Package ‘mosaic’

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Type Package

Title Project MOSAIC Statistics and Mathematics Teaching Utilities

Version 1.9.1

Description Data sets and utilities from Project MOSAIC (<http://www.mosaic-web.org>) used to teach mathematics, statistics, computation and modeling. Funded by the NSF, Project MOSAIC is a community of educators working to tie together aspects of quantitative work that students in science, technology, engineering and mathematics will need in their professional lives, but which are usually taught in isolation, if at all.

Depends R (>= 4.1),

Imports dplyr, tibble, lattice (>= 0.20-21), ggformula, mosaicData, Matrix, mosaicCore (>= 0.7.0), ggplot2, rlang (>= 0.4.7), purrr, MASS, grid, tidyr, methods, utils

Suggests ggstance, ggridges, vdiffr, lubridate, magrittr, NHANES, RCurl, sp, vcd, testthat (>= 3.0.0), knitr, tools, parallel, mapproj, rgl, rmarkdown, covr, formatR, palmerpenguins, ggrepel, readr, ggdendro, gridExtra, splines, latticeExtra, glue, broom, leaflet

Enhances manipulate

VignetteBuilder knitr

License GPL (>= 2)

LazyLoad yes

LazyData yes

URL https://github.com/ProjectMOSAIC/mosaic,

https://www.mosaic-web.org/mosaic/

BugReports https://github.com/ProjectMOSAIC/mosaic/issues

RoxygenNote 7.3.1

Encoding UTF-8

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NeedsCompilation no
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mosaic-package

mosaic: the Project MOSAIC package

Description
mosaic

Details
Data sets and utilities from Project MOSAIC (mosaic-web.org) used to teach mathematics, statistics, computation and modeling. Funded by the NSF, Project MOSAIC is a community of educators working to tie together aspects of quantitative work that students in science, technology, engineering and mathematics will need in their professional lives, but which are usually taught in isolation, if at all.

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adapt_seq

Adaptively generate sequences in an interval

Description

adapt_seq is similar to seq except that instead of selecting points equally spaced along an interval, it selects points such that the values of a function applied at those points are (very) roughly equally spaced. This can be useful for sampling a function in such a way that it can be plotted more smoothly, for example.

Usage

adapt_seq(
  from,
  to,
  length.out = 200,
  f = function(x, ...) {
    1
  },
  args = list(),
  quiet = FALSE
)

Arguments

from start of interval
to end of interval
length.out desired length of sequence
f a function
args arguments passed to f
quiet suppress warnings about NaNs, etc.

Value

a numerical vector
aggregatingFunction

1-ary Aggregating functions

Description

aggregatingFunction creates statistical summaries of one numerical vector that are formula aware.

Usage

aggregatingFunction(
  fun,
  output.multiple = FALSE,
  envir = parent.frame(),
  na.rm = getOption("na.rm", FALSE),
  style = c("formula1st", "formula", "flexible")
)

Arguments

fun          a function that takes a numeric vector and computes a summary statistic, returning a numeric vector.
output.multiple  a boolean indicating whether fun returns multiple values
envir          an environment in which evaluation takes place.
na.rm          the default value for na.rm in the resulting function.
style          one of "formula1st", "formula2nd" or "flexible". In the first two cases, the first argument must be a formula or evaluate to an object. In the latter case, bare names will be converted into formulas.

Details

The logic of the resulting function is this: 1) If the first argument is a formula, use that formula and data to create the necessary call(s) to fun; (2) Else simply pass everything to fun for evaluation.

Value

a function that generalizes fun to handle a formula/data frame interface.

Note

Earlier versions of this function supported a "bare name + data frame" interface. This functionality has been removed since it was (a) ambiguous in some cases, (b) unnecessary, and (c) difficult to maintain.

Examples

adapt_seq(0, pi, 25, sin)
agggregatingFunction1or2

Examples

```r
if (require(mosaicData)) {
  foo <- aggregatingFunction1(base::mean)
  foo(~ length, data = KidsFeet)
  base::mean(KidsFeet$length)
  foo(length ~ sex, data = KidsFeet)
}
```

agggregatingFunction1or2

1- or 2-ary aggregating functions

Description

agggregatingFunction1or2() creates statistical summaries for functions like `var()` that can have either 1 or 2 numeric vector inputs.

Usage

```r
agggregatingFunction1or2(
  fun,
  output.multiple = FALSE,
  na.rm = getOption("na.rm", FALSE)
)
```

Arguments

- `fun` a function that takes 1 or 2 numeric vectors and computes a summary statistic, returning a numeric vector of length 1.
- `output.multiple` a boolean indicating whether `fun` returns multiple values
- `na.rm` the default value for `na.rm` in the resulting function.

Details

This was designed primarily to support `var()` which can be used to compute either the variance of one variable or the covariance of two variables. The logic of the resulting function is this: 1) If the first two arguments are both formulas, then those formulas are evaluated (with `data`) to compute the covariance; (2) If the first argument is a formula, and the second is `NULL`, then the formula and `data` are used to create the necessary call(s) to `fun`; (3) Else everything is simply passed to `fun` for evaluation.

Note

Earlier versions of this function supported a "bare name + data frame" interface. This functionality has been removed since it was (a) ambiguous in some cases, (b) unnecessary, and (c) difficult to maintain.
aggregatingFunction2  2-ary aggregating functions

Description

aggregatingFunction2 creates statistical summaries of two numerical vectors that are formula aware.

Usage

aggregatingFunction2(fun)

Arguments

fun a function that takes two numeric vectors and computes a summary statistic, returning a numeric vector of length 1.

Details

This was designed to support functions like `cov()` which can be used to compute numerical summaries from two numeric vectors. The logic of the resulting function is this: 1) If the first two arguments are both formulas, then those formulas are evaluated (with data) to compute the covariance; (2) If the first argument is a formula, and the second is NULL, then the left and right sides of the formula and data are used to create the vectors passed to `fun`; (3) Else everything is simply passed to `fun` for evaluation.

Value

a function that generalizes `fun` to handle a formula/data frame interface.

Note

Earlier versions of this function supported a "bare name + data frame" interface. This functionality has been removed since it was (a) ambiguous in some cases, (b) unnecessary, and (c) difficult to maintain.

Examples

```r
if(require(mosaicData)) {
  foo <- aggregatingFunction2(stats::cor)
  foo(length ~ width, data = KidsFeet)
  stats::cor(KidsFeet$length, KidsFeet$width)
}
```
as.xtabs

Convert objects to xtabs format

Description

Convert a data frame or a matrix into an xtabs object.

Usage

as.xtabs(x, ...)

## S3 method for class 'data.frame'
as.xtabs(x, rowvar = NULL, colvar = NULL, labels = 1, ...)

## S3 method for class 'matrix'
as.xtabs(x, rowvar = NULL, colvar = NULL, ...)

Arguments

x  
object (typically a data frame) to be converted to xtabs format

...  
additional arguments to be passed to or from methods.

rowvar  
name of the row variable as character string

colvar  
name of the column variable as character string

labels  
column of data frame that contains the labels of the row variable.

Details

The intended use is to convert a two-way contingency table stored in a data frame or a matrix into an xtabs object.

Value

An xtabs object.

Examples

# example from example(fisher.test)
df <- data.frame( X=c('Tea','Milk'), Tea=c(3,1), Milk=c(1,3) )
xt <- as.xtabs(df, rowvar="Guess", colvar="Truth"); xt
if (require(vcd)) { mosaic(xt) }
ashplot

Average Shifted Histograms

Description

An ASH plot is the average over all histograms of a fixed bin width.

Usage

ashplot(
  x,
  data = data,
  ..., 
  width = NULL,
  adjust = NULL,
  panel = panel.ashplot,
  prepanel = prepanel.default.ashplot
)

prepanel.default.ashplot(x, darg, groups = NULL, subscripts = TRUE, ...)

panel.ashplot(
  x,
  darg = list(),
  plot.points = FALSE,
  ref = FALSE,
  groups = NULL,
  jitter.amount = 0.01 * diff(current.panel.limits()$ylim),
  type = "p",
  ..., 
  identifier = "ash"
)

Arguments

x A formula or numeric vector.
data A data frame.
... Additional arguments passed to panel and prepanel functions or data, a data frame in which to find the variables used for the plot.
width The histogram bin width.
adjust A numeric adjustment to width. Primarily useful when width is not specified. Increasing adjust makes the plot smoother.
panel A panel function.
prepanel A prepanel function.
darg a list of arguments for the function computing the ASH.
groups as in other lattice plots
subscripts as in other lattice prepanel functions
plot.points One of TRUE, FALSE, "jitter", or "rug"
ref a logical indicating whether a reference line should be displayed
jitter.amount when plot.points="jitter", the value to use as the amount argument to jitter().
type type argument used to plot points, if requested. This is not expected to be useful, it is available mostly to protect a type argument, if specified, from affecting the display of the ASH.
identifier A character string that is prepended to the names of i grobs that are created by this panel function.

Examples

ashplot(~age | substance, groups = sex, data = HELPrct)

bargraph
Create bar graphs from raw data

Description

lattice::barchart() from the lattice package makes bar graphs from pre-tabulated data. Raw data can be tabulated using xtabs(), but the syntax is unusual compared to the other lattice plotting functions. bargraph provides an interface that is consistent with the other lattice functions.

Usage

bargraph(
  x,
  data = parent.frame(),
  groups = NULL,
  horizontal = FALSE,
  origin = 0,
  ylab = ifelse(horizontal, "", type),
  xlab = ifelse(horizontal, type, ""),
  type = c("count", "frequency", "proportion", "percent"),
  auto.key = TRUE,
  scales = list(),
  ...
)
Arguments

- **x**: a formula describing the plot
- **data**: a data frame in which the formula `x` is evaluated
- **groups**: a variable or expression used for grouping. See `lattice::barchart()`.
- **horizontal**: a logical indicating whether bars should be horizontal
- **origin**: beginning point for bars. For the default behavior used by `lattice::barchart()` set `origin` to `NULL`, but 0 is often a better default. If 0 is not good, perhaps you should use a different kind of plot as the results may be misleading.
- **ylab**: a character vector of length one used for the y-axis label
- **xlab**: a character vector of length one used for the x-axis label
- **type**: one of "frequency", "count", "percent", or "proportion" indicating what type of scale to use. Unique prefixes are sufficient.
- **auto.key**: a logical expression indicating whether a legend should be automatically produced
- **scales**: is a list determining how the x- and y-axes are drawn
- **...**: additional arguments passed to `lattice::barchart()`

Details

`bargraph(formula, data=data, ...) works by creating a new data frame from xtabs(formula, data=data) and then calling `lattice::barchart()` using modified version of the formula and this new data frame as inputs. This has implications on, for example, conditional plots where one desires to condition on some expression that will be evaluated in data. This typically does not work because the required variables do not exist in the output of `xtabs`. One solution is to first add a new variable to `data` first and then to condition using this new variable. See the examples.

Value

a trellis object describing the plot

See Also

`lattice::barchart()`

Examples

```r
if (require(mosaicData)) {
  data(HELPrct)
  bargraph(~ substance, data = HELPrct)
  bargraph(~ substance, data = HELPrct, horizontal = TRUE)
  bargraph(~ substance | sex, groups = homeless, auto.key = TRUE, data = HELPrct)
  bargraph(~ substance, groups = homeless, auto.key=TRUE,
    data = HELPrct |> filter(sex == "male"))
  HELPrect2 <- mutate(HELPrct, older = age > 40)
  bargraph(~ substance | older, data = HELPrect2)
}
```
binom.test

---

**Description**

The `binom.test()` function performs an exact test of a simple null hypothesis about the probability of success in a Bernoulli experiment from summarized data or from raw data. The mosaic `binom.test` provides wrapper functions around the function of the same name in `stats`. These wrappers provide an extended interface (including formulas).

**Usage**

```r
binom.test(
  x,  # count of successes, length 2 vector of success and failure counts, a formula, or a character, numeric, or factor vector containing raw data.
  n = NULL,  # sample size (successes + failures) or a data frame (for the formula interface)
  p = 0.5,  # probability for null hypothesis
  alternative = c("two.sided", "less", "greater"),  # type of alternative hypothesis
  conf.level = 0.95,  # confidence level for confidence interval
  data = NULL,  # a data frame (if missing, n may be a data frame)
  success = NULL,  # level of variable to be considered success. All other levels are considered failure.
  ...  # additional arguments (often ignored)
)
```

**Arguments**

- `x` count of successes, length 2 vector of success and failure counts, a formula, or a character, numeric, or factor vector containing raw data.
- `n` sample size (successes + failures) or a data frame (for the formula interface)
- `p` probability for null hypothesis
- `alternative` type of alternative hypothesis
- `conf.level` confidence level for confidence interval
- `ci.method` a method to use for computing the confidence interval (case insensitive and may be abbreviated). See details below.
- `data` a data frame (if missing, n may be a data frame)
- `success` level of variable to be considered success. All other levels are considered failure.
- `...` additional arguments (often ignored)

**Details**

`binom.test()` is a wrapper around `stats::binom.test()` from the stats package to simplify its use when the raw data are available, in which case an extended syntax for `binom.test()` is provided. See the examples.
Also, five confidence interval methods are provided: *"Clopper-Pearson", "binom.test": This is the interval produced when using \texttt{stats::binom.test()} from the stats package. It guarantees a coverage rate at least as large as the nominal coverage rate, but may produce wider intervals than some of the methods below, which may either under- or over-cover depending on the data.

- "Score", "Wilson", "prop.test": This is the usual method used by \texttt{stats::prop.test()} and is computed by inverting p-values from score tests. It is often attributed to Edwin Wilson. If specified with "prop.test", the continuity correction is applied (as is the default in \texttt{prop.test()}), else the continuity correction is not applied.
  - "Wald": This is the interval traditionally taught in entry level statistics courses. It uses the sample proportion to estimate the standard error and uses normal theory to determine how many standard deviations to add and/or subtract from the sample proportion to determine an interval.
  - "Agresti-Coull": This is the Wald method after setting \(n' = n + z^2\) and \(p' = (x + z^2/2)/n'\) and using \(x' = n'p'\) and \(n'\) in place of \(x\) and \(n\).
  - "Plus4": This is Wald after adding in two artificial success and two artificial failures. It is nearly the same as the Agresti-Coull method when the confidence level is 95%. since \(z^2\) is approximately 4 and \(z^2/2\) is approximately 2.

\textbf{Value}

an object of class \texttt{htest}

\textbf{Note}

When \(x\) is a 0-1 vector, 0 is treated as failure and 1 as success. Similarly, for a logical vector \texttt{TRUE} is treated as success and \texttt{FALSE} as failure.

\textbf{See Also}

\texttt{prop.test()}, \texttt{stats::binom.test()}

\textbf{Examples}

```r
# Several ways to get a confidence interval for the proportion of Old Faithful
# eruptions lasting more than 3 minutes.
data(faithful)
binom.test(faithful$eruptions > 3)
binom.test(97, 272)
binom.test(c(97, 272-97))
faithful$long <- faithful$eruptions > 3
binom.test(faithful$long)
binom.test(resample(1:4, 400), p=.25)
binom.test(~ long, data = faithful)
binom.test(~ long, data = faithful, ci.method = "Wald")
binom.test(~ long, data = faithful, ci.method = "Plus4")
with(faithful, binom.test(~long))
with(faithful, binom.test(long))
```
**Broyden**

**Description**

Implementation of Broyden’s root finding function to numerically compute the root of a system of nonlinear equations

**Usage**

```r
Broyden(system, vars, x = 0, tol = .Machine$double.eps^0.4, maxiters = 10000)
```

**Arguments**

- `system` A list of functions
- `vars` A character string list of variables that appear in the functions
- `x` A starting vector
- `tol` The tolerance for the function specifying how precise it will be
- `maxiters` maximum number of iterations.

---

**cdist**

**Central portion of a distribution**

**Description**

This function determines the critical values for isolating a central portion of a distribution with a specified probability. This is designed to work especially well for symmetric distributions, but it can be used with any distribution.

**Usage**

```r
cdist(
  dist = "norm",
  p,
  plot = TRUE,
  verbose = FALSE,
  invisible = FALSE,
  digits = 3L,
  xlim = NULL,
  ylim = NULL,
  resolution = 500L,
  return = c("values", "plot"),
  pattern = c("rings", "stripes"),
  ...
)```

...
refinements = list()
)

xcgamma(
p,
shape,
rate = 1,
scale = 1/rate,
lower.tail = TRUE,
log.p = FALSE,
...
)

taxt(p, df, ncp, lower.tail = TRUE, log.p = FALSE, ...)

xcchisq(p, df, ncp = 0, lower.tail = TRUE, log.p = FALSE, ...)

xcf(p, df1, df2, lower.tail = TRUE, log.p = FALSE, ...)

xcbinom(p, size, prob, lower.tail = TRUE, log.p = FALSE, ...)

xcpois(p, lambda, lower.tail = TRUE, log.p = FALSE, ...)

xcgeom(p, prob, lower.tail = TRUE, log.p = FALSE, ...)

xcnbinom(p, size, prob, mu, lower.tail = TRUE, log.p = FALSE, ...)

xcbeta(p, shape1, shape2, ncp = 0, lower.tail = TRUE, log.p = FALSE, ...)

Arguments

dist a character string naming a distribution family (e.g., "norm"). This will work
for any family for which the usual d/p/q functions exist.
p the proportion to be in the central region, with equal proportions in either "tail".
plot a logical indicating whether a plot should be created
verbose a logical indicating whether a more verbose output value should be returned.
invisible a logical
digits the number of digits desired
xlim x limits. By default, these are chosen to show the central 99.8\% of the distribution.
ylim y limits
resolution number of points used for detecting discreteness and generating plots. The de-
default value of 5000 should work well except for discrete distributions that have
many distinct values, especially if these values are not evenly spaced.
return If "plot", return a plot. If "values", return a vector of numerical values.
pattern One of "stripes" or "rings". In the latter case, pairs of regions (from the out-
side to the inside) are grouped together for coloring and probability calculation.
additional arguments passed to the distribution functions. Typically these specify the parameters of the particular distribution desired. See the examples.

refinements A list of refinements to the plot. See `ggformula::gf_refine()`.

shape, scale shape and scale parameters. Must be positive, scale strictly.

rate an alternative way to specify the scale.

lower.tail logical; if TRUE (default), probabilities are \( P[X \leq x] \), otherwise, \( P[X > x] \).

log.p A logical indicating whether probabilities should be returned on the log scale.

df degrees of freedom (> 0, maybe non-integer). \( df = \infty \) is allowed.

ncp non-centrality parameter \( \delta \); currently except for \( \text{rt}() \), only for \( \text{abs}(ncp) \leq 37.62 \). If omitted, use the central \( t \) distribution.

df1, df2 degrees of freedom. \( \infty \) is allowed.

size number of trials (zero or more).

prob probability of success on each trial.

lambda vector of (non-negative) means.

mu alternative parametrization via mean: see ‘Details’.

shape1, shape2 non-negative parameters of the Beta distribution.

Value

a pair of numbers indicating the upper and lower bounds, unless `verbose` is `TRUE`, in which case a 1-row data frame is returned containing these bounds, the central probability, the tail probabilities, and the name of the distribution.

Note

This function is still experimental and changes the input or output formats are possible in future versions of the package.

Examples

cdist( "norm", .95)
cdist( "t", c(.90, .95, .99), df=5)
cdist( "t", c(.90, .95, .99), df=50)
# plotting doesn't work well when the parameters are not constant
cdist( "t", .95, df=c(3,5,10,20), plot = FALSE)
cdist( "norm", .95, mean=500, sd=100 )
cdist( "chisq", c(.90, .95), df=3 )
# CI
x <- rnorm(23, mean = 10, sd = 2)
cdist("t", p = 0.95, df=22)
mean(x) + cdist("t", p = 0.95, df=22) * sd(x) / sqrt(23)
confint(t.test(x))
cdist("t", p = 0.95, df=22, verbose = TRUE)
chisq  

Extract Chi-squared statistic

Description

Extract Chi-squared statistic

Usage

chisq(x, ...)

## S3 method for class 'htest'
chisq(x, ...)

## S3 method for class 'table'
chisq(x, correct = FALSE, ...)

## Default S3 method:
chisq(x, correct = FALSE, ...)

Arguments

x  An object of class "htest" a coming from a Chi-squared test, an object of class "table", or the inputs to tally().

...  additional arguments passed on to tally or chisq.test.

correct  a logical indicating whether a continuity correction should be applied.

See Also

after_stat()

Examples

if(require(mosaicData)) {
   Mites.table <- tally(~ outcome + treatment, data=Mites )
   chisq.test(Mites.table)
   chisq(Mites.table)
   chisq(chisq.test(Mites.table))
   ## Randomization test. Increase replications to decrease Monte Carlo error.
   do(3) * chisq( tally(~ outcome + shuffle(treatment), data=Mites ) )
   Mites.rand <- do(1000) * chisq( tally(~ outcome + shuffle(treatment), data=Mites ) )
   tally(~(X.squared >= chisq(Mites.table)), data=Mites.rand, format="proportion")
}
CIAdata

Return a dataset based on the CIA World Factbook

Description

This function can be used in two different ways. Without an argument, it returns a reference table that includes information about all the CIA World Factbook tables that are available through this function. Note the Name column that indicates a unique name for each available dataset. If this name is passed as an argument to the function, the function will return the corresponding dataset.

Usage

CIAdata(name = NULL)

Arguments

name

An optional parameter specifying the name of the desired dataset. If multiple names are given, a merge will be attempted on the individual data sets.

Examples

## Not run:
head(CIAdata())
Population <- CIAdata("pop")
nrow(Population)
head(Population)

PopArea <-
  CIAdata(c("pop","area")) |>
    mutate(density = pop / area)
nrow(PopArea)
head(PopArea)
PopArea |>  
  filter(!is.na(density)) |>  
    arrange(density) |>  
    tail()

## End(Not run)

CIsim

Compute confidence intervals from (multiple) simulated data sets

Description

This function automates the calculation of coverage rates for exploring the robustness of confidence interval methods.
Usage

CIsim(
  n,
  samples = 100,
  rdist = rnorm,
  args = list(),
  plot = if (samples <= 200) "draw" else "none",
  estimand = 0,
  conf.level = 0.95,
  method = t.test,
  method.args = list(),
  interval = function(x) {
    do.call(method, c(list(x, conf.level = conf.level),
                       method.args))$conf.int
  },
  estimate = function(x) {
    do.call(method, c(list(x, conf.level = conf.level),
                       method.args))$estimate
  },
  verbose = TRUE
)

Arguments

n  size of each sample
samples  number of samples to simulate
rdist  function used to draw random samples
args  arguments required by rdist
plot  one of "print", "return", "horizontal", or "none" describing whether a plot
       should be printed, returned, printed with horizontal intervals, or not generated
       at all.
estimand  true value of the parameter being estimated
conf.level  confidence level for intervals
method  function used to compute intervals. Standard functions that produce an object
         of class htest can be used here.
method.args  arguments required by method
interval  a function that computes a confidence interval from data. Function should return
           a vector of length 2.
estimate  a function that computes an estimate from data
verbose  print summary to screen?

Value

A data frame with variables lower, upper, estimate, cover ("Yes" or "No"), and sample is returned
invisibly. See the examples for a way to use this to display the intervals graphically.
Examples

```r
# 1000 95% intervals using t.test; population is N(0,1)
CIsim(n = 10, samples = 1000)
# this time population is Exp(1); fewer samples, so we get a plot
CIsim(n = 10, samples = 100, rdist = rexp, estimand = 1)
# Binomial treats 1 like success, 0 like failure
CIsim(n = 30, samples = 100, rdist = rbinom, args = list(size = 1, prob = .7),
       estimand = .7, method = binom.test, method.args = list(ci = "Plus4"))
```

---

**cnorm**  
*Central Probability in a Normal or T Distribution*

Description

These versions of the quantile functions take a vector of *central* probabilities as its first argument.

Usage

```r
cnorm(p, mean = 0, sd = 1, log.p = FALSE, side = c("both", "upper", "lower"))
ct(p, df, ncp, log.p = FALSE, side = c("upper", "lower", "both"))
```

Arguments

- `p`: vector of probabilities.
- `mean`: vector of means.
- `sd`: vector of standard deviations.
- `log.p`: logical. If TRUE, uses the log of probabilities.
- `side`: One of "upper", "lower", or "both" indicating whether a vector of upper or lower quantiles or a matrix of both should be returned.
- `df`: degrees of freedom (> 0, maybe non-integer). `df = Inf` is allowed.
- `ncp`: non-centrality parameter δ; currently except for `rt()`, only for `abs(ncp) <= 37.62`. If omitted, use the central t distribution.

See Also

`stats::qnorm()`, `cdist()`
Examples

```r
qnorm(.975)
cnorm(.95)
xcnorm(.95)
xcnorm(.95, verbose = FALSE, return = "plot") |> 
gf_refine(
  scale_fill_manual(values = c("navy", "limegreen")),
  scale_color_manual(values = c("black", "black"))
) cnorm(.95, mean = 100, sd = 10)
xcnorm(.95, mean = 100, sd = 10)
```

---

**compareMean**

**Defunct functions**

**Description**

The following functions were once a part of the mosaic package but have been removed. In some cases, an alternative is available and is suggested if you attempt to execute the function.

**Usage**

```r
compareMean(...) 
compareProportion(...) 
deltaMethod(...) 
gwm(...) 
r.squared(...) 
mm(...) 
perctable(...) 
proptable(...) 
xhistogram(...)
```

**Arguments**

```r
... arguments, ignored since the function is defunct
```
Description

Methods for `confint` to compute confidence intervals on numerical vectors and numerical components of data frames.

Usage

```r
## S3 method for class 'numeric'
confint(
  object,
  parm,
  level = 0.95,
  ...,  # ...;
  method = "percentile",
  margin.of.error = "stderr" %in% method == "stderr"
)

## S3 method for class 'do.tbl_df'
confint(
  object,
  parm,
  level = 0.95,
  ...,  # ...;
  method = "percentile",
  margin.of.error = "stderr" %in% method,
  df = NULL
)

## S3 method for class 'do.data.frame'
confint(
  object,
  parm,
  level = 0.95,
  ...,  # ...;
  method = "percentile",
  margin.of.error = "stderr" %in% method,
  df = NULL
)

## S3 method for class 'data.frame'
confint(object, parm, level = 0.95, ...)

## S3 method for class 'summary.lm'
confint(object, parm, level = 0.95, ...)
```
Arguments

object and R object
parm a vector of parameters
level a confidence level
... additional arguments
method a character vector of methods to use for creating confidence intervals. Choices are "percentile" (or "quantile") which is the default, "stderr" (or "se"), "bootstrap-t", and "reverse" (or "basic")
margin.of.error if true, report intervals as a center and margin of error.
df degrees for freedom. This is required when object was produced using link{do} when using the standard error to compute the confidence interval since typically this information is not recorded in these objects. The default (Inf) uses a normal critical value rather than a one derived from a t-distribution.

Details

The methods of producing confidence intervals from bootstrap distributions are currently quite naive. In particular, when using the standard error, assistance may be required with the degrees of freedom, and it may not be possible to provide a correct value in all situations. None of the methods include explicit bias correction. Let \( q_a \) be the \( a \) quantile of the bootstrap distribution, let \( t_a, df \) be the \( a \) quantile of the t distribution with \( df \) degrees of freedom, let \( SE_b \) be the standard deviation of the bootstrap distribution, and let \( \hat{\theta} \) be the estimate computed from the original data. Then the confidence intervals with confidence level \( 1 - 2a \) are

- **quantile** \( (q_a, q_{1-a}) \)
- **reverse** \( (2\hat{\theta} - q_{1-a}, 2\hat{\theta} - q_a) \)
- **stderr** \( (\hat{\theta} - t_{1-a,df}SE_b, \hat{\theta} + t_{1-a,df}SE_b) \). When \( df \) is not provided, at attempt is made to determine an appropriate value, but this should be double checked. In particular, missing data an lead to unreliable results.

The bootstrap-t confidence interval is computed much like the reverse confidence interval but the bootstrap t distribution is used in place of a theoretical t distribution. This interval has much better properties than the reverse (or basic) method, which is here for comparison purposes only and is not recommended. The t-statistic is computed from a mean, a standard deviation, a sample size which much be named "mean", "sd", and "n" as they are when using `favstats()`.

Value

When applied to a data frame, returns a data frame giving the confidence interval for each variable in the data frame using `t.test` or `binom.test`, unless the data frame was produced using do, in which case it is assumed that each variable contains resampled statistics that serve as an estimated sampling distribution from which a confidence interval can be computed using either a central proportion of this distribution or using the standard error as estimated by the standard deviation of the estimated sampling distribution. For the standard error method, the user must supply the correct
degrees of freedom for the t distribution since this information is typically not available in the output of `do()`.

When applied to a numerical vector, returns a vector.

**References**


**Examples**

```r
if (require(mosaicData)) {
  bootstrap <- do(500) * diffmean( age ~ sex, data = resample(HELPrct) )
  confint(bootstrap)
  confint(bootstrap, method = "percentile")
  confint(bootstrap, method = "boot")
  confint(bootstrap, method = "se", df = nrow(HELPrct) - 1)
  confint(bootstrap, margin.of.error = FALSE)
  confint(bootstrap, margin.of.error = TRUE, level = 0.99,
    method = c("se", "perc") )

  # bootstrap t method requires both mean and sd
  bootstrap2 <- do(500) * favstats(resample(1:10))
  confint(bootstrap2, method = "boot")
}
```

```r
lm(width ~ length * sex, data = KidsFeet) |> summary() |> confint()
```

---

**confint.h.test**

*Extract summary statistics*

**Description**

Extract confidence intervals, test statistics or p-values from an htest object.

**Usage**

```r
## S3 method for class 'htest'
confint(object, parm, level, ...)
pval(x, ...)

## S3 method for class 'htest'
pval(x, digits = 4, verbose = FALSE, ...)
stat(x, ...)
```
## S3 method for class 'htest'
stat(x, ...)

## S3 method for class 'uneval'
stat(x, ...)

### Arguments

- **object**: a fitted model object or an htest object.
- **parm**: a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
- **level**: the confidence level required.
- **...**: Additional arguments.
- **x**: An object of class htest.
- **digits**: number of digits to display in verbose output
- **verbose**: a logical

### Value

The extracted p-value, confidence interval, or test statistic

### Examples

```r
confint(t.test(rnorm(100)))
pval(t.test(rnorm(100)))
stat(t.test(rnorm(100)))
confint(var.test(rnorm(10, sd=1), rnorm(20, sd=2)))
pval(var.test(rnorm(10, sd=1), rnorm(20, sd=2)))
if (require(mosaicData)) {
data(HELPrct)
stat(t.test (age ~ shuffle(sex), data=HELPrct))
# Compare to test statistic computed with permuted values of sex.
do(10) * stat(t.test (age ~ shuffle(sex), data=HELPrct))
}
```

---

**cor_test.formula**  
*Alternative formula interface for cor.test*

### Description

The `stats::cor.test()` in `stats` accepts formulas of the shape `~ y + x`. The `mosaic` package allows the use of `y ~ x` as an alternative formula shape.
Usage

## S3 method for class 'formula'
cor.test(formula, ...)

cor.test(x, ...)

cor.test(x, y, ...)

## Default S3 method:
cor.test(x, y, ...)

Arguments

formula        a formula
...
other arguments passed to stats::cor.test().
x, y
numeric vectors of data values. x and y must have the same length.

See Also

stats::cor.test() in the stats package.

Examples

# This is an example from example(stats::cor.test) done in old and new style
require(graphics)
cor.test(~ CONT + INTG, data = USJudgeRatings)
cor.test(CONT ~ INTG, data = USJudgeRatings)

cross

Factor cross products

Description

Construct a product of factors.

Usage

cross(..., sep = ":", drop.unused.levels = FALSE)

Arguments

... factors to be crossed.
sep separator between levels
drop.unused.levels
should levels that do not appear in cross product be dropped?
Value

a factor

Examples

```r
x <- letters[1:3]
y <- c(1,2,1,1,3,1,3)
cross(x, y)
cross(x, y, drop.unused.levels=TRUE)
```

---

cull_for_do  

Cull objects used with do()

Description

The `do()` function facilitates easy replication for randomization tests and bootstrapping (among other things). Part of what makes this particularly useful is the ability to cull from the objects produced those elements that are useful for subsequent analysis. `cull_for_do` does this culling. It is generic, and users can add new methods to either change behavior or to handle additional classes of objects.

Usage

```r
cull_for_do(object, ...)
```

Arguments

- **object**: an object to be culled
- **...**: additional arguments (currently ignored)

Details

When `do(n) * expression` is evaluated, `expression` is evaluated `n` times to produce a list of `n` result objects. `cull_for_do` is then applied to each element of this list to extract from it the information that should be stored. For example, when applied to a object of class "lm", the default `cull_for_do` extracts the coefficients, coefficient of determinism, an the estimate for the variance, etc.

Examples

```r
cull_for_do(lm(length ~ width, data = KidsFeet))
do(1) * lm(length ~ width, data = KidsFeet)
```
deg2rad  

Convert between degrees and radians

Description
Facilitates conversion between degrees and radians.

Usage

deg2rad(x)

rad2deg(x)

Arguments

x a numeric vector

Value

a numeric vector

See Also

latlon2xyz(), googleMap(), and rgeo().

Examples

deg2rad(180)
rad2deg(2*pi)

derivedVariable  

Create new variables from logicals

Description
Utility functions for creating new variables from logicals describing the levels

Usage

derivedVariable(
  ..., .ordered = FALSE,
  .method = c("unique", "first", "last"),
  .debug = c("default", "always", "never"),
  .sort = c("given", "alpha"),
  .default = NULL,
...)

```r
.derivedVariable = FALSE
)

derivedFactor(..., .asFactor = TRUE)
```

**Arguments**

- `[...](#)` named logical “rules” defining the levels.
- `.ordered` a logical indicating whether the resulting factored should be ordered. Ignored if `.asFactor` is `FALSE`.
- `.method` one of "unique", "first", and "last". If "unique", exactly one rule must be `TRUE` for each position. If "first", the first `TRUE` rule defines the level. If "last", the last `TRUE` rule defines the level.
- `.debug` one of "default", "always", and "never", indicating whether debugging information should be printed. If "default", debugging information is printed only when multiple rules give conflicting definitions for some positions.
- `.sort` One of "given" (the default) or "alpha" or a vector of integers the same length as the number of levels indicating the order in which the levels should appear in the resulting factor. Ignored if `.asFactor` is `FALSE`.
- `.default` character vector of length 1 giving name of default level or `NULL` for no default.
- `.asFactor` A logical indicating whether the returned value should be a factor.

**Details**

Each logical “rule” corresponds to a level in the resulting variable. If `.default` is defined, an implicit rule is added that is `TRUE` whenever all other rules are `FALSE`. When there are multiple `TRUE` rules for a slot, the first or last such is used or an error is generated, depending on the value of `.method`.

derivedVariable is designed to be used with `transform()` or `dplyr::mutate()` to add new variables to a data frame. derivedFactor() is the same but that the default value for `.asFactor` is `TRUE`. See the examples.

**Examples**

```r
Kf <- mutate(KidsFeet, biggerfoot2 = derivedFactor(
  dom = biggerfoot == domhand,
  nondom = biggerfoot != domhand)
)
tally(~ biggerfoot + biggerfoot2, data = Kf)
tally(~ biggerfoot + domhand, data = Kf)

# Three equivalent ways to define a new variable
# Method 1: explicitly define all levels
modHELP <- mutate(HELPPrct, drink_status = derivedFactor(
  abstinent = i1 == 0,
  moderate = (i1>0 & i1<=1 & i2<=3 & sex==’female’) |
  (i1>0 & i1<=2 & i2<=4 & sex==’male’),
  highrisk = (((i1>1 | i2>3) & sex==’female’) |
```
design_plot

((i1>2 | i2>4) & sex=='male'),
.ordered = TRUE)
)
tally(~ drink_status, data = modHELP)

# Method 2: Use .default for last level
modHELP <- mutate(HELPrct, drink_status = derivedFactor(
  abstinent = i1 == 0,
  moderate = (i1<=1 & i2<=3 & sex=='female') |
    (i1<=2 & i2<=4 & sex=='male'),
  .ordered = TRUE,
  .method = "first",
  .default = "highrisk")
)
tally(~ drink_status, data = modHELP)

# Method 3: use TRUE to catch any fall through slots
modHELP <- mutate(HELPrct, drink_status = derivedFactor(
  abstinent = i1 == 0,
  moderate = (i1<=1 & i2<=3 & sex=='female') |
    (i1<=2 & i2<=4 & sex=='male'),
  highrisk=TRUE,
  .ordered = TRUE,
  .method = "first"
)
)
tally(~ drink_status, data = modHELP)
is.factor(modHELP$drink_status)

modHELP <- mutate(HELPrct, drink_status = derivedVariable(
  abstinent = i1 == 0,
  moderate = (i1<=1 & i2<=3 & sex=='female') |
    (i1<=2 & i2<=4 & sex=='male'),
  highrisk=TRUE,
  .ordered = TRUE,
  .method = "first"
)
)
is.factor(modHELP$drink_status)

**Description**

Proves a simple interface to let users interactively design plots in **ggformula**, **lattice**, or **ggplot2**. An option is available to show the code used to create the plot. This can be copied and pasted elsewhere to (into an RMarkdown document, for example) to recreate the plot. Only works in RStudio. Requires the **manipulate** package.
Usage

design_plot(
  data,
  format,
  default = format,
  system = system_choices()[1],
  show = FALSE,
  title = "",
  data_text = rlang::expr_deparse(substitute(data)),
  ...
)

Arguments

data  a data frame containing the variables that might be used in the plot. Note that for maps, the data frame must contain coordinates of the polygons comprising the map and a variable for determining which coordinates are part of the same region. See sp2df() for one way to create such a data frame. Typically merge() will be used to combine the map data with some auxiliary data to be displayed as fill color on the map, although this is not necessary if all one wants is a map.

format a synonym for default.

default default type of plot to create: one of "scatter", "jitter", "boxplot", "violin", "sina", "histogram", "density", "density (contours)", "density (filled)", "frequency polygon", "xyplot", or "map". Unique prefixes suffice.

system which graphics system to use (initially) for plotting (ggplot2 or lattice). A check box will allow on the fly change of plotting system.

show a logical, if TRUE, the code will be displayed each time the plot is changed.

title a title for the plot

data_text A text string describing the data. It must be possible to recover the data from this string using eval(). Typically users will not need to modify this from the default value.

Details

Currently maps are only supported in ggplot2 and not in lattice.

Due to an unresolved issue with RStudio, the first time this function is called, and additional plot is created to correctly initialize the manipulate framework.

Value

Nothing. Used for side effects.
diffmean

Examples

```r
## Not run:
mtcars2 <- mtcars |> mutate(
cyl2 = factor(cyl),
carb2 = factor(carb),
shape = c("V-shaped", "straight")[1 + vs],
gear2 = factor(gear),
transmission = c("automatic", "manual")[1 + am])
design_plot(mtcars2)

## End(Not run)
```

diffmean  Difference in means and proportions

Description

Wrappers around `diff(mean(...))` and `diff(prop(...))` that facilitate better naming of the result.

Usage

```r
diffmean(x, ..., data = parent.frame(), only.2 = TRUE)
diffprop(x, ..., data = parent.frame(), only.2 = TRUE)
```

Arguments

- `x, data, ...` as in `mean()` or `prop()`
- `only.2` a logical indicating whether differences should only be computed between two groups.

Examples

```r
if (require(mosaicData)) {
  diffprop(homeless ~ sex, data=HELPct)
do(3) * diffprop(homeless ~ shuffle(sex), data=HELPct)
diffmean(age ~ substance, data=HELPct, only.2=FALSE)
do(3) * diffmean(age ~ shuffle(substance), data=HELPct, only.2=FALSE)
diffmean(age ~ sex, data=HELPct)
do(3) * diffmean(age ~ shuffle(sex), data=HELPct)
}
```
**do**  

*Do Things Repeatedly*

**Description**

`do()` provides a natural syntax for repetition tuned to assist with replication and resampling methods.

**Usage**

```r
do(object, ...)
```

`## S3 method for class 'numeric'
do(object, ...)`

`## Default S3 method:
do(object, ...)`

`Do(n = 1L, cull = NULL, mode = "default", algorithm = 1, parallel = TRUE)`

`## S3 method for class 'repeater'
print(x, ...)`

`## S4 method for signature 'repeater,ANY'
e1 * e2`

**Arguments**

- **object**
  
an object

- **...**
  
additional arguments

- **n**
  
number of times to repeat

- **cull**
  
function for culling output of objects being repeated. If NULL, a default culling function is used. The default culling function is currently aware of objects of types `lme`, `lm`, `htest`, `table`, `cointoss`, and `matrix`.

- **mode**
  
target mode for value returned

- **algorithm**
  
a number used to select the algorithm used. Currently numbers below 1 use an older algorithm and numbers >=1 use a newer algorithm which is faster in some situations.

- **parallel**
  
a logical indicating whether parallel computation should be attempted using the `parallel` package (if it is installed and loaded).

- **x**
  
an object created by `do`.

- **e1**
  
an object (in cases documented here, the result of running `do`)

- **e2**
  
an object (in cases documented here, an expression to be repeated)
do

Value

do returns an object of class `repeater` which is only useful in the context of the operator `*`. See the examples.

Naming

The names used in the object returned from `do()` are inferred from the objects created in each replication. Roughly, this the strategy employed.

- If the objects have names, those names are inherited, if possible.
- If the objects do not have names, but `do()` is used with a simple function call, the name of that function is used. Example: `do(3) * mean(~height, data = Galton)` produces a data frame with a variable named `mean`.
- In cases where names are not easily inferred and a single result is produced, it is named `result`.

To get different names, one can rename the objects as they are created, or rename the result returned from `do()`. Example of the former: `do(3) * c(mean_height = mean(~height, data = resample(Galton)))`.

Note

do is a thin wrapper around `Do` to avoid collision with `dplyr::do()` from the `dplyr` package.

Author(s)

Daniel Kaplan (<kaplan@macalaster.edu>) and Randall Pruim (<rpruim@calvin.edu>)

See Also

`replicate()`, `set.rseed()`

Examples

```r
do(3) * rnorm(1)
do(3) * "hello"
do(3) * 1:4
do(3) * mean(rnorm(25))
do(3) * lm(shuffle(height) ~ sex + mother, Galton)
do(3) * anova(lm(shuffle(height) ~ sex + mother, Galton))
do(3) * c(sample.mean = mean(rnorm(25)))
# change the names on the fly
do(3) * mean(~height, data = resample(Galton))
do(3) * c(mean_height = mean(~height, data = resample(Galton)))
set.rseed(1234)
do(3) * tally(~sex|treat, data=resample(HELPct))
set.rseed(1234) # re-using seed gives same results again
do(3) * tally(~sex|treat, data=resample(HELPct))
```
**docFile**  
*Return the path to a documentation file in a package*

**Description**

Return the path to a documentation file in a package

**Usage**

```r
docFile(file, package = "mosaic", character.only = FALSE)
```

**Arguments**

- `file`: the name of a file
- `package`: the name of a package
- `character.only`: a logical. If TRUE package names must be specified as character, else names will be converted as a convenience as is `library()` and `library()`.

**Value**

a character vector specifying the path to the file on the user’s system.

---

**dotPlot**  
*Dotplots*

**Description**

A high level function and panel function for producing a variant of a histogram called a dotplot.

**Usage**

```r
dotPlot(x, breaks, ..., panel = panel.dotPlot)
```

```r
panel.dotPlot(
  x,
  breaks,
  equal.widths = TRUE,
  groups = NULL,
  nint = if (is.factor(x)) nlevels(x) else round(1.3 * log2(length(x)) + 4),
  pch,
  col,
  lty = trellis.par.get("dot.line")$lty,
  lwd = trellis.par.get("dot.line")$lwd,
  col.line = trellis.par.get("dot.line")$col,
  alpha = trellis.par.get("dot.symbol")$alpha,
```
**dpqrdist**

Distribution wrapper

**Description**

Utility function wrapping up the d/p/q/r distribution functions

**Usage**

dpqrdist(dist, type = c("d", "p", "q", "r"), ...)

---

**Arguments**

- **x**: a vector of values or a formula
  
  as in `histogram()`

- **...**: additional arguments
- **panel**: a panel function
- **nint**: the number of intervals to use
- **cex**: a ratio by which to increase or decrease the dot size

**Value**

a trellis object

**See Also**

`histogram()`

**Examples**

```r
if (require(mosaicData)) {
  dotPlot(~ age, data = HELPrct)
  dotPlot(~ age, nint=42, data = HELPrct)
  dotPlot(~ height | voice.part, data = singer, nint = 17,  
    endpoints = c(59.5, 76.5), layout = c(4,2), aspect = 1,  
    xlab = "Height (inches)")
}
```
Arguments

- **dist**: a character description of a distribution, for example "norm", "t", or "chisq"
- **type**: one of "x", "p", "q", or "r"
- **...**: additional arguments passed on to underlying distribution function. Note that one of d, p, q, or n must be a named argument in ...

Examples

```r
# 3 random draws from N(1,2)
dpqrdist("norm", "r", n = 3, mean = 1, sd = 2)
# These should all be the same
dpqrdist("norm", "d", x = 0) == dnorm(x = 0)
dpqrdist("norm", "p", q = 0, mean = 1, sd = 2) == pnorm(q = 0, mean = 1, sd = 2)
dpqrdist("norm", "q", p = 0.5, mean = 1, sd = 2) == qnorm(p = 0.5, mean = 1, sd = 2)
```

---

## expandFun

**Expand the left-hand side of a formula**

### Description

Expands the contents of functions used in a formula.

### Usage

```r
expandFun(formula, ...)
```

### Arguments

- **formula**: A mathematical expression (see examples and `plotFun()`)
- **...**: additional parameters

### Value

A list with the new expanded formula and the combined formals

### Examples

```r
f=makeFun(x^2-x)
expandFun(f(z)-z) #Returns z^2-z
```
factorize

Description

A generic function and several instances for creating factors from other sorts of data. The primary use case is for vectors that contain few unique values and might be better considered as factors. When applied to a data frame, this is applied to each variable in the data frame.

Usage

factorize(x, ...)

## Default S3 method:
factorize(x, ...)

## S3 method for class 'numeric'
factorize(x, max.levels = 5L, ...)

## S3 method for class 'character'
factorize(x, max.levels = 5L, ...)

## S3 method for class 'data.frame'
factorize(x, max.levels = 5L, ...)

factorise(x, ...)

Arguments

x       an object
...
additional arguments (currently ignored)
max.levels an integer. Only convert if the number of unique values is no more than max.levels.

Examples

data(KidsFeet, package="mosaicData")
str(KidsFeet)
factorize(KidsFeet$birthyear)
str(factorize(KidsFeet))
# alternative spelling
str(factorise(KidsFeet))
fav_stats

Some favorite statistical summaries

Description

Likely you mean to be using favstats(). Each of these computes the mean, standard deviation, quartiles, sample size and number of missing values for a numeric vector, but favstats() can take a formula describing how these summary statistics should be aggregated across various subsets of the data.

Usage

fav_stats(x, ..., na.rm = TRUE, type = 7)

Arguments

x numeric vector
... additional arguments (currently ignored)
na.rm boolean indicating whether missing data should be ignored
type an integer between 1 and 9 selecting one of the nine quantile algorithms detailed in the documentation for stats::quantile()

Value

A vector of statistical summaries

Examples

fav_stats(1:10)
fav_stats(faithful$eruptions)
data(penguins, package = "palmerpenguins")

# Note: this is favstats() rather than fav_stats()
favstats(bill_length_mm ~ species, data = penguins)

fetchData

Defunct functions now in the fetch package

Description

These functions have been moved to the fetch package.
findZeros

Usage

findZeros(
expr,
..., 
xlim = c(near - within, near + within), 
near = 0,
within = Inf,
earest = 10,
npts = 1000,
iterate = 1,
sortBy = c("byx", "byy", "radial")
)

## S3 method for class 'formula'
solve(
form,
..., 
near = 0,
within = Inf,
nearest = 10,
npts = 1000,
iterate = 1,
sortBy = c("byx", "byy", "radial")
)

Arguments

... arguments

Description

Compute numerically zeros of a function or simultaneous zeros of multiple functions.
Arguments

expr A formula. The right side names the variable with respect to which the zeros should be found. The left side is an expression, e.g. \( \sin(x) \sim x \). All free variables (all but the variable on the right side) named in the expression must be assigned a value via \( \ldots \)

... Formulas corresponding to additional functions to use in simultaneous zero finding and/or specific numerical values for the free variables in the expression.

xlim The range of the dependent variable to search for zeros. \( \text{Inf} \) is a legitimate value, but is interpreted in the numerical sense as the non-\( \text{Inf} \) largest floating point number. This can also be specified replacing \( x \) with the name of the variable. See the examples.

near a value near which zeros are desired

within only look for zeros at least this close to near. near and within provide an alternative to using xlim to specify the search space.

nearest the number of nearest zeros to return. Fewer are returned if fewer are found.

npts How many sub-intervals to divide the xlim into when looking for candidates for zeros. The default is usually good enough. If \( \text{Inf} \) is involved, the intervals are logarithmically spaced up to the largest finite floating point number. There is no guarantee that all the roots will be found.

iterate maximum number of times to iterate the search. Subsequent searches take place with the range of previously found zeros. Choosing a large number here is likely to kill performance without improving results, but a value of 1 (the default) or 2 works well when searching in \( c(-\text{Inf}, \text{Inf}) \) for a modest number of zeros near near.

sortBy specifies how the zeros found will be sorted. Options are 'byx', 'byy', or 'radial'.

form Expression to be solved

Details

Searches numerically using uniroot.

Uses findZerosMult of findZeros to solve the given expression

Value

A dataframe of zero or more numerical values. Plugging these into the expression on the left side of the formula should result in values near zero.

a dataframe with solutions to the expression.

Author(s)

Daniel Kaplan (<kaplan@macalester.edu>)

Cecyilia Bocovich
Examples

```r
findZeros( sin(t) ~ t, xlim=c(-10,10) )
# Can use tlim or t.lim instead of xlim if we prefer
findZeros( sin(t) ~ t, tlim=c(-10,10) )
findZeros( sin(theta) ~ theta, near=0, nearest=20)
findZeros( A*sin(2*pi*t/P) ~ t, xlim=c(0,100), P=50, A=2)
# Interval of a normal at half its maximum height.
findZeros( dnorm(x,mean=0,sd=10) - 0.5*dnorm(0,mean=0,sd=10) ~ x )
# A pathological example
# There are no "nearest" zeros for this function. Each iteration finds new zeros.
f <- function(x) { if (x==0) 0 else sin(1/x) }
findZeros( f(x) ~ x, near=0 )
# Better to look nearer to 0
findZeros( f(x) ~ x, near=0, within=100 )
findZeros( f(x) ~ x, near=0, within=100, iterate=0 )
findZeros( f(x) ~ x, near=0, within=100, iterate=3 )
# Zeros in multiple dimensions (not run: these take a long time)
# findZeros(x^2+y^2+z^2-5~x&y&z, nearest=3000, within = 5)
# findZeros(x+y+z^2~z&y&z, z+y=x&y&z, npts=10)
solve(3*x==3~x)
# plot out sphere (not run)
# sphere = solve(x^2+y^2+z^2==5~x&y&z, within=5, nearest=1000)
# cloud(z~x+y, data=sphere)
```

findZerosMult

Find the zeros of a function of two or more variables

Description

Compute numerically zeros of a function of two or more variables. All free variables (all but the variable on the right side) named in the expression must be assigned a value via `\ldots`

Usage

```r
findZerosMult(..., npts = 10, rad = 5, near = 0, sortBy = "byx")
```

Arguments

... arguments for values NOTE: if the system has more than one equation and the rhs variables do not match up, there will be an error.
npts number of desired zeros to return
rad radius around near in which to look for zeros
near center of search for zeros
sortBy options for sorting zeros for plotting. Options are 'byx', 'byy' and 'radial'. The default value is 'byx'.
Details

sorts points in the domain according to the sign of the function value at respective points. Use continuity and uniroot to find zeros between points of opposite signs. Returns any number of points which may be sorted and plotted according to x, y, or radial values.

Value

A data frame of numerical values which should all result in a value of zero when input into original function

Author(s)

Cecylia Bocovich

Examples

findZerosMult(a*x^2-8~a&x, npts = 50)
findZerosMult(a^2+x^2-8~a&x, npts = 100, sortBy='radial')
## Not run: findZerosMult(a^2+x^2-8~a&x, npts = 1000, sortBy='radial')

fitModel

Fit a nonlinear least squares model

Description

Allows you to specify a formula with parameters, along with starting guesses for the parameters. Refines those guesses to find the least-squares fit.

Usage

fitModel(formula, data = parent.frame(), start = list(), ...)

model(object, ...)

## S3 method for class 'nlsfunction'
model(object, ...)

## S3 method for class 'nlsfunction'
summary(object, ...)

## S3 method for class 'nlsfunction'
coef(object, ...)
Arguments

formula  formula specifying the model
data     dataframe containing the data to be used
start    passed as start to \texttt{nls()}. If and empty list, a simple starting point is used (thus
         avoiding the usual warning message).
...      additional arguments passed to \texttt{nls()}
object   an R object (typically a the result of \texttt{fitModel})

Details

Fits a nonlinear least squares model to data. In contrast to linear models, all the parameters (in-
cluding linear ones) need to be named in the formula. The function returned simply contains the
formula together with pre-assigned arguments setting the parameter value. Variables used in the
fitting (as opposed to parameters) are unassigned arguments to the returned function.

Value

a function

Note

This doesn’t work with categorical explanatory variables. Also, this does not work with synthetic
data that fit the model perfectly. See \texttt{link{nls}} for details.

See Also

\texttt{linearModel()}. \texttt{nls()}

Examples

if (require(mosaicData)) {
  f <- fitModel(temp ~ A+B*exp(-k*time), data=CoolingWater, start=list(A=50,B=50,k=1/20))
  f(time=50)
  coef(f)
  summary(f)
  model(f)
}

---

fitSpline  \hspace{1cm} \textit{Fit splines to data}

Description

These functions create mathematical functions from data, using splines.
Usage

fitSpline(
  formula,
  data = parent.frame(),
  df = NULL,
  knots = NULL,
  degree = 3,
  type = c("natural", "linear", "cubic", "polynomial"),
  ...
)

Arguments

  formula  a formula. Only one quantity is allowed on the left-hand side, the output quantity
  data     a data frame in which formula is evaluated.
  df        degrees of freedom (used to determine how many knots should be used)
  knots     a vector of knots
  degree    parameter for splines when type is "polynomial". 1 is locally linear, 2 is locally quadratic, etc.
  type      type of splines to use; one of "linear", "cubic", "natural" (cubic with linear tails, the default), or "polynomial".
  ...       additional arguments passed to spline basis functions (splines::ns() and splines::bs()).

Value

  a function of the explanatory variable

See Also

  splines::bs() and splines::ns() for the bases used to generate the splines.

Examples

  f <- fitSpline( weight ~ height, data=women, df=5 )
  xyplot( weight ~ height, data=women )
  plotFun(f(height) ~ height, add=TRUE)

  g <- fitSpline( length ~ width, data = KidsFeet, type='natural', df=5 )
  h <- fitSpline( length ~ width, data = KidsFeet, type='linear', df=5 )
  xyplot( length ~ width, data = KidsFeet, col='gray70', pch=16)
  plotFun(g, add=TRUE, col='navy')
  plotFun(h, add=TRUE, col='red')
Description

mosaic tools for clustering

Usage

```r
## S3 method for class 'hclust'
fortify(model, data, which = c("segments", "heatmap", "leaves", "labels", "data"), k = 1, ...)

## S3 method for class 'hclust'
mplot(object, data, colorize = TRUE, k = 1, labels = FALSE, heatmap = 0, enumerate = "white", ...)
```

Arguments

- `model`: a model
- `data`: a data-like object
- `which`: which kind of fortification to compute
- `k`: number of clusters
- `...`: additional arguments passed on to `link{dendro_data}`
- `object`: an object of class "hclust"
- `colorize`: whether to show clusters in different colors
- `labels`: a logical indicating whether labels should be used to identify leaves of the tree.
- `heatmap`: the ratio of size of heatmap to size of dendrogram. Use 0 or FALSE to omit the heatmap.
- `enumerate`: a color used for numbers within heatmap. Use "transparent" to hide.
Examples

```r
KidsFeet |> select(-name, -birthmonth) |> rescale() -> KidsFeet2
M <- dist(KidsFeet2)
Cl <- hclust(M)
fortify(Cl, k=5) |> head(3)
fortify(Cl, which="heatmap", data=KidsFeet2) |> head(3)
fortify(Cl, which="data", data=KidsFeet2) |> head(3)
fortify(Cl, which="labels") |> head(3)
mplot(Cl, data=KidsFeet2, k=4, heatmap=2)
mplot(Cl, data=KidsFeet2, k=4, heatmap=0.5, enumerate="transparent")
mplot(Cl, data=KidsFeet2, k=4, heatmap=2, type="triangle")
mplot(Cl, data=KidsFeet2, k=4, heatmap=0, type="triangle")
```

fortify.summary.lm  
*Extract data from R objects*

Description

Extract data from R objects

Usage

```r
## S3 method for class 'summary.lm'
fortify(model, data = NULL, level = 0.95, ...)

## S3 method for class 'summary.glm'
fortify(model, data = NULL, level = 0.95, ...)

## S3 method for class 'TukeyHSD'
fortify(model, data, order = c("asis", "pval", "difference"), ...)
```

Arguments

- `model`: an R object
- `data`: original data set, if needed
- `level`: confidence level
- `...`: additional arguments
- `order`: one of "pval", "diff", or "asis" determining the order of the pair factor, which determines the order in which the differences are displayed on the plot.
freqpoly

Turn histograms into frequency polygons

Description

Turn histograms into frequency polygons

Usage

freqpoly(x, plot = TRUE, ...) hist2freqpolygon(hist)

## S3 method for class 'freqpolygon'
plot(
x,
    freq = equidist,
    col = graphics::par("fg"),
    lty = NULL,
    lwd = 1,
    main = paste("Frequency polygon of", paste(x$xname, collapse = "\n")),
    sub = NULL,
    xlab = x$xname,
    ylab,
    xlim = range(x$x),
    ylim = NULL,
    axes = TRUE,
    labels = FALSE,
    add = FALSE,
    ann = TRUE,
    ...
)

Arguments

x a vector of values for which a frequency polygon is desired.
plot a logical indicating if a plot should be generated.
... additional arguments passed on to hist().
hist a histogram object produced by link{hist}().
freq A logical indicating whether the vertical scale should be frequency (count).
col A color for the frequency polygon.
lty An integer indicating the line type.
lwd An integer indicating the line width.
main A title for the plot.
sub  A sub-title for the plot.
xlab  Label for the horizontal axis.
ylab  Label for the vertical axis.
xlim  A numeric vector of length 2.
ylim  A numeric vector of length 2.
axes  A logical indicating whether axes should be drawn.
labels A logical indicating whether labels should be printed or a character vector of labels to add.
add  A logical indicating whether the plot should be added to the current plot
ann  A logical indicating whether annotations (titles and axis titles) should be plotted.

Value
An object of class "freqpoly" (invisibly). Additionally, if plot is TRUE, a plot is generated.

Examples
freqpolygon(faithful$eruptions)
bks <- c(0, 1, 1.5, 2, 3, 3.5, 4, 4.5, 5, 7)
hist(faithful$eruptions, breaks = bks)
freqpolygon(faithful$eruptions, col = rgb(0,0,1,.5), lwd = 5, breaks = bks, add = TRUE)

freqpolygon  Frequency Polygons

Description
Frequency polygons are an alternative to histograms that make it simpler to overlay multiple distributions.

Usage
freqpolygon(
x,
...,  
panel = "panel.freqpolygon",
prepanel = "prepanel.default.freqpolygon"
)

prepanel.default.freqpolygon(
x,
darg = list(),
plot.points = FALSE,
ref = FALSE,
freqpolygon

```r
groups = NULL,
subscripts = TRUE,
jitter.amount = 0.01 * diff(current.panel.limits()$ylim),
center = NULL,
nint = NULL,
breaks = NULL,
width = darg$width,
type = "density",
...
)

panel.freqpolygon(
  x,
  darg = list(),
  plot.points = FALSE,
  ref = FALSE,
  groups = NULL,
  weights = NULL,
  jitter.amount = 0.01 * diff(current.panel.limits()$ylim),
  type = "density",
  breaks = NULL,
  nint = NULL,
  center = NULL,
  width = darg$width,
  gcol = trellis.par.get("reference.line")$col,
  glwd = trellis.par.get("reference.line")$lwd,
  h,
  v,
  ...
  identifier = "freqpoly"
)
```

**Arguments**

- `x` a formula or a numeric vector
- `...` additional arguments passed on to `histogram()` and `panel`
- `panel` a panel function
- `prepanel` a prepanel function
- `darg` a list of arguments for the function computing the frequency polygon. This exists primarily for compatibility with `densityplot` and is unlikely to be needed by the end user.
- `plot.points` one of `TRUE`, `FALSE`, "jitter", or "rug" indicating how points are to be displayed
- `ref` a logical indicating whether a horizontal reference line should be added (roughly equivalent to `h=0`)
subscripts as in other lattice prepanel functions
center center of one of the bins
nint an approximate number of bins for the frequency polygon
breaks a vector of breaks for the frequency polygon bins
width width of the bins
type one of 'density', 'percent', or 'count'
gcol color of guidelines
glwd width of guidelines
h, v a vector of values for additional horizontal and vertical lines

Value
a trellis object

Note
This function make use of histogram to determine overall layout. Often this works reasonably well but sometimes it does not. In particular, when groups is used to overlay multiple frequency polygons, there is often too little head room. In the latter cases, it may be necessary to use ylim to determine an appropriate viewing rectangle for the plot.

Examples
freqpolygon(~age | substance, data=HELPrct, v=35)
freqpolygon(~age, data=HELPrct, labels=TRUE, type='count')
freqpolygon(~age | substance, data=HELPrct, groups=sex)
freqpolygon(~age | substance, data=HELPrct, groups=sex, ylim=c(0,0.11))
## comparison of histogram and frequency polygon
histogram(~eruptions, faithful, type='density', width=.5)
ladd( panel.freqpolygon(faithful$eruptions, width=.5 ))
Arguments

- **formula**: a formula. Only one quantity is allowed on the left-hand side, the output quantity.
- **data**: a data frame.
- **method**: a method for splining. See `spline()`.
- **monotonic**: a TRUE/FALSE flag specifying whether the spline should respect monotonicity in the data.
- **span**: parameter to smoother. How smooth it should be.
- **degree**: parameter to smoother. 1 is locally linear, 2 is locally quadratic.
- **...**: additional arguments to `stats::loess()` or `stats::lm()`.

Details

These functions use data to create a mathematical, single-valued function of the inputs. All return a function whose arguments are the variables used on the right-hand side of the formula. If the formula involves a transformation, e.g. $\sqrt{\text{age}}$ or $\log(\text{income})$, only the variable itself, e.g. age or income, is an argument to the function.

`linearModel` takes a linear combination of the vectors specified on the right-hand side. It differs from `project` in that `linearModel` returns a function whereas `project` returns the coefficients.

**NOTE**: An intercept term is not included unless that is explicitly part of the formula with `+1`. This conflicts with the standard usage of formulas as found in `lm`. Another option for creating such functions is to combine `lm()` and `makeFun()`.

`spliner` and `connector` currently work for only one input variable.

See Also

- `project()` method for formulas

Examples

```r
if (require(mosaicData)) {
  data(CPS85)
  f <- smoother(wage ~ age, span=.9, data=CPS85)
  f(40)
  g <- linearModel(log(wage) ~ age + educ + 1, data=CPS85)
  g(age=40, educ=12)
  # an alternative way to define g (Note: + 1 is the default for lm().)
  g2 <- makeFun(lm(log(wage) ~ age + educ, data=CPS85))
  g2(age=40, educ=12)
  x<-1:5; y=c(1, 2, 4, 8, 8.2)
  f1 <- spliner(y ~ x)
  f1(x=8:10)
  f2 <- connector(x-y)
}
```
getVarFormula

Extract data from a data frame using a formula interface

Description

Uses the full model syntax.

Usage

ggetVarFormula(formula, data = parent.frame(), intercept = FALSE)

Arguments

formula a formula. The right-hand side selects variables; the left-hand side, if present, is used to set row names. A . on the right-hand side indicates to use all variables not in the LHS.
data a data frame
intercept a logical indicating whether to include the intercept in the model default: FALSE (no intercept)

Examples

getVarFormula(~ wt + mpg, data = mtcars)

googleMap

Display a point on earth on a Google Map

Description

Creates a URL for Google Maps for a particular latitude and longitude position. This function has been deprecated due to changes in Google’s access policies. Give leaflet_map() a try as an alternative.

Usage

googleMap(
  latitude,
  longitude,
  position = NULL,
  zoom = 12,
  maptype = c("roadmap", "satellite", "terrain", "hybrid"),
  mark = FALSE,
  radius = 0,
  browse = TRUE,
  ...
)

...
Arguments

- **latitude, longitude**
  vectors of latitude and longitude values
- **position**
  a data frame containing latitude and longitude positions
- **zoom**
  zoom level for initial map (1-20)
- **maptype**
  one of 'roadmap', 'satellite', 'terrain', and 'hybrid'
- **mark**
  a logical indicating whether the location should be marked with a pin
- **radius**
  a vector of radii of circles centered at position that are displayed on the map
- **browse**
  a logical indicating whether the URL should be browsed (else only returned as a string)
- **...**
  additional arguments passed to browseURL

Value

a string containing a URL. Optionally, as a side-effect, the URL is visited in a browser

See Also

- `leaflet_map()`, `deg2rad()`, `latlon2xyz()` and `rgeo()`.

Examples

```r
## Not run:
googleMap(40.7566, -73.9863, radius=1) # Times Square
googleMap(position=rgeo(2), radius=1) # 2 random locations
## End(Not run)
```

Description

The primary purpose is for inferring argument settings from names derived from variables occurring in a formula. For example, the default use is to infer limits for variables without having to call them `xlim` and `ylim` when the variables in the formula have other names. Other uses could easily be devised by specifying different variants.

Usage

```r
inferArgs(
  vars,
  dots,
  defaults = alist(xlim = , ylim = , zlim = ),
  variants = c(".lim", "lim")
)
```
is.wholenumber

Arguments

vars a vector of variable names to look for
dots a named list of argument values
defualts named list or alist of default values for limits
variants a vector of optional postixes for limit-specifying variable names

Value

a named list or alist of limits. The names are determined by the names in defaults.
If multiple variants are matched, the first is used.

Examples

inferArgs(c('x','u','t'), list(t=c(1,3), x.lim=c(1,10), u=c(1,3), u.lim=c(2,4)))
inferArgs(c('x','u'), list(u=c(1,3)), defaults=list(xlim=c(0,1), ylim=NULL))

is.wholenumber Check for whole number values

Description

Unlike is.integer(), which checks the type of argument is integer, this function checks whether
the value of the argument is an integer (within a specified tolerance).

Usage

is.wholenumber(x, tol = .Machine$double.eps^0.5)

Arguments

x a vector
tol a numeric tolerance

Details

This function is borrowed from the examples for is.integer()

Value

a logical vector indicating whether x has a whole number value

Examples

is.wholenumber(1)
all(is.wholenumber(rbinom(100,10,.5)))
is.wholenumber((1:10)/2)
Add to Lattice Plots

Description

Simplified lattice plotting by adding additional elements to existing plots.

Usage

ladd(x, data = NULL, ..., plot = trellis.last.object())

Arguments

x          callable graphical element to be added to a panel or panels in a lattice plot
data       a list containing objects that can be referred to in x. Panel functions also have
            access to the data already used in the panel by the underlying lattice plot. See
            latticeExtra::layer() for details.
...       additional arguments passed to latticeExtra::layer().
plot      a lattice plot to add to. Defaults to previous lattice plot.

Details

ladd is a wrapper around latticeExtra::layer() that simplifies certain common plotting addi-
            tions. The same caveats that apply to that function apply here as well. In particular, ladd uses
            non-standard evaluation. For this reason care must be taken if trying to use ladd within other func-
            tions and the use of data may be required to pass information into the environment in which x will
            be evaluated.

Value

a trellis object

Author(s)

Randall Pruim (<rpruim@calvin.edu>)

See Also

latticeExtra::layer()

Examples

p <- xyplot(rnorm(100) ~ rnorm(100))
print(p)
ladd(panel.abline(a=0,b=1))
ladd(panel.abline(h=0,col='blue'))
ladd(grid.text('Hello'))
ladd(grid.text(x=.95,y=.05,'text here',just=c('right','bottom')))


q <- xyplot(rnorm(100) ~ rnorm(100) | factor(rbinom(100, 4, .5)))
q <- update(q, layout=c(3, 2))
ladd(panel.abline(a=0, b=1), plot=q)
ladd(panel.abline(h=0, col="blue"))
ladd(grid.text("(2,1)", gp=gpar(cex=3, alpha=.5)), columns=2, rows=1)
ladd(grid.text("p5", gp=gpar(cex=3, alpha=.5)), packets=5)
q
ladd(grid.text(paste(current.column(), current.row(), sep=''), gp=gpar(cex=3, alpha=.5)) )
histogram(~ eruptions, data=faithful )
# over would probably be better here, but the demonstrates what under=TRUE does.
ladd(panel.densityplot(faithful$eruptions, lwd=4, under=TRUE)

---

### leaflet_map

**Simple Leaflet Maps**

**Description**

Primarily designed to work with `rgeo()` to display randomly sampled points on the globe.

**Usage**

```
leaflet_map(
    latitude = NULL,
    longitude = NULL,
    position = NULL,
    zoom = 12,
    mark = FALSE,
    radius = 0,
    units = c("km", "miles", "meters", "feet"),
    ...
)
```

**Arguments**

- `latitude`, `longitude` vectors of latitude and longitude values. If `latitude` is a data frame, then it is treated as `position`. This facilitates "piping" from `rgeo()`. See examples.
- `position` a data frame containing latitude and longitude positions
- `zoom` zoom level for initial map (1-20)
- `mark` a logical indicating whether the location should be marked with a pin
- `radius` a vector of radii of circles (in miles) centered at position that are displayed on the map
- `units` units for radii of circles (km, miles, meters, or feet).
- ... additional arguments passed to `leaflet::addCircles()`
Value

- a leaflet map

See Also

deg2rad(), latlon2xyz() and rgeo().

Examples

```r
# the leaflet package is required
if (require(leaflet)) {
  # Times Square
  leaflet_map(40.7566, -73.9863, radius = 1, units = "miles")
  # 3 random locations; 5 km circles
  leaflet_map(position = rgeo(3), radius = 5, mark = TRUE, color = "red")
  # using pipes
  rgeo(4, latlim = c(25,50), lonlim = c(-65, -125)) |>  
    leaflet_map(radius = 5, mark = TRUE, color = "purple")
}
```

linear.algebra  

Functions for teaching linear algebra.

Description

These functions provide a formula based interface to the construction of matrices from data and for fitting. You can use them both for numerical vectors and for functions of variables in data frames. These functions are intended to support teaching basic linear algebra with a particular connection to statistics.

Usage

```r
mat(formula, data = parent.frame(), A = formula)
singvals(formula, data = parent.frame(), A = formula)
```

Arguments

- `formula` a formula. In mat and singvals, only the right-hand side is used.
- `data` a data frame from which to pull out numerical values for the variables in the formula
- `A` an alias for `formula` for backward compatibility.

mat returns a model matrix

To demonstrate singularity, use `singvals`.
Value

mat returns a matrix
singvals gives singular values for each column in the model matrix

See Also

project()
linearModel(), which returns a function.

Examples

a <- c(1,0,0); b <- c(1,2,3); c <- c(4,5,6); x <- rnorm(3)
# Formula interface
mat(~a+b)
mat(~a+b+1)
if (require(mosaicData)) {
  mat(~length+sex, data=KidsFeet)
singvals(~length*sex*width, data=KidsFeet)
}

MAD
All pairs mean and sum of absolute differences

Description

The functions compute the sum or mean of all pairwise absolute differences. This differs from stats::mad(), which computes the median absolute difference of each value from the median of all the values. See the ISIwithR package (and the textbook it accompanies) for examples using these functions in the context of simulation-based inference.

Usage

MAD(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
SAD(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))

Arguments

x a numeric vector or a formula.
... additional arguments passed through to MAD_ or SAD_. If x is a formula, ... should include an argument named data if the intent is to interpret the formula in a data frame.
data a data frame in which to evaluate formulas (or bare names). Note that the default is data = parent.frame(). This makes it convenient to use this function interactively by treating the working environment as if it were a data frame. But this may not be appropriate for programming uses. When programming, it is best to use an explicit data argument – ideally supplying a data frame that contains the variables mentioned.
### Description

All pairs mean and sum of absolute differences

### Usage

```r
MAD_(x, ..., na.rm = getOption("na.omit", FALSE))
SAD_(x, ..., na.rm = getOption("na.omit", FALSE))
```

### Arguments

- **x**: a numeric vector or a formula.
- **...**: additional arguments appended to `x`
- **na.rm**: a logical indicating whether NAs should be removed before calculating.

### Value

the mean or sum of the absolute differences between each pair of values in `c(x,...)`.

### See Also

`mad()`, `MAD()`
m agg r e g a t e  

**Aggregate for mosaic**

**Description**

Compute function on subsets of a variable in a data frame.

**Usage**

```r
m_agg r e g a t e ( 
  formula,  
  data = parent.frame(),  
  FUN,  
  groups = NULL,  
  subset,  
  drop = FALSE,  
  ...,  
  .format = c("default", "table", "flat"),  
  .overall = mosaic.par.get("aggregate.overall"),  
  .multiple = FALSE,  
  .name = deparse(substitute(FUN)),  
  .envir = parent.frame()  
)
```

**Arguments**

- **formula** a formula. Left side provides variable to be summarized. Right side and condition describe subsets. If the left side is empty, right side and condition are shifted over as a convenience.
- **data** a data frame. Note that the default is `data = parent.frame()`. This makes it convenient to use this function interactively by treating the working environment as if it were a data frame. But this may not be appropriate for programming uses. When programming, it is best to use an explicit `data` argument – ideally supplying a data frame that contains the variables mentioned in `formula`.
- **FUN** a function to apply to each subset
- **groups** grouping variable that will be folded into the formula (if there is room for it). This offers some additional flexibility in how formulas can be specified.
- **subset** a logical indicating a subset of data to be processed.
- **drop** a logical indicating whether unused levels should be dropped.
- **...** additional arguments passed to `FUN`
- **.format** format used for aggregation. "default" and "flat" are equivalent.
- **.overall** currently unused
- **.multiple** a logical indicating whether `FUN` returns multiple values. Ignored if `.multiple` is not `NULL`.
- **.name** a name used for the resulting object
- **.envir** an environment in which to evaluate expressions
makeColorscheme

Value

a vector

Examples

if (require(mosaicData)) {
maggregate( cesd ~ sex, HELPrct, FUN = mean )
# using groups instead
maggregate( ~ cesd, groups = sex, HELPrct, FUN = sd )
# the next four all do the same thing
maggregate( cesd ~ sex + homeless, HELPrct, FUN = mean )
maggregate( cesd ~ sex | homeless, HELPrct, FUN = sd )
maggregate( ~ cesd | sex , groups= homeless, HELPrct, FUN = sd )
# this is unusual, but also works.
maggregate( cesd ~ NULL , groups = sex, HELPrct, FUN = sd )
}

makeColorscheme Create a color generating function from a vector of colors

Description

Create a color generating function from a vector of colors

Usage

makeColorscheme(col)

Arguments

col a vector of colors

Value

a function that generates a vector of colors interpolated among the colors in col

Examples

cs <- makeColorscheme( c('red','white','blue') )
cs(10)
cs(10, alpha=.5)
Description

`makeMap` takes in two sources of data that refer to geographical regions and merges them together. Depending on the arguments passed, it returns this merged data or a ggplot object constructed with the data.

Usage

```r
makeMap(
  data = NULL,
  map = NULL,
  key = c(key.data, key.map),
  key.data,
  key.map,
  tr.data = identity,
  tr.map = identity,
  plot = c("borders", "frame", "none")
)
```

Arguments

data  A dataframe with regions as cases

map  An object that can be fortified to a dataframe (ex: a dataframe itself, or a SpatialPolygonsDataFrame)

key  The combination of key.data and key.map

key.data  The column name in the data that holds the unique names of each region

key.map  The column name in the map that holds the unique names of each region

tr.data  A function of the transformation to be performed to the key.data column

tr.map  A function of the transformation to be performed to the key.map column

plot  The plot desired for the output. plot = "none" returns the merged data that is the result of merging the data and map together; plot="frame" returns an empty (unplottable) ggplot object; plot = "border" (the default) returns a ggplot object with one geom_polygon layer that shows the borders of the regions.
Description

The mosaic package makes several summary statistic functions (like mean and sd) formula aware.

Usage

mean_(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
mean(x, ...)
median(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
range(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
sd(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
max(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
min(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
sum(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
IQR(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
fivenum(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
iqr(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
prod(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
sum(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
favstats(x, ..., data = NULL, groups = NULL, na.rm = TRUE)
quantile(x, ..., data = NULL, groups = NULL, na.rm = getOption("na.rm", FALSE))
var(x, y = NULL, na.rm = getOption("na.rm", FALSE), ..., data = NULL)
cor(x, y = NULL, ..., data = NULL)
cov(x, y = NULL, ..., data = NULL)

Arguments

x a numeric vector or a formula
Mean...

data  a data frame in which to evaluate formulas (or bare names). Note that the default is data = parent.frame(). This makes it convenient to use this function interactively by treating the working environment as if it were a data frame. But this may not be appropriate for programming uses. When programming, it is best to use an explicit data argument – ideally supplying a data frame that contains the variables mentioned.

groups  a grouping variable, typically a name of a variable in data

na.rm  a logical indicating whether NAs should be removed before computing

y  a numeric vector or a formula

Details

Many of these functions mask core R functions to provide an additional formula interface. Old behavior should be unchanged. But if the first argument is a formula, that formula, together with data are used to generate the numeric vector(s) to be summarized. Formulas of the shape \( x \sim a \) or \( x \mid a \) can be used to produce summaries of \( x \) for each subset defined by \( a \). Two-way aggregation can be achieved using formulas of the form \( x \sim a + b \) or \( x \sim a \mid b \). See the examples.

Note

Earlier versions of these functions supported a "bare name + data frame" interface. This functionality has been removed since it was (a) ambiguous in some cases, (b) unnecessary, and (c) difficult to maintain.

Examples

```r
mean(HELP$age)
mean( ~ age, data = HELP)
mean(~ drugrisk, na.rm = TRUE, data = HELP)
mean(age ~ shuffle(sex), data = HELP)
mean(age ~ shuffle(sex), data = HELP, .format = "table")
# wrap in data.frame() to auto-convert awkward variable names
data.frame(mean(age ~ shuffle(sex), data = HELP, .format = "table"))
mean(age ~ sex + substance, data = HELP)
mean(~ age | sex + substance, data = HELP)
mean(~ sqrt(age), data = HELP)
sum(~ age, data = HELP)
sd(HELP$age)
sd(~ age, data = HELP)
sd(age ~ sex + substance, data = HELP)
var(HELP$age)
var(~ age, data = HELP)
var(age ~ sex + substance, data = HELP)
IQR(width ~ sex, data = Kids)
iqr(width ~ sex, data = Kids)
favstats(width ~ sex, data = Kids)

cor(length ~ width, data = Kids)
cov(length ~ width, data = Kids)
```
mid

midpoints along a sequence

Description

Compute a vector of midpoints between values in a numeric vector.

Usage

mid(x)

Arguments

x  a numeric vector

Value

a vector of length 1 less than x

Examples

mid(1:5)
mid((1:5)^2)

mosaic.options

Setting options for mosaic package functions

Description

A mechanism for setting options in the mosaic package.

Usage

mosaic.options(...)

mosaic.getOption(name)

mosaic.par.set(name, value, ..., theme, warn = TRUE, strict = FALSE)

mosaic.par.get(name = NULL)
restoreLatticeOptions()
mosaicLatticeOptions()

Arguments

... additional arguments that are turned into a list if a list cannot be inferred from theme, name, and value.
name the name of the option being set
value the value to which to set the option
theme a list appropriate for a mosaic theme
warn a logical. UNUSED at present.
strict a logical or numeric.

Details

restoreLatticeOptions returns any lattice options that were changed when the mosaic package was loaded back to their pre-mosaic state.
mosaicLatticeOptions sets a number of defaults for lattice graphics.

Description

These functions provide a menu selection system (via manipulate) so that different aspects of a plot can be selected interactively. The ggplot2 or lattice command for generating the plot currently being displayed can be copied to the console, whence it can be copied to a document for later direct, non-interactive use.

Usage

mPlot(
    data,
    format,
    default = format,
    system = system_choices()[1],
    show = FALSE,
    title = "",
    data_text = rlang::expr_deparse(substitute(data)),
    ...
)

mMap(
    data,
Arguments

data a data frame containing the variables that might be used in the plot. Note that for maps, the data frame must contain coordinates of the polygons comprising the map and a variable for determining which coordinates are part of the same region. See `sp2df()` for one way to create such a data frame. Typically `merge()` will be used to combine the map data with some auxiliary data to be displayed as fill color on the map, although this is not necessary if all one wants is a map.

format a synonym for `default`.

default the default type of plot to create; one of "scatter", "jitter", "boxplot", "violin", "sina", "density", "density (contours)", "density (filled)", "frequency polygon", "xyplot", or "map". Unique prefixes suffice.

system which graphics system to use (initially) for plotting (`ggplot2` or `lattice`). A check box will allow on the fly change of plotting system.

show a logical; if `TRUE`, the code will be displayed each time the plot is changed.

title a title for the plot.

data_text A text string describing the data. It must be possible to recover the data from this string using `eval()`. Typically users will not need to modify this from the default value.

... additional arguments
Details

Only mPlot is required by end users. The other plotting functions are dispatched based on the value of default. Furthermore, mplot() will dispatch mPlot when provided a data frame.

Currently maps are only supported in ggplot2 and not in lattice.
Due to an unresolved issue with RStudio, the first time this function is called, and additional plot is created to correctly initialize the manipulate framework.

Value

Nothing. Just for side effects.

Note

Due to an unresolved issue with RStudio, the first time this function is called, and additional plot is created to correctly initialize the manipulate framework.

Examples

```r
## Not run:
mPlot(HELPrct, format = "scatter")
mPlot(HELPrct, format = "density")

## End(Not run)
```

mplot

Generic plotting

Description

Generic function plotting for R objects. Currently plots exist for data.frames, lms, (including glms).

Usage

```r
mplot(object, ...)
```

```r
## Default S3 method:
mplot(object, ...)
```

```r
## S3 method for class 'lm'
mplot(
    object,
    which = c(1:3, 7),
    system = c("ggplot2", "lattice", "base"),
    ask = FALSE,
    multiplot = "package:gridExtra" %in% search(),
    par.settings = theme.mosaic(),
)```
level = 0.95,
title = paste("model: ", deparse(object$call), "\n"),
rows = TRUE,
id.n = 3L,
id.size = 5,
id.color = "red",
id.nudge = 1,
add.smooth = TRUE,
smooth.color = "red",
smooth.alpha = 0.6,
smooth.size = 0.7,
span = 3/4,
...
)

## S3 method for class 'data.frame'
mplot(
  object,
  format,
  default = format,
  system = c("ggformula", "ggplot2", "lattice"),
  show = FALSE,
  data_text = rlang::expr_deparse(substitute(object)),
  title = "",
  ...)

## S3 method for class 'summary.lm'
mplot(
  object,
  system = c("ggplot2", "lattice"),
  level = 0.95,
  par.settings = trellis.par.get(),
  rows = TRUE,
  ...
)

## S3 method for class 'TukeyHSD'
mplot(
  object,
  system = c("ggplot2", "lattice"),
  ylab = "",
xlab = "difference in means",
title = paste0(attr(object, "conf.level") * 100, "% family-wise confidence level"),
par.settings = trellis.par.get(),
order = c("asis", "pval", "difference"),
...
**Arguments**

- **object**
  - an R object from which a plot will be constructed.
  - additional arguments. If `object` is an `lm`, subsets of these arguments are passed to `gridExtra::grid.arrange` and to the `lattice` plotting routines; in particular, `nrow` and `ncol` can be used to control the number of rows and columns used.

- **which**
  - a numeric vector used to select from 7 potential plots

- **system**
  - which graphics system to use (initially) for plotting (`ggplot2` or `lattice`). A check box will allow on the fly change of plotting system.

- **ask**
  - if TRUE, each plot will be displayed separately after the user responds to a prompt.

- **multiplot**
  - if TRUE and `ask == FALSE`, all plots will be displayed together.

- **par.settings**
  - `lattice` theme settings

- **level**
  - a confidence level

- **title**
  - title for plot

- **rows**
  - rows to show. This may be a numeric vector, TRUE (for all rows), or a character vector of row names.

- **id.n**
  - Number of id labels to display.

- **id.size**
  - Size of id labels.

- **id.color**
  - Color of id labels.

- **id.nudge**
  - a numeric used to increase (>1) or decrease (<1) the amount that observation labels are nudged. Use a negative value to nudge down instead of up.

- **add.smooth**
  - A logical indicating whether a LOESS smooth should be added (where this makes sense to do). Currently ignored for lattice plots.

- **smooth.color, smooth.size, smooth.alpha**
  - Color, size, and alpha used for LOESS curve. Currently ignored for lattice plots.

- **span**
  - A positive number indicating the amount of smoothing. A larger number indicates more smoothing. See `stats::loess()` for details. Currently ignored for lattice plots.

- **format, default**
  - default type of plot to create; one of "scatter", "jitter", "boxplot", "violin", "histogram", "density", "frequency polygon", or "map". Unique prefixes suffice.

- **show**
  - a logical, if TRUE, the code will be displayed each time the plot is changed.

- **data_text**
  - text representation of the data set. In typical use cases, the default value should suffice.

- **ylab**
  - label for y-axis

- **xlab**
  - label for x-axis

- **order**
  - one of "pval", "diff", or "asis" determining the order of the pair factor, which determines the order in which the differences are displayed on the plot.

- **data**
  - a data frame containing the variables that might be used in the plot.
Details

The method for models (lm and glm) is still a work in progress, but should be usable for relatively simple models. When the results for a logistic regression model created with `glm()` are satisfactory will depend on the format and structure of the data used to fit the model.

Due to a bug in RStudio 1.3, the method for data frames may not display the controls consistently. We have found that executing this code usually fixes the problem:

```r
library(manipulate)
manipulate(plot(A), A = slider(1, 10))
```

Value

Nothing. Just for side effects.

Examples

```
lm( width ~ length * sex, data = KidsFeet) |> mplot(which = 1:3, id.n = 5)
lm( width ~ length * sex, data = KidsFeet) |> mplot(smooth.color = "blue", smooth.size = 1.2, smooth.alpha = 0.3, id.size = 3)
lm(width ~ length * sex, data = KidsFeet) |> mplot(rows = 2:3, which = 7)
## Not run:
mplot( HELPrct )
mplot( HELPrct, "histogram" )
## End(Not run)
lm(width ~ length * sex, data = KidsFeet) |> summary() |> mplot()
lm(width ~ length * sex, data = KidsFeet) |> summary() |> mplot(rows = c("sex", "length"))
lm(width ~ length * sex, data = KidsFeet) |> summary() |> mplot(rows = TRUE)
lm(age ~ substance, data = HELPrct) |> TukeyHSD() |> mplot()
fm(age ~ substance, data = HELPrct) |> TukeyHSD() |> mplot(system = "lattice")
```
mUSMap

Make a US map with ggplot2

Description

mUSMap takes in one dataframe that includes information about different US states. It merges this dataframe with a dataframe that includes geographical coordinate information. Depending on the arguments passed, it returns this data or a ggplot object constructed with the data.

Usage

mUSMap(
  data = NULL,
  key,
  fill = NULL,
  plot = c("borders", "frame", "none"),
  style = c("compact", "real")
)

Arguments

data A dataframe with US states as cases
key The column name in the data that holds the unique names of each state
fill A variable in the data used to specify the fill color of states in the map (note: if fill is not null, then plot cannot be set to "none")
plot The plot desired for the output. plot = "none" returns the merged data that is the result of merging the data and the dataframe with the geographical coordinate information; plot = "frame" returns an empty (unplottable) ggplot object; plot = "border" (the default) returns a ggplot object with one geom_polygon layer that shows the borders of the states
style The style in which to display the map. compact gives a polyconic projection with Alaska and Hawaii on the lower left corner; real gives the real size and position of all states without any projection.

Examples

USArrests2 <- USArrests |> tibble::rownames_to_column("state")
mUSMap(USArrests2, key="state", fill = "UrbanPop")
Mustangs

Mustangs

<table>
<thead>
<tr>
<th>Mustang Prices</th>
</tr>
</thead>
</table>

**Description**

Mustang Prices

**Usage**

data(Mustangs)

**Format**

A data frame with 25 observations on the following 3 variables.

- **Age**  age of vehicle in years
- **Miles** 1000s of miles driven
- **Price** selling price in 1000s USD

**Details**

`#' @docType data
A student collected data on the selling prices for a sample of used Mustang cars being offered for sale at an internet website.

**Source**

These data were used in a "resampling bake-off" hosted by Robin Lock.

mWorldMap

Make a world map with ggplot2

**Description**

mWorldMap takes in one dataframe that includes information about different countries. It merges this dataframe with a dataframe that includes geographical coordinate information. Depending on the arguments passed, it returns this data or a ggplot object constructed with the data.

**Usage**

mWorldMap(
  data = NULL,
  key = NA,
  fill = NULL,
  plot = c("borders", "frame", "none")
)
Arguments

data A dataframe with countries as cases
key The column name in the data that holds the unique names of each country
fill A variable in the data used to specify the fill color of countries in the map (note: if fill is not null, then plot cannot be set to "none")
plot The plot desired for the output. plot = "none" returns the merged data that is the result of merging the data and the dataframe with the geographical coordinate information; plot = "frame" returns an empty (unplottable) ggplot object; plot = "border" (the default) returns a ggplot object with one geom_polygon layer that shows the borders of the countries

Examples

```r
## Not run:
gdpData <- CIAdata("GDP") # load some world data
mWorldMap(gdpData, key="country", fill="GDP")
gdpData <- gdpData | mutate(GDP5 = ntiles(-GDP, 5, format="rank"))
mWorldMap(gdpData, key="country", fill="GDP5")
mWorldMap(gdpData, key="country", plot="frame") + geom_point()
mergedData <- mWorldMap(gdpData, key="country", plot="none")
ggplot(mergedData, aes(x=long, y=lat, group=group, order=order)) + geom_polygon(aes(fill=GDP5), color="gray70", size=.5) + guides(fill=FALSE)
## End(Not run)
```

ntiles Create vector based on roughly equally sized groups

Description

Create vector based on roughly equally sized groups

Usage

```r
ntiles(
x,
  n = 3,
  format = c("rank", "interval", "mean", "median", "center", "left", "right"),
  digits = 3
)
```
Arguments

- x: a numeric vector
- n: (approximate) number of quantiles
- format: a specification of desired output format.
- digits: desired number of digits for labeling of factors.

Value

a vector. The type of vector will depend on format.

Examples

```r
if (require(mosaicData)) {
  tally(~ ntiles(age, 4), data=HELPrct)
  tally(~ ntiles(age, 4, format="center"), data=HELPrct)
  tally(~ ntiles(age, 4, format="interval"), data=HELPrct)
  tally(~ ntiles(age, 4, format="left"), data=HELPrct)
  tally(~ ntiles(age, 4, format="right"), data=HELPrct)
  tally(~ ntiles(age, 4, format="mean"), data=HELPrct)
  tally(~ ntiles(age, 4, format="median"), data=HELPrct)
  bwplot(i2 ~ ntiles(age, n=5, format="interval"), data=HELPrct)
}
```

orrr  Odds Ratio and Relative Risk for 2 x 2 Contingency Tables

Description

This function calculates the odds ratio and relative risk for a 2 x 2 contingency table and a confidence interval (default `conf.level` is 95 percent) for the each estimate. `x` should be a matrix, data frame or table. "Successes" should be located in column 1 of `x`, and the treatment of interest should be located in row 2. The odds ratio is calculated as `(Odds row 2) / (Odds row 1)`. The confidence interval is calculated from the log(OR) and backtransformed.

Usage

```r
orrr(
  x,
  conf.level = 0.95,
  verbose = !quiet,
  quiet = TRUE,
  digits = 3,
  relrisk = FALSE
)
```

```r
oddsRatio(x, conf.level = 0.95, verbose = !quiet, quiet = TRUE, digits = 3)
```
relrisk(x, conf.level = 0.95, verbose = !quiet, quiet = TRUE, digits = 3)

## S3 method for class 'oddsRatio'
print(x, digits = 4, ...)

## S3 method for class 'relrisk'
print(x, digits = 4, ...)

## S3 method for class 'oddsRatio'
summary(object, digits = 4, ...)

## S3 method for class 'relrisk'
summary(object, digits = 4, ...)

Arguments

x
a 2 x 2 matrix, data frame, or table of counts

conf.level
the confidence interval level

verbose
a logical indicating whether verbose output should be displayed

quiet
a logical indicating whether verbose output should be suppressed

digits
number of digits to display

relrisk
a logical indicating whether the relative risk should be returned instead of the
odds ratio

...additional arguments

object
an R object to print or summarise. Here an object of class "oddsRatio" or "relrisk".

Value

an odds ratio or relative risk. If verbose is true, more details and the confidence intervals are
displayed.

Author(s)

Kevin Middleton (<kmm@csusb.edu>); modified by R Pruim.

See Also

chisq.test(), fisher.test()

Examples

M1 <- matrix(c(14, 38, 51, 11), nrow = 2)
M1
oddsRatio(M1)

M2 <- matrix(c(18515, 18496, 1427, 1438), nrow = 2)
rownames(M2) <- c("Placebo", "Aspirin")
colnames(M2) <- c("No", "Yes")
M2
oddsRatio(M2)
oddsRatio(M2, verbose = TRUE)
relrisk(M2, verbose = TRUE)
if (require(mosaicData)) {
  relrisk(tally(~ homeless + sex, data = HELPrct) )
do(3) * relrisk( tally(~ homeless + shuffle(sex), data = HELPrct) )
}

panel.levelcontourplot

Lattice plot that draws a filled contour plot

Description

Used within plotFun

Usage

panel.levelcontourplot(
  x,
  y,
  z,
  subscripts = 1,
  at,
  shrink,
  labels = TRUE,  
  label.style = c("mixed", "flat", "align"),
  contour = FALSE,
  region = TRUE,
  col = add.line$col,
  lty = add.line$lty,
  lwd = add.line$lwd,
  border = "transparent",
  ...
  col.regions = regions$col,
  filled = TRUE,
  alpha.regions = regions$alpha
)

Arguments

x x on a grid
y y on a grid
z zvalues for the x and y
subscripts which points to plot
at
cuts for the contours
shrink
what does this do?
labels
draw the contour labels
label.style
where to put the labels
contour
logical draw the contours
region
logical color the regions
col
color for contours
lty
type for contours
lwd
width for contour
border
type of border
...
dots additional arguments
col.regions
a vector of colors or a function (topo.colors by default) for generating such
filled
whether to fill the contours with color
alpha.regions
transparency of regions

panel.lmband <- show confidence and prediction bands on plots

Description

show confidence and prediction bands on plots

Usage

panel.lmband(
  x,
  y,
  interval = "confidence",
  level = 0.95,
  model = lm(y ~ x),
  band.col = c(conf = slcol[3], pred = slcol[2]),
  band.lty = c(conf = slty[3], pred = slty[2]),
  band.show = TRUE,
  fit.show = TRUE,
  band.alpha = 0.6,
  band.lwd = 1,
  npts = 100,
  ...
)
)
Panel function for plotting functions

Description

Panel function for plotting functions

Usage

```R
panel.plotFun(
  object,
  ..., type = "l",
  npts = NULL,
  zlab = NULL,
  filled = TRUE,
  levels = NULL,
  nlevels = 10,
  surface = FALSE,
  col.regions = topo.colors,
  lwd = trellis.par.get("superpose.line")$lwd,
  lty = trellis.par.get("superpose.line")$lty,
  alpha = NULL,
  discontinuity = NULL,
  discontinuities = NULL
)
```
Arguments

- object: an object (e.g., a formula) describing a function
- ...: additional arguments, typically processed by lattice panel functions such as `lattice::panel.xyplot()` or `lattice::panel.levelplot()`. Frequently used arguments include:
  - lwd: line width
  - lty: line type
  - col: a color
- type: type of plot ("l" by default)
- npts: an integer giving the number of points (in each dimension) to sample the function
- zlab: label for z axis (when in surface-plot mode)
- filled: fill with color between the contours (TRUE by default)
- levels: levels at which to draw contours
- nlevels: number of contours to draw (if levels not specified)
- surface: a logical indicating whether to draw a surface plot rather than a contour plot
- col.regions: a vector of colors or a function (topo.colors by default) for generating such colors
- lwd: width of the line
- lty: line type
- alpha: number from 0 (transparent) to 1 (opaque) for the fill colors
- discontinuity: a positive number determining how sensitive the plot is to potential discontinuity. Larger values result in less sensitivity. The default is 1. Use discontinuity = Inf to disable discontinuity detection. Discontinuity detection uses a crude numerical heuristic and may not give the desired results in all cases.
- discontinuities: a vector of input values at which a function is discontinuous or NULL to use a heuristic to auto-detect.

See Also

- plotFun

Examples

```r
x <- runif(30,0,2*pi)
d <- data.frame( x = x, y = sin(x) + rnorm(30,sd=.2) )
xyplot( y ~ x, data=d )
ladd(panel.plotFun( sin(x) ~ x, col='red' ) )
xyplot( y ~ x | rbinom(30,1,.5), data=d )
ladd(panel.plotFun( sin(x) ~ x, col='red', lty=2 ) )  # plots sin(x) in each panel
```
panel.plotFun1

Panel function for plotting functions

Description
Panel function for plotting functions

Usage
panel.plotFun1(
  ..f..,
  ..., 
  x,
  y,
  type = "l",
  lwd = trellis.par.get("superpose.line")$lwd,
  lty = trellis.par.get("superpose.line")$lty,
  col = trellis.par.get("superpose.line")$col,
  npts = NULL,
  zlab = NULL,
  filled = TRUE,
  levels = NULL,
  nlevels = 10,
  surface = FALSE,
  alpha = NULL,
  discontinuity = NULL,
  discontinuities = NULL
)

Arguments
..f.. an object (e.g., a formula) describing a function
... additional arguments, typically processed by lattice panel functions such as
lattice::panel.xyplot() or lattice::panel.levelplot(). Frequently used arguments include
lwd line width
lty line type
col a color
x, y ignored, but there for compatibility with other lattice panel functions
type type of plot ("l" by default)
lwd width of the line
lty line type
col a vector of colors
npts an integer giving the number of points (in each dimension) to sample the function
Illustrated probability calculations from distributions

Function pdist

Description

Illustrated probability calculations from distributions

Usage

```r
pdist(
  dist = "norm",
  q,
  plot = TRUE,
  verbose = FALSE,
  invisible = FALSE,
  digits = 3L,
  xlim,
  ylim,
  resolution = 500L,
)```

Examples

```r
x <- runif(30,0,2*pi)
d <- data.frame( x = x, y = sin(x) + rnorm(30,sd=.2) )
xyplot( y ~ x, data=d )
ladd(panel.plotFun1( sin, col="red" ))
```

---

**pdist**

Illustrated probability calculations from distributions

**Description**

Illustrated probability calculations from distributions

**Usage**

```r
pdist(
  dist = "norm",
  q,
  plot = TRUE,
  verbose = FALSE,
  invisible = FALSE,
  digits = 3L,
  xlim,
  ylim,
  resolution = 500L,
)```

**Examples**

```r
x <- runif(30,0,2*pi)
d <- data.frame( x = x, y = sin(x) + rnorm(30,sd=.2) )
xyplot( y ~ x, data=d )
ladd(panel.plotFun1( sin, col="red" ))
```
return = c("values", "plot"),
    ...,
    refinements = list()
)

xpgamma(
    q,
    shape,
    rate = 1,
    scale = 1/rate,
    lower.tail = TRUE,
    log.p = FALSE,
    ...)

xpt(q, df, ncp, lower.tail = TRUE, log.p = FALSE, ...)

xpchisq(q, df, ncp = 0, lower.tail = TRUE, log.p = FALSE, ...)

xpf(q, df1, df2, lower.tail = TRUE, log.p = FALSE, ...)

xpbinom(q, size, prob, lower.tail = TRUE, log.p = FALSE, ...)

xpgeom(q, prob, lower.tail = TRUE, log.p = FALSE, ...)

xpgeometric(q, prob, lower.tail = TRUE, log.p = FALSE, ...)

xpgeom(q, size, prob, mu, lower.tail = TRUE, log.p = FALSE, ...)

xpbeta(q, shape1, shape2, ncp = 0, lower.tail = TRUE, log.p = FALSE, ...)

Arguments

dist a character description of a distribution, for example "norm", "t", or "chisq"
q a vector of quantiles
plot a logical indicating whether a plot should be created
verbose a logical
invisible a logical
digits the number of digits desired
xlim x limits
ylim y limits
resolution Number of points used for detecting discreteness and generating plots. The
default value of 5000 should work well except for discrete distributions that
have many distinct values, especially if these values are not evenly spaced.
return If "plot", return a plot. If "values", return a vector of numerical values.
... Additional arguments, typically for fine tuning the plot.
refinements A list of refinements to the plot. See `ggformula::gf_refine()`.
shape, scale shape and scale parameters. Must be positive, scale strictly.
rate an alternative way to specify the scale.
lower.tail logical; if TRUE (default), probabilities are \( P[X \leq x] \), otherwise, \( P[X > x] \).
log.p A logical indicating whether probabilities should be returned on the log scale.
df degrees of freedom (> 0, maybe non-integer). \( df = \text{Inf} \) is allowed.
ncp non-centrality parameter \( \delta \); currently except for \( \text{rt()} \), only for \( \text{abs(ncp)} \leq \text{37.62} \). If omitted, use the central t distribution.
df1, df2 degrees of freedom. \( \text{Inf} \) is allowed.
size number of trials (zero or more).
prob probability of success on each trial.
lambda vector of (non-negative) means.
mu alternative parametrization via mean: see ‘Details’.
shape1, shape2 non-negative parameters of the Beta distribution.

Details
The most general function is \( \text{pdist} \) which can work with any distribution for which a p-function exists. As a convenience, wrappers are provided for several common distributions.

Value
A vector of probabilities; a plot is printed as a side effect.

See Also
\( \text{qdist()} \), \( \text{xpnorm()} \), \( \text{xqnorm()} \).

Examples
\( \text{pdist("norm", -2:2)} \)
\( \text{pdist("norm", seq(80,120, by = 10), mean = 100, sd = 10)} \)
\( \text{pdist("chisq", 2:4, df = 3)} \)
\( \text{pdist("f", 1, df1 = 2, df2 = 10)} \)
\( \text{pdist("gamma", 2, shape = 3, rate = 4)} \)
plotCumfreq

Cumulative frequency plots

Description

A high-level function for producing a cumulative frequency plot using lattice graphics.

Usage

plotCumfreq(x, data, ...)  
## S3 method for class 'formula'
plotCumfreq(x, data = NULL, subscripts, ...)

## Default S3 method:
plotCumfreq(x, ...)

prepanel.cumfreq(x, ...)

panel.cumfreq(x, type = c("smooth", "step"), groups = NULL, ...)

Arguments

x a formula or numeric vector

data a data frame in which x is evaluated if x is a formula.

... other lattice arguments

subscripts as in lattice plots

type smooth or step-function?

groups grouping variable

Value

A plot of the empirical cumulative distribution function for sample values specified in x.

See Also

histogram(), densityplot()

Examples

plotCumfreq(~eruptions, faithful, xlab = 'duration of eruptions')
plotDist  

Plots of Discrete and Continuous Distributions

Description

Provides a simple way to generate plots of pdfs, probability mass functions, cdfs, probability histograms, and normal-quantile plots for distributions known to R.

Usage

plotDist(
  dist,
  ..., 
  xlim = NULL, 
  ylim = NULL, 
  add, 
  under = FALSE, 
  packets = NULL, 
  rows = NULL, 
  columns = NULL, 
  kind = c("density", "cdf", "qq", "histogram"), 
  xlab = ", "
  ylab = ", "
  breaks = NULL, 
  type, 
  resolution = 5000L, 
  params = NULL
)

Arguments

dist  
A string identifying the distribution. This should work with any distribution that has associated functions beginning with 'd', 'p', and 'q' (e.g, dnorm(), pnorm(), and qnorm()). dist should match the name of the distribution with the initial 'd', 'p', or 'q' removed.

...  
other arguments passed along to lattice graphing routines

xlim  
a numeric vector of length 2 or NULL, in which case the central 99.8 of the distribution is used.

ylim  
a numeric vector of length 2 or NULL, in which case a heuristic is used to avoid chasing asymptotes in distributions like the F distributions with 1 numerator degree of freedom.

add  
a logical indicating whether the plot should be added to the previous lattice plot. If missing, it will be set to match under.

under  
a logical indicating whether adding should be done in a layer under or over the existing layers when add = TRUE.
packets, rows, columns

- specification of which panels will be added to when add is TRUE. See `latticeExtra::layer()`.

- kind
  - one of "density", "cdf", "qq", or "histogram" (or prefix of any of these)

- xlab, ylab
  - as per other lattice functions

- breaks
  - a vector of break points for bins of histograms, as in `histogram()`

- type
  - passed along to various lattice graphing functions

- resolution
  - number of points to sample when generating the plots

- params
  - a list containing parameters for the distribution. If NULL (the default), this list is created from elements of \dots that are either unnamed or have names among the formals of the appropriate distribution function. See the examples.

Details

`plotDist()` determines whether the distribution is continuous or discrete by seeing if all the sampled quantiles are unique. A discrete random variable with many possible values could fool this algorithm and be considered continuous.

The plots are done referencing a data frame with variables x and y giving points on the graph of the pdf, pmf, or cdf for the distribution. This can be useful in conjunction with the groups argument. See the examples.

See Also

- `ggformula::gf_dist()`

Examples

```r
plotDist('norm')
plotDist('norm', type='h')
plotDist('norm', kind='cdf')
plotDist('exp', kind='histogram')
plotDist('binom', params=list(25, .25)) # explicit params
plotDist('binom', 25, .25) # params inferred
plotDist('norm', mean=100, sd=10, kind='cdf') # params inferred
plotDist('binom', 25, .25, xlim=c(-1,26) ) # params inferred
plotDist('binom', params=list(25, .25), kind='cdf')
plotDist('beta', params=list(3, 10), kind='density')
plotDist('beta', params=list(3, 10), kind='cdf')
plotDist( "binom", params=list(35,.25),
    groups= y < dbinom(qbinom(0.05, 35, .25), 35,.25) )
plotDist( "binom", params=list(35,.25),
    groups= y < dbinom(qbinom(0.05, 35, .25), 35,.25),
    kind='hist')
plotDist("norm", mean=10, sd=2, col="blue", type="h")
plotDist("norm", mean=12, sd=2, col="red", type="h", under=TRUE)
plotDist("binom", size=100, prob=.30) +
    plotDist("norm", mean=30, sd=sqrt(100 * .3 * .7))
plotDist("chisq", df=4, groups = x > 6, type="h")
plotDist("f", df1=1, df2 = 99)
if (require(mosaicData)) {
```
```r
histogram(~age|sex, data=HELPrct)

m <- mean(~age|sex, data=HELPrct)
s <- sd(~age|sex, data=HELPrct)
plotDist("norm", mean=m[1], sd=s[1], col="red", add=TRUE, packets=1)
plotDist("norm", mean=m[2], sd=s[2], col="blue", under=TRUE, packets=2)
```

---

**plotFun**

*Plotting mathematical expressions*

**Description**

Plots mathematical expressions in one and two variables.

**Usage**

```r
plotFun(
  object, ...
  plot = trellis.last.object(),
  add = NULL,
  under = FALSE,
  xlim = NULL,
  ylim = NULL,
  npts = NULL,
  ylab = NULL,
  xlab = NULL,
  zlab = NULL,
  filled = TRUE,
  levels = NULL,
  nlevels = 10,
  labels = TRUE,
  surface = FALSE,
  groups = NULL,
  col = trellis.par.get("superpose.line")$col,
  col.regions = topo.colors,
  type = "l",
  lwd = trellis.par.get("superpose.line")$lwd,
  lty = trellis.par.get("superpose.line")$lty,
  alpha = NULL,
  discontinuities = NULL,
  discontinuity = 1,
  interactive = rstudio_is_available()
)
```
**Arguments**

**object**

a mathematical expression or a function "of one variable" which will converted
to something intuitively equivalent to object(x) \sim x. (See examples)

... additional parameters, typically processed by lattice functions such as `lattice::xyplot()`,
`lattice::levelplot()` or their panel functions. Frequently used parameters include

- **main** main title for plot
- **sub** subtitle for plot
- **lwd** line width
- **lty** line type
- **col** a color or a (small) integer indicating which color in the current color
  scheme is desired.

Additionally, these arguments can be used to specify parameters for the function
being plotted and to specify the plotting window with natural names. See the
examples for such usage.

**plot**

a trellis object; by default, the most recently created trellis plot. When `add` is
TRUE, the new function will be plotted into a layer added to this object.

**add**

if TRUE, then add a layer to an existing plot rather than creating a new plot. If
NULL, this will be determined by the value of `under`.

**under**

if TRUE, then new layer is added beneath existing layers

**xlim**

limits for x axis (or use variable names, see examples)

**ylim**

limits for y axis (or use variable names, see examples)

**npts**

number of points for plotting.

**ylab**

label for y axis

**xlab**

label for x axis

**zlab**

label for z axis (when in surface-plot mode)

**filled**

fill with color between the contours (TRUE by default)

**levels**

levels at which to draw contours

**nlevels**

number of contours to draw (if `levels` not specified)

**labels**

if FALSE, don’t label contours

**surface**

draw a surface plot rather than a contour plot

**groups**

grouping argument ala lattice graphics

**col**

vector of colors for line graphs and contours

**col.regions**

a vector of colors or a function (`topo.colors` by default) for generating such

**type**

type of plot ("l" by default)

**lwd**

vector of line widths for line graphs

**lty**

vector of line types for line graphs

**alpha**

number from 0 (transparent) to 1 (opaque) for the fill colors

**discontinuities**

a vector of input values at which a function is discontinuous or NULL to use a
heuristic to auto-detect.
discontinuity  a positive number determining how sensitive the plot is to potential discontinuity. Larger values result in less sensitivity. The default is 1. Use discontinuity = Inf to disable discontinuity detection. Discontinuity detection uses a crude numerical heuristic and may not give the desired results in all cases.

interactive  a logical indicating whether the surface plot should be interactive.

Details

makes plots of mathematical expressions using the formula syntax. Will draw both line plots and contour/surface plots (for functions of two variables). In RStudio, the surface plot comes with sliders to set orientation. If the colors in filled surface plots are too blocky, increase npts beyond the default of 50, though npts=300 is as much as you’re likely to ever need. See examples for overplotting a constraint function on an objective function.

Value

a trellis object

Examples

plotFun( a*sin(x^2)~x, xlim=range(-5,5), a=2 )  # setting parameter value
plotFun( u^2 ~ u, ulim=c(-4,4) )  # limits in terms of u
# Note roles of ylim and y.lim in this example
plotFun( y^2 ~ y, ylim=c(-2,20), y.lim=c(-4,4) )
# Combining plot elements to show the solution to an inequality
plotFun( x^2 -3 ~ x, xlim=c(-4,4), grid=TRUE )
ladd( panel.abline(h=0,v=0,col='gray50') )
plotFun( (x^2 -3) * (x^2 > 3) ~ x, type='h', alpha=.1, lwd=4, col='lightblue', add=TRUE )
plotFun( sin(x) ~ x,
groups=cut(x, findZeros(sin(x) ~ x, within=10)$x),
col=c('blue','green'), lty=2, lwd=3, xlim=c(-10,10) )
plotFun( sin(x) ~ x,
groups=cut(x, findZeros(sin(x) ~ x, within=10)$x),
col=c(1,2), lty=2, lwd=3, xlim=c(-10,10) )
## plotFun( sin(2*pi*x/P)*exp(-k*t)~x+t, k=2, P=.3)
f <- rfun( ~ u & v )
plotFun( f(u=u,v=v) ~ u & v, u.lim=range(-3,3), v.lim=range(-3,3) )
plotFun( u^2 + v < 3 ~ u & v, add=TRUE, npts=200 )
if (require(mosaicData)) {
  # display a linear model using a formula interface
  model <- lm(wage ~ poly(exper,degree=2), data=CPS85)
  fit <- makeFun(model)
  xyplot(wage ~ exper, data=CPS85)
  plotFun(fit(exper) ~ exper, add=TRUE, lwd=3, col="red")
  # Can also just give fit since it is a "function of one variable"
  plotFun(fit, add=TRUE, lwd=2, col="white")
}
# Attempts to find sensible axis limits by default
plotFun( sin(k*x)~x, k=0.01 )
# Plotting a linear model with multiple predictors.
mod <- lm(length ~ width * sex, data=KidsFeet)
fitted.length <- makeFun(mod)
xyplot(length ~ width, groups=sex, data=KidsFeet, auto.key=TRUE)
plotFun(fitted.length(width, sex="B") ~ width, add=TRUE, col=1)
plotFun(fitted.length(width, sex="G") ~ width, add=TRUE, col=2)

---

plotModel  
*Plot a regression model*

**Description**

Visualize a regression model amid the data that generated it.

**Usage**

```r
plotModel(mod, ...)  
```

## Default S3 method:
```r
plotModel(mod, ...)  
```

## S3 method for class `parsedModel`
```r
plotModel(
  mod,
  formula = NULL,
  ...,  
  auto.key = NULL,
  drop = TRUE,
  max.levels = 9L,
  system = c("ggplot2", "lattice")
)
```

**Arguments**

- `mod` A model of type `lm()` or `glm()`
- `...` arguments passed to `xyplot()` or `rgl::plot3d`.
- `formula` a formula indicating how the variables are to be displayed. In the style of `lattice` and `ggformula`.
- `auto.key` If TRUE, automatically generate a key.
- `drop` If TRUE, unused factor levels are dropped from `interaction()`.
- `max.levels` currently unused
- `system` which of `ggplot2` or `lattice` to use for plotting
Details

The goal of this function is to assist with visualization of statistical models. Namely, to plot the model on top of the data from which the model was fit.

The primary plot type is a scatter plot. The x-axis can be assigned to one of the predictors in the model. Additional predictors are thought of as co-variates. The data and fitted curves are partitioned by these covariates. When the number of components to this partition is large, a random subset of the fitted curves is displayed to avoid visual clutter.

If the model was fit on one quantitative variable (e.g. SLR), then a scatter plot is drawn, and the model is realized as parallel or non-parallel lines, depending on whether interaction terms are present.

Eventually we hope to support 3-d visualizations of models with 2 quantitative predictors using the rgl package.

Currently, only linear regression models and generalized linear regression models are supported.

Value

A lattice or ggplot2 graphics object.

Caution

This is still underdevelopment. The API is subject to change, and some use cases may not work yet. Watch for improvements in subsequent versions of the package.

Author(s)

Ben Baumer, Galen Long, Randall Pruim

See Also

plotPoints(), plotFun()

Examples

```r
require(mosaic)
mod <- lm( mpg ~ factor(cyl), data = mtcars)
plotModel(mod)

# SLR
mod <- lm( mpg ~ wt, data = mtcars)
plotModel(mod, pch = 19)

# parallel slopes
mod <- lm( mpg ~ wt + factor(cyl), data=mtcars)
plotModel(mod)

## Not run:
# multiple categorical vars
```
mod <- lm( mpg ~ wt + factor(cyl) + factor(vs) + factor(am), data = mtcars)
plotModel(mod)
plotModel(mod, mpg ~ am)

# interaction
mod <- lm( mpg ~ wt + factor(cyl) + wt:factor(cyl), data = mtcars)
plotModel(mod)

# polynomial terms
mod <- lm( mpg ~ wt + I(wt^2), data = mtcars)
plotModel(mod)

# GLM
mod <- glm(vs ~ wt, data=mtcars, family = 'binomial')
plotModel(mod)

# GLM with interaction
mod <- glm(vs ~ wt + factor(cyl), data=mtcars, family = 'binomial')
plotModel(mod)

# 3D model
mod <- lm( mpg ~ wt + hp, data = mtcars)
plotModel(mod)

# parallel planes
mod <- lm( mpg ~ wt + hp + factor(cyl) + factor(vs), data = mtcars)
plotModel(mod)

# interaction planes
mod <- lm( mpg ~ wt + hp + wt * factor(cyl), data = mtcars)
plotModel(mod)
plotModel(mod, system='g') + facet_wrap(~ cyl

## End(Not run)

---

**plotPoints**  
*Scatter plot of points*

**Description**

Make or add a scatter plot in a manner coordinated with plotFun.

**Usage**

```r
plotPoints(
  x,
  data = parent.frame(),
  add = NULL,
  under = FALSE,
  panelfun = panel.xyplot,
  plotfun = xyplot,
  ...,
)```
plotPoints

...,
  plot = trellis.last.object()
)

Arguments

   x  A formula specifying y ~ x or z ~ x&y
 data  Data frame containing the variables to be plotted. If not specified, the variables
       will be looked up in the local environment
  add  If TRUE, add points as a new layer to an existing plot. If NULL, the value of under
       will be used.
    under  If TRUE, the new layer will be underneath existing layers.
   panelfun  Lattice panel function to be used for adding. Set only if you want something
             other than a scatter plot. Mainly, this is intended to add new functionality
             through other functions.
  plotfun  Lattice function to be used for initial plot creation. Set only if you want some-
           thing other than a scatter plot. Mainly, this is intended to add new functionality
           through other functions.
      ...  additional arguments
         plot  a trellis plot, by default the most recently created one. If add is TRUE, new points
       will be added as a new layer to plot.

Value

A trellis graphics object

See Also

   plotFun()

Examples

if (require(mosaicData)) {
  plotPoints( width ~ length, data=KidsFeet, groups=sex, pch=20)
  f <- makeFun( lm( width ~ length * sex, data=KidsFeet))
  plotFun( f(length=length,sex="G")~length, add=TRUE, col="pink")
  plotFun( f(length=length,sex="B")~length, add=TRUE)
}
**Description**

Compute projections onto the span of a vector or a model space, dot products, and vector lengths in Euclidean space.

**Usage**

```
project(x, ...)
```

## S4 method for signature 'formula'
```
project(x, u = NULL, data = parent.frame(2), coefficients = TRUE, ...)
```

## S4 method for signature 'numeric'
```
project(x, u = rep(1, length(x)), type = c("vector", "length", "coef"), ...)
```

## S4 method for signature 'matrix'
```
project(x, u, data = parent.frame())
```

`vlength(x, ...)`

`dot(u, v)`

**Arguments**

- `x` a numeric vector (all functions) or a formula (only for `project`). Left-hand sides of formulas should be a single quantity
- `...` additional arguments
- `u` a numeric vector
- `data` a data frame.
- `coefficients` For `project(y ~ x)` indicates whether the projection coefficients should be returned or the projection vector.
- `type` one of "length" or "vector" determining the type of the returned value
- `v` a numeric vector

**Details**

`project` (preferably pronounced "pro-JECT" as in "projection") does either of two related things: (1) Given two vectors as arguments, it will project the first onto the second, returning the point in the subspace of the second that is as close as possible to the first vector. (2) Given a formula as an argument, will work very much like `lm()`, constructing a model matrix from the right-hand side of the formula and projecting the vector on the left-hand side onto the subspace of that model matrix.

In (2), rather than returning the projected vector, `project()` returns the coefficients on each of the vectors in the model matrix. UNLIKE `lm()`, the intercept vector is NOT included by default. If you want an intercept vector, include `+1` in your formula.
Value

project returns the projection of x onto u (or its length if u and v are numeric vectors and type == "length")

vlength returns the length of the vector (i.e., the square root of the sum of the squares of the components)

dot returns the dot product of u and v

See Also

link{project}

Examples

```r
x1 <- c(1,0,0); x2 <- c(1,2,3); y1 <- c(3,4,5); y2 <- rnorm(3)
# projection onto the 1 vector gives the mean vector
mean(y2)
project(y2, 1)
# return the length of the vector, rather than the vector itself
project(y2 - x1 + x2) -> pr; pr
# recover the projected vector
cbind(x1,x2) %*% pr -> v; v
project( y1 - x1 + x2, coefficients=FALSE)
# left over should be orthogonal to projection, so this should be ~ 0
if (require(mosaicData)) {
  project(width~length+sex, data=KidsFeet)
}
vlength(rep(1,4))
if (require(mosaicData)) {
  m <- lm( length ~ width, data=KidsFeet )
  # These should be the same
  vlength( m$effects )
  vlength( KidsFeet$length)
  # So should these
  vlength( tail(m$effects, -2) )
  sqrt(sum(resid(m)^2))
}

v <- c(1,1,1); w <- c(1,2,3)
u <- v / vlength(v) # make a unit vector
# The following should be the same:
project(w,v, type="coef") * v
project(w,v)
# The following are equivalent
abs(dot( w, u ))
vlength( project( w, u ) )
vlength( project( w, v ) )
project( w, v, type='length' )
```
prop.test

Exact and Approximate Tests for Proportions

Description

The mosaic prop.test provides wrapper functions around the function of the same name in stats. These wrappers provide an extended interface (including formulas). prop.test performs an approximate test of a simple null hypothesis about the probability of success in a Bernoulli or multinomial experiment from summarized data or from raw data.

Usage

prop.test(
  x,
  n,
  p = NULL,
  alternative = c("two.sided", "less", "greater"),
  conf.level = 0.95,
  data = NULL,
  success = NULL,
  ...
)

Arguments

  x  count of successes, length 2 vector of success and failure counts, a formula, or a character, numeric, or factor vector containing raw data.

  n  sample size (successes + failures) or a data frame (for the formula interface)

  p  a vector of probabilities of success. The length of p must be the same as the number of groups specified by x, and its elements must be greater than 0 and less than 1.

  alternative  character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter. Only used for testing the null that a single proportion equals a given value, or that two proportions are equal; ignored otherwise.

  conf.level  confidence level of the returned confidence interval. Must be a single number between 0 and 1. Only used when testing the null that a single proportion equals a given value, or that two proportions are equal; ignored otherwise.

  data  a data frame (if missing, n may be a data frame)

  success  level of variable to be considered success. All other levels are considered failure.

  ...  additional arguments (often ignored). When x is a formula, groups can be used to compare groups: x = ~ var, groups=g is equivalent to x = var ~ g. na.rm can be a logical or an integer vector of length 1 or 2 to indicate dimension along which NA’s are removed before computing the test. See the examples.
Details

conf.level = 0.95, ...)

This is a wrapper around `prop.test()` to simplify its use when the raw data are available, in which case an extended syntax for prop.test is provided.

Value

an htest object

Note

When x is a 0-1 vector, 0 is treated as failure and 1 as success. Similarly, for a logical vector TRUE is treated as success and FALSE as failure.

See Also

`binom.test()`, `stats::prop.test()`

Examples

# Several ways to get a confidence interval for the proportion of Old Faithful # eruptions lasting more than 3 minutes.
prop.test( faithful$eruptions > 3 )
prop.test(97,272)
faithful$long <- faithful$eruptions > 3
prop.test( faithful$long )
prop.test( ~long , data = faithful )
prop.test( ~ homeless ~ sex , data = HELPrct )
prop.test( ~ homeless | sex , data = HELPrct )
prop.test( ~ homeless , groups = sex , data = HELPrct )
prop.test( anysub ~ link , data = HELPrct , na.rm = TRUE)
prop.test( link ~ anysub , data = HELPrct , na.rm = 1)
prop.test( link ~ anysub , data = HELPrct , na.rm = TRUE)
Usage

\[
\text{prop.test(} \\
\quad x, \\
\quad n, \\
\quad p = \text{NULL}, \\
\quad \text{alternative} = c(\text{"two.sided"}, \text{"less"}, \text{"greater"}), \\
\quad \text{conf.level} = 0.95, \\
\quad \ldots \\
\)
\]

Arguments

- \(x\): a vector, count, or formula.
- \(n\): a vector of counts of trials (not needed when \(x\) is a table or matrix).
- \(p\): a vector of probabilities of success (for the null hypothesis). The length must be the same as the number of groups specified by \(x\).
- \(\text{alternative}\): a character string specifying the alternative hypothesis, must be one of \"two.sided\" (default), \"greater\" or \"less\". You can specify just the initial letter. Only used for testing the null that a single proportion equals a given value, or that two proportions are equal; ignored otherwise.
- \(\text{conf.level}\): confidence level of the returned confidence interval. Must be a single number between 0 and 1. Only used when testing the null that a single proportion equals a given value, or that two proportions are equal; ignored otherwise.
- \(\ldots\): additional arguments passed to methods.

qdata

The Data Distribution

Description

Density, distribution function, quantile function, and random generation from data.

Usage

- \(\text{qdata(formula, p = seq(0, 1, 0.25), data = NULL, \ldots)}\)
- \(\text{cdata(formula, p = 0.95, data = NULL, \ldots)}\)
- \(\text{pdata(formula, q, data = NULL, \ldots)}\)
- \(\text{rdata(formula, n, data = NULL, \ldots)}\)
- \(\text{ddata(formula, q, data = NULL, \ldots)}\)
Arguments

- **formula**: a formula or a vector
- **p**: a vector of probabilities
- **data**: a data frame in which to evaluate `formula`
- **...**: additional arguments passed to `quantile` or `sample`
- **q**: a vector of quantiles
- **n**: number of values to sample

Value

For `qdata`, a vector of quantiles
for `cdata`, a data frame giving upper and lower limits and the central proportion requested
For `pdata`, a vector of probabilities
For `rdata`, a vector of sampled values.
For `ddata`, a vector of probabilities (empirical densities)

Examples

data(penguins, package = "palmerpenguins")
qdata(flipper_length_mm ~ species, 0.5, data = penguins)
qdata(~ flipper_length_mm, p = 0.5, groups = species, data = penguins)
qdata(penguins$flipper_length_mm, p = 0.5)
qdata(~ flipper_length_mm, p = 0.5, data = penguins)
qdata(~ flipper_length_mm, p = 0.5, groups = species, data = penguins)
data(penguins, package = 'palmerpenguins')
cdata(penguins$flipper_length_mm, 0.5)
cdata(~ flipper_length_mm, 0.5, data = penguins)
cdata(~ flipper_length_mm, 0.5, data = penguins)
cdata(~ flipper_length_mm | species, data = penguins, p = .5)
data(penguins, package = 'palmerpenguins')
pdata(penguins$flipper_length_mm, 3:6)
pdata(~ flipper_length_mm, 3:6, data = penguins)
data(penguins, package = 'palmerpenguins')
rdata(penguins$species, 10)
rdata(~ species, n = 10, data = penguins)
rdata(flipper_length_mm ~ species, n = 5, data = penguins)
data(penguins, package = 'palmerpenguins')
ddata(penguins$species, 'setosa')
ddata(~ species, 'setosa', data = penguins)
Description

Utility functions for density, distribution function, quantile function, and random generation from data.

Usage

qdata_v(x, p = seq(0, 1, 0.25), na.rm = TRUE, ...)
qdata_f(x, ..., data = NULL, groups = NULL, na.rm = TRUE)
cdata_v(x, p = 0.95, na.rm = TRUE, ...)
cdata_f(x, ..., data = NULL, groups = NULL, na.rm = TRUE)
pdata_v(x, q, lower.tail = TRUE, ...)
pdata_f(x, ..., data = NULL, groups = NULL, na.rm = TRUE)
rdata_v(x, n, replace = TRUE, ...)
rdata_f(x, ..., data = NULL, groups = NULL, na.rm = TRUE)
ddata_v(x, q, ..., data = NULL, log = FALSE, na.rm = TRUE)
ddata_f(x, ..., data = NULL, groups = NULL, na.rm = TRUE)

Arguments

x a vector containing the data
p a vector of probabilities
na.rm a logical indicating whether NAs should be removed before computing.
... additional arguments passed to quantile or sample
data a data frame in which to evaluate formula
groups a grouping variable, typically the name of a variable in data
q a vector of quantiles
lower.tail a logical indicating whether to use the lower or upper tail probability
n number of values to sample
replace a logical indicating whether to sample with replacement
log a logical indicating whether the result should be log transformed
See Also

data(), pdata(), qdata(), rdata(), cdata()

---

qdist

Illustrated quantile calculations from distributions

Description

Illustrated quantile calculations from distributions

Usage

qdist(
  dist = "norm",
  p,
  plot = TRUE,
  verbose = FALSE,
  invisible = FALSE,
  resolution = 500L,
  digits = 3L,
  xlim,
  ylim,
  return = c("values", "plot"),
  refinements = list(),
  ...
)

xqgamma(
  p,
  shape,
  rate = 1,
  scale = 1/rate,
  lower.tail = TRUE,
  log.p = FALSE,
  ...
)

xqt(p, df, ncp, lower.tail = TRUE, log.p = FALSE, ...)

xqchisq(p, df, ncp = 0, lower.tail = TRUE, log.p = FALSE, ...)

xqf(p, df1, df2, lower.tail = TRUE, log.p = FALSE, ...)

xqbinom(p, size, prob, lower.tail = TRUE, log.p = FALSE, ...)

xqpois(p, lambda, lower.tail = TRUE, log.p = FALSE, ...)
xqgeom(p, prob, lower.tail = TRUE, log.p = FALSE, ...)

xqnbinom(p, size, prob, mu, lower.tail = TRUE, log.p = FALSE, ...)

xqbeta(p, shape1, shape2, ncp = 0, lower.tail = TRUE, log.p = FALSE, ...)

Arguments

dist a character description of a distribution, for example "norm", "t", or "chisq"
p a vector of probabilities
plot a logical indicating whether a plot should be created
verbose a logical
invisible a logical
resolution number of points used for detecting discreteness and generating plots. The default value of 5000 should work well except for discrete distributions that have many distinct values, especially if these values are not evenly spaced.
digits the number of digits desired
xlim x limits. By default, these are chosen to show the central 99.8% of the distribution.
ylim y limits
return If "plot", return a plot. If "values", return a vector of numerical values.
refinements A list of refinements to the plot. See ggformula::gf_refine().
... additional arguments, including parameters of the distribution and additional options for the plot. To help with name collisions (eg size for binomial distributions and shape for gamma distributions), argument names beginning plot_ will be renamed to remove plot_ and passed only to the plot. The unprefixed version will used as a parameter for the the distribution.
shape, scale shape and scale parameters. Must be positive, scale strictly.
rate an alternative way to specify the scale.
lower.tail logical; if TRUE (default), probabilities are \( P[X \leq x] \), otherwise, \( P[X > x] \).
log.p A logical indicating whether probabilities should be returned on the log scale.
df degrees of freedom (> 0, maybe non-integer). \( df = \infty \) is allowed.
ncp non-centrality parameter \( \delta \); currently except for \( rt() \), only for \( \text{abs(ncp)} \leq 37.62 \). If omitted, use the central t distribution.
df1, df2 degrees of freedom. \( \infty \) is allowed.
size number of trials (zero or more).
prob probability of success on each trial.
lambda vector of (non-negative) means.
mu alternative parametrization via mean: see ‘Details’.
shape1, shape2 non-negative parameters of the Beta distribution.
Details

The most general function is `qdist` which can work with any distribution for which a q-function exists. As a convenience, wrappers are provided for several common distributions.

Value

a vector of quantiles; a plot is printed as a side effect

Examples

```r
qdist("norm", seq(.1, .9, by = 0.10),
       title = "Deciles of a normal distribution", show.legend = FALSE,
       pattern = "rings")
xqnorm(seq(.2, .8, by = 0.20), mean = 100, sd = 10)
qdist("unif", .5)
xqgamma(.5, shape = 3, scale = 4)
xqgamma(.5, shape = 3, scale = 4, color = "black")
xqbeta(.5, shape1 = .9, shape2 = 1.4, dlwd = 1)
xqchisq(c(.25,.5,.75), df = 3)
xcbinom(c(0.80, 0.90), size = 1000, prob = 0.40)
# displayed as if continuous
xcbinom(c(0.80, 0.90), size = 5000, prob = 0.40)
xpbinom(c(480, 500, 520), size = 1000, prob = 0.48)
xpbinom(c(40, 60), size = 100, prob = 0.5)
xqpois(c(0.25, 0.5, 0.75), lambda = 12)
xcpois(0.50, lambda = 12)
xcpois(0.50, lambda = 12, refinements = list(scale_color_brewer(type = "qual", palette = 5)))
```

rand

**Random Regressors**

Description

A utility function for producing random regressors with a specified number of degrees of freedom.

Usage

```r
rand(df = 1, rdist = rnorm, args = list(), nrow, seed = NULL)
```

Arguments

df degrees of freedom, i.e., number of random regressors
rdist random distribution function for sampling
args arguments for rdist
nrow number of rows in resulting matrix. This can often be omitted in the context of functions like `lm` where it is inferred from the data frame, if one is provided.
seed seed for random number generation
Value

A matrix of random variates with df columns. In its intended use, the number of rows will be selected to match the size of the data frame supplied to lm.

Examples

```r
rand(2,nrow=4)
rand(2,rdist=rpois, args=list(lambda=3), nrow=4)
summary(lm( waiting ~ eruptions + rand(1), faithful))
```

---

**read.file**

*Read data files*

**Description**

A wrapper around various file reading functions.

**Usage**

```r
read.file(
  file,
  header = T,
  na.strings = "NA",
  comment.char = NULL,
  filetype = c("default", "csv", "txt", "tsv", "fw", "rdata"),
  stringsAsFactors = FALSE,
  readr = FALSE,
  package = NULL,
  ...
)
```

**Arguments**

- `file` character: The name of the file which the data are to be read from. This may also be a complete URL or a path to a compressed file. If it does not contain an absolute path, the file name is relative to the current working directory, `getwd()`. Tilde-expansion is performed where supported. See `read.table()` for more details.
- `header` logical: For `.txt` and `.csv` files, this indicates whether the first line of the file includes variables names.
- `na.strings` character: strings that indicate missing data.
- `comment.char` character: a character vector of length one containing a single character or an empty string. Use "" to turn off the interpretation of comments altogether.
- `filetype` character: one of "default", "csv", "txt", or "rdata" indicating the type of file being loaded. The default is to use the filename to guess the type of file.
relm

Resample a Linear Model

Description

Fit a new model to data created using resample(model).

Usage

relm(model, ..., envir = environment(formula(model)))
Arguments

model: a linear model object produced using `lm()`.

...: additional arguments passed through to `resample()`.

envir: an environment in which to (re)evaluate the linear model.

See Also

resample()

Examples

```r
mod <- lm(length ~ width, data = KidsFeet)
do(1) * mod
do(3) * relm(mod)
# use residual resampling to estimate standard error (very crude because so few replications)
Boot <- do(100) * relm(mod)
sd(~ width, data = Boot)
# standard error as produced by summary() for comparison
mod |> summary() |> coef()
```

Repeater objects

Repeater objects can be used with the `*` operator to repeat things multiple time using a different syntax and different output format from that used by, for example, `replicate()`.

Slots

n: Object of class "numeric" indicating how many times to repeat something.
cull: Object of class "function" that culls the output from each repetition.
mode: Object of class "character" indicating the output mode ('default', 'data.frame', 'matrix', 'vector', or 'list'). For most purposes 'default' (the default) should suffice.
algorithm: an algorithm number.
parallel: a logical indicating whether to attempt parallel execution.

See Also

do()
Description

These functions simplify and unify sampling in various ways.

Usage

resample(..., replace = TRUE)
deal(...)
shuffle(x, replace = FALSE, prob = NULL, groups = NULL, orig.ids = FALSE)
sample(x, size, replace = FALSE, ...)

## Default S3 method:
sample(
  x,
  size,
  replace = FALSE,
  prob = NULL,
  groups = NULL,
  orig.ids = FALSE,
  ...
)

## S3 method for class 'data.frame'
sample(
  x,
  size,
  replace = FALSE,
  prob = NULL,
  groups = NULL,
  orig.ids = TRUE,
  fixed = names(x),
  shuffled = c(),
  invisibly.return = NULL,
  ...
)

## S3 method for class 'matrix'
sample(
  x,
  size,
  replace = FALSE,
Arguments

... additional arguments passed to base::sample() or sample().
replace Should sampling be with replacement?
x Either a vector of one or more elements from which to choose, or a positive integer.
prob A vector of probability weights for obtaining the elements of the vector being sampled.
groups a vector (or variable in a data frame) specifying groups to sample within. This will be recycled if necessary.
orig.ids a logical; should original ids be included in returned data frame?
size a non-negative integer giving the number of items to choose.
fixed a vector of column names. These variables are shuffled en masse, preserving associations among these columns.
resample

shuffled a vector of column names. These variables are reshuffled individually (within
   groups if groups is specified), breaking associations among these columns. ex-
   amples.

invisibly.return a logical, should return be invisible?

drop.unused.levels a logical, should unused levels be dropped?

parametric A logical indicating whether the resampling should be done parametrically.

transformation NULL or a function providing a transformation to be applied to the synthetic
   responses. If NULL, an attempt it made to infer the appropriate transformation
   from the original call as recorded in x.

Details

These functions are wrappers around sample() providing different defaults and natural names.

Examples

# 100 Bernoulli trials -- no need for replace=TRUE
resample(0:1, 100)
tally(resample(0:1, 100))
if (require(mosaicData)) {
  Small <- sample(KidsFeet, 10)
  resample(Small)
tally(~ sex, data=resample(Small))
tally(~ sex, data=resample(Small))
  # fixed marginals for sex
tally(~ sex, data=Small)
tally(~ sex, data=resample(Small, groups=sex))
  # shuffled can be used to reshuffle some variables within groups
  # orig.id shows where the values were in original data frame.
  Small <- mutate(Small,
  id1 = paste(sex,1:10, sep=":"),
  id2 = paste(sex,1:10, sep=":"))
  resample(Small, groups=sex, shuffled=c("id1","id2"))
} deal(Cards, 13)  # A Bridge hand
shuffle(Cards)
model <- lm(width ~ length * sex, data = KidsFeet)
KidsFeet |> head()
resample(model) |> head()
Boot <- do(500) * lm(width ~ length * sex, data = resample(KidsFeet))
df_stats(~ Intercept + length + sexG + length.sexG, data = Boot, sd)
head(Boot)
summary(coef(model))
rescale

Rescale vectors or variables within data frames. This can be useful for comparing vectors that are on different scales, for example in parallel plots or heatmaps.

Usage

```
rescale(x, range, domain = NULL, ...)
```

```
## S3 method for class 'data.frame'
rescale(x, range = c(0, 1), domain = NULL, ...)
```

```
## S3 method for class 'factor'
rescale(x, range, domain = NULL, ...)
```

```
## S3 method for class 'numeric'
rescale(x, range = c(0, 1), domain = NULL, ...)
```

```
## Default S3 method:
rescale(x, range = c(0, 1), domain = NULL, ...)
```

```
## S3 method for class 'character'
rescale(x, range = c(0, 1), domain = NULL, ...)
```

Arguments

- **x**: an R object to rescale
- **range**: a numeric vector of length 2
- **domain**: a numeric vector of length 2 or NULL
- **...**: additional arguments

rflip

Tossing Coins

Description

These functions simplify simulating coin tosses for those (students primarily) who are not yet familiar with the binomial distributions or just like this syntax and verbosity better.
Usage

```r
rflip(
  n = 1,
  prob = 0.5,
  quiet = FALSE,
  verbose = !quiet,
  summarize = FALSE,
  summarise = summarize
)
```

## S3 method for class 'cointoss'
print(x, ...)

```r
nflip(n = 1, prob = 0.5, ...)
```

Arguments

- `n` the number of coins to toss
- `prob` probability of heads on each toss
- `quiet` a logical. If TRUE, less verbose output is used.
- `verbose` a logical. If TRUE, more verbose output is used.
- `summarize` if TRUE, return a summary (as a data frame).
- `summarise` alternative spelling for `summarize`.
- `x` an object
- `...` additional arguments

Value

- for `rflip`, a `cointoss` object
- for `nflip`, a numeric vector

Examples

```r
rflip(10)
rflip(10, prob = 1/6, quiet = TRUE)
rflip(10, prob = 1/6, summarize = TRUE)
do(5) * rflip(10)
as.numeric(rflip(10))
nflip(10)
```
**rfun**  
*Generate a natural-looking function*

---

**Description**

Produce a random function that is the sum of Gaussian random variables

`rpol2y` generates a random 2nd degree polynomial (as a function)

**Usage**

```r
rfun(vars = ~x & y, seed = NULL, n = 0)
rpol2y(vars = ~x & y, seed = NULL)
```

**Arguments**

- `vars`: a formula; the LHS is empty and the RHS indicates the variables used for input to the function (separated by `&`).
- `seed`: seed for random number generator, passed to `set.seed()`. 
- `n`: the number of Gaussians. By default, this will be selected randomly.

**Details**

`rfun` is an easy way to generate a natural-looking but random function with ups and downs much as you might draw on paper. In two variables, it provides a good way to produce a random landscape that is smooth. Things happen in the domain -5 to 5. The function is pretty flat outside of that. Use seed to create a fixed function that will be the same for everybody.

These functions are particularly useful for teaching calculus.

**Value**

- a function with the appropriate number of inputs
- a function defined by a 2nd degree polynomial with coefficients selected randomly according to a `Unif(-1,1)` distribution.

**Examples**

```r
f <- rfun(~ u & v)
plotFun(f(u,v)~u&v,u=range(-5,5),v=range(-5,5))
myfun <- rfun(~ u & v, seed=1959)
g <- rpol2y(~ x&y&z, seed=1964)
plotFun(g(x,y,z=2)~x&y,xlim=range(-5,5),ylim=range(-5,5))
```
Sample longitude and latitude on a sphere

Description

Randomly samples longitude and latitude on earth so that equal areas are (approximately) equally likely to be sampled. (Approximation assumes earth as a perfect sphere.)

Usage

```r
rlatlon(...) rlonlat(...) rgeo(n = 1, latlim = c(-90, 90), lonlim = c(-180, 180), verbose = FALSE) rgeo2(n = 1, latlim = c(-90, 90), lonlim = c(-180, 180), verbose = FALSE)
```

Arguments

- `...`: arguments passed through to other functions
- `n`: number of random locations
- `latlim, lonlim`: range of latitudes and longitudes to sample within, only implemented for `rgeo`.
- `verbose`: return verbose output that includes Euclidean coordinates on unit sphere as well as longitude and latitude.

Details

`rgeo` and `rgeo2` differ in the algorithms used to generate random positions. Each assumes a spherical globe. `rgeo` uses that fact that each of the x, y and z coordinates is uniformly distributed (but not independent of each other). Furthermore, the angle about the z-axis is uniformly distributed and independent of z. This provides a straightforward way to generate Euclidean coordinates using `runif`. These are then translated into latitude and longitude.

`rlatlon` is an alias for `rgeo` and `rlonlat` is too, expect that it reverses the order in which the latitude and longitude values are returned.

`rgeo2` samples points in a cube by independently sampling each coordinate. It then discards any point outside the sphere contained in the cube and projects the non-discarded points to the sphere. This method must oversample to allow for the discarded points.

Value

A data frame with variables `long` and `lat`. If `verbose` is `TRUE`, then x, y, and z coordinates are also included in the data frame.

See Also

deg2rad(), googleMap() and latlon2xyz().
Examples

rgeo(4)
# sample from a region that contains the continental US
rgeo(4, latlim = c(25,50), lonlim = c(-65, -125))

rgeo2(4)

---

rspin

Simulate spinning a spinner

Description

This is essentially rmultinom with a different interface.

Usage

rspin(n, probs, labels = 1:length(probs))

Arguments

n  number of spins of spinner
probs  a vector of probabilities. If the sum is not 1, the probabilities will be rescaled.
labels  a character vector of labels for the categories

Examples

rspin(20, prob=c(1,2,3), labels=c("Red", "Blue", "Green"))
do(2) * rspin(20, prob=c(1,2,3), labels=c("Red", "Blue", "Green"))

---

rsquared  Extract r-squared value

Description

Attempts to extract an r-squared value from a model or model-like object.

Usage

rsquared(x, ...)

Arguments

x  an object
...  additional arguments
rstudio_is_available  
*Check whether RStudio is in use*

**Description**

This function checks that RStudio is in use. It will likely be removed from this package once the versions of RStudio in popular use rely on the manipulate package on CRAN which will provide its own version.

**Usage**

```r
rstudio_is_available()
```

**Value**

a logical

---

set.rseed  
*Set seed in parallel compatible way*

**Description**

When the parallel package is used, setting the RNG seed for reproducibility involves more than simply calling `set.seed()`. `set.rseed` takes care of the additional overhead.

**Usage**

```r
set.rseed(seed)
```

**Arguments**

- `seed`  
  seed for the random number generator

**Details**

If the parallel package is not on the search path, then `set.seed()` is called. If `parallel` is on the search path, then the RNG kind is set to "L'Ecuyer-CMRG", the seed is set and `mc.reset.stream` is called.

**Examples**

```r
# These should give identical results, even if the 'parallel' package is loaded.
set.rseed(123); do(3) * resample(1:10, 2)
set.rseed(123); do(3) * resample(1:10, 2)
```
Description

Sleep and Memory

Usage
data(Sleep)

Format

A data.frame with 24 observations on the following 2 variables.

- Group  treatment group of the subject
- Words  number of words recalled

Details

In an experiment on memory (Mednicj et al, 2008), students were given lists of 24 words to memorize. After hearing the words they were assigned at random to different groups. One group of 12 students took a nap for 1.5 hours while a second group of 12 students stayed awake and was given a caffeine pill. The data set records the number of words each participant was able to recall after the break.

Source

These data were used in a "resampling bake-off" hosted by Robin Lock.

sp2df

Transforms a shapefile into a dataframe

Description

This function takes in a shapefile (formal class of SpatialPolygonsDataFrame) and transforms it into a dataframe

Usage

sp2df(map, ...)

Arguments

- map  A map object of class SpatialPolygonsDataFrame
- ...  Other arguments, currently ignored
Value

A dataframe, in which the first 7 columns hold geographical information (ex: long and lat)

Examples

```r
## Not run:
if(require(maptools)) {
  data(wrld_simpl)
  worldmap <- sp2df(wrld_simpl)
}

if ( require(ggplot2) && require(maptools) ) {
  data(wrld_simpl)
  World <- sp2df(wrld_simpl)
  World2 <- merge(World, Countries, by.x="NAME", by.y="maptools", all.y=FALSE)
  Mdata <- merge(Alcohol, World2, by.x="country", by.y="gapminder", all.y=FALSE)
  Mdata <- Mdata[order(Mdata$order),]
  qplot( x=long, y=lat, fill=ntiles(alcohol,5),
         data=subset(Mdata, year==2008), group = group,
         geom="polygon")
}
```

## End(Not run)

---

**standardName**                        **Standardization of Geographic Names**

**Description**

Often different sources of geographical data will use different names for the same region. These utilities make it easier to merge data from different sources by converting names to standardized forms.

**Usage**

```r
standardName(
  x,
  standard,
  ignore.case = TRUE,
  returnAlternatives = FALSE,
  quiet = FALSE
)
```

```r
standardCountry(
  x,
  ignore.case = TRUE,
  returnAlternatives = FALSE,
```
 Arguments

 x  A vector with the region names to standardize
 standard  a named vector providing the map from non-standard names (names of vector) to standard names (values of vector)
 ignore.case  a logical indicating whether case should be ignored when matching.
 returnAlternatives  a logical indicating whether all alternatives should be returned in addition to the standard name.
 quiet  a logical indicating whether warnings should be suppressed

 Details

 standardName  This is the most general standardizing function. In addition to x, this function requires another argument: standard - a named vector in which each name is a particular spelling of the region name in question and the corresponding value is the standardized version of that region name

 standardCountry  This function will standardize the country names in x to the standard ISO_a3 country code format. If returnAlternatives is set to TRUE, this function will also return the the named vector used to standardize the country names

 standardState  This function will standardize the US state names in x to the standard two-letter abbreviations. If returnAlternatives is set to TRUE, this function will also return the the named vector used to standardize the state names

 In all three cases, any names not found in standard will be left unaltered. Unless suppressed, a warning message will indicate the number of such cases, if there are any.

Description

 Tally test statistics from data and from multiple draws from a simulated null distribution

Usage

statTally(sample, rdata, FUN, direction = NULL,
alternative = c("default", "two.sided", "less", "greater"),
sig.level = 0.1,
system = c("gg", "lattice"),
shade = "navy",
alpha = 0.1,
binwidth = NULL,
bins = NULL,
fill = "gray80",
color = "black",
center = NULL,
stemplot = dim(rdata)[direction] < 201,
q = c(0.5, 0.9, 0.95, 0.99),
fun = function(x) x,
xlim,
quiet = FALSE,
...
)

Arguments

sample      sample data
rdata       a matrix of randomly generated data under null hypothesis.
FUN         a function that computes the test statistic from a data set. The default value does
            nothing, making it easy to use this to tabulate precomputed statistics into a null
            distribution. See the examples.
direction   1 or 2 indicating whether samples in rdata are in rows (1) or columns (2).
alternative one of default, two.sided, less, or greater
sig.level   significance threshold for wilcox.test used to detect lack of symmetry
system      graphics system to use for the plot
shade       a color to use for shading.
alpha       opacity of shading.
binwidth    bin width for histogram.
bins        number of bins for histogram.
fill        fill color for histogram.
color       border color for histogram.
center      center of null distribution
stemplot    indicates whether a stem plot should be displayed
q           quantiles of sampling distribution to display
fun         same as FUN so you don’t have to remember if it should be capitalized
xlim        limits for the horizontal axis of the plot.
quiet       a logical indicating whether the text output should be suppressed
...         additional arguments passed to lattice::histogram() or ggplot2::geom_histogram()
surround

Value
A lattice or ggplot showing the sampling distribution.
As side effects, information about the empirical sampling distribution and (optionally) a stem plot are printed to the screen.

Examples

# is my spinner fair?
x <- c(10, 18, 9, 15)  # counts in four cells
rdata <- rmultinom(999, sum(x), prob = rep(.25, 4))
statTally(x, rdata, fun = max, binwidth = 1)  # unusual test statistic
statTally(x, rdata, fun = var, shade = "red", binwidth = 2)  # equivalent to chi-squared test
# Can also be used with test stats that are precomputed.
if (require(mosaicData)) {
  D <- diffmean( age ~ sex, data = HELPrct); D
  nullDist <- do(999) * diffmean( age ~ shuffle(sex), data = HELPrct)
  statTally(D, nullDist)
  statTally(D, nullDist, system = "lattice")
}

---

surround

Format strings for pretty output

Description
Format strings for pretty output

Usage

surround(x, pre = " ", post = " ", width = 8, ...)

Arguments

x a vector
pre text to prepend onto string
post text to postpend onto string
width desired width of string
... additional arguments passed to format()

Value

a vector of strings padded to the desired width

Examples

surround(rbinom(10,20,.5), " ", " ", width=4)
surround(rnorm(10), " ", " ", width=8, digits = 2, nsmall = 2)
swap

*Swap values among columns of a data frame*

**Description**

Swap values among columns of a data frame

**Usage**

\[
\text{swap(data, which)}
\]

**Arguments**

- `data`: a data frame
- `which`: a formula or an integer or character vector specifying columns in `data`

**Details**

`swap` is not a particularly speedy function. It is intended primarily as an aid for teaching randomization for paired designs. Used this way, the number of randomizations should be kept modest (approximately 1000) unless you are very patient.

**Examples**

```r
if (require(tidyr)) {
  Sleep2 <- sleep |>
  spread(key=group, val=extra)
  names(Sleep2) <- c("subject", "drug1", "drug2")
  swap(Sleep2, drug1 ~ drug2)
  mean(~(drug1 - drug2), data=Sleep2)
  do(3) * mean(~(drug1 - drug2), data=Sleep2 |> swap(drug1 ~ drug2))
}
```

---

theme.mosaic

*Lattice Theme*

**Description**

A theme for use with lattice graphics.

**Usage**

```r
theme.mosaic(bw = FALSE, lty = if (bw) 1:7 else 1, lwd = 2, ...)

col.mosaic(bw = FALSE, lty = if (bw) 1:7 else 1, lwd = 2, ...)
```
theme_map

**Arguments**

- **bw**
  - whether color scheme should be "black and white"
- **lty**
  - vector of line type codes
- **lwd**
  - vector of line widths
- ... additional named arguments passed to `trellis.par.set()`

**Value**

Returns a list that can be supplied as the theme to `trellis.par.set()`.

**Note**

These two functions are identical. `col.mosaic` is named similarly to `lattice::col.whitebg()`, but since more than just colors are set, `theme.mosaic` is a preferable name.

**See Also**

`trellis.par.set()`, `show.settings()`

**Examples**

```r
library(lattice)

theme_map()
show.settings()

theme_map(bw = TRUE)
show.settings()
```

---

### theme_map

**ggplot2 theme for maps**

**Description**

A very plain `ggplot2` theme that is good for maps.

**Usage**

```r
theme_map(base_size = 12)
```

**Arguments**

- **base_size**
  - the base font size for the theme.

**Details**

This theme is largely based on an example posted by Winston Chang at the `ggplot2` Google group forum.
TukeyHSD.lm

Additional interfaces to TukeyHSD

Description

TukeyHSD() requires use of aov(). Since this is a hindrance for beginners, wrappers have been provided to remove this need.

Usage

## S3 method for class 'lm'
TukeyHSD(x, which, ordered = FALSE, conf.level = 0.95, ...)

## S3 method for class 'formula'
TukeyHSD(
  x,
  which, 
  ordered = FALSE,
  conf.level = 0.95,
  data = parent.frame(),
  ...
)

Arguments

x an object, for example of class lm or formula
which, ordered, conf.level, ...
just as in TukeyHSD() from the base package
data a data frame. NB: This does not come second in the argument list.

Examples

## These should all give the same results
if (require(mosaicData)) {
  model <- lm(age ~ substance, data=HELPrct)
  TukeyHSD(model)
  TukeyHSD(age ~ substance, data=HELPrct)
  TukeyHSD(aov(age ~ substance, data=HELPrct))
}
**Description**

Performs one and two sample t-tests. The mosaic t.test provides wrapper functions around the function of the same name in stats. These wrappers provide an extended interface that allows for a more systematic use of the formula interface.

**Usage**

```r
# S3 method for class 'formula'
t_test(formula, data, ..., groups = NULL)
```

```r
## Default S3 method:
t_test(
  x,                                                
  y = NULL,                                          
  alternative = c("two.sided", "less", "greater"), 
  mu = 0,                                            
  paired = FALSE,                                    
  var.equal = FALSE,                                 
  conf.level = 0.95,                                 
  ...                                               
)
```

**Arguments**

- `x`: a (non-empty) numeric vector of data values.
- `y`: further arguments to be passed to or from methods.
- `formula`: a formula of the form `lhs ~ rhs` where `lhs` is a numeric variable giving the data values and `rhs` either 1 for a one-sample or paired test or a factor with two levels giving the corresponding groups. If `lhs` is of class "Pair" and `rhs` is 1, a paired test is done.
- `data`: an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
- `groups`: When `x` is a formula, groups can be used to compare groups: `x ~ var`, `groups = g` is equivalent to `x = var ~ g`. See the examples.
- `alternative`: a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
mu

a number indicating the true value of the mean (or difference in means if you are performing a two sample test).

paired

a logical indicating whether you want a paired t-test.

var.equal

a logical variable indicating whether to treat the two variances as being equal. If TRUE then the pooled variance is used to estimate the variance otherwise the Welch (or Satterthwaite) approximation to the degrees of freedom is used.

conf.level

confidence level of the interval.

Details

This is a wrapper around `stats::t.test()` from the `stats` package to extend the functionality of the formula interface. In particular, one can now use the formula interface for a 1-sample t-test. Before, the formula interface was only permitted for a 2-sample test. The type of formula that can be used for the 2-sample test has also been broadened. See the examples.

Value

an object of class htest

See Also

`prop.test()`, `binom.test()`, `stats::t.test()`

Examples

t.test(HELPrct$age)
  # We can now do this with a formula
t.test(~ age, data = HELPrct)
  # data = can be omitted, but it is better to use it
t.test(~ age, HELPrct)
  # the original 2-sample formula
  t.test(age ~ sex, data = HELPrct)
  # alternative 2-sample formulas
  t.test(~ age | sex, data = HELPrct)
t.test(~ age, groups = sex, data = HELPrct)
  # 2-sample t from vectors
  with(HELPrct, t.test(age[sex == "male"], age[sex == "female"]))
  # just the means
  mean(age ~ sex, data = HELPrct)

Description

Update the confidence interval portion of an object returned from `binom.test` using one of several alternative methods.
Usage

update_ci(
  object,
  method = c("clopper-pearson", "wald", "agresti-coull", "plus4", "score", "prop.test")
)

Arguments

object An "htest" object produced by \texttt{binom.test()}
method a method for computing a confidence interval for a proportion.

Value

an "htest" object with an updated confidence interval

See Also

\texttt{binom.test()}

\begin{longtable}{ll}
\textbf{value} & \textit{Extract value from an object} \\
\end{longtable}

Description

Functions like \texttt{integrate()} and \texttt{nlm()} return objects that contain more information than simply the value of the integration or optimization. \texttt{value()} extracts the primary value from such objects. Currently implemented situations include the output from \texttt{integrate()}, \texttt{nlm()}, \texttt{cubature::adaptIntegrate()}, and \texttt{uniroot()}.

Usage

value(object, ...)

## S3 method for class 'integrate'
value(object, ...)

## Default S3 method:
value(object, ...)

Arguments

object an object from which a "value" is to be extracted.
... additional arguments (currently ignored).
Examples

integrate(sin, 0, 1) |> value()
nlm(cos, p = 0) |> value()
unioorot(cos, c(0, 2)) |> value()

xchisq.test

Augmented Chi-squared test

Description

This augmented version of chisq.test() provides more verbose output.

Usage

xchisq.test(
x, 
y = NULL,
correct = TRUE,
p = rep(1/length(x), length(x)),
rescale.p = FALSE,
simulate.p.value = FALSE,
B = 2000,
data = environment(x)
)

Arguments

x, y, correct, p, rescale.p, simulate.p.value, B

as in chisq.test(), but x may also be a formula, in which case x is replaced
by tally(x, data) prior to the call to chisq.test().

data a data frame for use when x is a formula.

See Also

chisq.test()

Examples

# Physicians' Health Study data
phs <- cbind(c(104,189),c(10933,10845))
rownames(phs) <- c("aspirin","placebo")
colnames(phs) <- c("heart attack","no heart attack")
phs
xchisq.test(phs)
xchisq.test(sex ~ substance, data = HELPct)
Augmented histograms

Description

The mosaic package adds some additional functionality to lattice::histogram(), making it simpler to obtain certain common histogram adornments. This is done by resetting the default panel and prepanel functions used by histogram.

Usage

xhistogramBreaks(x, center = NULL, width = NULL, nint, ...)

prepanel.xhistogram(x, breaks = xhistogramBreaks, ...)

panel.xhistogram(
  x,
  dcol = trellis.par.get("plot.line")$col,
  dalpha = 1,
  dlwd = 2,
  gcol = trellis.par.get("add.line")$col,
  glwd = 2,
  fcol = trellis.par.get("superpose.polygon")$col,
  dmath = dnorm,
  verbose = FALSE,
  dn = 100,
  args = NULL,
  labels = FALSE,
  density = NULL,
  under = FALSE,
  fit = NULL,
  start = NULL,
  type = "density",
  v,
  h,
  groups = NULL,
  center = NULL,
  width = NULL,
  breaks,
  nint = round(1.5 * log2(length(x)) + 1),
  stripes = c("vertical", "horizontal", "none"),
  alpha = 1,
  ...
)

Arguments

x a formula or a numeric vector
center  center of one of the bins
width  width of the bins
nint  approximate number of bins
...  additional arguments passed from lattice::histogram() to the panel function; by default when the mosaic package has been loaded this will be panel.xhistogram().
breaks  break points for histogram bins, a function for computing such, or a method hist() knows about given as a character string. When using the mosaic package defaults, xhistogramBreaks() is used.
dcol  color of density curve
dalpha  alpha for density curve
dlwd, glwd  like lwd but affecting the density line and guide lines, respectively
gcol  color of guidelines
fcol  fill colors for histogram rectangles when using groups. (Use col, which is passed through to the histogram panel function, when not using groups.)
dmath  density function for density curve overlay
verbose  be verbose?
dn  number of points to sample from density curve
args  a list of additional arguments for dmath
labels  should counts/densities/percent be displayed or each bin?
density  a logical indicating whether to overlay a density curve
under  a logical indicating whether the density layers should be under or over other layers of the plot.
fit  a character string describing the distribution to fit. Known distributions include "exponential", "normal", "lognormal", "poisson", "beta", "geometric", "t", "weibull", "cauchy", "gamma", "chisq" and "chi-squared"
start  numeric value passed to MASS::fitdistr()
type  one of 'density', 'count', or 'percent'
h, v  a vector of values for additional horizontal and vertical lines
groups  as per lattice::histogram()
stripes  one of "vertical", "horizontal", or "none", indicating how bins should be striped when groups is not NULL
alpha  transparency level
panel  a panel function

Details

The primary additional functionality added to histogram() are the arguments width and center which provide a simple way of describing equal-sized bins, and fit which can be used to overlay the density curve for one of several distributions. The groups argument can be used to color the bins. The primary use for this is to shade tails of histograms, but there may be other uses as well.
Value

xhistogramBreaks returns a vector of break points

Note

Versions of lattice since 0.20-21 support setting custom defaults for breaks, panel, and prepanel used by histogram(), so xhistogram() is no longer needed. As a result, xhistogram() (which was required in earlier versions of mosaic is no longer needed and has been removed.

See Also

lattice::histogram(), mosaicLatticeOptions(), and restoreLatticeOptions().

Examples

```r
if (require(mosaicData)) {
  histogram(~age | substance, HELPrct, v=35, fit='normal')
  histogram(~age, HELPrct, labels=TRUE, type='count')
  histogram(~age, HELPrct, groups=cut(age, seq(10,80,by=10)))
  histogram(~age, HELPrct, groups=sex, stripes='horizontal')
  histogram(~racegrp, HELPrct, groups=substance,auto.key=TRUE)
  xhistogramBreaks(1:10, center=5, width=1)
  xhistogramBreaks(1:10, center=5, width=2)
  xhistogramBreaks(0:10, center=15, width=3)
  xhistogramBreaks(1:100, center=50, width=3)
  xhistogramBreaks(0:10, center=5, nint=5)
}
```

xpnorm
Augmented versions of pnorm and qnorm

Description

These functions behave similarly to the functions with the initial x removed from their names but add more verbose output and graphics.

Usage

```r
xpnorm(
  q,
  mean = 0,
  sd = 1,
  plot = TRUE,
  verbose = TRUE,
  invisible = FALSE,
  digits = 4,
  lower.tail = TRUE,
  log.p = FALSE,
)```
Arguments

- `q` quantile
- `mean, sd` parameters of normal distribution.
- `plot` logical. If TRUE, show an illustrative plot.
- `verbose` logical. If TRUE, display verbose output.
- `invisible` logical. If TRUE, return value invisibly.
Augmented version of `qqmath`

**Description**

Augmented version of `qqmath`
Usage

\texttt{xqqmath(x, data = NULL, panel = "panel.xqqmath", \ldots)}

\texttt{panel.xqqmath(}
\begin{verbatim}
x, qmathline = !(fitline || idline), idline = FALSE, fitline = NULL, slope = NULL, intercept = NULL, overlines = FALSE, groups = NULL,
\ldots,
col.line = trellis.par.get("add.line")$col, pch = 16, lwd = 2, lty = 2
\end{verbatim}
\texttt{)}

Arguments

\texttt{x, data, panel, \ldots}

as in \texttt{lattice::qqmath()}

\texttt{qqmathline} a logical: should line be displayed passing through first and third quartiles?

\texttt{idline} a logical: should the line y=x be added to the plot?

\texttt{fitline} a logical: should a fitted line be added to plot? Such a line will use slope and intercept if provided, else the standard deviation and mean of the data. If slope is specified, the line will be added unless \texttt{fitline} is \texttt{FALSE}.

\texttt{slope} slope for added line

\texttt{intercept} intercept for added line

\texttt{overlines} a logical: should lines be on top of qq plot?

\texttt{groups, pch, lwd, lty} as in lattice plots

\texttt{col.line} color to use for added lines

Value

a trellis object

Examples

\begin{verbatim}
x <- rnorm(100)
xqqmath(~ x) # with quartile line
xqqmath(~ x, fitline = TRUE) # with fitted line
xqqmath(~ x, idline = TRUE) # with y = x
x <- rexp(100, rate = 10)
xqqmath(~ x, distribution = qexp) # with quartile line
\end{verbatim}
xyz2latlon

Convert back and forth between latitude/longitude and XYZ-space

Description

Convert back and forth between latitude/longitude and XYZ-space

Usage

xyz2latlon(x, y, z)
latlon2xyz(latitude, longitude)
lonlat2xyz(longitude, latitude)

Arguments

x, y, z numeric vectors
latitude, longitude vectors of latitude and longitude values

Value

a matrix each row of which describes the latitudes and longitudes
a matrix each row of which contains the x, y, and z coordinates of a point on a unit sphere

See Also

deg2rad(), googleMap(), and rgeo().

Examples

xyz2latlon(1, 1, 1) # point may be on sphere of any radius
xyz2latlon(0, 0, 0) # this produces a NaN for latitude
latlon2xyz(30, 45)
lonlat2xyz(45, 30)
### Description

Compute z-scores

### Usage

```r
zscore(x, na.rm = getOption("na.rm", FALSE))
```

### Arguments

- `x` a numeric vector
- `na.rm` a logical indicating whether missing values should be removed

### Examples

```r
data(penguins, package = "palmerpenguins")
penguins |> 
  group_by(species) |> 
  mutate(zbill_length_mm = zscore(bill_length_mm, na.rm = TRUE)) |> 
  head()
```
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