code> columns of <code>nobs</code> values each giving the simulations on the link scale by applying each set of simulated coefficients to <code>newdata</code> (or to the training set of <code>newdata</code> is not supplied).
<code>response</code>	a <code>data.frame</code> with <code>nsim</code> columns of <code>nobs</code> values each giving the simulations on the response scale, being <code>linkinv</code> of the simulations on the link scale.
<code>if length(type)>1</code>	a list with simulations on the desired scales.

The value also has an attribute "seed". If argument `seed` is `NULL`, the attribute is the value of `.Random.seed` before the simulation started. Otherwise it is the value of the argument with a `kind` attribute with value `as.list(RNGkind())`.

NOTE: This function currently may not work with a model fit that involves a multivariate link or response.

Author(s)

Spencer Graves

See Also

[simulate.glm](#) [predict.glm](#) [set.seed](#)

Examples

```
library(mvtnorm)
##
## 1. a factor and a numeric
##
PoisReg2 <- data.frame(y=1:6,
  x=factor(rep(0:2, 2)), x1=rep(1:2, e=3))
GLMpoisR2 <- glm(y~x+x1, poisson, PoisReg2)
```

```

newDat. <- data.frame(
  x=factor(rep(c(0, 2), 2), levels=0:2),
  x1=3:6)
# NOTE: Force newDat2['x'] to have the same levels
# as PoisReg2['x']

GLMsim2n <- simulate(GLMpoisR2, nsim=3, seed=2,
  newdata=newDat.)

##
## 2. One variable: BMA returns
## a mixture of constant & linear models
##
PoisRegDat <- data.frame(x=1:2, y=c(5, 10))
GLMex <- glm(y~x, poisson, PoisRegDat)

# Simulate for the model data
GLMsig <- simulate(GLMex, nsim=2, seed=1)

# Simulate for new data
newDat <- data.frame(x=3:4,
  row.names=paste0('f', 3:4))
GLMsio <- simulate(GLMex, nsim=3, seed=2,
  newdata=newDat)

##
## 2a. Compute the correct answers manually
##
newMat <- model.matrix(~., newDat)
RNGstate <- structure(2, kind = as.list(RNGkind()))
set.seed(2)

sim <- mvtnorm::rmvnorm(3, coef(GLMex),
  vcov(GLMex))
rownames(sim) <- paste0('sim_', 1:3)
simDF <- data.frame(t(sim))

GLMsim.l <- tcrossprod(newMat, sim)
colnames(GLMsim.l) <- paste0('sim_', 1:3)
GLMsim.r <- exp(GLMsim.l)
GLMsim2 <- list(coef=simDF,
  link=data.frame(GLMsim.l),
  response=data.frame(GLMsim.r) )
attr(GLMsim2, 'seed') <- RNGstate

all.equal(GLMsio, GLMsim2)

```

Description

Split the first field from `x`, identified as all the characters preceding the first unquoted occurrence of `split`.

Usage

```
strsplit1(x, split=',', Quote='', ...)
```

Arguments

<code>x</code>	a character vector to be split
<code>split</code>	the split character
<code>Quote</code>	a quote character: Occurrences of <code>split</code> between pairs of <code>Quote</code> are ignored.
<code>...</code>	optional arguments for <code>grep</code>

Details

This function was written to help parse data from the US Department of Health and Human Services on [cyber-security breaches affecting 500 or more individuals](#). As of 2014-06-03 the csv version of these data included commas in quotes that are not sep characters. This function was written to split the fields one at a time to allow manual processing to make it easier to correct parsing errors.

Algorithm:

1. `spl1 <- regexpr(split, x, ...)`
2. `Qt1 <- regexpr(Quote, x, ...)`
3. For any (`Qt1 < spl1`), look for `Qt2 <- regexpr(Quote, substring(x, Qt1+1))`, then look for `spl1 <- regexpr(split, substring(x, Qt1+Qt2+1))`
4. `out <- list(substr(x, 1, spl1-1), substr(x, spl1+1))`

Value

A list of length 2: The first component of the list contains the character strings found before the first unquoted occurrence of `split`. The second component contains the character strings remaining after the characters up to the identified `split` are removed.

Author(s)

Spencer Graves

See Also

[strsplit](#) [substring](#) [grep](#)

Examples

```
chars2split <- c(qs00='abcdefg', qs01='abc,def',
  qs10a='"abcdefg', qs10b='abc"defg',
  qs1.1='"abc,def', qs20='"abc" def',
  qs2.1='"ab,c" def', qs21='"abc", def', qs22.1='"a,b",c')

split <- strsplit1(chars2split)

# answer
split. <- list(c(qs00='abcdefg', qs01='abc', qs10a='"abcdefg',
  qs10b='abc"defg', qs1.1='"abc,def', qs20='"abc" def',
  qs2.1='"ab,c" def', qs21='"abc"', qs22.1='"a,b"'),
  c(qs00='', qs01='def', qs10a='',
  qs10b='', qs1.1='', qs20='', qs2.1='',
  qs21=' def', qs22.1='c') )

all.equal(split, split.)
```

 subNonStandardCharacters

sub nonstandard characters with replacement

Description

First convert to ASCII, stripping standard accents and special characters. Then find the first and last character not in standardCharacters and replace all between them with replacement. For example, a string like "Ruben" where "e" carries an accent and is mangled by some software would become something like "Rub_n" using the default values for standardCharacters and replacement.

Usage

```
subNonStandardCharacters(x,
  standardCharacters=c(letters, LETTERS,
    '!', '.', '?', '!', ',', 0:9, '/', '*',
    '$', '%', '\\', '\\', '-', '+', '&',
    '_', ';', '(', ')', '[', ']', '\\n'),
  replacement='_',
  gsubList=list(list(pattern =
    '\\\\\\\\\\\\|\\\\\\\\',
    replacement='\\')), ... )
```

Arguments

x character vector in which it is desired to find the first and last character not in standardCharacters and replace that substring by replacement.

standardCharacters a character vector of acceptable characters to keep.

replacement	a character to replace the substring starting and ending with characters not in standardCharacters.
gsubList	list of lists of pattern and replacement arguments to be called in succession before looking for nonStandardCharacters
...	optional arguments passed to strsplit

Details

1. `for(il in 1:length(gsubList)) x <- gsub(gsubList[[il]][["pattern"]], gsubList[[il]][['replacement']] x)`
2. `x <- stringi::stri_trans_general(x, "Latin-ASCII")`
3. `nx <- length(x)`
4. `x. <- strsplit(x, "", ...)`
5. `for(ix in 1:nx)` find the first and last standardCharacters in `x.[ix]` and substitute replacement for everything in between.

NOTES:

** To find the elements of `x` that have changed, use either `subNonStandardCharacters(x) != x` or `grep(replacement, subNonStandardCharacters(x))`, where `replacement` is the replacement argument = "_" by default.

** On 13 May 2013 Jeff Newmiller at the University of California, Davis, wrote, 'I think it is a fools errand to think that you can automatically "normalize" arbitrary Unicode characters to an ASCII form that everyone will agree on.' (This was a reply on r-help@r-project.org, subject: "Re: [R] Matching names with non-English characters".)

** On 2014-12-15 Ista Zahn suggested [stri_trans_general](#). (This was a reply on r-help@r-project.org, subject: "[R] Comparing Latin characters with and without accents?".)

Value

a character vector with everything between the first and last character not in `standardCharacters` replaced by `replacement`.

Author(s)

Spencer Graves with thanks to Jeff Newmiller, who described this as a "fool's errand", Milan Bouchet-Valat, who directed me to [iconv](#), and Ista Zahn, who suggested [stri_trans_general](#).

See Also

[sub](#), [strsplit](#), [grepNonStandardCharacters](#), [subNonStandardNames](#) [subNonStandardNames](#) [iconv](#) in the base package does some conversion, but is not consistent across platforms, at least using R 3.1.2 on 2015-01.25. [stri_trans_general](#) seems better.

Examples

```
##
## 1. Consider Names = Ruben, Avila and Jose, where
## "e" and "A" in these examples carry an accent.
## With the default values for standardCharacters and
## replacement, these might be converted to something
## like Rub_n, _vila, and Jos_, with different software
## possibly mangling the names differently. (The
## standard checks for R packages in an English locale
## complains about non-ASCII characters, because they
## are not portable.)
##
nonstdNames <- c('Ra`l', 'Ra`', '`l', 'Torres, Raul',
                "Robert C. \\Bobby\\\\" , NA, '', ' ',
                '$12', '12%')
# confusion in character sets can create
# names like Names[2]
Name2 <- subNonStandardCharacters(nonstdNames)
str(Name2)

# check
Name2. <- c('Ra_l', 'Ra_', '_l', nonstdNames[4],
            'Robert C. "Bobby"', NA, '', ' ',
            '$12', '12%')
str(Name2.)

all.equal(Name2, Name2.)

##
## 2. Example from iconv
##
icx <- c("Ekstr\u{f8}m", "J\u{f6}reskog",
        "bi\u{df}chen Z\u{fc}rcher")
icx2 <- subNonStandardCharacters(icx)

# check
icx. <- c('Ekstrom', 'Joreskog', 'bisschen Zurcher')

all.equal(icx2, icx.)
```

subNonStandardNames *sub for nonstandard names*

Description

```
sub(nonStandardNames[, 1], nonStandardNames[, 2], x)
```

Accented characters common in non-English languages often get mangled in different ways by different software. For example, the "e" in "Andre" may carry an accent that gets replaced by other characters by different software.

This function first converts "Andr*" to "Andr_" for any character "*" not in standardCharacters. It then looks for "Andr_" in nonStandardNames. By default, it will find that and replace it with "Andre".

Usage

```
subNonStandardNames(x,
  standardCharacters=c(letters, LETTERS, ' ',
    '.', '?', '!', ',', '0:9', '/', '*', '$',
    '%', '\\', "\\'", '-', '+', '&', '_', ';',
    '(', ')', '[', ']', '\\n'),
  replacement='_',
  gsubList=list(list(pattern=
    '\\\\\\\\\\\\\\\\\\\\|\\\\\\\\\\\\\\\\\\\\',
    replacement='\\')),
  removeSecondLine=TRUE,
  nonStandardNames=Ecdat::nonEnglishNames,
  namesNotFound="attr.replacement", ...)
```

Arguments

x character vector or matrix or a data.frame of character vectors in which it is desired to replace `nonStandardNames[, 1]` in `subNonStandardCharacters(x, ...)` with the corresponding element of `nonStandardNames[, 2]`.

`standardCharacters`, `replacement`, `gsubList`, ... arguments passed to [subNonStandardCharacters](#)

`removeSecondLine` logical: If TRUE, delete anything following "\n" and return it as an attribute `secondLine`.

`nonStandardNames` data.frame or character matrix with two columns: Replace any substring of `x` matching `nonStandardNames[, 1]` with the corresponding element of `nonStandardNames[, 2]`

`namesNotFound` character vector describing how to treat substitutions not found in `nonStandardNames[, 1]`:

- `attr.replacement`: Return an attribute `namesNotFound` with `grep(replacement, subNonStandardCharacters(...))`, if any.
- `attr.notFound`: Return an attribute `namesNotFound` with `x != subNonStandardCharacters(...)`, if any.
- "print": Print the elements of `x` not found per either `attr.replacement` or `attr.notFound`, as requested.
- "": Do not report any notFound elements of `x`.

NOTE: `x = "_"` will be identified by `attr.replacement` but not by `attr.notfound` assuming the default value for replacement.

Details

1. removeSecondLines
2. `x. <- subNonStandardCharacters(x, standardCharacters, replacement, ...)`
3. Loop over all rows of `nonStandardNames` substituting anything matching `nonStandardNames[i, 1]` with `nonStandardNames[i, 2]`.
4. Eliminate leading and trailing blanks.
5. `if(is.matrix(x)) return a matrix; if(is.data.frame(x)) return a data.frame(..., stringsAsFactors=FALSE)`

NOTE: On 13 May 2013 Jeff Newmiller at the University of California, Davis, wrote, 'I think it is a fools errand to think that you can automatically "normalize" arbitrary Unicode characters to an ASCII form that everyone will agree on.' (This was a reply on `r-help@r-project.org`, subject: "Re: [R] Matching names with non-English characters".) Doubtless someone has software to do a better job of this than what this function does, but I've so far been unable to find it in R. If you know of a better solution to this problem, I'd be pleased to hear from you. Spencer Graves

Value

a character vector with all `nonStandardCharacters` replaced first by `replacement` and then by the second column of `nonStandardNames` for any that match the first column. If a `secondLine` is found on any elements, it is returned as a `secondLine` attribute.

If any names with `nonStandardCharacters` are not found in `nonStandardNames[, 1]`, they are identified in an optional attribute per the `namesNotFound` argument.

Author(s)

Spencer Graves

See Also

[sub nonEnglishNames](#) [subNonStandardCharacters](#) [stripBlanks](#)

Examples

```
##
## 1. Example
##
tstSNSN <- c('Raul', 'Ra`l', 'Torres,Raul',
            'Torres, Ra`l', "Robert C. \\Bobby\\\\" ,
            'Ed \n --Vacancy', '', ' ')
# confusion in character sets can create
# names like Names[2]
##
## 2. subNonStandardNames(vector)
##
SNS2 <- subNonStandardNames(tstSNSN)
SNS2

# check
SNS2. <- c('Raul', 'Raul', 'Torres,Raul', 'Torres, Raul',
```



```

      'Robert C. "Bobby"', 'Ed', '', '')
  attr(SNS2., 'secondLine') <- c(rep(NA, 5), '--Vacancy',
    NA, NA)

  all.equal(SNS2, SNS2.)

##
## 3. subNonStandardNames(matrix)
##
tstmat <- parseName(tstSNSN, surnameFirst=TRUE)
submat <- subNonStandardNames(tstmat)

# check
SNSmat <- parseName(SNS2., surnameFirst=TRUE)

all.equal(submat, SNSmat)

##
## 4. subNonStandardNames(data.frame)
##
tstdf <- as.data.frame(tstmat)
subdf <- subNonStandardNames(tstdf)

# check
SNSdf <- as.data.frame(SNSmat, stringsAsFactors=FALSE)

all.equal(subdf, SNSdf)

##
## 5. namesNotFound
##
noSub <- subNonStandardNames('xx_x')

# check
noSub. <- 'xx_x'
attr(noSub., 'namesNotFound') <- 'xx_x'

all.equal(noSub, noSub.)

```

trimImage

Trim zero rows or columns from an object of class Image.

Description

Identify rows or columns of a matrix or 3-dimensional array that are all 0 and remove them.

Usage

```
trimImage(x, max2trim=.Machine$double.eps,
          na.rm=TRUE, returnIndices2Keep=FALSE,
          ...)
```

Arguments

<code>x</code>	a numeric matrix or 3-dimensional array or an object with subscripting defined so it acts like such.
<code>max2trim</code>	a single number indicating the max absolute numeric value to trim.
<code>na.rm</code>	logical: If TRUE, NAs will be ignored in determining the max absolute value for the row. If a row or column is all NA, it will be treated as all 0 in deciding whether to trim. If FALSE, any row or column containing an NA will be retained.
<code>returnIndices2Keep</code>	if TRUE, return a list with 2 integer vectors giving row and column indices to use in selecting the desired subset of <code>x</code> . This allows an array <code>y</code> to be trimmed to match <code>x</code> . If FALSE, return the desired trimmed version of <code>x</code> . If this is a list with two two integer vectors, use them to trim <code>x</code> .
<code>...</code>	Optional arguments; not currently used.

Details

1. Check arguments: `2 <= length(dim(x)) <= 3? is.logical(na.rm)? returnIndices2Keep = logical or list of 2 integer vectors, all the same sign, not exceeding dim(x)?`
2. `if(is.list(returnIndices2Keep))` check that `returnIndices2Keep` is a list with 2 integer vectors, all the same sign, not exceeding `dim(x)`. If yes, return `x` appropriately subsetted.
3. `if(!is.logical(returnIndices2Keep))` throw an error message.
4. Compute `indices2Keep`.
5. `If(returnIndices2Keep) return (indices2Keep) else return x appropriately subsetted.`

Value

`if(returnIndices2Keep==TRUE)` return a list with 2 integer vectors to use as subscripts in trimming objects like `x`.

Otherwise, return an object like `x` appropriately trimmed.

Author(s)

Spencer Graves

See Also

[trim](#) trims raster images, similar to `trimImage`.

[trimws](#) trims leading and trailing spaces from character strings and factors. Similar `trim` functions exist in other packages but without obvious, explicit consideration of factors.

Examples

```
##
## 1. trim a simple matrix
##
tst1 <- matrix(.Machine$double.eps, 3, 3,
  dimnames=list(letters[1:3], LETTERS[1:3]))
tst1[2,2] <- 1
tst1t <- trimImage(tst1)

# check
tst1. <- matrix(1, 1, 1,
  dimnames=list(letters[2], LETTERS[2]))

all.equal(tst1t, tst1.)

##
## 2. returnIndices2Keep
##
tst2i <- trimImage(tst1, returnIndices2Keep=TRUE)
tst2a <- trimImage(tst1, returnIndices2Keep=tst2i)

tst2i. <- list(index1=2, index2=2)

# check

all.equal(tst2i, tst2i.)

all.equal(tst2a, tst1.)

##
## 3. trim 0's only
##
tst3 <- array(0, dim=3:5)
tst3[2, 2:3, ] <- 0.5*.Machine$double.eps
tst3[3,, ] <- 1

tst3t <- trimImage(tst3, 0)

# check
tst3t. <- tst3[2:3,, ]

# check

all.equal(tst3t, tst3t.)

##
## 4. trim NAs
```

```

##
tst4 <- tst1
tst4[1,1] <- NA
tst4[3,] <- NA

tst4t <- trimImage(tst4)
# tst4o == tst4
tst4o <- trimImage(tst4, na.rm=FALSE)

# check

all.equal(tst4t, tst1[2, 2, drop=FALSE])

all.equal(tst4o, tst4)

##
## 5. trim all
##
tst4a <- trimImage(tst1, 1)

tst4a. <- matrix(0,0,0,
               dimnames=list(NULL, NULL))

all.equal(tst4a, tst4a.)

```

truncdist

Truncated distribution

Description

The cumulative distribution function for a truncated distribution is 0 for $x \leq \text{truncmin}$, 1 for $\text{truncmax} < x$, and in between is as follows:

$$(\text{pdist}(x, \dots) - \text{pdist}(\text{truncmin}, \dots)) / (\text{pdist}(\text{truncmax}, \dots) - \text{pdist}(\text{truncmin}, \dots))$$

The density, quantile, and random number generation functions are similarly defined from this.

Usage

```

dtruncdist(x, ..., dist='norm', truncmin=-Inf,
           truncmax=Inf)
ptruncdist(q, ..., dist='norm', truncmin=-Inf,
           truncmax=Inf)
qtruncdist(p, ..., dist='norm', truncmin=-Inf,

```

```

      truncmax=Inf)
rtruncdist(n, ..., dist='norm', truncmin=-Inf,
           truncmax=Inf)

```

Arguments

x, q	numeric vector of quantiles
p	numeric vector of probabilities
n	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required.
...	other arguments to be passed to the corresponding function for the indicated <code>dist</code>
dist	Standard R name for the family of functions for the desired distribution. By default, this is <code>norm</code> , so the corresponding function for <code>dtruncdist</code> is <code>dnorm</code> , the corresponding function for <code>ptruncdist</code> is <code>pnorm</code> , etc.
truncmin, truncmax	lower and upper truncation points, respectively.

Details

NOTE: Truncation is different from "censoring", where it's known that an observation lies between certain limits; it's just not known exactly where it lies between those limits.

By contrast, with a truncated distribution, events below `truncmin` and above `truncmax` may exist but are not observed. Thus, it's not known how many events occur outside the given range, `truncmin` to `truncmax`, if any. Given data believed to come from a truncated distribution, estimating the parameters provide a means of estimating the number of unobserved events, assuming a particular form for their distribution.

1. Setup

```
dots <- list(...)
```

2. For `dtruncdist`, return 0 for all `x` outside `truncmin` and `truncmax`. For all others, compute as follows:

```

dots$x <- truncmin ddist <- paste0('d', dist) pdist <- paste0('p', dist) p.min <- do.call(pdist,
dots) dots$x <- truncmax p.max <- do.call(pdist, dots) dots$x <- x dx <- do.call(ddist,
dots)

```

```
return(dx / (p.max-p.min))
```

NOTE: Adjustments must be made if 'log' appears in `names(dots)`

3. The computations for `ptruncdist` are similar.

4. The computations for `qtruncdist` are complementary.

5. For `rtruncdist`, use `qtruncdist(runif(n), ...)`.

Value

`dtruncdist` gives the density, `ptruncdist` gives the distribution function, `qtruncdist` gives the quantile function, and `rtruncdist` generates random deviates.

The length of the result is determined by `n` for `rtruncdist` and is the maximum of the lengths of the numerical arguments for the other functions.

Author(s)

Spencer Graves

See Also[Distributions Normal](#)**Examples**

```
##
## 1. dtruncdist
##
# 1.1. Normal
dx <- dtruncdist(1:4)

# check

all.equal(dx, dnorm(1:4))

# 1.2. Truncated normal between 0 and 1
dx01 <- dtruncdist(seq(-1, 2, .5), truncmin=0, truncmax=1)

# check
dx01. <- c(0, 0, 0, dnorm(c(.5, 1))/(pnorm(1)-pnorm(0)),
           0, 0)

all.equal(dx01, dx01.)

# 1.3. lognormal meanlog=log(100), sdlog = 2, truncmin=500
x10 <- 10^(0:9)
dx10 <- dtruncdist(x10, log(100), 2, dist='lnorm',
                  truncmin=500)

# check
dx10. <- (dtruncdist(log(x10), log(100), 2,
                    truncmin=log(500)) / x10)

all.equal(dx10, dx10.)

# 1.4. log density of the previous example
dx10log <- dtruncdist(x10, log(100), 2, log=TRUE,
                    dist='lnorm', truncmin=500)

all.equal(dx10log, log(dx10))

# 1.5. Poisson without 0.
dPois0.9 <-dtruncdist(0:9, lambda=1, dist='pois', truncmin=0)
```

```
# check
dP0.9 <- c(0, dpois(1:9, lambda=1)/ppois(0, lambda=1, lower.tail=FALSE))

all.equal(dPois0.9, dP0.9)

##
## 2. ptruncdist
##
# 2.1. Normal
px <- ptruncdist(1:4)

# check

all.equal(px, pnorm(1:4))

# 2.2. Truncated normal between 0 and 1
px01 <- ptruncdist(seq(-1, 2, .5), truncmin=0, truncmax=1)

# check
px01. <- c(0, 0, (pnorm(c(0, .5, 1)) - pnorm(0))
          /(pnorm(1)-pnorm(0)), 1, 1)

all.equal(px01, px01.)

# 2.3. lognormal meanlog=log(100), sdlog = 2, truncmin=500
x10 <- 10^(0:9)
px10 <- ptruncdist(x10, log(100), 2, dist='lnorm',
                  truncmin=500)

# check
px10. <- (ptruncdist(log(x10), log(100), 2,
                    truncmin=log(500)))

all.equal(px10, px10.)

# 2.4. log of the previous probabilities
px10log <- ptruncdist(x10, log(100), 2, log=TRUE,
                    dist='lnorm', truncmin=500)

all.equal(px10log, log(px10))

##
## 3. qtruncdist
##
# 3.1. Normal
qx <- qtruncdist(seq(0, 1, .2))
```

```

# check

all.equal(qx, qnorm(seq(0, 1, .2)))

# 3.2. Normal truncated outside (0, 1)
qx01 <- qtruncdist(seq(0, 1, .2),
                  truncmin=0, truncmax=1)

# check
pxmin <- pnorm(0)
pxmax <- pnorm(1)
unp <- (pxmin + seq(0, 1, .2)*(pxmax-pxmin))
qx01. <- qnorm(unp)

all.equal(qx01, qx01.)

# 3.3. lognormal meanlog=log(100),
#       sdlog=2, truncmin=500
qlx10 <- qtruncdist(seq(0, 1, .2), log(100), 2,
                   dist='lnorm', truncmin=500)

# check
plxmin <- plnorm(500, log(100), 2)
unp. <- (plxmin + seq(0, 1, .2)*(1-plxmin))

qlx10. <- qlnorm(unp., log(100), 2)

all.equal(qlx10, qlx10.)

# 3.4. previous example with log probabilities
qlx101 <- qtruncdist(log(seq(0, 1, .2)),
                   log(100), 2, log.p=TRUE, dist='lnorm',
                   truncmin=500)

# check

all.equal(qlx10, qlx101)

##
## 4. rtruncdist
##
# 4.1. Normal
set.seed(1)
rx <- rtruncdist(9)

# check
set.seed(1)

all.equal(rx[1], rnorm(1))

```



```

# Only the first observation matches; check that.

# 4.2. Normal truncated outside (0, 1)
set.seed(1)
rx01 <- rtruncdist(9, truncmin=0, truncmax=1)

# check
pxmin <- pnorm(0)
pxmax <- pnorm(1)
set.seed(1)
rnp <- (pxmin + runif(9)*(pxmax-pxmin))
rx01. <- qnorm(rnp)

all.equal(rx01, rx01.)

# 4.3. lognormal meanlog=log(100), sdlog=2, truncmin=500
set.seed(1)
rlx10 <- rtruncdist(9, log(100), 2,
                    dist='lnorm', truncmin=500)

# check
plxmin <- plnorm(500, log(100), 2)
set.seed(1)
rnp. <- (plxmin + runif(9)*(1-plxmin))

rlx10. <- qlnorm(rnp., log(100), 2)

all.equal(rlx10, rlx10.)

```

whichAeqB

Index of a single match

Description

Return which(A %in% B) if it has length 1; give an error message otherwise.

Usage

```

whichAeqB(A, B, errNoMatch='no match',
          err2Match='more than one match')

```

Arguments

A	A vector which may have a single match in B.
B	A vector of possible matches for A.
errNoMatch	a character string: error message if no match found.
err2Match	a character string: error message if multiple matches found.

Value

a single integer giving the index of the match in A.

Author(s)

Spencer Graves

See Also

[interpPairs](#)

Examples

```
a2b <- whichAeqB(letters, 'b')
```

```
all.equal(a2b, 2)
```

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