Package 'HelpersMG'

August 24, 2026

Type Package

Title Tools for Various R Functions Helpers

Version 2026.8.24

Date 2026-08-24

Depends R (>= 4.1), MASS, rlang, coda, Matrix, ggplot2

Suggests lme4, RNetCDF, ncdf4, maps, fields, shiny, ppcor, pbmcapply, pbapply, parallel, visNetwork, igraph, shinyWidgets, cranlogs

Description Contains miscellaneous functions useful for managing 'NetCDF' files (see <https://en.wikipedia.org/wiki/NetCDF>), get moon phase and time for sun rise and fall, tide level, analyse and reconstruct periodic time series of temperature with irregular sinusoidal pattern, show scales and wind rose in plot with change of color of text, Metropolis-Hastings algorithm for Bayesian MCMC analysis, plot graphs or boxplot with error bars, search files in disk by there names or their content, read the contents of all files from a folder at one time.

License GPL-2

LazyLoad yes

Encoding UTF-8

NeedsCompilation no

Config/roxygen2/version 8.1.0

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Repository CRAN

Date/Publication 2026-08-24 13:10:02 UTC

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`HelpersMG-package` *Tools for Environmental Analyses, Ecotoxicology and Various R Functions*

Description

Contains miscellaneous functions useful for managing
'NetCDF' files (see http://en.wikipedia.org/wiki/NetCDF),
get tide levels on any point of the globe,
get moon phase and time for sun rise and fall,
analyse and reconstruct daily time series of temperature
with irregular sinusoidal pattern,
show scales and wind rose in plot with change of color of text,
Metropolis-Hastings algorithm for Bayesian MCMC analysis,
plot graphs or boxplot with error bars,
search files in disk by there names or their content,
read the contents of all files from a folder at one time,
calculate IC50 for ecotoxicological studies,
calculate the probability mass function of the sum of negative binomial
distributions, calculate distribution of unobserved values in censored or truncated distributions.
The latest version of this package can always be installed using:
install.packages("http://marc.girondot.free.fr/CRAN/HelpersMG.tar.gz", repos=NULL, type="source")

Details

Helpers functions for several packages

Package:	HelpersMG
Type:	Package
Version:	2026.8.24 build 1817
Date:	2026-08-24
License:	GPL (>= 2)
LazyLoad:	yes

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
## Not run:
library(HelpersMG)
```

```
print('---------------------------------')
print('Examples for mcmcComposite objects')
print('---------------------------------')
require(coda)
x <- rnorm(30, 10, 2)
dnormx <- function(x, par) return(-sum(dnorm(x, mean=par['mean'], sd=par['sd'], log=TRUE)))
parameters_mcmc <- data.frame(Density=c('dnorm', 'dlnorm'),
Prior1=c(10, 0.5), Prior2=c(2, 0.5), SDProp=c(0.35, 0.2),
Min=c(-3, 0), Max=c(100, 10), Init=c(10, 2), stringsAsFactors = FALSE,
row.names=c('mean', 'sd'))
mcmc_run <- MHalgoGen(n.iter=100000, parameters=parameters_mcmc, data=x,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=1)
plot(mcmc_run, xlim=c(0, 20))
plot(mcmc_run, xlim=c(0, 10), parameters="sd")
mcmcforcoda <- as.mcmc(mcmc_run)
# Optimal rejection rate should be 0.234
rejectionRate(mcmcforcoda)
heidel.diag(mcmcforcoda)
raftery.diag(mcmcforcoda)
autocorr.diag(mcmcforcoda)
acf(mcmcforcoda[[1]][,"mean"], lag.max=20, bty="n", las=1)
acf(mcmcforcoda[[1]][,"sd"], lag.max=20, bty="n", las=1)
batchSE(mcmcforcoda, batchSize=100)
# The batch standard error procedure is usually thought to
# be not as accurate as the time series methods used in summary
summary(mcmcforcoda)$statistics[,"Time-series SE"]
summary(mcmc_run)
as.parameters(mcmc_run)
lastp <- as.parameters(mcmc_run, index="last")
parameters_mcmc[,"Init"] <- lastp
# The n.adapt set to 1 is used to not record the first set of parameters
# then it is not duplicated (as it is also the last one for
# the object mcmc_run)
mcmc_run2 <- MHalgoGen(n.iter=10000, parameters=parameters_mcmc, data=x,
likelihood=dnormx, n.chains=1, n.adapt=1, thin=1, trace=1)
mcmc_run3 <- merge(mcmc_run, mcmc_run2)
####### no adaptation, n.adapt must be 0
parameters_mcmc[,"Init"] <- c(mean(x), sd(x))
mcmc_run3 <- MHalgoGen(n.iter=10000, parameters=parameters_mcmc, data=x,
likelihood=dnormx, n.chains=1, n.adapt=0, thin=1, trace=1)
print('-----------------------------------------')
print('Examples for Daily patterns of temperature')
print('-----------------------------------------')
# Generate a timeserie of time
time.obs <- NULL
for (i in 0:9) time.obs <- c(time.obs, c(0, 6, 12, 18)+i*24)
# For these time, generate a timeseries of temperatures
temp.obs <- rep(NA, length(time.obs))
temp.obs[3+(0:9)*4] <- rnorm(10, 25, 3)
temp.obs[1+(0:9)*4] <- rnorm(10, 10, 3)
for (i in 1:(length(time.obs)-1))
  if (is.na(temp.obs[i]))
  temp.obs[i] <- mean(c(temp.obs[i-1], temp.obs[i+1]))
```

```
  if (is.na(temp.obs[length(time.obs)]))
  temp.obs[length(time.obs)] <- temp.obs[length(time.obs)-1]/2
observed <- data.frame(time=time.obs, temperature=temp.obs)
# Search for the minimum and maximum values
r <- minmax.periodic(time.minmax.daily=c(Min=2, Max=15),
observed=observed, period=24)

# Estimate all the temperatures for these values
t <- temperature.periodic(minmax=r)

plot_errbar(x=t[,"time"], y=t[,"temperature"],
errbar.y=ifelse(is.na(t[,"sd"]), 0, 2*t[,"sd"]),
type="l", las=1, bty="n", errbar.y.polygon = TRUE,
xlab="hours", ylab="Temperatures", ylim=c(0, 35),
errbar.y.polygon.list = list(col="grey"))

plot_add(x=t[,"time"], y=t[,"temperature"], type="l")

# How many times this package has been download
library(cranlogs)
HelpersMG <- cran_downloads("HelpersMG", from = "2015-04-07",
                            to = Sys.Date() - 1)
sum(HelpersMG$count)
plot(HelpersMG$date, HelpersMG$count, type="l", bty="n")

## End(Not run)
```

`+.PriorsmcmcComposite` *Set priors for MHalgoGen()*

Description

Construct priors for MHalgoGen()
A check is done to verify that parameter names are not duplicated.

Usage

```
## S3 method for class 'PriorsmcmcComposite'
prior1 + prior2
```

Arguments

`prior1`	The first prior.
`prior2`	The second prior.

Details

+.PriorsmcmcComposite is a general function to set priors for MHalgoGen()

Value

Return a data.frame with the formatted priors

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other mcmcComposite functions: MHalgoGen(), PPD(), as.mcmc.mcmcComposite(), as.parameters(), merge.mcmcComposite(), plot.PriorsmcmcComposite(), plot.mcmcComposite(), setPriors(), setPriors1(), summary.mcmcComposite()

Examples

```
## Not run:
library(HelpersMG)
Priors <- setPriors1(Name="a0", Prior1=0, Prior2=1, Density="dunif",
                     SDProp=0.1, Min=0, Max=1, Init=0.5)
Priors <- Priors + setPriors1(Name="a1", Prior1=0.5, Prior2=0.1, Density="dnorm",
                     SDProp=0.05, Min=0, Max=1, Init=0.5)
# Using Parameters
Priors <- setPriors1(Name="a0", Parameters=c(min=0, max=1), Density="dunif",
                     SDProp=0.1, Min=0, Max=1, Init=0.5)
Priors <- Priors + setPriors1(Name="a1", Parameters=c(mean=0.5, sd=0.1), Density="dnorm",
                     SDProp=0.05, Min=0, Max=1, Init=0.5)

## End(Not run)
```

---

addS3Class *Add a S3 class to an object.*

Description

Add a S3 class as first class to an object.

Usage

```
addS3Class(x, class = NULL)
```

Arguments

x	The object to add class.
class	The class to add.

Details

addS3Class add a S3 class to an object

Value

The same object with the new class as first class

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
print.CF <- function(x) {cat("print.CF ", x)}
result <- "Je suis donc je pense"
result <- addS3Class(result, class="CF")
class(result)
print(result)
result <- addS3Class(result, class=c("ECF", "OCF"))
class(result)
print(result)
```

---

as.mcmc.mcmcComposite *Extract mcmc object from a mcmcComposite object*

Description

Take a mcmcComposite object and create a mcmc.list object to be used with coda package.

Usage

```
## S3 method for class 'mcmcComposite'
as.mcmc(x, ...)
```

Arguments

x	A mcmcComposite obtained as a result of MHalgoGen() function
...	Not used

Details

as.mcmc Extract mcmc object from the result of phenology_MHmcmc to be used with coda package

Value

A mcmc.list object

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other mcmcComposite functions: +.PriorsmcmcComposite(), MHalgoGen(), PPD(), as.parameters(), merge.mcmcComposite(), plot.PriorsmcmcComposite(), plot.mcmcComposite(), setPriors(), setPriors1(), summary.mcmcComposite()

Examples

```
## Not run:
library(HelpersMG)
require(coda)
x <- rnorm(30, 10, 2)
dnormx <- function(data, x) {
 data <- unlist(data)
 return(-sum(dnorm(data, mean=x['mean'], sd=x['sd'], log=TRUE)))
}
parameters_mcmc <- data.frame(Density=c('dnorm', 'dlnorm'),
Prior1=c(10, 0.5), Prior2=c(2, 0.5), SDProp=c(1, 1),
Min=c(-3, 0), Max=c(100, 10), Init=c(10, 2), stringsAsFactors = FALSE,
row.names=c('mean', 'sd'))
mcmc_run <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, data=x,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=1)
plot(mcmc_run, xlim=c(0, 20))
plot(mcmc_run, xlim=c(0, 10), parameters="sd")
mcmcforcoda <- as.mcmc(mcmc_run)
#' heidel.diag(mcmcforcoda)
raftery.diag(mcmcforcoda)
autocorr.diag(mcmcforcoda)
acf(mcmcforcoda[[1]][,"mean"], lag.max=20, bty="n", las=1)
acf(mcmcforcoda[[1]][,"sd"], lag.max=20, bty="n", las=1)
batchSE(mcmcforcoda, batchSize=100)
# The batch standard error procedure is usually thought to
# be not as accurate as the time series methods used in summary
summary(mcmcforcoda)$statistics[,"Time-series SE"]
summary(mcmc_run)
as.parameters(mcmc_run)
lastp <- as.parameters(mcmc_run, index="last")
parameters_mcmc[,"Init"] <- lastp
# The n.adapt set to 1 is used to not record the first set of parameters
# then it is not duplicated (as it is also the last one for
# the object mcmc_run)
mcmc_run2 <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, data=x,
likelihood=dnormx, n.chains=1, n.adapt=1, thin=1, trace=1)
mcmc_run3 <- merge(mcmc_run, mcmc_run2)
####### no adaptation, n.adapt must be 0
parameters_mcmc[,"Init"] <- c(mean(x), sd(x))
mcmc_run3 <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, data=x,
likelihood=dnormx, n.chains=1, n.adapt=0, thin=1, trace=1)

## End(Not run)
```

`as.parameters` *Extract parameters from mcmcComposite object*

Description

Take a mcmcComposite object and create a vector object with parameter value at specified iteration.
If `index="best"`, the function will return the parameters for the highest likelihood. It also indicates at which iteration the maximum lihelihood has been observed.
If `index="last"`, the function will return the parameters for the last likelihood.
If `index="median"`, the function will return the median value of the parameter.
if `index="quantile"`, the function will return the `probs` defined by quantiles parameter.
If `index="mode"`, the function will return the mode value of the parameter based on Asselin de Beauville (1978) method.
`index` can also be a numeric value. It uses all the chains being concatanated.
This function uses the complete iterations available if total is TRUE. The adaptation part is never used.
`index` can also be a function applied to the iterations.

Usage

```
as.parameters(
  x = stop("A result obtained after a MCMC analysis must be given."),
  total = FALSE,
  index = "median",
  chain = "all",
  probs = c(0.025, 0.5, 0.975),
  silent = FALSE
)
```

Arguments

`x`	A mcmcComposite obtained as a result of `MHalgoGen()` function
`total`	If TRUE, does not use the thinned results.
`index`	At which iteration the parameters must be taken, see description.
`chain`	The chain in which to get parameters; "all" is for all chains.
`probs`	Quantiles to be returned, see description.
`silent`	If TRUE, does not print any information.

Value

A vector with parameters at maximum likelihood or index position

Author(s)

Marc Girondot <marc.girondot@gmail.com>

References

Asselin de Beauville J.-P. (1978). Estimation non paramétrique de la densité et du mode, exemple de la distribution Gamma. Revue de Statistique Appliquée, 26(3):47-70.

See Also

Other mcmcComposite functions: `+.PriorsmcmcComposite()`, `MHalgoGen()`, `PPD()`, `as.mcmc.mcmcComposite()`, `merge.mcmcComposite()`, `plot.PriorsmcmcComposite()`, `plot.mcmcComposite()`, `setPriors()`, `setPriors1()`, `summary.mcmcComposite()`

Examples

```
## Not run:
library(HelpersMG)
require(coda)
x <- rnorm(30, 10, 2)
dnormx <- function(data, x) {
 data <- unlist(data)
 return(-sum(dnorm(data, mean=x['mean'], sd=x['sd'], log=TRUE)))
}
parameters_mcmc <- data.frame(Density=c('dnorm', 'dlnorm'),
                              Prior1=c(10, 0.5),
                              Prior2=c(2, 0.5),
                              SDProp=c(1, 1),
                              Min=c(-3, 0),
                              Max=c(100, 10),
                              Init=c(10, 2),
                              stringsAsFactors = FALSE,
                              row.names=c('mean', 'sd'))
mcmc_run <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, data=x,
                      likelihood=dnormx, n.chains=1, n.adapt=100,
                      thin=1, trace=1)
plot(mcmc_run, xlim=c(0, 20))
plot(mcmc_run, xlim=c(0, 10), parameters="sd")
mcmcforcoda <- as.mcmc(mcmc_run)
#' heidel.diag(mcmcforcoda)
raftery.diag(mcmcforcoda)
autocorr.diag(mcmcforcoda)
acf(mcmcforcoda[[1]][,"mean"], lag.max=20, bty="n", las=1)
acf(mcmcforcoda[[1]][,"sd"], lag.max=20, bty="n", las=1)
batchSE(mcmcforcoda, batchSize=100)

# The batch standard error procedure is usually thought to
# be not as accurate as the time series methods used in summary
summary(mcmcforcoda)$statistics[,"Time-series SE"]
summary(mcmc_run)
as.parameters(mcmc_run)
lastp <- as.parameters(mcmc_run, index="last")
parameters_mcmc[,"Init"] <- lastp

# The n.adapt set to 1 is used to not record the first set of parameters
# then it is not duplicated (as it is also the last one for
```

```
# the object mcmc_run)
mcmc_run2 <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, data=x,
                       likelihood=dnormx, n.chains=1, n.adapt=1,
                       thin=1, trace=1)
mcmc_run3 <- merge(mcmc_run, mcmc_run2)

####### no adaptation, n.adapt must be 0
parameters_mcmc[,"Init"] <- c(mean(x), sd(x))
mcmc_run3 <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, data=x,
                       likelihood=dnormx, n.chains=1, n.adapt=0,
                       thin=1, trace=1)
# With index being median, it returns the median value for each parameter
as.parameters(mcmc_run3, index="median")
as.parameters(mcmc_run3, index="mode")
as.parameters(mcmc_run3, index="best")
as.parameters(mcmc_run3, index="quantile", probs=0.025)
as.parameters(mcmc_run3, index="quantile", probs=0.975)
as.parameters(mcmc_run3, index="quantile", probs=c(0.025, 0.975))
d(as.parameters(mcmc_run3, index = function(x) mean(x)))

## End(Not run)
```

`asc` *Return the codes (in UTF-8) of a string*

Description

Return the codes (in UTF-8) of a string.

Usage

```
asc(x)
```

Arguments

`x`	The string to be analyzed

Details

asc returns the codes (in UTF-8) of a string

Value

A vector with ITF-8 codes of a string

Author(s)

Based on this blog: http://datadebrief.blogspot.com/2011/03/ascii-code-table-in-r.html

See Also

Other Characters: `char()`, `d()`, `tnirp()`

Examples

```
asc("abcd")
asc("ABCD")
```

`barplot_errbar` *Plot a barplot graph with error bar on y*

Description

To plot data, just use it as a normal barplot but add the errbar.y values or errbar.y.minus, errbar.y.plus if bars for y axis are asymetric. Use y.plus and y.minus to set absolut limits for error bars. Note that y.plus and y.minus have priority over errbar.y, errbar.y.minus and errbar.y.plus.

Usage

```
barplot_errbar(
  ...,
  errbar.y = NULL,
  errbar.y.plus = NULL,
  errbar.y.minus = NULL,
  y.plus = NULL,
  y.minus = NULL,
  errbar.tick = 1/50,
  errbar.lwd = par("lwd"),
  errbar.lty = par("lty"),
  errbar.col = par("fg"),
  add = FALSE
)
```

Arguments

`...`	Parameters for barplot() such as main= or ylim=
`errbar.y`	The length of error bars for y. Recycled if necessary.
`errbar.y.plus`	The length of positive error bars for y. Recycled if necessary.
`errbar.y.minus`	The length of negative error bars for y. Recycled if necessary.
`y.plus`	The absolut position of the positive error bar for y. Recycled if necessary.
`y.minus`	The absolut position of the nagative error bar for y. Recycled if necessary.
`errbar.tick`	Size of small ticks at the end of error bars defined as a proportion of total width or height graph size.
`errbar.lwd`	Error bar line width, see par("lwd")
`errbar.lty`	Error bar line type, see par("lwd")
`errbar.col`	Error bar line color, see par("col")
`add`	If true, add the graph to the previous one.

Details

barplot_errbar plot a barplot with error bar on y

Value

A numeric vector (or matrix, when beside = TRUE), say mp, giving the coordinates of all the bar midpoints drawn, useful for adding to the graph.
If beside is true, use colMeans(mp) for the midpoints of each group of bars, see example.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

plot_errorbar

Other plot and barplot functions: ScalePreviousPlot(), plot_add(), plot_errbar(), show_name()

Examples

```
## Not run:
barplot_errbar(rnorm(10, 10, 3),
 xlab="axe x", ylab="axe y", bty="n",
  errbar.y.plus=rnorm(10, 1, 0.1), col=rainbow(10),
  names.arg=paste("Group",1:10), cex.names=0.6)
y <- rnorm(10, 10, 3)
barplot_errbar(y,
                xlab="axe x", ylab="axe y", bty="n",
              y.plus=y+2)

## End(Not run)
```

---

cArrows *Draw curved lines with arrowhead*

Description

Draw a curved line with arrowhead.

Usage

```
cArrows(
  x1,
  y1,
  x2,
  y2,
  code = 2,
  size = 1,
```

```
  width = 1.2/4/cin,
  open = TRUE,
  sh.adj = 0.1,
  sh.lwd = 1,
  sh.col = par("fg"),
  sh.lty = 1,
  h.col = sh.col,
  h.col.bo = sh.col,
  h.lwd = sh.lwd,
  h.lty = sh.lty,
  curved = FALSE,
  beautiful.arrow = 2/3
)
```

Arguments

x1	coordinates of points from which to draw.
y1	coordinates of points from which to draw.
x2	coordinates of points to which to draw.
y2	coordinates of points to which to draw.
code	integer code (1, 2, or 3), determining kind of arrows to be drawn.
size	size of the arrowhead.
width	width of the arrowhead.
open	shape of the arrowhead.
sh.adj	Shift the beginning of the line.
sh.lwd	width of the line.
sh.col	color of the line.
sh.lty	type of line.
h.col	color of the arrowhead.
h.col.bo	color of the arrowhead border.
h.lwd	width of the arrowhead.
h.lty	type of line for the arrowhead.
curved	0 is a straigth line, positive of negative value make the line curved.
beautiful.arrow	if open is false, make the arrowhead more beautiful.

Details

cArrows draws curved lines with arrowhead

Value

A list wit lab.x and lab.y being the position where to draw label

Author(s)

Modified from iGraph

Examples

```
plot(c(1, 10), c(1, 10), type="n", bty="n")
cArrows(x1=2, y1=2, x2=6, y2=6, curved=1)
cArrows(x1=2, y1=2, x2=6, y2=6, curved=0)
cArrows(x1=2, y1=2, x2=6, y2=6, curved=1, sh.adj=1)
cArrows(x1=2, y1=2, x2=6, y2=6, curved=-1, open=FALSE)
cArrows(x1=9, y1=2, x2=6, y2=6, curved=-1, open=FALSE, sh.col="red")
cArrows(x1=9, y1=9, x2=6, y2=6, curved=-1, open=FALSE, h.col="red")
cArrows(x1=2, y1=9, x2=6, y2=6, curved=1, open=FALSE, h.col="red", h.col.bo="red")
```

ChangeCoordinate *Return a value in a changed coordinate*

Description

Return a value in a changed coordinate system.

Usage

```
ChangeCoordinate(
  x = stop("At least one value to convert must be provided"),
  initial = stop("Set of two values must be provided as references"),
  transformed = stop("Set of two transformed values must be provided")
)
```

Arguments

x	value to convert
initial	Set of two values in the original system
transformed	Set of the two values in the converted system

Details

ChangeCoordinate returns a value in a changed coordinate

Value

A value in the new system

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
ChangeCoordinate(x=c(10, 20), initial=c(1, 100), transformed=c(0, 1))
```

`char` *Return the characters defined by the codes*

Description

Return a string with characters defined by the codes.

Usage

```
char(n)
```

Arguments

`n`	The code to be used to return a character

Details

char returns the characters defined by the codes

Value

A string with characters defined by the codes

Author(s)

Based on this blog: http://datadebrief.blogspot.com/2011/03/ascii-code-table-in-r.html

See Also

Other Characters: `asc()`, `d()`, `tnirp()`

Examples

```
char(65:75)
char(unlist(tapply(144:175, 144:175, function(x) {c(208, x)})))
```

compare *Run a shiny application for basic functions of comparison*

Description

Run a shiny application for basic functions of comparison.

Usage

```
compare()
```

Details

compare runs a shiny application for basic functions of comparison

Value

Nothing

Author(s)

Marc Girondot <marc.girondot@gmail.com>

References

Girondot, M., Guillon, J.-M., 2018. The w-value: An alternative to t- and X2 tests. Journal of Biostatistics & Biometrics 1, 1-3.

See Also

Other w-value functions: `contingencyTable.compare()`, `series.compare()`

Examples

```
## Not run:
library(HelpersMG)
compare()

## End(Not run)
```

compare_AIC *Compares the AIC of several outputs*

Description

This function is used to compare the AIC of several outputs obtained with the same data but with different set of parameters.
The parameters must be lists with $aic or $AIC or $value and $par elements or if AIC(element) is defined.
if `$value` and `$par` are present in the object, the AIC is calculated as `2*factor.value*value+2*length(par)`.
If `$value` is -log(likeihood), then factor.value must be 1 and if `$value` is log(likeihood), then factor.value must be -1.
If several objects are within the same list, their AIC are summed.
For example, compare_AIC(g1=list(group), g2=list(separe1, separe2)) can be used to compare a single model onto two different sets of data against each set of data fited with its own set of parameters.
Take a look at `ICtab` in package `bbmle` which is similar.

Usage

```
compare_AIC(
  ...,
  factor.value = 1,
  silent = FALSE,
  FUN = function(x) specify_decimal(x, decimals = 2)
)
```

Arguments

`...`	Successive results to be compared as lists.
`factor.value`	The $value of the list object is multiplied by factor.value to calculate AIC.
`silent`	If TRUE, nothing is displayed.
`FUN`	Function used to show values

Details

compare_AIC compares the AIC of several outputs obtained with the same data.

Value

A list with DeltaAIC and Akaike weight for the models.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other AIC: ELPDweight(), ExtractAIC.glm(), FormatCompareAIC(), compare_AICc(), compare_BIC()

Examples

```
## Not run:
library("HelpersMG")
# Here two different models are fitted
x <- 1:30
y <- rnorm(30, 10, 2)+log(x)
plot(x, y)
d <- data.frame(x=x, y=y)
m1 <- lm(y ~ x, data=d)
m2 <- lm(y ~ log(x), data=d)
compare_AIC(linear=m1, log=m2)
# Here test if two datasets can be modeled with a single model
x2 <- 1:30
y2 <- rnorm(30, 15, 2)+log(x2)
plot(x, y, ylim=c(5, 25))
plot_add(x2, y2, col="red")
d2 <- data.frame(x=x2, y=y2)
m1_2 <- lm(y ~ x, data=d2)
x_grouped <- c(x, x2)
y_grouped <- c(y, y2)
d_grouped <- data.frame(x=x_grouped, y=y_grouped)
m1_grouped <- lm(y ~ x, data=d_grouped)
compare_AIC(separate=list(m1, m1_2), grouped=m1_grouped)

## End(Not run)
```

---

compare_AICc *Compares the AICc of several outputs*

Description

This function is used to compare the AICc of several outputs obtained with the same data but with different set of parameters.
Each object must have associated `logLik()` method with df and nobs attributes.
AICc for object x will be calculated as `2*factor.value*logLik(x)+(2*attributes(logLik(x))$df*(attributes(logL`

Usage

```
compare_AICc(
  ...,
  factor.value = -1,
  silent = FALSE,
  FUN = function(x) specify_decimal(x, decimals = 2)
)
```

Arguments

...	Successive results to be compared as lists.
factor.value	The $value of the list object is multiplied by factor.value to calculate BIC.
silent	If TRUE, nothing is displayed.
FUN	Function used to show values

Details

compare_AICc compares the AICc of several outputs obtained with the same data.

Value

A list with DeltaAICc and Akaike weight for the models.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other AIC: ELPDweight(), ExtractAIC.glm(), FormatCompareAIC(), compare_AIC(), compare_BIC()

Examples

```
## Not run:
library("HelpersMG")
# Here two different models are fitted
x <- 1:30
y <- rnorm(30, 10, 2)+log(x)
plot(x, y)
d <- data.frame(x=x, y=y)
m1 <- lm(y ~ x, data=d)
m2 <- lm(y ~ log(x), data=d)
compare_BIC(linear=m1, log=m2, factor.value=-1)
# Here test if two datasets can be modeled with a single model
x2 <- 1:30
y2 <- rnorm(30, 15, 2)+log(x2)
plot(x, y, ylim=c(5, 25))
plot_add(x2, y2, col="red")
d2 <- data.frame(x=x2, y=y2)
m1_2 <- lm(y ~ x, data=d2)
x_grouped <- c(x, x2)
y_grouped <- c(y, y2)
d_grouped <- data.frame(x=x_grouped, y=y_grouped)
m1_grouped <- lm(y ~ x, data=d_grouped)
compare_AICc(separate=list(m1, m1_2), grouped=m1_grouped, factor.value=-1)
# Or simply
compare_AICc(m1=list(AICc=100), m2=list(AICc=102))

## End(Not run)
```

compare_BIC *Compares the BIC of several outputs*

Description

This function is used to compare the BIC of several outputs obtained with the same data but with different set of parameters.
Each object must have associated `logLik()` method with df and nobs attributes.
BIC for object x will be calculated as `2*factor.value*sum(logLik(x))+sum(attributes(logLik(x))$df)*log(attrib`
When several data (i..n) are included, the global BIC is calculated as:
`2*factor.value*sum(logLik(x))` for `i..n+sum(attributes(logLik(x))$df)` for `i..n*log(attributes(logLik(x` for `i..n))`

Usage

```
compare_BIC(
  ...,
  factor.value = -1,
  silent = FALSE,
  FUN = function(x) specify_decimal(x, decimals = 2)
)
```

Arguments

`...`	Successive results to be compared as lists.
`factor.value`	The $value of the list object is multiplied by factor.value to calculate BIC.
`silent`	If TRUE, nothing is displayed.
`FUN`	Function used to show values

Details

compare_BIC compares the BIC of several outputs obtained with the same data.

Value

A list with DeltaBIC and Akaike weight for the models.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other AIC: `ELPDweight()`, `ExtractAIC.glm()`, `FormatCompareAIC()`, `compare_AIC()`, `compare_AICc()`

Examples

```
## Not run:
library("HelpersMG")
# Here two different models are fitted
x <- 1:30
y <- rnorm(30, 10, 2)+log(x)
plot(x, y)
d <- data.frame(x=x, y=y)
m1 <- lm(y ~ x, data=d)
m2 <- lm(y ~ log(x), data=d)
compare_BIC(linear=m1, log=m2, factor.value=-1)
# Here test if two datasets can be modeled with a single model
x2 <- 1:30
y2 <- rnorm(30, 15, 2)+log(x2)
plot(x, y, ylim=c(5, 25))
plot_add(x2, y2, col="red")
d2 <- data.frame(x=x2, y=y2)
m1_2 <- lm(y ~ x, data=d2)
x_grouped <- c(x, x2)
y_grouped <- c(y, y2)
d_grouped <- data.frame(x=x_grouped, y=y_grouped)
m1_grouped <- lm(y ~ x, data=d_grouped)
compare_BIC(separate=list(m1, m1_2), grouped=m1_grouped, factor.value=-1)

## End(Not run)
```

---

contingencyTable.compare

Contingency table comparison using Akaike weight

Description

This function is used as a replacement of chisq.test() to not use p-value.

Usage

```
contingencyTable.compare(
  table,
  criterion = c("AIC", "AICc", "BIC"),
  probs = NULL
)
```

Arguments

table	A matrix or a data.frame with series in rows and number of each category in column
criterion	Which criterion is used for model selection
probs	Series of probabilities used for conformity comparison

Details

contingencyTable.compare compares contingency table using Akaike weight.

Value

The probability that a single proportion model is sufficient to explain the data

Author(s)

Marc Girondot <marc.girondot@gmail.com>

References

Girondot, M., Guillon, J.-M., 2018. The w-value: An alternative to t- and X2 tests. Journal of Biostatistics & Biometrics 1, 1-4.

See Also

Other w-value functions: compare(), series.compare()

Examples

```
## Not run:
library("HelpersMG")

# Symmetry of Lepidochelys olivacea scutes
table <- t(data.frame(SriLanka=c(200, 157), AfricaAtl=c(19, 12),
                      Guyana=c(8, 6), Suriname=c(162, 88),
                      MexicoPac1984=c(42, 34), MexicoPac2014Dead=c(8, 9),
                      MexicoPac2014Alive=c(13, 12),
                      row.names =c("Symmetric", "Asymmetric")))
table
contingencyTable.compare(table)

table <- t(data.frame(SriLanka=c(200, 157), AfricaAtl=c(19, 12), Guyana=c(8, 6),
                      Suriname=c(162, 88), MexicoPac1984=c(42, 34),
                      MexicoPac2014Dead=c(8, 9),
                      MexicoPac2014Alive=c(13, 12), Lepidochelys.kempii=c(99, 1),
                      row.names =c("Symmetric", "Asymmetric")))
table
contingencyTable.compare(table)

# Conformity to a model
table <- matrix(c(33, 12, 25, 75), ncol = 2, byrow = TRUE)
probs <- c(0.5, 0.5)
contingencyTable.compare(table, probs=probs)

# Conformity to a model
table <- matrix(c(33, 12), ncol = 2, byrow = TRUE)
probs <- c(0.5, 0.5)
contingencyTable.compare(table, probs=probs)
```

```
# Conformity to a model
table <- matrix(c(33, 12, 8, 25, 75, 9), ncol = 3, byrow = TRUE)
probs <- c(0.8, 0.1, 0.1)
contingencyTable.compare(table, probs=probs)

# Comparison of chisq.test() and this function
table <- matrix(c(NA, NA, 25, 75), ncol = 2, byrow = TRUE)

pv <- NULL
aw <- NULL
par(new=FALSE)
n <- 100

for (GroupA in 0:n) {
  table[1, 1] <- GroupA
  table[1, 2] <- n-GroupA
  pv <- c(pv, chisq.test(table)$p.value)
  aw <- c(aw, contingencyTable.compare(table, criterion="BIC")[1])
}

x <- 0:n
y <- pv
y2 <- aw
plot(x=x, y=y, type="l", bty="n", las=1, xlab="Number of type P in Group B", ylab="Probability",
     main="", lwd=2)
lines(x=x, y=y2, type="l", col="red", lwd=2)

# w-value
(l1 <- x[which(aw>0.05)[1]])
(l2 <- rev(x)[which(rev(aw)>0.05)[1]])

aw[l1]
pv[l1]

aw[l2+2]
pv[l2+2]

# p-value
l1 <- which(pv>0.05)[1]
l2 <- max(which(pv>0.05))

aw[l1]
pv[l1]

aw[l2]
pv[l2]

y[which(y2>0.05)[1]]
y[which(rev(y2)>0.05)[1]]

par(xpd=TRUE)
text(x=25, y=1.15, labels="Group A: 25 type P / 100", pos=1)
```

```
segments(x0=25, y0=0, x1=25, y1=1, lty=3)

# plot(1, 1)

v1 <- c(expression(italic("p")*"-value"), expression("after "*chi^2*"-test"))
v2 <- c(expression(italic("w")*"-value for A"), expression("and B identical models"))
legend("topright", legend=c(v1, v2),
       y.intersp = 1,
       col=c("black", "black", "red", "red"), bty="n", lty=c(1, 0, 1, 0))

segments(x0=0, x1=n, y0=0.05, y1=0.05, lty=2)
text(x=101, y=0.05, labels = "0.05", pos=4)

## End(Not run)
```

`convert.tz` *Convert one Date-Time from one timezone to another*

Description

Convert one Date-Time from one timezone to another.
Available timezones can be shown using OlsonNames().

Usage

```
convert.tz(x, tz = Sys.timezone())
```

Arguments

`x`	The date-time in POSIXlt or POSIXct format
`tz`	The timezone

Details

convert.tz Convert one Date-Time from one timezone to another

Value

A POSIXlt or POSIXct date converted

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Function `with_tz()` from `lubridate` package does the same. I keep it here only for compatibility with old scripts.

Examples

```
d <- as.POSIXlt("2010-01-01 17:34:20", tz="UTC")
convert.tz(d, tz="America/Guatemala")
```

`cutter` *Distribution of the fitted distribution without cut.*

Description

If observations is a data.frame, it can have 4 columns:
A column for the measurements;
A column for the lower detection limit;
A column for the upper detection limit;
A column for the truncated of censored nature of the data.
The names of the different columns are in the observations.colname, lower_detection_limit.colname, upper_detection_limit.colname and cut_method.colname.
If lower_detection_limit.colname is NULL or if the column does not exist, the data are supposed to not be left-cut and if upper_detection_limit.colname is NULL or if the column does not exist, the data are supposed to not be right-cut.
If observations is a vector, then the parameters lower_detection_limit and/or upper_detection_limit must be given. Then cut_method must be also provided.
In observations, -Inf must be used to indicate a value below the lower detection limit and +Inf must be used for a value above the upper detection limit.
Be careful: NA is used to represent a missing data and not a value below of above the detection limit.
If lower_detection_limit, upper_detection_limit or cut_method are only one value, they are supposed to be used for all the observations.
Definitions for censored or truncated distribution vary, and the two terms are sometimes used interchangeably. Let the following data set:
1 1.25 2 4 5

Censoring: some observations will be censored, meaning that we only know that they are below (or above) some bound. This can for instance occur if we measure the concentration of a chemical in a water sample. If the concentration is too low, the laboratory equipment cannot detect the presence of the chemical. It may still be present though, so we only know that the concentration is below the laboratory's detection limit.

If the detection limit is 1.5, so that observations that fall below this limit is censored, our example data set would become:
<1.5 <1.5 2 4 5; that is, we don't know the actual values of the first two observations, but only that they are smaller than 1.5.

Truncation: the process generating the data is such that it only is possible to observe outcomes above (or below) the truncation limit. This can for instance occur if measurements are taken using a detector which only is activated if the signals it detects are above a certain limit. There may be lots of weak incoming signals, but we can never tell using this detector.

If the truncation limit is 1.5, our example data set would become: 2 4 5; and we would not know that there in fact were two signals which were not recorded.
If n.iter is NULL, no Bayesian MCMC is performed but credible interval will not be available.

Usage

```
cutter(
  observations = stop("Observations must be provided"),
  observations.colname = "Observations",
  lower_detection_limit.colname = "LDL",
  upper_detection_limit.colname = "UDL",
  cut_method.colname = "Cut",
  par = NULL,
  lower_detection_limit = NULL,
  upper_detection_limit = NULL,
  cut_method = "censored",
  distribution = "gamma",
  n.mixture = 1,
  n.iter = 5000,
  n.adapt = 100,
  debug = FALSE,
  progress.bar = TRUE,
  priors = NULL,
  adaptive = TRUE,
  session = NULL
)
```

Arguments

observations	The observations; see description
observations.colname	If observations is a data.frame, the name of column with observations
lower_detection_limit.colname	If observations is a data.frame, the name of column with lower detection limit
upper_detection_limit.colname	If observations is a data.frame, the name of column with upper detection limit
cut_method.colname	If observations is a data.frame, the name of column with cut method, being "censored" or "truncated"
par	Initial values for parameters of distribution
lower_detection_limit	Value for lower detection limit
upper_detection_limit	Value for upper detection limit
cut_method	Value for cut method, being "censored" or "truncated"
distribution	Can be gamma, normal, weibull, lognormal, or generalized.gamma

n.mixture	Number of distributions
n.iter	Number of iteration for Bayesian MCMC and to estimate the goodness-of-fit
n.adapt	Number of burn-in iterations Bayesian MCMC
debug	If TRUE, show some information
progress.bar	If TRUE, show a progress bar for MCMC
priors	A dataframe with priors.
adaptive	Should the adaptive methodologie for SDprop be used
session	The session of a shiny process

Details

cutter returns the fitted distribution without cut

Value

The parameters of distribution of values below or above the detection limit.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Distributions: dSnbinom(), dbeta_new(), dcutter(), dggamma(), dnbinom_new(), logLik.cutter(), plot.cutter(), print.cutter(), r2norm(), rcutter(), rmnorm(), rnbinom_new()

Examples

```
## Not run:
library(HelpersMG)
# ________________________________________________________________
# right censored distribution with gamma distribution
# ________________________________________________________________
# Detection limit
DL <- 100
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# remove the data below the detection limit
obc[obc>DL] <- +Inf
# search for the parameters the best fit these censored data
result <- cutter(observations=obc, upper_detection_limit=DL,
                           cut_method="censored")
result
plot(result, xlim=c(0, 150), breaks=seq(from=0, to=150, by=10), col.mcmc=NULL)
plot(result, xlim=c(0, 150), breaks=seq(from=0, to=150, by=10))
# ________________________________________________________________
# The same data seen as truncated data with gamma distribution
# ________________________________________________________________
obc <- obc[is.finite(obc)]
```

```
# search for the parameters the best fit these truncated data
result <- cutter(observations=obc, upper_detection_limit=DL,
                          cut_method="truncated")
result
plot(result, xlim=c(0, 150), breaks=seq(from=0, to=150, by=10))
# ____________________________________________________________
# left censored distribution with gamma distribution
# ____________________________________________________________
# Detection limit
DL <- 10
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# remove the data below the detection limit
obc[obc<DL] <- -Inf
# search for the parameters the best fit these truncated data
result <- cutter(observations=obc, lower_detection_limit=DL,
                         cut_method="censored")
result
plot(result, xlim=c(0, 200), breaks=seq(from=0, to=300, by=10))
# ____________________________________________________________
# left censored distribution with mixture of gamma distribution
# ____________________________________________________________
#' # Detection limit
library(HelpersMG)
# Generate 200 random data from a gamma distribution
set.seed(1234)
obc <- c(rgamma(100, scale=10, shape=5), rgamma(100, scale=20, shape=10))
LDL <- 20
l <- seq(from=0, to=LDL, length.out=1001)
p <- pgamma(l, scale=10, shape=5)*0.5+pgamma(l, scale=20, shape=10)
deltal <- l[2]-l[1]
expected_LDL <- sum((l[-1]-deltal/2)*(p[-1]-p[-length(p)]))/sum((p[-1]-p[-length(p)]))
# remove the data below the detection limit
obc[obc<LDL] <- -Inf

UDL <- 300
l <- seq(from=UDL, to=1000, length.out=1001)
p <- pgamma(l, scale=10, shape=5)*0.5+pgamma(l, scale=20, shape=10)
deltal <- l[2]-l[1]
expected_UDL <- sum((l[-1]-deltal/2)*(p[-1]-p[-length(p)]))/sum((p[-1]-p[-length(p)]))
obc[obc>UDL] <- +Inf

# search for the parameters the best fit these truncated data
result1_gamma <- cutter(observations=obc, lower_detection_limit=LDL,
                         upper_detection_limit = UDL,
                         distribution="gamma",
                         cut_method="censored", n.iter=5000, debug=0)
result1_normal <- cutter(observations=obc, lower_detection_limit=LDL,
                         upper_detection_limit = UDL,
                         distribution="normal",
                         cut_method="censored", n.iter=5000)
result1_lognormal <- cutter(observations=obc, lower_detection_limit=LDL,
                         upper_detection_limit = UDL,
```

```
                          distribution="lognormal",
                          cut_method="censored", n.iter=5000)
result1_Weibull <- cutter(observations=obc, lower_detection_limit=LDL,
                          upper_detection_limit = UDL,
                          distribution="Weibull",
                          cut_method="censored", n.iter=5000)
result1_generalized.gamma <- cutter(observations=obc, lower_detection_limit=LDL,
                          upper_detection_limit = UDL,
                          distribution="generalized.gamma",
                          cut_method="censored", n.iter=5000)
result2_gamma <- cutter(observations=obc, lower_detection_limit=LDL,
                          upper_detection_limit = UDL,
                          distribution="gamma",
                          n.mixture=2,
                          cut_method="censored", n.iter=5000)
result2_normal <- cutter(observations=obc, lower_detection_limit=LDL,
                          upper_detection_limit = UDL,
                          distribution="normal",
                          n.mixture=2,
                          cut_method="censored", n.iter=5000)
result2_lognormal <- cutter(observations=obc, lower_detection_limit=LDL,
                          upper_detection_limit = UDL,
                          distribution="lognormal",
                          n.mixture=2,
                          cut_method="censored", n.iter=5000)
result2_Weibull <- cutter(observations=obc, lower_detection_limit=LDL,
                          upper_detection_limit = UDL,
                          distribution="Weibull",
                          n.mixture=2,
                          cut_method="censored", n.iter=5000)
result2_generalized.gamma <- cutter(observations=obc, lower_detection_limit=LDL,
                          upper_detection_limit = UDL,
                          distribution="generalized.gamma",
                          n.mixture=2,
                          cut_method="censored", n.iter=5000)

compare_AIC(nomixture.gamma=result1_gamma,
             nomixture.normal=result1_normal,
             nomixture.lognormal=result1_lognormal,
             nomixture.Weibull=result1_Weibull,
             nomixture.generalized.gamma=result1_generalized.gamma,
             mixture.gamma=result2_gamma,
             mixture.normal=result2_normal,
             mixture.lognormal=result2_lognormal,
             mixture.Weibull=result2_Weibull,
             mixture.generalized.gamma=result2_generalized.gamma)

plot(result2_gamma, xlim=c(0, 600), breaks=seq(from=0, to=600, by=10))
plot(result2_generalized.gamma, xlim=c(0, 600), breaks=seq(from=0, to=600, by=10))

# ____________________________________________________________
# left and right censored distribution
# ____________________________________________________________
```

```
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# Detection limit
LDL <- 10
# remove the data below the detection limit
obc[obc<LDL] <- -Inf
# Detection limit
UDL <- 100
# remove the data below the detection limit
obc[obc>UDL] <- +Inf
# search for the parameters the best fit these censored data
result <- cutter(observations=obc, lower_detection_limit=LDL,
                          upper_detection_limit=UDL,
                         cut_method="censored")
result
plot(result, xlim=c(0, 150), col.DL=c("black", "grey"),
                            col.unobserved=c("green", "blue"),
     breaks=seq(from=0, to=150, by=10))
# ____________________________________________________________
# Example with two values for lower detection limits
# corresponding at two different methods of detection for example
# with gamma distribution
# ____________________________________________________________
obc <- rgamma(50, scale=20, shape=2)
# Detection limit for sample 1 to 50
LDL1 <- 10
# remove the data below the detection limit
obc[obc<LDL1] <- -Inf
obc2 <- rgamma(50, scale=20, shape=2)
# Detection limit for sample 1 to 50
LDL2 <- 20
# remove the data below the detection limit
obc2[obc2<LDL2] <- -Inf
obc <- c(obc, obc2)
# search for the parameters the best fit these censored data
result <- cutter(observations=obc,
                           lower_detection_limit=c(rep(LDL1, 50), rep(LDL2, 50)),
                         cut_method="censored")
result
# It is difficult to choose the best set of colors
plot(result, xlim=c(0, 150), col.dist="red",
     col.unobserved=c(rgb(red=1, green=0, blue=0, alpha=0.1),
                      rgb(red=1, green=0, blue=0, alpha=0.2)),
     col.DL=c(rgb(red=0, green=0, blue=1, alpha=0.5),
                      rgb(red=0, green=0, blue=1, alpha=0.9)),
     breaks=seq(from=0, to=200, by=10))

# ____________________________________________________________________
# left censored distribution comparison of normal, lognormal,
# weibull, generalized gamma, and gamma without Bayesian MCMC
# Comparison with Akaike Information Criterion
# ____________________________________________________________________
# Detection limit
```

```
DL <- 10
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# remove the data below the detection limit
obc[obc<DL] <- -Inf

result_gamma <- cutter(observations=obc, lower_detection_limit=DL,
                          cut_method="censored", distribution="gamma",
                          n.iter=NULL)
plot(result_gamma)

result_lognormal <- cutter(observations=obc, lower_detection_limit=DL,
                          cut_method="censored", distribution="lognormal",
                          n.iter=NULL)
plot(result_lognormal)

result_weibull <- cutter(observations=obc, lower_detection_limit=DL,
                          cut_method="censored", distribution="weibull",
                          n.iter=NULL)
plot(result_weibull)

result_normal <- cutter(observations=obc, lower_detection_limit=DL,
                          cut_method="censored", distribution="normal",
                          n.iter=NULL)
plot(result_normal)

result_generalized.gamma <- cutter(observations=obc, lower_detection_limit=DL,
                          cut_method="censored", distribution="generalized.gamma",
                          n.iter=NULL)
plot(result_generalized.gamma)

compare_AIC(gamma=result_gamma,
            lognormal=result_lognormal,
            normal=result_normal,
            Weibull=result_weibull,
            Generalized.gamma=result_generalized.gamma)

# ____________________________________________________________________________
# left censored distribution comparison of normal, lognormal,
# weibull, generalized gamma, and gamma
# ____________________________________________________________________________
# Detection limit
DL <- 10
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# remove the data below the detection limit
obc[obc<DL] <- -Inf
# search for the parameters the best fit these truncated data
result_gamma <- cutter(observations=obc, lower_detection_limit=DL,
                          cut_method="censored", distribution="gamma")
result_gamma
plot(result_gamma, xlim=c(0, 250), breaks=seq(from=0, to=250, by=10))
```

```
result_lognormal <- cutter(observations=obc, lower_detection_limit=DL,
                           cut_method="censored", distribution="lognormal")
result_lognormal
plot(result_lognormal, xlim=c(0, 250), breaks=seq(from=0, to=250, by=10))

result_weibull <- cutter(observations=obc, lower_detection_limit=DL,
                           cut_method="censored", distribution="weibull")
result_weibull
plot(result_weibull, xlim=c(0, 250), breaks=seq(from=0, to=250, by=10))

result_normal <- cutter(observations=obc, lower_detection_limit=DL,
                           cut_method="censored", distribution="normal")
result_normal
plot(result_normal, xlim=c(0, 250), breaks=seq(from=0, to=250, by=10))

result_generalized.gamma <- cutter(observations=obc, lower_detection_limit=DL,
                           cut_method="censored", distribution="generalized.gamma")
result_generalized.gamma
plot(result_generalized.gamma, xlim=c(0, 250), breaks=seq(from=0, to=250, by=10))

# ____________________________________________________________________
# Test for similarity in gamma left censored distribution between two
# datasets
# ____________________________________________________________________
obc1 <- rgamma(100, scale=20, shape=2)
# Detection limit for sample 1 to 50
LDL <- 10
# remove the data below the detection limit
obc1[obc1<LDL] <- -Inf
obc2 <- rgamma(100, scale=10, shape=2)
# remove the data below the detection limit
obc2[obc2<LDL] <- -Inf
# search for the parameters the best fit these censored data
result1 <- cutter(observations=obc1,
                  distribution="gamma",
                  lower_detection_limit=LDL,
                  cut_method="censored", n.iter=NULL)
logLik(result1)
plot(result1, xlim=c(0, 200),
     breaks=seq(from=0, to=200, by=10))
result2 <- cutter(observations=obc2,
                  distribution="gamma",
                  lower_detection_limit=LDL,
                  cut_method="censored", n.iter=NULL)
logLik(result2)
plot(result2, xlim=c(0, 200),
     breaks=seq(from=0, to=200, by=10))
result_totl <- cutter(observations=c(obc1, obc2),
                      distribution="gamma",
                      lower_detection_limit=LDL,
                      cut_method="censored", n.iter=NULL)
logLik(result_totl)
plot(result_totl, xlim=c(0, 200),
```

```
     breaks=seq(from=0, to=200, by=10))

compare_AIC(Separate=list(result1, result2),
            Common=result_totl, factor.value=1)
compare_BIC(Separate=list(result1, result2),
            Common=result_totl, factor.value=1)

## End(Not run)
```

---

d *Write an ASCII Representation of a vector object*

Description

Writes an ASCII text representation of an R object.
It can be used as a replacement of dput() for named vectors.
The controls "keepNA", "keepInteger" and "showAttributes" are utilized for named vectors.

Usage

```
d(
  x,
  file = "",
  control = c("keepNA", "keepInteger", "showAttributes"),
  collapse = ", \n  "
)
```

Arguments

x	A named vector object
file	either a character string naming a file or a connection. "" indicates output to the console.
control	character vector indicating deparsing options. See .deparseOpts for their description.
collapse	Characters used to separate values.

Details

d Write an ASCII Representation of a vector object

Value

A string

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Characters: `asc()`, `char()`, `tnirp()`

Examples

```
d(c(A=10, B=20))
dput(c(A=10, B=20))
```

`dbeta_new` *Density for the Beta distributions.*

Description

Density for the Beta distribution with parameters mu and v or shape1 and shape2 (and optional non-centrality parameter ncp).
The returned object has three attributes:
shape1, shape2, and ncp
Note that if x has other attributes, they are preserved.

Usage

```
dbeta_new(
  x,
  mu = NULL,
  v = NULL,
  shape1,
  shape2,
  ncp = 0,
  log = FALSE,
  silent = FALSE
)
```

Arguments

`x`	vector of quantiles.
`mu`	mean of the Beta distribution.
`v`	variance of the Beta distribution.
`shape1`	non-negative parameters of the Beta distribution.
`shape2`	non-negative parameters of the Beta distribution.
`ncp`	non-centrality parameter.
`log`	logical; if TRUE, probabilities p are given as log(p).
`silent`	If FALSE, show the shape1 and shape 2 values.

Details

dbeta_new returns the density for the Beta distributions

The Beta distribution with parameters shape1 = a and shape2 = b has density
gamma(a+b)/(gamma(a)gamma(b))x^(a-1)(1-x)^(b-1)
for a > 0, b > 0 and 0 <= x <= 1 where the boundary values at x=0 or x=1 are defined as by continuity (as limits).
The mean is a/(a+b) and the variance is ab/((a+b)^2 (a+b+1)). These moments and all distributional properties can be defined as limits.

Value

dbeta_new gives the density for the Beta distributions

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Distributions: cutter(), dSnbinom(), dcutter(), dggamma(), dnbinom_new(), logLik.cutter(), plot.cutter(), print.cutter(), r2norm(), rcutter(), rmnorm(), rnbinom_new()

Examples

```
pi <- rbeta(100, shape1=0.48, shape2=0.12)
hist(pi, freq=FALSE, breaks=seq(from=0, to=1, by=0.1), ylim=c(0, 8), las=1)
library("HelpersMG")
mx <- ScalePreviousPlot()$ylim["end"]/
      max(dbeta_new(seq(from=0.01, to=0.99, by=0.01), mu = 0.8, v=0.1))
curve(dbeta_new(x, mu = 0.8, v=0.1)*mx, add=TRUE, col="red")
out <- dbeta_new(0.1, mu = 0.8, v=0.1)
out
attributes(out)$shape1; attributes(out)$shape2; attributes(out)$ncp
dbeta(0.1, shape1=attributes(out)$shape1, shape2=attributes(out)$shape2,
      ncp=attributes(out)$ncp)

# It can be used to generate random numbers using mu and v
out <- dbeta_new(0.1, mu = 0.8, v=0.1, silent=TRUE)
pi <- rbeta(100, shape1=attributes(out)$shape1, shape2=attributes(out)$shape2,
      ncp=attributes(out)$ncp)
hist(pi, freq=FALSE, breaks=seq(from=0, to=1, by=0.1), ylim=c(0, 8), las=1)
```

---

dcutter *Distribution of the fitted distribution without cut.*

Description

If observations must be a data.frame with 4 columns:
observations: A column for the measurements;
LDL: A column for the lower detection limit;
UDL: A column for the upper detection limit;
Cut: A column for the truncated of censored nature of the data.

Usage

```
dcutter(
  par,
  observations = NULL,
  distribution = "gamma",
  n.mixture = NULL,
  debug = FALSE,
  limits.lower = NULL,
  limits.upper = NULL,
  log = TRUE
)
```

Arguments

par	Values for parameters of distribution
observations	The observations; see description.
distribution	Can be gamma, normal, weibull, lognormal, or generalized.gamma.
n.mixture	Number of distributions
debug	If TRUE, show some information. If 2, show more information.
limits.lower	Value for lower detection limit
limits.upper	Value for upper detection limit
log	If TRUE, return the log likelihood

Details

dcutter returns the density of the cutter function

Value

The density of the cutter function according to observations.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Distributions: cutter(), dSnbinom(), dbeta_new(), dggamma(), dnbinom_new(), logLik.cutter(), plot.cutter(), print.cutter(), r2norm(), rcutter(), rmnorm(), rnbinom_new()

Examples

```
## Not run:
library(HelpersMG)
par <- c('shape1' = 0.42265849507444225,
         'scale1' = 14.139457094879594,
         'shape2' = 1.667131542489706,
         'scale2' = 0.10763344388223803,
         'p1' = 0.12283307526788023)
obs <- data.frame(Observations=c(0.755, 1.013, 2.098, 6.265, 4.708, 0.078, 2.169, 0.403, 1.251,
                          0.008, 1.419, 1.078, 2.744, 81.534, 1.426, 13.486, 7.813, 0.165,
                           0.118, 0.864, 0.369, 7.159, 2.605, 1.579, 1.646, 0.484, 4.492,
                            0.139, 0.28, 0.154, 0.106, 0.104, 4.185, 0.735, 0.149, 0.183,
                           0.062, 8.246, 0.165, 0.121, 0.109, 0.092, 0.162, 0.108, 0.139,
                            0.141, 0.124, 0.124, 0.151, 0.141, 0.364, 0.295, 0.09, 0.135,
                            0.154, 0.218, 0.167, -Inf, 0.203, 0.228, 0.107, 0.162, 0.194,
                         0.322, 0.351, 0.17, 0.236, 0.176, 0.107, 0.12, 0.095, 0.27, 0.194,
                                 0.125, 0.123, 0.085, 0.164, 0.106, 0.079, 0.162),
                  LDL=0.001, UDL=NA, Cut="censored")
dcutter(par=par, observations=obs, distribution="gamma",
        n.mixture=NULL, debug=FALSE, limits.lower=NULL,
        limits.upper=NULL,log=FALSE)
dcutter(par=par, observations=obs, distribution="gamma",
        n.mixture=NULL, debug=FALSE, limits.lower=NULL,
        limits.upper=NULL, log=TRUE)


## End(Not run)
```

---

dggamma *Generalized gamma distribution.*

Description

Generalized gamma distribution

Usage

```
dggamma(x, theta, kappa, delta, log = FALSE)

pggamma(q, theta, kappa, delta, lower.tail = TRUE, log.p = FALSE)

qggamma(p, theta, kappa, delta, lower.tail = TRUE, log.p = FALSE)

rggamma(n, theta, kappa, delta)
```

Arguments

x, q	vector of quantiles.
theta	scale parameter.

kappa	shape parameter.
delta	shape parameter.
log, log.p	logical; if TRUE, probabilities *p* are given as *log(p)*.
lower.tail	logical; if TRUE (default), probabilities are *P[X <= x]* otherwise, *P[X > x]*.
p	vector of probabilities.
n	number of observations.

Details

pggamma, qggamma, dggamma, and rggamma are used to model the generalized gamma distribution.

The code is modified from https://rpubs.com/FJRubio/GG.

Value

dggamma gives the density, pggamma gives the distribution function, qggamma gives the quantile function, and rggamma generates random deviates.

Functions

- dggamma(): Density of the generalized gamma.
- pggamma(): Distribution function of the generalized gamma.
- qggamma(): Quantile of the generalized gamma.
- rggamma(): Random of the generalized gamma.

More details here

The generalized gamma is described here https://en.wikipedia.org/wiki/Generalized_gamma_distribution.
With a being theta, b being kappa, and p being delta.
theta, kappa and delta must be all > 0.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Distributions: cutter(), dSnbinom(), dbeta_new(), dcutter(), dnbinom_new(), logLik.cutter(), plot.cutter(), print.cutter(), r2norm(), rcutter(), rmnorm(), rnbinom_new()

Examples

```
# To reproduce the wikipedia page graphic
x <- seq(from=0, to=8, by=0.1)
plot(x, dggamma(x, theta=2, kappa=0.5, delta=0.5), lty=1, col="blue",
     type="l", lwd=2, xlab="x", ylab="PDF")
lines(x, dggamma(x, theta=1, kappa=1, delta=0.5), lty=1, col="green", lwd=2)
lines(x, dggamma(x, theta=2, kappa=1, delta=2), lty=1, col="red", lwd=2)
```

```
lines(x, dggamma(x, theta=5, kappa=1, delta=5), lty=1, col="yellow", lwd=2)
lines(x, dggamma(x, theta=7, kappa=1, delta=7), lty=1, col="grey", lwd=2)
legend("topright", legend=c("a=2, d=0.5, p=0.5", "a=1, d=1, p=0.5",
                            "a=2, d=1, p=2", "a=5, d=1, p=5", "a=7, d=1, p=7"),
                            col=c("blue", "green", "red", "yellow", "grey"),
                            lty=1, lwd=2, bty="n")
par <- c(theta=2, kappa=0.5, delta=0.5)
# Mean, var and sd
mean.ggamma <- function(theta, kappa, delta)
       return(theta*(gamma((kappa+1)/delta))/gamma(kappa/delta))
var.ggamma <- function(theta, kappa, delta)
       return(theta^2* ( ( (gamma((kappa+2)/delta))/gamma(kappa/delta) ) -
                ( (gamma((kappa+1)/delta))/gamma(kappa/delta) )^2 ) )
sd.ggamma <- function(theta, kappa, delta)
       return(sqrt(theta^2* ( ( (gamma((kappa+2)/delta))/gamma(kappa/delta) ) -
                ( (gamma((kappa+1)/delta))/gamma(kappa/delta) )^2 ) ))
```

DIx *Return an index of quantitative asymmetry and complexity named Developmental Instability Index (DIx)*

Description

Return an index of quantitative asymmetry and complexity.
Higher is the value, higher is the complexity (number of objects) and diversity (difference between them).
The indice is based on the product of the average angular distance of Edwards (1971) for all permutations of measures for both sides with the geometric mean of the inverse of Shannon entropy H for both sides. Let p1 and p2 two vectors of relative measures of objects with sum(p1) = 1 and sum(p2)=1 and n1 being the number of objects in p1 and n2 being the number of objects in p2.
Edwards distance for all permutations of p1 and p2 objects are computed and the average value E is calculated.
The maximun possible Shannon index for identical n1 is max1 = sum((1/n1) * log(1/n1)).
Shannon index is v1 = sum(p1 * log(p1)).
If version == 2, the complementary of Shannon index for these n1 objects is used: c1 = 2 * max1 - v1
If version == 1, the Shannon index is used directly.
The geometry mean between both sides defined the measure of diversity within each side: S=sqrt(c1 * c2)
The Developmental Instability Index is then S * E

Usage

```
DIx(l1, l2, details = FALSE, version = 1)
```

Arguments

l1	Set of measures at one side of an organism

l2	Set of measures at the other side of an organism
details	If TRUE, will show the details of computing
version	Can be 1 or 2; see description

Details

DIx returns an index of quantitative asymmetry and complexity

Value

A numeric value

Author(s)

Marc Girondot <marc.girondot@gmail.com>

References

Edwards, A.W.F., 1971. Distances between populations on the basis of gene frequencies. Biometrics 27, 873–881.
Shannon C.E. 1948 A mathematical theory of communication. Bell System Technical Journal 27(3), 379-423.

Examples

```
## Not run:
l1 <- c(0.1, 0.1, 0.05, 0.2, 0.3, 0.25)
l2 <- c(0.2, 0.3, 0.5)
DIx(l1, l2)

l1 <- c(0.1, 0.1, 0.05, 0.2, 0.3, 0.25)
l2 <- c(0.1, 0.1, 0.05, 0.2, 0.3, 0.25)
DIx(l1, l2)

l1 <- c(0.2, 0.3, 0.5)
l2 <- c(0.2, 0.3, 0.5)
DIx(l1, l2)

l1 <- c(0.2, 0.2, 0.2, 0.2, 0.2)
l2 <- c(0.2, 0.3, 0.5)
DIx(l1, l2)

l1 <- c(0.2, 0.2, 0.2, 0.2, 0.2)
l2 <- c(0.3333, 0.3333, 0.3333)
DIx(l1, l2)

l1 <- c(0.2, 0.2, 0.2, 0.2, 0.2)
l2 <- c(0.2, 0.2, 0.2, 0.2, 0.2)
DIx(l1, l2)
```

```
l1 <- c(0.3333, 0.3333, 0.3333)
l2 <- c(0.3333, 0.3333, 0.3333)
DIx(l1, l2)

## End(Not run)
```

`dnbinom_new` *Density for the negative binomial distribution - Alternative parametrization.*

Description

Density for the negative binomial distribution with parameters mu, sd, var, size or prob. See `dnbinom`.

Usage

```
dnbinom_new(
  x,
  size = NULL,
  prob = NULL,
  mu = NULL,
  sd = NULL,
  var = NULL,
  log = FALSE
)
```

Arguments

`x`	vector of (non-negative integer) quantiles.
`size`	target for number of successful trials, or dispersion parameter (the shape parameter of the gamma mixing distribution). Must be strictly positive, need not be integer.
`prob`	probability of success in each trial. 0 < prob <= 1.
`mu`	alternative parametrization via mean.
`sd`	alternative parametrization via standard deviation.
`var`	alternative parametrization via variance.
`log`	logical; if TRUE, probabilities p are given as log(p).

Details

dnbinom_new returns density for the negative binomial distribution

Value

Density for the negative binomial distribution - Alternative parametrization.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Distributions: cutter(), dSnbinom(), dbeta_new(), dcutter(), dggamma(), logLik.cutter(), plot.cutter(), print.cutter(), r2norm(), rcutter(), rmnorm(), rnbinom_new()

Examples

```
## Not run:
library("HelpersMG")
set.seed(1)
x <- rnbinom_new(n=100, mu=2, sd=3)
LnL <- NULL
df <- data.frame(mu=seq(from=0.1, to=8, by=0.1), "-LnL"=NA)
for (mu in df[, "mu"])
LnL <- c(LnL, -sum(dnbinom_new(x=x, mu=mu, sd=3, log=TRUE)))
df[, "-LnL"] <- LnL
ggplot(data = df, aes(x = .data[["mu"]], y = .data[["-LnL"]])) + geom_line()
# Examples of wrong parametrization
dnbinom_new(x=x, mu=c(1, 2), sd=3, log=TRUE)

## End(Not run)
```

---

dSnbinom *Distribution of the sum independent negative binomial random variables.*

Description

Distribution of the sum of random variable with negative binomial distributions.
Technically the sum of random variable with negative binomial distributions is a convolution of negative binomial random variables.
dSnbinom returns the density for the sum of random variable with negative binomial distributions.
pSnbinom returns the distribution function for the sum of random variable with negative binomial distributions.
qSnbinom returns the quantile function for the sum of random variable with negative binomial distributions.
rSnbinom returns random numbers for the sum of random variable with negative binomial distributions.
If all prob values are the same, exact probabilities are estimated.
Estimate using Vellaisamy&Upadhye method uses parallel computing depending on value of parallel.
The number of cores in usage can be defined using options(mc.cores = c) with c being the number of cores to be used. By default it will use all the available cores. Forking will be used in Unix system and no forking on Windows systems.
When Furman method is in use, it will return the progress of Pr(S = x) during recursion in an attribute if verbose is TRUE (see examples).

Usage

```
dSnbinom(
  x = stop("You must provide at least one x value"),
  size = NULL,
  prob = NULL,
  mu = NULL,
  log = FALSE,
  tol = NULL,
  method = "Furman",
  normalize = TRUE,
  max.iter = NULL,
  mean = NULL,
  sd = NULL,
  n.random = 1e+06,
  parallel = FALSE,
  verbose = FALSE
)

pSnbinom(
  q = stop("At least one quantile must be provided"),
  size = NULL,
  prob = NULL,
  mu = NULL,
  lower.tail = TRUE,
  log.p = FALSE,
  tol = NULL,
  method = "Furman",
  normalize = TRUE
)

qSnbinom(
  p = stop("At least one probability must be provided"),
  size = stop("size parameter is mandatory"),
  prob = NULL,
  mu = NULL,
  lower.tail = TRUE,
  log.p = FALSE,
  tol = NULL,
  method = "Furman"
)

rSnbinom(n = 1, size = NULL, prob = NULL, mu = NULL)
```

Arguments

x	vector of (non-negative integer) quantiles.
size	target for number of successful trials, or dispersion parameter (the shape parameter of the gamma mixing distribution). Must be strictly positive, need not be

	integer.
prob	probability of success in each trial. 0 < prob <= 1.
mu	alternative parametrization via mean.
log, log.p	logical; if TRUE, probabilities *p* are given as *log(p)*.
tol	Tolerance for recurrence for Furman (2007) method. If NULL, will use a saddlepoint estimation.
method	Can be Furman (default), Vellaisamy&Upadhye or exact, approximate.normal, approximate.negativebinomial, approximate.RandomObservations, or saddlepoint.
normalize	If TRUE (default) will normalize the saddlepoint approximation estimate.
max.iter	Number of maximum iterations for Furman method. Can be NULL.
mean	Mean of the distribution for approximate.normal method. If NULL, the theoretical mean will be used.
sd	Standard deviation of the distribution for approximate.normal method. If NULL, the theoretical sd will be used.
n.random	Number of random numbers used to estimate parameters of distribution for approximate.RandomObservations method.
parallel	logical; if FALSE (default), parallel computing is not used for Vellaisamy&Upadhye methods.
verbose	Give more information on the method.
q	vector of quantiles.
lower.tail	logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x].
p	vector of probabilities.
n	number of observations.

Details

Distribution of the Sum of Independent Negative Binomial Random Variables.

Value

`dSnbinom` gives the density, `pSnbinom` gives the distribution function, `qSnbinom` gives the quantile function, and `rSnbinom` generates random deviates.

Functions

- `dSnbinom()`: Density for the sum of random variable with negative binomial distributions.
- `pSnbinom()`: Distribution function for the sum of random variable with negative binomial distributions.
- `qSnbinom()`: Quantile function for the sum of random variable with negative binomial distributions.
- `rSnbinom()`: Random numbers for the sum of random variable with negative binomial distributions.

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References

Furman, E., 2007. On the convolution of the negative binomial random variables. Statistics & Probability Letters 77, 169-172.

Vellaisamy, P. & Upadhye, N.S. 2009. On the sums of compound negative binomial and gamma random variables. Journal of Applied Probability, 46, 272-283.

Girondot M, Barry J. 2023. Computation of the distribution of the sum of independent negative binomial random variables. Mathematical and Computational Applications 2023, 28, 63, doi:10.3390/mca28030063

See Also

Other Distributions: cutter(), dbeta_new(), dcutter(), dggamma(), dnbinom_new(), logLik.cutter(), plot.cutter(), print.cutter(), r2norm(), rcutter(), rmnorm(), rnbinom_new()

Examples

```
## Not run:
library(HelpersMG)
alpha <- c(1, 2, 5, 1, 2)
p <- c(0.1, 0.12, 0.13, 0.14, 0.14)
# By default, the Furman method with tol=1E-40 is used
dSnbinom(20, size=alpha, prob=p)
# Note the attribute is the dynamics of convergence of Pr(X=x)
attributes(dSnbinom(20, size=alpha, prob=p, verbose=TRUE))$Pk[, 1]

mutest <- c(0.01, 0.02, 0.03)
sizetest <- 2
x <- 20
# Exact probability
dSnbinom(x, size=sizetest, mu=mutest, method="vellaisamy&upadhye")
dSnbinom(x, size=sizetest, mu=mutest, method="vellaisamy&upadhye", log=TRUE)
# With Furman method and tol=1E-12, when probability
# is very low, it will be biased
dSnbinom(x, size=sizetest, mu=mutest, method="Furman", tol=1E-12)
# The solution is to use a tolerance lower than the estimate
dSnbinom(x, size=sizetest, mu=mutest, method="Furman", tol=1E-45)
# Here the estimate used a first estimation by saddlepoint approximation
dSnbinom(x, size=sizetest, mu=mutest, method="Furman", tol=NULL)
# Or a huge number of iterations; but it is not the best solution
dSnbinom(x, size=sizetest, mu=mutest, method="Furman",
         tol=1E-12, max.iter=10000)
# With the saddle point approximation method
dSnbinom(x, size=sizetest, mu=mutest, method="saddlepoint", log=FALSE)
dSnbinom(x, size=sizetest, mu=mutest, method="saddlepoint", log=TRUE)

# Another example
```

```
sizetest <- c(1, 1, 0.1)
mutest <- c(2, 1, 10)
x <- 5
(exact <- dSnbinom(x=x, size=sizetest, mu=mutest, method="Vellaisamy&Upadhye"))
(sp <- dSnbinom(x=x, size=sizetest, mu=mutest, method="saddlepoint"))
paste0("Saddlepoint approximation: Error of ", specify_decimal(100*abs(sp-exact)/exact, 2), "%")
(furman <- dSnbinom(x=x, size=sizetest, mu=mutest, method="Furman"))
paste0("Inversion of mgf: Error of ", specify_decimal(100*abs(furman-exact)/exact, 2), "%")
(na <- dSnbinom(x=x, size=sizetest, mu=mutest, method="approximate.normal"))
paste0("Gaussian approximation: Error of ", specify_decimal(100*abs(na-exact)/exact, 2), "%")
(nb <- dSnbinom(x=x, size=sizetest, mu=mutest, method="approximate.negativebinomial"))
paste0("NB approximation: Error of ", specify_decimal(100*abs(nb-exact)/exact, 2), "%")

plot(0:20, dSnbinom(0:20, size=sizetest, mu=mutest, method="furman"), bty="n", type="h",
     xlab="x", ylab="Density", ylim=c(0, 0.2), las=1)
points(x=0:20, y=dSnbinom(0:20, size=sizetest, mu=mutest,
                          method="saddlepoint"), pch=1, col="blue")
points(x=0:20, y=dSnbinom(0:20, size=sizetest, mu=mutest,
                          method="approximate.negativebinomial"),
                          col="red")
points(x=0:20, y=dSnbinom(0:20, size=sizetest, mu=mutest,
                          method="approximate.normal"),
                          col="green")

# Test with a single distribution
dSnbinom(20, size=1, mu=20)
# when only one distribution is available, it is the same as dnbinom()
dnbinom(20, size=1, mu=20)

# If a parameter is supplied as only one value, it is supposed to be constant
dSnbinom(20, size=1, mu=c(14, 15, 10))
dSnbinom(20, size=c(1, 1, 1), mu=c(14, 15, 10))

# The functions are vectorized:
plot(0:200, dSnbinom(0:200, size=alpha, prob=p, method="furman"), bty="n", type="h",
     xlab="x", ylab="Density")
points(0:200, dSnbinom(0:200, size=alpha, prob=p, method="saddlepoint"),
     col="red", pch=3)

# Comparison with simulated distribution using rep replicates
alpha <- c(2.1, 2.05, 2)
mu <- c(10, 30, 20)
rep <- 100000
distEmpirique <- rSnbinom(rep, size=alpha, mu=mu)
tabledistEmpirique <- rep(0, 301)
names(tabledistEmpirique) <- as.character(0:300)
tabledistEmpirique[names(table(distEmpirique))] <- table(distEmpirique)/rep

plot(0:300, dSnbinom(0:300, size=alpha, mu=mu, method="furman"), type="h", bty="n",
   xlab="x", ylab="Density", ylim=c(0,0.02))
plot_add(0:(length(tabledistEmpirique)-1), tabledistEmpirique, type="l", col="red")
legend(x=200, y=0.02, legend=c("Empirical", "Theoretical"),
   text.col=c("red", "black"), bty="n")
```

```
# Example from Vellaisamy, P. & Upadhye, N.S. (2009) - Table 1
# Note that computing time for k = 7 using exact method is very long
k <- 2:7
x <- c(3, 5, 8, 10, 15)
table1_Vellaisamy <- matrix(NA, ncol=length(x), nrow=length(k))
rownames(table1_Vellaisamy) <- paste0("n = ", as.character(k))
colnames(table1_Vellaisamy) <- paste0("x = ", as.character(x))
table1_approximateObservations <- table1_Vellaisamy
table1_Furman3 <- table1_Vellaisamy
table1_Furman6 <- table1_Vellaisamy
table1_Furman9 <- table1_Vellaisamy
table1_Furman12 <- table1_Vellaisamy
table1_Furman40 <- table1_Vellaisamy
table1_Furman40 <- table1_Vellaisamy
table1_FurmanAuto <- table1_Vellaisamy
table1_FurmanAuto_iter <- table1_Vellaisamy
table1_Vellaisamy_parallel <- table1_Vellaisamy
table1_Approximate_Normal <- table1_Vellaisamy
table1_saddlepoint <- table1_Vellaisamy

st_Furman3 <- rep(NA, length(k))
st_Furman6 <- rep(NA, length(k))
st_Furman9 <- rep(NA, length(k))
st_Furman12 <- rep(NA, length(k))
st_Furman40 <- rep(NA, length(k))
st_FurmanAuto <- rep(NA, length(k))
st_approximateObservations <- rep(NA, length(k))
st_Vellaisamy <- rep(NA, length(k))
st_Vellaisamy_parallel <- rep(NA, length(k))
st_Approximate_Normal <- rep(NA, length(k))
st_saddlepoint <- rep(NA, length(k))

for (n in k) {
    print(n)
    alpha <- 1:n
    p <- (1:n)/10
    st_Vellaisamy[which(n == k)] <-
        system.time({
        table1_Vellaisamy[which(n == k), ] <- dSnbinom(x=x, prob=p, size=alpha,
                                method="Vellaisamy&Upadhye", log=FALSE, verbose=FALSE)
        })[1]
    st_Vellaisamy_parallel[which(n == k)] <-
        system.time({
        table1_Vellaisamy_parallel[which(n == k), ] <- dSnbinom(x=x, prob=p, size=alpha,
                                   parallel=TRUE,
                                method="Vellaisamy&Upadhye", log=FALSE, verbose=FALSE)
        })[1]
    st_approximateObservations[which(n == k)] <-
        system.time({
      table1_approximateObservations[which(n == k), ] <- dSnbinom(x=x, prob=p, size=alpha,
                                  method="approximate.RandomObservations", log=FALSE,
```

```
                                verbose=FALSE)
    })[1]
st_Furman3[which(n == k)] <-
    system.time({
        table1_Furman3[which(n == k), ] <- dSnbinom(x=x, prob=p, size=alpha,
                                method="Furman", tol=1E-3, log=FALSE,
                                verbose=FALSE)
    })[1]
st_Furman6[which(n == k)] <-
    system.time({
        table1_Furman6[which(n == k), ] <- dSnbinom(x=x, prob=p, size=alpha,
                                method="Furman", tol=1E-6, log=FALSE,
                                verbose=FALSE)
    })[1]
st_Furman9[which(n == k)] <-
    system.time({
        table1_Furman9[which(n == k), ] <- dSnbinom(x=x, prob=p, size=alpha,
                                method="Furman", tol=1E-9, log=FALSE,
                                verbose=FALSE)
    })[1]
st_Furman12[which(n == k)] <-
    system.time({
        table1_Furman12[which(n == k), ] <- dSnbinom(x=x, prob=p, size=alpha,
                                method="Furman", tol=1E-12, log=FALSE,
                                verbose=FALSE)
    })[1]
st_Furman40[which(n == k)] <-
    system.time({
        table1_Furman40[which(n == k), ] <- dSnbinom(x=x, prob=p, size=alpha,
                                method="Furman", tol=1E-40, log=FALSE,
                                verbose=FALSE)
    })[1]

st_FurmanAuto[which(n == k)] <-
    system.time({
        table1_FurmanAuto[which(n == k), ] <- dSnbinom(x=x, prob=p, size=alpha,
                                method="Furman", tol=NULL, log=FALSE,
                                verbose=FALSE)
    })[1]

st_Approximate_Normal[which(n == k)] <-
    system.time({
      table1_Approximate_Normal[which(n == k), ] <- dSnbinom(x=x, prob=p, size=alpha,
                                method="approximate.normal", tol=1E-12, log=FALSE,
                                verbose=FALSE)
    })[1]
    st_saddlepoint[which(n == k)] <-
    system.time({
        table1_saddlepoint[which(n == k), ] <- dSnbinom(x=x, prob=p, size=alpha,
                                method="saddlepoint", tol=1E-12, log=FALSE,
                                verbose=FALSE)
    })[1]
```

```
for (xc in x) {
 essai <- dSnbinom(x=xc, prob=p, size=alpha, method="Furman", tol=NULL, log=FALSE, verbose=TRUE)
 table1_FurmanAuto_iter[which(n == k), which(xc == x)] <- nrow(attributes(essai)[[1]])
}
}

cbind(table1_Vellaisamy, st_Vellaisamy)
cbind(table1_Vellaisamy_parallel, st_Vellaisamy_parallel)
cbind(table1_Furman3, st_Furman3)
cbind(table1_Furman6, st_Furman6)
cbind(table1_Furman9, st_Furman9)
cbind(table1_Furman12, st_Furman12)
cbind(table1_Furman40, st_Furman40)
cbind(table1_FurmanAuto, st_FurmanAuto)
cbind(table1_approximateObservations, st_approximateObservations)
cbind(table1_Approximate_Normal, st_Approximate_Normal)
cbind(table1_saddlepoint, st_saddlepoint)


# Test of different methods
n <- 9
x <- 17
alpha <- 1:n
p <- (1:n)/10

# Parallel computing is not always performant
# Here it is very performant
system.time({print(dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye", log=FALSE,
         verbose=TRUE, parallel=TRUE))})
system.time({print(dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye", log=FALSE,
         verbose=TRUE, parallel=FALSE))})

# Test of different methods
n <- 7
x <- 8
alpha <- 1:n
p <- (1:n)/10

# Parallel computing is not always performant
# Here it is approximately the same time of execution
system.time({print(dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye", log=FALSE,
         verbose=TRUE, parallel=TRUE))})
system.time({print(dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye", log=FALSE,
         verbose=TRUE, parallel=FALSE))})

# Test of different methods
n <- 7
x <- 15
alpha <- 1:n
p <- (1:n)/10

# Parallel computing is sometimes very performant
# Here parallel computing is 7 times faster (with a 8 cores computer)
```

```
#             for vellaisamy&upadhye method
system.time(dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye", log=FALSE,
         verbose=TRUE, parallel=TRUE))
system.time(dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye", log=FALSE,
         verbose=TRUE, parallel=FALSE))

# Test of different methods
n <- 2
x <- 3
alpha <- 1:n
p <- (1:n)/10

# Parallel computing is sometimes very performant
# Here parallel computing is 7 times faster (with a 8 cores computer)
#             for vellaisamy&upadhye method
system.time(dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye", log=FALSE,
         verbose=TRUE, parallel=TRUE))
system.time(dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye", log=FALSE,
         verbose=TRUE, parallel=FALSE))

# Test for different tolerant values
n <- 7
x <- 8
alpha <- 1:n
p <- (1:n)/10
dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye", log=FALSE, verbose=TRUE)
as.numeric(dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE, tol=1E-3, verbose=TRUE))
as.numeric(dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE, tol=1E-6, verbose=TRUE))
as.numeric(dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE, tol=1E-9, verbose=TRUE))
as.numeric(dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE, verbose=TRUE))
as.numeric(dSnbinom(x=x, prob=p, size=alpha, method="Saddlepoint", log=FALSE, verbose=TRUE))
as.numeric(dSnbinom(x=x, prob=p, size=alpha, method="approximate.RandomObservations",
         log=FALSE, verbose=TRUE))

# Test for criteria of convergence
Pr_exact <- dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye",
                  log=FALSE, verbose=TRUE)
Pr_Furman <- dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE,
                verbose=TRUE)
Pr_exact;as.numeric(Pr_Furman)
plot(1:length(attributes(Pr_Furman)$Pk),
     log10(abs(attributes(Pr_Furman)$Pk-Pr_exact)), type="l", xlab="Iterations",
     ylab="Abs log10", bty="n")
lines(1:(length(attributes(Pr_Furman)$Pk)-1),
      log10(abs(diff(attributes(Pr_Furman)$Pk))), col="red")
legend("bottomleft", legend=c("Log10 Convergence to true value", "Log10 Rate of change"),
       col=c("black", "red"),
       lty=1)

n <- 7
x <- 6
alpha <- 1:n
p <- (1:n)/10
```

```
Pr_exact <- dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye",
                  log=FALSE, verbose=TRUE)
Pr_Furman <- dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE,
                verbose=TRUE)
Pr_saddlepoint <- dSnbinom(x=x, prob=p, size=alpha, method="saddlepoint", log=FALSE,
                verbose=TRUE)

# pdf("figure.pdf", width=7, height=7, pointsize=14)
ylab <- as.expression(bquote(.("P(S=6) x 10")^"6"))
layout(1:2)
par(mar=c(3, 4, 1, 1))
plot(1:length(attributes(Pr_Furman)$Pk),
     attributes(Pr_Furman)$Pk*1E6, type="l", xlab="",
     ylab="", bty="n", las=1, xlim=c(0, 80))
mtext(text=ylab, side=2, line=2.5)
segments(x0=25, x1=80, y0=Pr_exact*1E6, y1=Pr_exact*1E6, lty=3)
par(xpd=TRUE)
text(x=0, y=6, labels="Exact probability", pos=4)
txt <- "       Approximate probability\n    based on Furman (2007)\nrecursive iterations"
text(x=20, y=2, labels=txt, pos=4)
text(x=75, y=5, labels="A", cex=2)
par(mar=c(4, 4, 1, 1))
ylab <- as.expression(bquote("log"["10"]*""*"(P"["k+1"]*""*" - P"["k"]*""*")"))
plot(1:(length(attributes(Pr_Furman)$Pk)-1),
      log10(diff(attributes(Pr_Furman)$Pk)), col="black", xlim=c(0, 80), type ="l",
      bty="n", las=1, xlab="Iterations", ylab="")
mtext(text=ylab, side=2, line=2.5)
 peak <- (1:(length(attributes(Pr_Furman)$Pk)-1))[which.max(
            log10(abs(diff(attributes(Pr_Furman)$Pk))))]
segments(x0=peak, x1=peak, y0=-12, y1=-5, lty=2)
text(x=0, y=-6, labels="Positive trend", pos=4)
text(x=30, y=-6, labels="Negative trend", pos=4)
segments(x0=0, x1=43, y0=-12, y1=-12, lty=4)
segments(x0=62, x1=80, y0=-12, y1=-12, lty=4)
text(x=45, y=-12, labels="Tolerance", pos=4)
text(x=75, y=-7, labels="B", cex=2)
# dev.off()

# pdf("figure 2.pdf", width=7, height=7, pointsize=14)
ylab <- as.expression(bquote(.("P(S=6) x 10")^"6"))
layout(1:2)
par(mar=c(3, 4, 1, 1))
plot(1:length(attributes(Pr_Furman)$Pk),
     attributes(Pr_Furman)$Pk*1E6, type="l", xlab="",
     ylab="", bty="n", las=1, xlim=c(0, 80))
mtext(text=ylab, side=2, line=2.5)
segments(x0=25, x1=80, y0=Pr_exact*1E6, y1=Pr_exact*1E6, lty=3)
par(xpd=TRUE)
text(x=0, y=6, labels="Exact probability", pos=4)
txt <- "       Approximate probability\n    based on Furman (2007)\nrecursive iterations"
text(x=20, y=2, labels=txt, pos=4)
text(x=75, y=5, labels="A", cex=2)
par(mar=c(4, 4, 1, 1))
```

```
ylab <- as.expression(bquote("(P"["k+1"]*""*" - P"["k"]*""*") x 10"^"7"))
plot(1:(length(attributes(Pr_Furman)$Pk)-1),
      diff(attributes(Pr_Furman)$Pk)*1E7,
      col="black", xlim=c(0, 80), type ="l",
      bty="n", las=1, xlab="Iterations", ylab="")
mtext(text=ylab, side=2, line=2.5)
 peak <- (1:(length(attributes(Pr_Furman)$Pk)-1))[which.max(diff(attributes(Pr_Furman)$Pk))]
segments(x0=peak, x1=peak, y0=0, y1=3.5, lty=2)
text(x=-2, y=3.5, labels="Positive trend", pos=4)
text(x=30, y=3.5, labels="Negative trend", pos=4)
segments(x0=0, x1=22, y0=1E-12, y1=1E-12, lty=4)
segments(x0=40, x1=80, y0=1E-12, y1=1E-12, lty=4)
text(x=22, y=1E-12+0.2, labels="Tolerance", pos=4)
text(x=75, y=3, labels="B", cex=2)
# dev.off()

# Test of different methods
n <- 2
x <- 15
alpha <- 1:n
p <- (1:n)/10
dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye", log=FALSE, verbose=TRUE)
as.numeric(dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE, tol=1E-3, verbose=TRUE))
as.numeric(dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE, tol=1E-6, verbose=TRUE))
as.numeric(dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE, tol=1E-9, verbose=TRUE))
as.numeric(dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE, verbose=TRUE))
dSnbinom(x=x, prob=p, size=alpha, method="approximate.RandomObservations",
         log=FALSE, verbose=TRUE)


n <- 50
x <- 300
alpha <- (1:n)/100
p <- (1:n)/1000
# Produce an error
Pr_exact <- dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye",
                  log=FALSE, verbose=TRUE)
Pr_Furman <- dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE,
                 verbose=FALSE)
Pr_ApproximateNormal <- dSnbinom(x=x, prob=p, size=alpha, method="approximate.normal",
                        log=FALSE,
                        verbose=TRUE)
Pr_ApproximateRandom <- dSnbinom(x=x, prob=p, size=alpha, method="approximate.RandomObservations",
                        log=FALSE, n.random=1E6,
                        verbose=TRUE)

n <- 500
x <- 3000
alpha <- (1:n)/100
p <- (1:n)/1000
# Produce an error
Pr_exact <- dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye",
                  log=FALSE, verbose=TRUE)
```

```
Pr_Furman <- dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE,
                 verbose=FALSE)
Pr_ApproximateNormal <- dSnbinom(x=x, prob=p, size=alpha, method="approximate.normal",
                         log=FALSE,
                         verbose=TRUE)
Pr_ApproximateNegativeBinomial <- dSnbinom(x=x, prob=p, size=alpha,
                         method="approximate.negativebinomial",
                         log=FALSE,
                         verbose=TRUE)
Pr_ApproximateRandom <- dSnbinom(x=x, prob=p, size=alpha,
                         method="approximate.RandomObservations",
                         log=FALSE, n.random=1E6,
                         verbose=TRUE)
Pr_ApproximateSaddlepoint <- dSnbinom(x=x, prob=p, size=alpha,
                         method="saddlepoint",
                         log=FALSE,
                         verbose=TRUE)



layout(matrix(1:4, ncol=2, byrow=TRUE))
par(mar=c(3, 4.5, 1, 1))
alpha <- seq(from=10, to=100, length.out=3)
p <- seq(from=0.5, to=0.9, length.out=3)

p_nb <- dSnbinom(0:100, prob=p, size=alpha, method="vellaisamy&upadhye", verbose=TRUE)
p_Furman <- dSnbinom(0:100, prob=p, size=alpha, method="Furman", verbose=FALSE)
p_normal <- dSnbinom(0:100, prob=p, size=alpha, method="approximate.normal", verbose=TRUE)
p_aNB <- dSnbinom(0:100, prob=p, size=alpha, method="approximate.negativebinomial", verbose=TRUE)
p_SA <- dSnbinom(0:100, prob=p, size=alpha, method="saddlepoint", verbose=TRUE)

lab_PSnx <- bquote(italic("P(S"* "" [n] * "=x)"))

plot(1, 1, las=1, bty="n", col="grey", xlab="",
       xlim=c(10, 70), ylim=c(0, 0.05),
       ylab=lab_PSnx, type="n")
par(xpd=FALSE)
segments(x0=(0:100), x1=(0:100),
         y0=0, y1=as.numeric(p_nb), col="black")

plot(x=p_nb, y=p_normal, pch=4, cex=0.5, las=1, bty="n",
     xlab=bquote(italic("P" * "" [exact] * "(S"* "" [n] * "=x)")),
     ylab=bquote(italic("P" * "" [approximate] * "(S"* "" [n] * "=x)")),
     xlim=c(0, 0.05), ylim=c(0, 0.05))
points(x=p_nb, y=p_aNB, pch=5, cex=0.5)
points(x=p_nb, y=p_SA, pch=6, cex=0.5)
points(x=p_Furman, y=p_SA, pch=19, cex=0.5)

n <- 2
x <- 15
alpha <- 1:n
p <- (1:n)/10
```

```
p_nb <- dSnbinom(0:80, prob=p, size=alpha, method="vellaisamy&upadhye", verbose=TRUE)
p_Furman <- dSnbinom(0:80, prob=p, size=alpha, method="Furman", verbose=FALSE)
p_normal <- dSnbinom(0:80, prob=p, size=alpha, method="approximate.normal", verbose=TRUE)
p_aNB <- dSnbinom(0:80, prob=p, size=alpha, method="approximate.negativebinomial", verbose=TRUE)
p_SA <- dSnbinom(0:80, prob=p, size=alpha, method="saddlepoint", verbose=TRUE)


par(mar=c(4, 4.5, 1, 1))
plot(1, 1, las=1, bty="n", col="grey", xlab="x",
       xlim=c(0, 60), ylim=c(0, 0.05),
       ylab=lab_PSnx, type="n")
par(xpd=FALSE)
segments(x0=(0:80), x1=(0:80),
         y0=0, y1=as.numeric(p_nb), col="black")

plot(x=p_nb, y=p_normal, pch=4, cex=0.5, las=1, bty="n",
     xlab=bquote(italic("P" * "" [exact] * "(S"* "" [n] * "=x)")),
     ylab=bquote(italic("P" * "" [approximate] * "(S"* "" [n] * "=x)")),
     xlim=c(0, 0.05), ylim=c(0, 0.05))
points(x=p_nb, y=p_aNB, pch=5, cex=0.5)
points(x=p_nb, y=p_SA, pch=6, cex=0.5)
points(x=p_Furman, y=p_SA, pch=19, cex=0.5)

# pdf("figure 1.pdf", width=7, height=7, pointsize=14)

layout(1:2)
par(mar=c(3, 4, 1, 1))
alpha <- seq(from=10, to=100, length.out=3)
p <- seq(from=0.5, to=0.9, length.out=3)

p_nb <- dSnbinom(0:100, prob=p, size=alpha, method="vellaisamy&upadhye", verbose=TRUE)
p_Furman <- dSnbinom(0:100, prob=p, size=alpha, method="Furman", verbose=FALSE)
p_normal <- dSnbinom(0:100, prob=p, size=alpha, method="approximate.normal", verbose=TRUE)
p_aNB <- dSnbinom(0:100, prob=p, size=alpha, method="approximate.negativebinomial", verbose=TRUE)
p_SA <- dSnbinom(0:100, prob=p, size=alpha, method="saddlepoint", verbose=TRUE)

lab_PSnx <- bquote(italic("P(S"* "" [n] * "=x)"))

plot(1, 1, las=1, bty="n", col="grey", xlab="",
       xlim=c(10, 70), ylim=c(0, 0.09),
       ylab="", type="n", yaxt="n")
axis(2, at=seq(from=0, to=0.05, by=0.01), las=1)
mtext(lab_PSnx, side = 2, adj=0.3, line=3)
par(xpd=FALSE)
segments(x0=(0:100), x1=(0:100),
         y0=0, y1=as.numeric(p_nb), col="black")
errr <- (abs((100*(p_Furman-p_nb)/p_nb)))/1000+0.055
errr <- ifelse(is.infinite(errr), NA, errr)
lines(x=(0:100), y=errr, lty=5, col="red", lwd=2)
errr <- (abs((100*(p_normal-p_nb)/p_nb)))/1000+0.055
lines(x=(0:100), y=errr, lty=2, col="blue", lwd=2)
errr <- (abs((100*(p_aNB-p_nb)/p_nb)))/1000+0.055
lines(x=(0:100), y=errr, lty=3, col="purple", lwd=2)
```

```
errr <- (abs((100*(p_SA-p_nb)/p_nb)))/1000+0.055
lines(x=(0:100), y=errr, lty=4, col="green", lwd=2)
axis(2, at=seq(from=0, to=40, by=10)/1000+0.055, las=1,
     labels=as.character(seq(from=0, to=40, by=10)))
mtext("|% error|", side = 2, adj=0.9, line=3)
par(xpd=TRUE)
legend(x=30, y=0.1, legend=c("Inversion of mgf", "Saddlepoint", "Normal", "Negative binomial"),
      lty=c(5, 4, 2, 3), bty="n", cex=0.8, col=c("red", "green", "blue", "purple"), lwd=2)
legend(x=10, y=0.05, legend=c("Exact"), lty=c(1), bty="n", cex=0.8)
par(xpd=TRUE)
text(x=ScalePreviousPlot(x = 0.95, y = 0.1)$x,
     y=ScalePreviousPlot(x = 0.95, y = 0.1)$y, labels="A", cex=2)


# When normal approximation will fail
n <- 2
x <- 15
alpha <- 1:n
p <- (1:n)/10

p_nb <- dSnbinom(0:80, prob=p, size=alpha, method="vellaisamy&upadhye", verbose=TRUE)
p_Furman <- dSnbinom(0:80, prob=p, size=alpha, method="Furman", verbose=FALSE)
p_normal <- dSnbinom(0:80, prob=p, size=alpha, method="approximate.normal", verbose=TRUE)
p_aNB <- dSnbinom(0:80, prob=p, size=alpha, method="approximate.negativebinomial", verbose=TRUE)
p_SA <- dSnbinom(0:80, prob=p, size=alpha, method="saddlepoint", verbose=TRUE)

par(mar=c(4, 4, 1, 1))
plot(1, 1, las=1, bty="n", col="grey", xlab="x",
       xlim=c(0, 60), ylim=c(0, 0.09),
       ylab="", type="n", yaxt="n")
axis(2, at=seq(from=0, to=0.05, by=0.01), las=1)
mtext(lab_PSnx, side = 2, adj=0.3, line=3)
par(xpd=FALSE)
segments(x0=(0:80), x1=(0:80),
         y0=0, y1=as.numeric(p_nb), col="black")
errr <- (abs((100*(p_Furman-p_nb)/p_nb)))/1000+0.055
errr <- ifelse(is.infinite(errr), NA, errr)
lines(x=(0:80), y=errr, lty=5, col="red", lwd=2)
errr <- (abs((100*(p_normal-p_nb)/p_nb)))/1000+0.055
lines(x=(0:80), y=errr, lty=2, col="blue", lwd=2)
errr <- (abs((100*(p_aNB-p_nb)/p_nb)))/1000+0.055
lines(x=(0:80), y=errr, lty=3, col="purple", lwd=2)
errr <- (abs((100*(p_SA-p_nb)/p_nb)))/1000+0.055
lines(x=(0:80), y=errr, lty=4, col="green", lwd=2)
axis(2, at=seq(from=0, to=40, by=10)/1000+0.055, las=1,
     labels=as.character(seq(from=0, to=40, by=10)))
mtext("|% error|", side = 2, adj=0.9, line=3)
legend(x=30, y=0.055,
     legend=c("Exact", "Inversion of mgf", "Saddlepoint", "Normal", "Negative binomial"),
     lty=c(1, 5, 4, 2, 3), bty="n", cex=0.8, col=c("black", "red", "green", "blue", "purple"),
       lwd=c(1, 2, 2, 2, 2))
par(xpd=TRUE)
text(x=ScalePreviousPlot(x = 0.95, y = 0.1)$x,
```

```
     y=ScalePreviousPlot(x = 0.95, y = 0.1)$y, labels="B", cex=2)


# dev.off()


# Test for criteria of convergence
Pr_exact <- dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye",
                  log=FALSE, verbose=TRUE)
Pr_Furman <- dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE,
                verbose=TRUE)
Pr_exact;as.numeric(Pr_Furman)
plot(1:length(attributes(Pr_Furman)$Pk),
     log10(abs(attributes(Pr_Furman)$Pk-Pr_exact)), type="l", xlab="Iterations",
     ylab="Abs log10", bty="n")
lines(1:(length(attributes(Pr_Furman)$Pk)-1),
      log10(abs(diff(attributes(Pr_Furman)$Pk))), col="red")
legend("bottomleft", legend=c("Log10 Convergence to true value", "Log10 Rate of change"),
       col=c("black", "red"),
       lty=1)


# Test of different methods
alpha <- c(2.05, 2)
mu <- c(10, 30)
test <- rSnbinom(n=100000, size=alpha, mu=mu)
plot(0:200, table(test)[as.character(0:200)]/sum(table(test), na.rm=TRUE),
     bty="n", type="h", xlab="x", ylab="Density")
lines(x=0:200, dSnbinom(0:200, size=alpha, mu=mu, log=FALSE, method="Furman"), col="blue")
lines(x=0:200, y=dSnbinom(0:200, size=alpha, mu=mu, log=FALSE,
                          method="vellaisamy&upadhye"), col="red")
lines(x=0:200, y=dSnbinom(0:200, size=alpha, mu=mu, log=FALSE,
                          method="approximate.randomobservations"), col="green")

# Test for criteria of convergence for x = 50
x <- 50
# Test for criteria of convergence
Pr_exact <- dSnbinom(x=x, prob=p, size=alpha, method="vellaisamy&upadhye",
                  log=FALSE, verbose=TRUE)
Pr_Furman <- dSnbinom(x=x, prob=p, size=alpha, method="Furman", log=FALSE, tol=1E-12,
                verbose=TRUE)
Pr_exact;as.numeric(Pr_Furman)
plot(1:length(attributes(Pr_Furman)$Pk),
     log10(abs(attributes(Pr_Furman)$Pk-Pr_exact)), type="l", xlab="Iterations",
     ylab="Abs log10", bty="n")
lines(1:(length(attributes(Pr_Furman)$Pk)-1),
      log10(abs(diff(attributes(Pr_Furman)$Pk))), col="red")
legend("bottomleft", legend=c("Log10 Convergence to true value", "Log10 Rate of change"),
       col=c("black", "red"),
       lty=1)

# Another example more complicated
set.seed(2)
```

```
mutest <- c(56, 6.75, 1)
ktest <- c(50, 50, 50)
nr <- 100000
test <- rSnbinom(nr, size=ktest, mu=mutest)
system.time({pr_vellaisamy <- dSnbinom(x=0:150, size=ktest, mu=mutest,
                         method = "vellaisamy&upadhye", verbose=FALSE, parallel=FALSE)})
# Parallel computing is not efficient
system.time({pr_vellaisamy <- dSnbinom(x=0:150, size=ktest, mu=mutest,
                          method = "vellaisamy&upadhye", verbose=FALSE, parallel=TRUE)})
system.time({pr_furman <- dSnbinom(x=0:150, size=ktest, mu=mutest, prob=NULL,
                       method = "furman", verbose=FALSE, log=FALSE)})
pr_approximateObservations <- dSnbinom(0:150, size=ktest, mu=mutest,
                                       method = "approximate.randomobservations")

plot(table(test), xlab="N", ylab="Density", las=1, bty="n", ylim=c(0, 4000), xlim=c(0, 150))
lines(0:150, pr_vellaisamy*nr, col="red")
lines(0:150, pr_furman*nr, col="blue")
lines(0:150, pr_approximateObservations*nr, col="green")

dSnbinom(x=42, size=ktest, mu=mutest, prob=NULL,
         method = "vellaisamy&upadhye", verbose=TRUE)
as.numeric(dSnbinom(x=42, size=ktest, mu=mutest, prob=NULL,
           method = "Furman", verbose=TRUE))
dSnbinom(x=42, size=ktest, mu=mutest, prob=NULL,
         method = "approximate.randomobservations", verbose=TRUE)

x <- 100
# Test for criteria of convergence
Pr_exact <- dSnbinom(x=x, size=ktest, mu=mutest, method="vellaisamy&upadhye",
                    log=FALSE, verbose=TRUE)
Pr_Furman <- dSnbinom(x=x, size=ktest, mu=mutest, method="Furman", log=FALSE,
                 verbose=TRUE)
Pr_exact;as.numeric(Pr_Furman)
plot(1:length(attributes(Pr_Furman)$Pk),
     log10(abs(attributes(Pr_Furman)$Pk-Pr_exact)), type="l", xlab="Iterations",
     ylab="Abs log10", bty="n", ylim=c(-100, 0))
lines(1:(length(attributes(Pr_Furman)$Pk)-1),
      log10(abs(diff(attributes(Pr_Furman)$Pk))), col="red")
legend("bottomright", legend=c("Log10 Convergence to true value", "Log10 Rate of change"),
       col=c("black", "red"),
       lty=1)


# example to fit a distribution
data <- rnbinom(1000, size=1, mu=10)
hist(data)
ag <- rep(1:100, 10)
r <- aggregate(data, by=list(ag), FUN=sum)
hist(r[,2])

parx <- c(size=1, mu=10)

dSnbinomx <- function(x, par) {
```

```
  -sum(dSnbinom(x=x[,2], mu=rep(par["mu"], 10), size=par["size"], log=TRUE))
}

fit_mu_size <- optim(par = parx, fn=dSnbinomx, x=r, method="BFGS", control=c(trace=TRUE))
fit_mu_size$par

alpha <- c(2.1, 2.05, 2)
mu <- c(10, 30, 20)
p <- pSnbinom(q=10, size=alpha, mu=mu, lower.tail = TRUE)

alpha <- c(2.1, 2.05, 2)
mu <- c(10, 30, 20)
q <- qSnbinom(p=0.1, size=alpha, mu=mu, lower.tail = TRUE)

alpha <- c(2.1, 2.05, 2)
mu <- c(10, 30, 20)
rep <- 100000
distEmpirique <- rSnbinom(n=rep, size=alpha, mu=mu)
tabledistEmpirique <- rep(0, 301)
names(tabledistEmpirique) <- as.character(0:300)
tabledistEmpirique[names(table(distEmpirique))] <- table(distEmpirique)/rep

plot(0:300, dSnbinom(0:300, size=alpha, mu=mu), type="h", bty="n",
   xlab="x", ylab="Density", ylim=c(0,0.02))
plot_add(0:300, tabledistEmpirique, type="l", col="red")
legend(x=200, y=0.02, legend=c("Empirical", "Theoretical"),
   text.col=c("red", "black"), bty="n")


# Test if saddlepoint approximation must be normalized
# Yes, it must be
n <- 7
alpha <- 1:n
p <- (1:n)/10
dSnbinom(x=10, prob=p, size=alpha, method="saddlepoint", log=FALSE,
                 verbose=TRUE)
dSnbinom(x=10, prob=p, size=alpha, method="saddlepoint", log=FALSE,
                 verbose=TRUE, normalize=FALSE)

# Test for saddlepoint when x=0
n <- 7
alpha <- 1:n
p <- (1:n)/10
dSnbinom(x=0, prob=p, size=alpha, method="saddlepoint", log=FALSE,
                 verbose=TRUE)
dSnbinom(x=1, prob=p, size=alpha, method="saddlepoint", log=FALSE,
                 verbose=TRUE)
dSnbinom(x=c(0, 1), prob=p, size=alpha, method="saddlepoint", log=FALSE,
                 verbose=TRUE)
dSnbinom(x=c(0, 1), prob=p, size=alpha, method="saddlepoint", log=FALSE,
                 verbose=FALSE)

# Test when prob are all the same
```

```
p <- rep(0.2, 7)
n <- 7
alpha <- 1:n
dSnbinom(x=0:10, prob=p, size=alpha, method="saddlepoint", log=FALSE,
                 verbose=TRUE)
dSnbinom(x=0:10, prob=p, size=alpha, method="furman", log=FALSE,
                 verbose=TRUE)
dSnbinom(x=0:10, prob=p, size=alpha, method="exact", log=FALSE,
                 verbose=TRUE)

# Test when n=1
p <- 0.2
n <- 1
alpha <- 1:n
dSnbinom(x=0:10, prob=p, size=alpha, method="saddlepoint", log=FALSE,
                 verbose=TRUE)
dSnbinom(x=0:10, prob=p, size=alpha, method="furman", log=FALSE,
                 verbose=TRUE)
dSnbinom(x=0:10, prob=p, size=alpha, method="exact", log=FALSE,
                 verbose=TRUE)

# Poisson distribution
dpois(20, lambda =sum(c(14, 10)))
dnbinom(20, size=+Inf, mu=sum(c(14, 10)))
dSnbinom(20, size=+Inf, mu=c(14, 10))

## End(Not run)
```

`duplicated_packages` *List the duplicated packages with their locations*

Description

A data.frame with the duplicated packages and their locations and version.
The columns Lib1 and Version1 should have the oldest version of the packages.

Usage

```
duplicated_packages()
```

Details

duplicated_packages lists the duplicated packages with their locations

Value

A data.frame with 4 elements for each duplicated packages:

- versions: the version of the packages
- libraries: the locations

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
## Not run:
library(HelpersMG)
duplicated_packages()
# To remove the oldest versions of the installed packages, use
li <- duplicated_packages()
if (nrow(li) != 0)
    for (i in 1:nrow(li))
        remove.packages(rownames(li)[i], lib=li[i, "Lib1"])

## End(Not run)
```

`ellipse` *Plot an ellipse*

Description

Plot a ellipse defined by the center and the radius. The options for binomial confidence parameters are:

- conf.level
- method must be one of these "wald", "wilson", "wilsoncc", "agresti-coull", "jeffreys", "modified wilson", "modified jeffreys", "clopper-pearson", "arcsine", "logit", "witting", "pratt", "midp", "lik" and "blaker". Defaults to "wilson". Abbreviation of method is accepted. See details.
  Default is wilsoncc (Wilson with continuity correction) col parameter can be a list of colors. See examples

Usage

```
ellipse(
  center.x = 0,
  center.y = 0,
  radius.x = 1,
  radius.y = 1,
  radius.x.lower = NULL,
```

```
  radius.x.upper = NULL,
  radius.y.lower = NULL,
  radius.y.upper = NULL,
  alpha = 0,
  binconf.x = NULL,
  binconf.y = NULL,
  control.binconf = list(conf.level = 0.95, method = "wilsoncc"),
  length = 100,
  ...
)
```

Arguments

center.x	Center of the ellipse on x axis
center.y	Center of the ellipse on y axis
radius.x	Radius along the x axis
radius.y	Radius along the y axis
radius.x.lower	Radius along the x axis, at left of center
radius.x.upper	Radius along the x axis, at right of center
radius.y.lower	Radius along the y axis, at bottom of center
radius.y.upper	Radius along the y axis, at top of center
alpha	Rotation in radians
binconf.x	A data.frame or a matrix with two columns, x and n or with three columns, PointEst, Lower, and Upper
binconf.y	A data.frame or a matrix with two columns, x and n or with three columns, PointEst, Lower, and Upper
control.binconf	A list with options for binomial confidence
length	Number of points to draw the ellipse
...	Graphical parameters

Details

ellipse plots an ellipse

Value

Nothing

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
plot(0:1, 0:1, xlim=c(0, 1), ylim=c(0,1), lty=2, type="l", las=1, bty="n",
     xlab="Variable x", ylab="variable y")

ellipse(center.x = c(0.2, 0.3, 0.25), center.y = c(0.7, 0.6, 0.55),
        radius.x = c(0.1, 0.1, 0.1), radius.y = c(0.15, 0.2, 0.4),
        border=NA, col=rgb(red = 0.1, green = 0.1, blue = 0.1, alpha = 0.1))

ellipse(center.x = 0.5, center.y = 0.5,
        radius.x.lower = 0.1, radius.x.upper = 0.3,
        radius.y = 0.2,
        border=NA, col=rgb(red = 0.1, green = 0.1, blue = 0.1, alpha = 0.1))

ellipse(center.x = 0.6, center.y = 0.3,
        radius.x.lower = 0.3, radius.x.upper = 0.3,
        radius.y.lower = 0.2, radius.y.upper = 0.4,
        border=NA, col=rgb(red = 0.1, green = 0.1, blue = 0.1, alpha = 0.1))

plot(0:1, 0:1, xlim=c(0, 1), ylim=c(0,1), lty=2, type="l", bty="n", asp=1,
     xlab="Variable x", ylab="variable y", axes=FALSE)
axis(1, at=c(0, 0.25, 0.5, 0.75, 1))
axis(2, at=c(0, 0.25, 0.5, 0.75, 1), las=1)

ellipse(center.x = 0.5, center.y = 0.5, radius.x = 0.2, radius.y = 0.4,
       border=NA, col=rgb(red = 0.1, green = 0.1, blue = 0.1, alpha = 0.1))
ellipse(center.x = 0.5, center.y = 0.5, radius.x = 0.2, radius.y = 0.4,
       border=NA, col=rgb(red = 0.1, green = 0.1, blue = 0.1, alpha = 0.1), alpha = pi/4)

plot(0:1, 0:1, xlim=c(0, 1), ylim=c(0,1), lty=2, type="l", las=1, bty="n",
     xlab="Variable x", ylab="variable y")

for (k in 0:8)
  ellipse(center.x=0.5, center.y=0.5, radius.x=0.1, radius.y=0.4,
          alpha=seq(from=0, to=pi/4, length=9)[k],
          border=rainbow(9)[k])

# Exemple with confidence of proportions
males <- c(10, 25, 3, 4)
N <- c(12, 52, 17, 10)

males2 <- c(12, 20, 3, 6)
N2 <- c(15, 50, 20, 12)

plot(0:1, 0:1, xlim=c(0, 1), ylim=c(0,1), lty=2, type="l", las=1, bty="n",
     xlab="Variable x", ylab="variable y")

ellipse(binconf.x = data.frame(x=males, n=N), binconf.y = data.frame(x=males2, n=N2),
        border=NA, col=rgb(red = 0.1, green = 0.5, blue = 0.1, alpha = 0.1))

plot(0:1, 0:1, xlim=c(0, 1), ylim=c(0,1), lty=2, type="l", las=1, bty="n",
     xlab="Variable x", ylab="variable y")
```

```
ellipse(binconf.x = data.frame(x=males, n=N),
        binconf.y = data.frame(PointEst=c(0.1, 0.2, 0.3, 0.5),
                               Lower=c(0.02, 0.12, 0.25, 0.30),
                               Upper=c(0.18, 0.29, 0.35, 0.67)),
        border=NA, col=rgb(red = 0.1, green = 0.5, blue = 0.1, alpha = 0.1))

# Examples with a gradient
plot(0:1, 0:1, xlim=c(0, 1), ylim=c(0,1), lty=2, type="l", las=1, bty="n",
     xlab="Variable x", ylab="variable y")
ellipse(center.x = 0.6, center.y = 0.3,
        radius.x.lower = 0.3, radius.x.upper = 0.3,
        radius.y.lower = 0.2, radius.y.upper = 0.4,
        border=NA, col=grey.colors(100, alpha = 0.1))

plot(0:1, 0:1, xlim=c(0, 1), ylim=c(0,1), lty=2, type="l", las=1, bty="n",
     xlab="Variable x", ylab="variable y")
ellipse(binconf.x = data.frame(x=males, n=N), binconf.y = data.frame(x=males2, n=N2),
        border=NA, col=grey.colors(100, alpha = 0.1))
```

`ELPDweight` *Return the probability of models compared with loo being the best for prediction*

Description

Calculate the probability of models compared with loo being the best for prediction. It uses simulation using the pointwise LOO log-predictive densities. This preserves the correlation between models, because all models are evaluated on the same observations. This is the approach recommended by Aki Vehtari et al. (2017) when uncertainty in model comparison matters.

Usage

```
ELPDweight(
  loos = stop("A named list of loo data must be provided."),
  nreplicates = 10000
)
```

Arguments

`loos`	A named list of loos
`nreplicates`	Number of replicates.

Details

ELPDweight calculates the probability that each model is best for prediction

Value

A vector with the probabilities

Author(s)

Marc Girondot <marc.girondot@gmail.com>

References

Vehtari, A., Gelman, A., & Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. Statistics and Computing, 27(5), 1413-1432. https://doi.org/10.1007/s11222-016-9696-4

See Also

Other AIC: ExtractAIC.glm(), FormatCompareAIC(), compare_AIC(), compare_AICc(), compare_BIC()

Examples

```
## Not run:
model1_loo <- loo::loo(model1)
model2_loo <- loo::loo(model2)
ELPDweight(list(model1=model1_loo, model2=model2_loo))

## End(Not run)
```

ExtractAIC.glm *Return AIC, AICc or BIC from a glm object*

Description

For glm fits the family's aic() function is used to compute the AIC.
The choice between different criteria is done by setting a global option AIC. It can be checked using show.option=TRUE. Indeed, it is not possible to use the ... parameter due to a bug in some functions of MASS package. If you want to use this function as a replacement for setpAIC(), do extractAIC.glm <- ExtractAIC.glm before.

Usage

```
ExtractAIC.glm(fit, scale = 0, k = 2, ...)
```

Arguments

fit	fitted model, the result of a fitter glm.
scale	unused for glm.
k	numeric specifying the 'weight' of the equivalent degrees of freedom (=: edf) part in the AIC formula.
...	further arguments (currently unused because addterm.glm and dropterm.glm using this function do not transmit them).

Details

ExtractAIC.glm returns AIC, AICc or BIC from a glm object

Value

A numeric named vector of length 2, with first and second elements giving
edf the 'equivalent degrees of freedom' for the fitted model fit.
x the Information Criterion for fit.

Author(s)

Modified from stats:::extract.AIC.glm

See Also

Other AIC: `ELPDweight()`, `FormatCompareAIC()`, `compare_AIC()`, `compare_AICc()`, `compare_BIC()`

Examples

```
## Not run:
extractAIC.glm <- ExtractAIC.glm
n <- 100
x <- rnorm(n, 20, 2)
A <- rnorm(n, 20, 5)
g <- glm(x ~ A)
extractAIC(g, show.option=TRUE)
options(AIC="AIC")
extractAIC(g)
options(AIC="BIC")
extractAIC(g)
options(AIC="AICc")
extractAIC(g)

## End(Not run)
```

---

fitdistrquantiles *Parameters of beta, normal or gamma distribution based on quantiles.*

Description

Return the parameters of beta or gamm that fits the best the quantiles. The vector of probabilities can be obtained from names of quantiles.

Usage

```
fitdistrquantiles(
  quantiles = stop("At least two quantiles must be provided"),
  probs = NULL,
  scaled = FALSE,
  distribution = "beta"
)
```

Arguments

quantiles	Vector of quantiles.
probs	Numeric vector of probabilities with values in [0,1].
scaled	Used scaled least-square.
distribution	Distribution to be fitted: beta, normal, or gamma.

Details

fitdistrquantiles returns the parameters of beta, normal or gamma distribution

Value

Parameters of beta, normal or gamma distribution based on quantiles.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
## Not run:
rd <- rbeta(100000, shape1 = 0.7, shape2 = 6.2, ncp=0)
(q <- quantile(rd, probs=c(0.025, 0.5, 0.975)))

(best <- fitdistrquantiles(quantiles = q, probs = c(0.025, 0.5, 0.975),
                           scaled=FALSE, distribution = "beta"))
rd10000 <- rbeta(10000, shape1 = best["shape1"], shape2 = best["shape2"], ncp=best["ncp"])
quantile(rd10000, probs=c(0.025, 0.5, 0.975))

# Here the probabilities are obtained from names of quantiles
(best <- fitdistrquantiles(quantiles = q, scaled=FALSE, distribution = "beta"))
rd10000 <- rbeta(10000, shape1 = best["shape1"], shape2 = best["shape2"], ncp=best["ncp"])
quantile(rd10000, probs=c(0.025, 0.5, 0.975))

# If only two quantiles are provided, ncp cannot be fitted
(q2 <- quantile(rd, probs=c(0.025, 0.975)))
(best <- fitdistrquantiles(quantiles = q2, scaled=FALSE, distribution = "beta"))
rd10000 <- rbeta(10000, shape1 = best["shape1"], shape2 = best["shape2"])
quantile(rd10000, probs=c(0.025, 0.975))
x <- seq(from=0.00, to=1, by=0.001)
plot(x=x, y=pbeta(x, shape1 = best["shape1"], shape2 = best["shape2"]),
```

```
     las=1, bty="n", type="l", ylim=c(0, 1))
segments(x0=q2[1], x1=q2[1], y0=0, y1=1, lty=2)
segments(x0=q2[2], x1=q2[2], y0=0, y1=1, lty=2)

(best <- fitdistrquantiles(quantiles = q, probs = c(0.025, 0.5, 0.975),
                           scaled=FALSE, distribution = "gamma"))
rd10000 <- rgamma(10000, shape = best["shape"], scale = best["scale"])
quantile(rd10000, probs=c(0.025, 0.5, 0.975))

(best <- fitdistrquantiles(quantiles = c(10, 20, 30), probs = c(0.025, 0.5, 0.975),
                           scaled=FALSE, distribution = "normal"))
rd10000 <- rnorm(10000, mean = best["mean"], sd = best["sd"])
quantile(rd10000, probs=c(0.025, 0.5, 0.975))

## End(Not run)
```

`flexit` *Return the flexit*

Description

Return a vector with the probabilities. The flexit equation is published in:
Abreu-Grobois, F.A., Morales-Mérida, B.A., Hart, C.E., Guillon, J.-M., Godfrey, M.H., Navarro, E. & Girondot, M. (2020) Recent advances on the estimation of the thermal reaction norm for sex ratios. PeerJ, 8, e8451.
If dose < P then $(1 + (2^K1 - 1) * exp(4 * S1 * (P - x)))^(- 1/K1)$
If dose > P then $1 - ((1 + (2^K2 - 1) * exp(4 * S2 * (x - P)))^(- 1/K2)$
with:

$$S1 = (2^(K1 - 1) * S * K1)/(2^K1 - 1)$$
$$S2 = (2^(K2 - 1) * S * K2)/(2^K2 - 1)$$

If 2^K1 is too large to be estimated, the approximation $S1 = S * K1/2$ is used.
Demonstration:

$$S1 = (2^(K1 - 1) * S * K1)/(2^K1 - 1)$$
$$S1 = exp(log((2^(K1 - 1) * S * K1)/(2^K1 - 1)))$$
$$S1 = exp(log(2^(K1 - 1)) + log(S * K1) - log(2^K1 - 1))$$

When $K1$ is very large, $2^K1 - 1 = 2^K1$ then

$$S1 = exp((K1 - 1) * log(2) + log(S * K1) - K1 * log(2))$$
$$S1 = exp((K1 * log(2) - log(2) + log(S * K1) - K1 * log(2))$$
$$S1 = exp(log(S * K1) - log(2))$$
$$S1 = S * K1/2$$

If 2^K2 is too large to be estimated, the approximation $S2 = S * K2/2$ is used.
If $(1+(2^K1-1)*exp(4*S1*(P-x)))^(-1/K1)$ is not finite, the following approximation is used:

$$exp((-1/K1) * (K1 * log(2) + (4 * S1 * (P - x))))$$

If $1-((1+(2^K2-1)*exp(4*S2*(x-P)))^(-1/K2)$ is not finite, the following approximation is used:

$$1 - exp((-1/K2) * (K2 * log(2) + (4 * S2 * (x - P))))$$

Usage

```
flexit(
  x,
  par = NULL,
  P = NULL,
  S = NULL,
  K1 = NULL,
  K2 = NULL,
  Min = 0,
  Max = 1,
  zero = 1e-09,
  error0 = 0,
  error1 = 1
)
```

Arguments

x	The values at which the flexit model must be calculated
par	The vector with P, S, K1, and K2 values
P	P value
S	S value
K1	K1 value
K2	K2 value
Min	Min value for scaled flexit model
Max	Max value for scaled flexit model
zero	Value to replace zero
error0	Value to return if an error is observed toward 0
error1	Value to return if an error is observed toward 1

Details

Return the flexit value

Value

A vector with the probabilities

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other logit: invlogit(), logit()

Examples

```
## Not run:
n <- flexit(x=1:100, par=c(P=50, S=0.001, K1=0.01, K2=0.02))
n <- flexit(x=1:100, P=50, S=0.001, K1=0.01, K2=0.02)

1/(1+exp(0.01*4*(50-1:100)))
flexit(1:100, P=50, S=0.01, K1=1, K2=1)

## End(Not run)
```

FormatCompareAIC *Format data to be used with compare_AIC()*

Description

Format data to be used with compare_AIC(), compare_AICc() and compare_BIC().
Note that logLik is supposed to not be -logLik.

Usage

```
FormatCompareAIC(logLik, nobs, df)
```

Arguments

logLik	The log likelihood
nobs	Number of observations
df	Number of parameters

Details

FormatCompareAIC formats data to be used with compare_AIC()

Value

An object to be used with compare_AIC()

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other AIC: ELPDweight(), ExtractAIC.glm(), compare_AIC(), compare_AICc(), compare_BIC()

Examples

```
## Not run:
ED <- FormatCompareAIC(logLik=-140, nobs=100, df=3)
L <- FormatCompareAIC(logLik=-145, nobs=100, df=4)
compare_AIC(L=L, ED=ED)
compare_AICc(L=L, ED=ED)
compare_BIC(L=L, ED=ED)

## End(Not run)
```

---

format_ncdf *Return an array with ncdf data*

Description

Return a list with two elements: data is an array and time is the POSIX.lt time.
Or if label.time is NULL or if bathy is TRUE, a bathy object.
If varid is NULL, it shows the available variable and dimensions of the file.
Bathymetry data can be download here:
https://www.gebco.net/data_and_products/gridded_bathymetry_data/#global

Usage

```
format_ncdf(
  ncdf,
  label.latitude = "latitude",
  label.longitude = "longitude",
  label.time = "time",
  varid = NULL,
  longitude1 = NA,
  latitude1 = NA,
  longitude2 = NA,
  latitude2 = NA,
  package = "ncdf4",
  bathy = TRUE
)
```

Arguments

ncdf	An object read from package ncdf4 or a file name of ncdf file
label.latitude	Label of latitude
label.longitude	Label of longitude

label.time	Label of time
varid	Name of variable to extract
longitude1	Longitude for first corner
latitude1	latitude for first corner
longitude2	Longitude for second corner
latitude2	latitude for second corner
package	If ncdf is a file, give the package to use to open the file
bathy	If TRUE, return a bathy object

Details

format_ncdf is used extract information from ncdf file

Value

A list with two element: data is an array and time is the POSIX.lt time

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other ncdf: ind_long_lat()

Examples

```
## Not run:
url <- "https://downloads.psl.noaa.gov/Datasets/noaa.oisst.v2.highres/"
url <- paste0(url, "sst.day.mean.2012.v2.nc")
dest <- paste(Sys.getenv("HOME"), "/sst.day.mean.2012.v2.nc", sep="")
download.file(url, dest)
format_ncdf(dest)

## End(Not run)
```

---

from_min_max *Distribution from minimum and maximum*

Description

Bayesian estimate of distribution when minimum, maximum, median or mean are known.
If D="norm**" or "lnorm**", it will use the approximation of Gumbel based on D.
If D="norm*" or "lnorm*", it will generate D distribution using replicates number of random numbers, and estimate Gumbel parameters from the simulated D distribution.
Otherwise it will estimate parameters of Gumbel distribution based on maximum likelihood.
For D="pois", "beta" or "chisq" only second (D="pois*", "beta*" or "chisq*") and third solutions are available.
The observed.Quantiles parameter must be a named value, for example observed.Quantiles = c(Q0.025=17, Q0.975=26)

Usage

```
from_min_max(
  n = stop("n must be known."),
  fitted.parameters = stop("At least one parameter must be supplied."),
  observed.Minimum,
  observed.Maximum,
  observed.Median = NULL,
  observed.Mean = NULL,
  observed.Quantiles = NULL,
  priors = "dnorm",
  fixed.parameters = NULL,
  D = "norm**",
  n.iter = 10000,
  n.chains = 1,
  n.adapt = 100,
  thin = 30,
  adaptive = FALSE,
  trace = 100,
  replicates = 10000,
  silent = FALSE
)
```

Arguments

n	Number of observations
fitted.parameters	The initial value to fit
observed.Minimum	The observed minimum
observed.Maximum	The observed maximum
observed.Median	The observed median (can be omitted)
observed.Mean	The observed mean (can be omitted)

observed.Quantiles
: Observed quantiles with names being the values of quantiles with Q being first letter (can be omitted; see description)

priors
: The priors (see MHAlgogen()) or character "dnorm" or "dunif"

fixed.parameters
: The fixed parameters

D
: The distribution to fit as character. ex "norm" or "lnorm"

n.iter
: Number of iterations for each chain

n.chains
: Number of chains

n.adapt
: Number of iteration to stabilize likelihood

thin
: Interval for thinning likelihoods

adaptive
: Should an adaptive process for SDProp be used

trace
: Or FALSE or period to show progress

replicates
: Number of replicates to model D

silent
: If TRUE, do not print information

Details

from_min_max returns standard deviation and/or mean from minimum and maximum

Value

from_min_max returns a list with output, ML, Bayesian results

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
## Not run:
minobs <- 5
maxobs <- 25
# These two values are not mandatory
meanobs <- 15
medianobs <- 16
n <- 10
# To estimate only the sd of the distribution; mean is fixed
# Note that there is an obligation to have mean even if it
# is in fixed.parameters
# By defaut a normal distribution is fitted

out_sd <- from_min_max(n=n                                ,
                       observed.Minimum=minobs           ,
                       observed.Maximum=maxobs           ,
                       fitted.parameters=c(sd=5)         ,
                       fixed.parameters=c(mean=meanobs)  ,
                       n.iter=10000                      ,
```

```
                        trace=TRUE                                    )

plot(out_sd, what="MarkovChain", parameters="sd")
plot(out_sd, what="posterior", parameters="sd")
as.parameters(out_sd, index="quantile")

# To estimate both the sd and mean of the distribution

out_sd_mean_norm <- from_min_max(n=n,
                            observed.Minimum=minobs                   ,
                            observed.Maximum=maxobs                   ,
                            fitted.parameters=c(mean=15, sd=5)         ,
                            fixed.parameters=NULL                     ,
                            n.iter=10000                              ,
                            D="norm**"                                ,
                            trace=FALSE                               )

plot(out_sd_mean_norm, what="MarkovChain", parameters="sd", ylim=c(0, 10))
plot(out_sd_mean_norm, what="MarkovChain", parameters="mean", ylim=c(10, 20))
plot(out_sd_mean_norm, what="posterior", parameters="mean",
     breaks=seq(from=0, to=100, by=1), xlim=c(10, 20))
as.parameters(out_sd_mean_norm, index="quantile")

# Let see what's happened for a lognormal distribution

out_sd_mean_lnorm <- from_min_max(n=n,
                            observed.Minimum=minobs                   ,
                            observed.Maximum=maxobs                   ,
                            fitted.parameters=c(meanlog=15, sdlog=5)   ,
                            fixed.parameters=NULL                     ,
                            n.iter=10000                              ,
                            D="lnorm**"                               ,
                            trace=FALSE                               )

plot(out_sd_mean_lnorm, what="MarkovChain", parameters="sdlog", ylim=c(0, 10))
plot(out_sd_mean_lnorm, what="MarkovChain", parameters="meanlog", ylim=c(10, 20))
plot(out_sd_mean_lnorm, what="posterior", parameters="meanlog", xlim=c(0, 20),
     breaks=seq(from=0, to=100, by=1))
as.parameters(out_sd_mean_lnorm, index="quantile")

# To be compared with the rule of thumb:
print(paste0("mean = ", as.character((maxobs + minobs) / 2))) # Mean Not so bad
print(paste0("sd = ", as.character((maxobs - minobs) / 4))) # SD Clearly biased

# Covariation of sd and mean is nearly NULL
cor(x=as.parameters(out_sd_mean_norm, index="all")[, "mean"],
    y=as.parameters(out_sd_mean_norm, index="all")[, "sd"])^2
plot(x=as.parameters(out_sd_mean_norm, index="all")[, "mean"],
     y=as.parameters(out_sd_mean_norm, index="all")[, "sd"],
     xlab="mean", ylab="sd")

# Example when minimum, maximum and mean are known
```

```
out_sd_mean2 <- from_min_max(n=n                                    ,
                             observed.Minimum=minobs                ,
                             observed.Maximum=maxobs                ,
                             observed.Mean=meanobs                  ,
                             fitted.parameters=c(mean=15, sd=5)     ,
                             fixed.parameters=NULL                  ,
                             n.iter=10000                           ,
                             trace=FALSE                             )

# Example when minimum, maximum, mean and median are known

out_sd_mean3 <- from_min_max(n=n                                    ,
                             observed.Minimum=minobs                ,
                             observed.Maximum=maxobs                ,
                             observed.Mean=meanobs                  ,
                             observed.Median=medianobs              ,
                             fitted.parameters=c(mean=15, sd=5)     ,
                             fixed.parameters=NULL                  ,
                             n.iter=10000                           ,
                             trace=FALSE                             )

plot(out_sd_mean2, what="MarkovChain", parameters="sd")
plot(out_sd_mean2, what="MarkovChain", parameters="mean")
plot(out_sd_mean2, what="posterior", parameters="mean", xlim=c(0, 100),
     breaks=seq(from=0, to=100, by=5))
as.parameters(out_sd_mean2, index="quantile")

# Example of GEV density function
# Parametrisation from https://en.wikipedia.org/wiki/Generalized_extreme_value_distribution
dGEV <- getFromNamespace(".dGEV", ns="HelpersMG")
x <- seq(from=-4, to=4, by=0.1)
plot(x, y=dGEV(x=x,
               location=0, scale=1, shape=-1/2, log=FALSE, sum=FALSE),
     type="l", col="green", xlab="x", ylab="Density")
lines(x, y=dGEV(x=x,
                location=0, scale=1, shape=0, log=FALSE, sum=FALSE), col="red")
lines(x, y=dGEV(x=x,
                location=0, scale=1, shape=1/2, log=FALSE, sum=FALSE), col="blue")
legend("topleft", legend=c("shape=-1/2", "shape=0", "shape=1/2"),
       lty=1, col=c("green", "red", "blue"))

# Note the different parametrisation about shape
dGEV <- getFromNamespace("dgevd", ns="EnvStats")
x <- seq(from=-4, to=4, by=0.1)
plot(x, y=dGEV(x=x,
               location=0, scale=1, shape=-1/2),
     type="l", col="green", xlab="x", ylab="Density")
lines(x, y=dGEV(x=x,
                location=0, scale=1, shape=0), col="red")
lines(x, y=dGEV(x=x,
                location=0, scale=1, shape=1/2), col="blue")
legend("topleft", legend=c("shape=-1/2", "shape=0", "shape=1/2"),
       lty=1, col=c("green", "red", "blue"))
```

```
# Compute dn using the approximation from Wan et al. (2014)
   get_dn <- function(n) {
     if (n < 2) {
       stop("Sample size n must be at least 2.")
     }
     qnorm((n - 0.375) / (n + 0.25)) * 2
   }

   # Estimate standard deviation from min and max
   estimate_sd_from_range <- function(min_val, max_val, n) {
     dn <- get_dn(n)
     range <- max_val - min_val
     sd_estimate <- range / dn
     return(sd_estimate)
   }

   # Example usage:
   n <- 10
   min_val <- 5
   max_val <- 25

   dn_value <- get_dn(n)
   sd_estimate <- estimate_sd_from_range(min_val, max_val, n)

   cat("dn =", dn_value, "\n")
   cat("Estimated SD =", sd_estimate, "\n")

   # To generate data from publication

   library(parallel)
   library(embryogrowth)

   # Values for the prior of SD
   outSD <- subset(DatabaseTSD, subset = (((!is.na(IP.SD)) |
                   (!is.na(IP.SE))) & (!is.na(Hatched))),
                   select=c("Hatched", "IP.SE", "IP.SD", "IP.mean"))
  outSD$IP.SD <- ifelse(is.na(outSD$IP.SD), outSD$IP.SE*sqrt(outSD$Hatched), outSD$IP.SD)

   # Model estimation

   Example <- subset(DatabaseTSD, subset = (!is.na(IP.min)) &
                       ((is.na(IP.SE)) & (is.na(IP.SD)) & (!is.na(Hatched)) &
                     (is.na(IP.mean))), select=c("Species", "Incubation.temperature.set",
                                                 "Hatched", "IP.min", "IP.max",
                                                 "Reference"))

   out <- universalmclapply(X=1:nrow(Example), FUN=function(i) {
     n <- Example[i, "Hatched"]

     priors <- structure(list(Density = c("dunif", "dlnorm"),
                              Prior1 = c(30, log(mean(outSD$IP.SD))),
                              Prior2 = c(120, log(sd(outSD$IP.SD))),
```

```
                              SDProp = c(1, 1),
                              Min = c(30, 0.1),
                              Max = c(120, 6),
                          Init = c((Example[i, "IP.min"]+ Example[i, "IP.max"])/2, log(2))),
                            row.names = c("mean", "sd"),
                            class = c("PriorsmcmcComposite", "data.frame"))


  out_sd_mean_mcmc <- from_min_max(n=n, observed.Minimum=Example[i, "IP.min"],
                                   observed.Maximum=Example[i, "IP.max"],
                                   fitted.parameters=c(mean=(Example[i, "IP.min"]+
                                                               Example[i, "IP.max"])/2,
                                                       sd=log(2)),
                                   priors = priors,
                                   D="norm**",
                                   n.iter = 10000, n.adapt=15000, thin=30,
                                   trace=100, adaptive = TRUE)

  # plot(out_sd_mean_mcmc, what = "MarkovChain", parameters = "sd")

  assign(paste0("out_sd_mean_mcmc_", as.character(i)), out_sd_mean_mcmc)
  save(list = paste0("out_sd_mean_mcmc_", as.character(i)),
    file = file.path("dataOut", paste0("out_sd_mean_mcmc_", as.character(i), ".Rdata")))
  # rm(list=paste0("out_sd_mean_mcmc_", as.character(i)))
}, progressbar = TRUE)

# Generate table with all results

Example <- subset(DatabaseTSD, subset = (!is.na(IP.min)) &
((is.na(IP.SE)) & (is.na(IP.SD)) & (!is.na(Hatched)) &
  (is.na(IP.mean))), select=c("Species", "Incubation.temperature.set",
                              "Hatched", "IP.min", "IP.max",
                              "Reference"))

Example <- cbind(Example, dn=NA)
Example <- cbind(Example, "SD(Hozo 2005)"=NA)
Example <- cbind(Example, "SD(Wan 2014)"=NA)
Example <- cbind(Example, "mean(Wan 2014)"=NA)
Example <- cbind(Example, "median(SD)"=NA)
Example <- cbind(Example, "2.5%(SD)"=NA)
Example <- cbind(Example, "97.5%(SD)"=NA)
Example <- cbind(Example, "25%(SD)"=NA)
Example <- cbind(Example, "75%(SD)"=NA)
Example <- cbind(Example, "median(mean)"=NA)
Example <- cbind(Example, "2.5%(mean)"=NA)
Example <- cbind(Example, "97.5%(mean)"=NA)
Example <- cbind(Example, "25%(mean)"=NA)
Example <- cbind(Example, "75%(mean)"=NA)
Example <- cbind(Example, "z(mean)"=NA)
Example <- cbind(Example, "z(SD)"=NA)


library(coda)
```

```
for (i in 1:nrow(Example)) {

  n <- Example[i, "Hatched"]
  if (n<= 15) {
    Example[i, "SD(Hozo 2005)"] <- (1/sqrt(12))*sqrt(((Example[i, "IP.max"] -
     Example[i, "IP.min"]))^2+((Example[i, "IP.max"] - Example[i, "IP.min"]))^2/4)
  } else {
    if (n<=70) {
      Example[i, "SD(Hozo 2005)"] <- (Example[i, "IP.max"] - Example[i, "IP.min"])/4
    } else {
      Example[i, "SD(Hozo 2005)"] <- (Example[i, "IP.max"] - Example[i, "IP.min"])/6
    }
  }

  Example[i, "dn"] <- get_dn(n)
  Example[i, "SD(Wan 2014)"] <- estimate_sd_from_range(Example[i, "IP.min"],
         Example[i, "IP.max"], n)
  Example[i, "mean(Wan 2014)"] <- (Example[i, "IP.min"]+ Example[i, "IP.max"])/2
 load(file = file.path("dataOut", paste0("out_sd_mean_mcmc_", as.character(i), ".Rdata")))
  out_sd_mean_mcmc <- get(paste0("out_sd_mean_mcmc_", as.character(i)))
 k <- as.parameters(out_sd_mean_mcmc, index="quantile", probs=c(0.025, 0.25, 0.5, 0.75, 0.975))
  outgk <- geweke.diag(as.mcmc(out_sd_mean_mcmc))
  rm(out_sd_mean_mcmc)
  rm(list=paste0("out_sd_mean_mcmc_", as.character(i)))
  Example[i, "median(SD)"] <- k["50%", "sd"]
  Example[i, "2.5%(SD)"] <- k["2.5%", "sd"]
  Example[i, "97.5%(SD)"] <- k["97.5%", "sd"]
  Example[i, "25%(SD)"] <- k["25%", "sd"]
  Example[i, "75%(SD)"] <- k["75%", "sd"]
  Example[i, "median(mean)"] <- k["50%", "mean"]
  Example[i, "2.5%(mean)"] <- k["2.5%", "mean"]
  Example[i, "97.5%(mean)"] <- k["97.5%", "mean"]
  Example[i, "25%(mean)"] <- k["25%", "mean"]
  Example[i, "75%(mean)"] <- k["75%", "mean"]
  Example[i, "z(mean)"] <- outgk$`1`$z["mean"]
  Example[i, "z(SD)"] <- outgk$`1`$z["sd"]
}

 rownames(Example) <- as.character(1:nrow(Example))

# Figure 1
layout(mat = matrix(1:4, nrow=2))
par(mar=c(4, 4, 0, 0))
plot(out_sd_mean_mcmc_11, what = "MarkovChain", parameters = "mean", ylim=c(70, 76))
text(x=ScalePreviousPlot(x=0.05, y=0.95)$x, y=ScalePreviousPlot(x=0.85, y=0.95)$y,
   labels = "A: mean", cex=1.5, pos=4)
plot(out_sd_mean_mcmc_8, what = "MarkovChain", parameters = "mean", ylim=c(50, 52))
text(x=ScalePreviousPlot(x=0.05, y=0.95)$x, y=ScalePreviousPlot(x=0.85, y=0.95)$y,
    labels = "C: mean", cex=1.5, pos=4)
plot(out_sd_mean_mcmc_11, what = "MarkovChain", parameters = "sd")
text(x=ScalePreviousPlot(x=0.05, y=0.95)$x, y=ScalePreviousPlot(x=0.85, y=0.95)$y,
    labels = "B: sd", cex=1.5, pos=4)
```

```
plot(out_sd_mean_mcmc_8, what = "MarkovChain", parameters = "sd")
text(x=ScalePreviousPlot(x=0.05, y=0.95)$x, y=ScalePreviousPlot(x=0.85, y=0.95)$y,
    labels = "D: sd", cex=1.5, pos=4)

# Figure 2
dtafigure2 <- matrix(NA, nrow=nrow(as.parameters(out_sd_mean_mcmc, index = "all")),
                     ncol=nrow(Example))

for (i in 1:nrow(Example)) {
  # i <- 1
 load(file=file.path("dataOut", paste0("out_sd_mean_mcmc_", as.character(i), ".Rdata")))
  out_sd_mean_mcmc <- get(paste0("out_sd_mean_mcmc_", as.character(i)))
  PPM <- rnorm(nrow(as.parameters(out_sd_mean_mcmc, index = "all")),
     mean = as.parameters(out_sd_mean_mcmc, index = "all")[, "mean"],
     sd=as.parameters(out_sd_mean_mcmc, index = "all")[, "sd"])
  dtafigure2[, i] <- PPM
}

layout(mat = 1)
par(mar=c(3, 4, 0, 0))
boxplot(dtafigure2, outline=FALSE, las=1, bty="n", xaxt="n", frame=FALSE, ylim=c(40, 90),
  col=sapply(as.character(Example$Species),
    FUN=function(i) switch(i, "Caretta caretta"="white",
                              "Chelonia mydas"="green",
                              "Dermochelys coriacea"="lightblue")),
  ylab="Incubation duration in days")
axis(1, at=1:30, labels = rep(NA, 30))
Cc <- sum(as.character(Example$Species) == "Caretta caretta")
CcCm <- sum(as.character(Example$Species) == "Caretta caretta" |
            as.character(Example$Species) == "Chelonia mydas")
segments(x0= Cc + 0.5,
         x1= Cc + 0.5,
         y0=40, y1=90, lty = 2)

segments(x0= CcCm + 0.5,
         x1= CcCm + 0.5,
         y0=40, y1=90, lty = 2)

par(xpd=TRUE)
text(x=Cc/2, y=33, labels = expression(italic("Caretta caretta")), cex=0.9)

text(x=Cc+(CcCm-Cc)/2, y=32, labels = expression(italic("Chelonia\n  mydas")), cex=0.9)
text(x=CcCm+(30-CcCm)/2, y=32, labels = expression(italic("Dermochelys\n coriacea")), cex=0.9)

# With Lognormal
 # To generate data from publication

 library(parallel)
 library(embryogrowth)

 # Values for the prior of SD
 outSD <- subset(DatabaseTSD, subset = (((!is.na(IP.SD)) |
                 (!is.na(IP.SE))) & (!is.na(Hatched))),
```

```
                  select=c("Hatched", "IP.SE", "IP.SD", "IP.mean"))
outSD$IP.SD <- ifelse(is.na(outSD$IP.SD), outSD$IP.SE*sqrt(outSD$Hatched), outSD$IP.SD)

# Model estimation

Example <- subset(DatabaseTSD, subset = (!is.na(IP.min)) &
                    ((is.na(IP.SE)) & (is.na(IP.SD)) & (!is.na(Hatched)) &
                  (is.na(IP.mean))), select=c("Species", "Incubation.temperature.set",
                                              "Hatched", "IP.min", "IP.max",
                                              "Reference"))

out <- universalmclapply(X=1:nrow(Example), FUN=function(i) {
  n <- Example[i, "Hatched"]

  priors <- structure(list(Density = c("dunif", "dlnorm"),
                           Prior1 = c(30, log(mean(outSD$IP.SD))),
                           Prior2 = c(120, log(sd(outSD$IP.SD))),
                           SDProp = c(1, 1),
                           Min = c(30, 0.1),
                           Max = c(120, 6),
                      Init = c((Example[i, "IP.min"]+ Example[i, "IP.max"])/2, log(2))),
                        row.names = c("meanlog", "sdlog"),
                        class = c("PriorsmcmcComposite", "data.frame"))


  out_sd_mean_mcmc_LN <- from_min_max(n=n, observed.Minimum=Example[i, "IP.min"],
                                      observed.Maximum=Example[i, "IP.max"],
                                      fitted.parameters=c(mean=(Example[i, "IP.min"]+
                                                          Example[i, "IP.max"])/2,
                                                        sd=log(2)),
                                      priors = priors,
                                      D="lnorm**",
                                      n.iter = 10000, n.adapt=15000, thin=30,
                                      trace=100, adaptive = TRUE)

  # plot(out_sd_mean_mcmc, what = "MarkovChain", parameters = "sd")

  assign(paste0("out_sd_mean_mcmc_LN_", as.character(i)), out_sd_mean_mcmc_LN)
  save(list = paste0("out_sd_mean_mcmc_LN_", as.character(i)),
    file = file.path("dataOut", paste0("out_sd_mean_mcmc_LN_", as.character(i), ".Rdata")))
  # rm(list=paste0("out_sd_mean_mcmc_LN_", as.character(i)))
}, progressbar = TRUE)


## End(Not run)
```

---

iCutter *Run a shiny application to fit bone section*

Description

Run a shiny application to fit bone section

Usage

```
iCutter()
```

Details

BP runs a shiny application to fit bone section

Value

Nothing

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
## Not run:
# Not run:
library(HelpersMG)
iCutter()

## End(Not run)
```

IC_clean_data *Clean the dataframe before to be used with IC_threshold_matrix*

Description

This function must be used if missing values are present in the dataset.
It ensures that all correlations and partial correlations can be calculated. The columns of the dataframe are removed one per one until all can be calculated without error. It is possible to say that one or more columns must be retained because they are of particular importance in the analysis. The use and method parameters are used by cor() function. The function uses by default a parallel computing in Unix or MacOSX systems. If progress is TRUE and the package pbmcapply is present, a progress bar is displayed. If debug is TRUE, some informations are shown during the process. https://fr.wikipedia.org/wiki/Iconographie_des_corrélations

Usage

```
IC_clean_data(
  data = stop("A dataframe object is required"),
  use = c("pairwise.complete.obs", "everything", "all.obs", "complete.obs",
    "na.or.complete"),
  method = c("pearson", "kendall", "spearman"),
  variable.retain = NULL,
  test.partial.correlation = TRUE,
  progress = TRUE,
```

```
  debug = FALSE
)
```

Arguments

data	The data.frame to be cleaned
use	an optional character string giving a method for computing covariances in the presence of missing values. This must be (an abbreviation of) one of the strings "everything", "all.obs", "complete.obs", "na.or.complete", or "pairwise.complete.obs".
method	a character string indicating which correlation coefficient (or covariance) is to be computed. One of "pearson" (default), "kendall", or "spearman": can be abbreviated.
variable.retain	a vector with the name of columns to keep
test.partial.correlation	should the partial correlations be tested ?
progress	Show a progress bar
debug	if TRUE, information about progression of cleaning are shown

Details

IC_clean_data checks and corrects the dataframe to be used with IC_threshold_matrix

Value

A dataframe

Author(s)

Marc Girondot <marc.girondot@gmail.com>

References

Lesty, M., 1999. Une nouvelle approche dans le choix des régresseurs de la régression multiple en présence d'interactions et de colinéarités. Revue de Modulad 22, 41-77.

See Also

Other Iconography of correlations: IC_correlation_simplify(), IC_threshold_matrix(), plot.IconoCorel()

Examples

```
## Not run:
library("HelpersMG")
# based on https://fr.wikipedia.org/wiki/Iconographie_des_corrélations
es <- structure(list(Student = c("e1", "e2", "e3", "e4", "e5", "e6", "e7", "e8"),
                     Mass = c(52, 59, 55, 58, 66, 62, 63, 69),
                     Age = c(12, 12.5, 13, 14.5, 15.5, 16, 17, 18),
                     Assiduity = c(12, 9, 15, 5, 11, 15, 12, 9),
```

```
                    Note = c(5, 5, 9, 5, 13.5, 18, 18, 18)),
                    row.names = c(NA, -8L), class = "data.frame")
es

df_clean <- IC_clean_data(es, debug = TRUE)
cor_matrix <- IC_threshold_matrix(data=df_clean, threshold = NULL, progress=FALSE)
cor_threshold <- IC_threshold_matrix(data=df_clean, threshold = 0.3)
plot(cor_threshold, show.legend.strength=FALSE, show.legend.direction = FALSE)
cor_threshold_Note <- IC_correlation_simplify(matrix=cor_threshold, variable="Note")
plot(cor_threshold_Note, show.legend.strength=FALSE, show.legend.direction = FALSE)

cor_threshold <- IC_threshold_matrix(data=df_clean, threshold = 0.6)
plot(cor_threshold,
layout=matrix(data=c(53, 53, 55, 55,
                    55, 53, 55, 53), ncol=2, byrow=FALSE),
show.legend.direction = FALSE,
show.legend.strength = FALSE, xlim=c(-2, 2), ylim=c(-2, 2))

## End(Not run)
```

`IC_correlation_simplify` *Simplify the correlation matrix*

Description

This function can be used to simplify the network of correlations.
If no vector of variables is given, the variables not linked to any other variable are removed. If a vector of variables is given, only link to these variables are retained. https://fr.wikipedia.org/wiki/Iconographie_des_c

Usage

```
IC_correlation_simplify(matrix, variable = NULL)
```

Arguments

matrix	The correlation matrix to simplify
variable	a vector with the name of columns to keep

Details

IC_correlation_simplify simplifies the correlation matrix

Value

A list

Author(s)

Marc Girondot <marc.girondot@gmail.com>

References

Lesty, M., 1999. Une nouvelle approche dans le choix des régresseurs de la régression multiple en présence d'interactions et de colinéarités. Revue de Modulad 22, 41-77.

See Also

Other Iconography of correlations: IC_clean_data(), IC_threshold_matrix(), plot.IconoCorel()

Examples

```
## Not run:
library("HelpersMG")
es <- structure(list(Student = c("e1", "e2", "e3", "e4", "e5", "e6", "e7", "e8"),
                 Mass = c(52, 59, 55, 58, 66, 62, 63, 69),
                 Age = c(12, 12.5, 13, 14.5, 15.5, 16, 17, 18),
                 Assiduity = c(12, 9, 15, 5, 11, 15, 12, 9),
                 Note = c(5, 5, 9, 5, 13.5, 18, 18, 18)),
                 row.names = c(NA, -8L), class = "data.frame")

es

df <- IC_clean_data(es, debug = TRUE)
cor_matrix <- IC_threshold_matrix(data=df, threshold = NULL, progress=FALSE)
cor_threshold <- IC_threshold_matrix(data=df, threshold = 0.3)
par(mar=c(1,1,1,1))
set.seed(4)
plot(cor_threshold)
cor_threshold_Note <- IC_correlation_simplify(matrix=cor_threshold, variable="Note")
plot(cor_threshold_Note)

## End(Not run)
```

`IC_threshold_matrix` *Calculate correlation matrix*

Description

This function calculates the matrix of correlations thresholded using partial correlation.
If the threshold is not given, the object that is produced can be used later for thresholding.
For model OAT: The link between A and B is "remarkable" if and only if the total correlation between them is higher than a given threshold and if the partial correlation between A and B in respect to any other variable C is also higher in absolute values than this threshold and with the same sign as the total correlation. For model AAT: A correlation is retained if it is higher than the threshold and the partial correlation is lower than the threshold. In this case, no missing value is accepted.
The use and method parameters are used by cor() function. The function uses by default a parallel computing in Unix or MacOSX systems. If progress is TRUE and the package pbmcapply is present, a progress bar is displayed. If debug is TRUE, some informations are shown during the process but parallel computing is not used.
https://fr.wikipedia.org/wiki/Iconographie_des_corrélations

Usage

```
IC_threshold_matrix(
  data = stop("A dataframe or an IconoCorel object is required"),
  threshold = NULL,
  use = c("pairwise.complete.obs", "everything", "all.obs", "complete.obs",
    "na.or.complete"),
  method = c("pearson", "kendall", "spearman"),
  model = c("OAT", "ATT"),
  significance.level = FALSE,
  correction.multiple.comparisons = "fdr",
  progress = TRUE,
  debug = FALSE
)
```

Arguments

data	A dataframe or an IconoCorel object from a previous run of IC_threshold_matrix
threshold	threshold for partial and full correlations
use	an optional character string giving a method for computing covariances in the presence of missing values. This must be (an abbreviation of) one of the strings "everything", "all.obs", "complete.obs", "na.or.complete", or "pairwise.complete.obs".
method	a character string indicating which correlation coefficient (or covariance) is to be computed. One of "pearson" (default), "kendall", or "spearman": can be abbreviated.
model	a character string indicating if linear model uses all variables at a time (AAT) or one at a time (OAT).
significance.level	if FALSE, does not use significance level; or use this significance level.
correction.multiple.comparisons	"holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", or "none".
progress	show a progress bar
debug	display information about progression of computing

Details

IC_threshold_matrix calculates correlation matrix thresholed by partial correlation

Value

A list

Author(s)

Marc Girondot <marc.girondot@gmail.com>

References

Lesty, M., 1999. Une nouvelle approche dans le choix des régresseurs de la régression multiple en présence d'interactions et de colinéarités. Revue de Modulad 22, 41-77.

See Also

Other Iconography of correlations: IC_clean_data(), IC_correlation_simplify(), plot.IconoCorel()

Examples

```
## Not run:
library("HelpersMG")
es <- structure(list(Student = c("e1", "e2", "e3", "e4", "e5", "e6", "e7", "e8"),
                Mass = c(52, 59, 55, 58, 66, 62, 63, 69),
                Age = c(12, 12.5, 13, 14.5, 15.5, 16, 17, 18),
                Assiduity = c(12, 9, 15, 5, 11, 15, 12, 9),
                Note = c(5, 5, 9, 5, 13.5, 18, 18, 18)),
                row.names = c(NA, -8L), class = "data.frame")

es

df_clean <- IC_clean_data(es, debug = TRUE)
cor_matrix <- IC_threshold_matrix(data=df_clean, threshold = NULL, progress=FALSE)
cor_threshold <- IC_threshold_matrix(data=df_clean, threshold = 0.3)
plot(cor_threshold, show.legend.strength=FALSE, show.legend.direction = FALSE)
cor_threshold_Note <- IC_correlation_simplify(matrix=cor_threshold, variable="Note")
plot(cor_threshold_Note)

cor_threshold <- IC_threshold_matrix(data=df_clean, threshold = 0.8, progress=FALSE)
gr <- plot(cor_threshold, plot=FALSE)
ly <- getFromNamespace("layout_nicely", ns="igraph")(gr)
plot(cor_threshold,
layout=matrix(data=c(53, 53, 55, 55,
                     55, 53, 55, 53), ncol=2, byrow=FALSE),
show.legend.direction = FALSE,
show.legend.strength = FALSE, xlim=c(-2, 2), ylim=c(-2, 2))

# Using significance level

cor_threshold <- IC_threshold_matrix(data=df_clean,
                                     significance.level=0.05, debug=TRUE)
plot(cor_threshold, show.legend.strength=FALSE, show.legend.direction = FALSE)
cor_threshold_Note <- IC_correlation_simplify(matrix=cor_threshold, variable="Note")
plot(cor_threshold_Note)

# Using the model All at a time

cor_threshold_AAT <- IC_threshold_matrix(data=df_clean, threshold = 0.3, model="AAT")
par(mar=c(1,1,1,1))
set.seed(4)
plot(cor_threshold_AAT, show.legend.strength="bottomleft")
```

```
############
dta <- structure(list(Student = c("e1", "e2", "e3", "e4", "e5", "e6", "e7", "e8"),
                      Mass = c(52, 59, 55, 58, 66, 62, 63, 69),
                      Age = c(12, 12.5, 13, 14.5, 15.5, 16, 17, 18),
                      Assiduity = c(12, 9, 15, 5, 11, 15, 12, 9),
                      Note = c(5, 5, 9, 5, 13.5, 18, 18, 18)),
                      row.names = c(NA, -8L), class = "data.frame")

dta0 <- dta[, 2:ncol(dta)]
ic0 <- IC_threshold_matrix(data = dta0)
cor_threshold <- IC_threshold_matrix(data=ic0, threshold = 0.3)
par(mar=c(1,1,1,1))
set.seed(4)
library("igraph")

plot(cor_threshold, vertex.color="red", show.legend.strength = FALSE)
plot(IC_correlation_simplify(matrix=cor_threshold),
     show.legend.strength = FALSE, show.legend.direction = FALSE)


## End(Not run)
```

`index.periodic` *Estimate indices in periodic timeseries based on anchored minimum and maximum*

Description

Estimate indices in periodic timeseries based on anchored minimum and maximum.
The data.frame minmax can be generated manually. It should have three columns (time, index, SD), with all the successive minimum and maximum indices.
It can be used with sun.info() to get the time of minimum and maximum air temperature or with getTide() to reconstruct the sea level.

Usage

```
index.periodic(minmax, time = NULL, replicates = 100, progressbar = FALSE)
```

Arguments

`minmax`	A data.frame returned by minmax.periodic
`time`	The time at which produced the estimate
`replicates`	Number of replicates to estimate SD
`progressbar`	Does a progression bar must be shown

Details

index.periodic estimate indices in periodic timeseries based on anchored minimum and maximum

Value

A data.frame with a column time and a column index

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Periodic patterns of indices: minmax.periodic(), moon.info(), sun.info(), tide.info()

Examples

```
## Not run:
# Generate a timeserie of time
time.obs <- NULL
for (i in 0:9) time.obs <- c(time.obs, c(0, 6, 12, 18)+i*24)
# For these time, generate a timeseries of temperatures
temp.obs <- rep(NA, length(time.obs))
temp.obs[3+(0:9)*4] <- rnorm(10, 25, 3)
temp.obs[1+(0:9)*4] <- rnorm(10, 10, 3)
for (i in 1:(length(time.obs)-1))
  if (is.na(temp.obs[i]))
  temp.obs[i] <- mean(c(temp.obs[i-1], temp.obs[i+1]))
  if (is.na(temp.obs[length(time.obs)]))
  temp.obs[length(time.obs)] <- temp.obs[length(time.obs)-1]/2
observed <- data.frame(time=time.obs, temperature=temp.obs)
# Search for the minimum and maximum values
r <- minmax.periodic(time.minmax.daily=c(Min=2, Max=15),
observed=observed, period=24, colname.index="temperature")

# Estimate all the temperatures for these values
t <- index.periodic(minmax=r)

plot_errbar(x=t[,"time"], y=t[,"index"],
errbar.y=ifelse(is.na(t[,"sd"]), 0, 2*t[,"sd"]),
type="l", las=1, bty="n", errbar.y.polygon = TRUE,
xlab="hours", ylab="Temperatures", ylim=c(0, 35),
errbar.y.polygon.list = list(col="grey"))

plot_add(x=t[,"time"], y=t[,"index"], type="l")

plot_add(observed$time, observed$temperature, pch=19, cex=0.5)

## End(Not run)
```

`ind_long_lat` *Return or the index in ncdf object from lat/longitude or inverse*

Description

Return or the index in ncdf object from lat/longitude or reverse.

Usage

```
ind_long_lat(
  ncdf = stop("The ncdf data must be supplied"),
  long = NULL,
  lat = NULL,
  indice.long = NULL,
  indice.lat = NULL,
  label.longitude = "lon",
  label.latitude = "lat"
)
```

Arguments

`ncdf`	An object read from package ncdf4, ncdf or RNetCDF
`long`	Longitude in decimal format
`lat`	Latitude in decimal format
`indice.long`	Index of longitude
`indice.lat`	Index of latitude
`label.longitude`	Name of argument for longitude, default is lon
`label.latitude`	Name of argument for latitude, default is lat

Details

ind_long_lat is used to manage ncdf information

Value

Or the index in ncdf object from lat/longitude or inverse

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other ncdf: `format_ncdf()`

Examples

```
## Not run:
url <- "https://downloads.psl.noaa.gov/Datasets/noaa.oisst.v2.highres/"
url <- paste0(url, "sst.day.mean.2012.v2.nc")
dest <- paste(Sys.getenv("HOME"), "/sst.day.mean.2012.v2.nc", sep="")
download.file(url, dest)
library("ncdf4")
dta2012 <- nc_open(dest)
indices <- ind_long_lat(ncdf=dta2012, lat=5.89, long=-20.56)
coordinates <- ind_long_lat(ncdf=dta2012, indice.lat=20, indice.long=30)
# library("RNetCDF")
# dta2012 <- open.nc(dest)
# indices <- ind_long_lat(ncdf=dta2012, lat=5.89, long=-20.56)
# coordinates <- ind_long_lat(ncdf=dta2012, indice.lat=20, indice.long=30)
# ncdf library is depreciated in CRAN
# library("ncdf")
# dta2012 <- open.ncdf(dest)
# indices <- ind_long_lat(ncdf=dta2012, lat=5.89, long=-20.56)
# coordinates <- ind_long_lat(ncdf=dta2012, indice.lat=20, indice.long=30)

## End(Not run)
```

---

inside *Search a string within files of a folder*

Description

Search for a string inside the files of a folder and return where the string is found.
The pattern for files that must be included uses regex for filtering.

Usage

```
inside(
  text = stop("A text to be searched for is necessary"),
  path = ".",
  pattern = "*\\.R$",
  showallfilenames = FALSE,
  ...,
  fixed = TRUE,
  ignore.case = FALSE
)
```

Arguments

text	Text to search in files
path	Path of the folder to search in
pattern	Pattern for file names to search in

showallfilenames	logical. Show all the filenames search for in
...	Options for readLines(), example warn = FALSE
fixed	logical. If TRUE, pattern is a string to be matched as is. Overrides all conflicting arguments (see gsub)
ignore.case	logical. if FALSE, the pattern matching for text is case sensitive and if TRUE, case is ignored during matching.

Details

inside Search a string within files of a folder

Value

Return an invisible vector with filenames in which the pattern occurs

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
## Not run:
library(HelpersMG)
# Search for files in path with names based on pattern that have the string search inside.
inside("embryogrowth", path=".", pattern="*\\.R$")

## End(Not run)
```

---

invlogit *Return the inverse logit*

Description

Return the inverse logit.

Usage

```
invlogit(n)
```

Arguments

n	The value to inverse to get the probability

Details

invlogit returns the inverse logit

Value

A value

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other logit: flexit(), logit()

Examples

```
n <- logit(0.5)
invlogit(n)
```

LD50 *Estimate the parameters that best describe LD50*

Description

Estimate the parameters that best describe LD50
Logistic and logit models are the same but with different parametrization:
logistic = 1/(1+exp((1/S)*(P-d)))*
*logit = 1/(1+exp(P+d*S))
See these publications for the description of equations:
Girondot, M. 1999. Statistical description of temperature-dependent sex determination using maximum likelihood. Evolutionary Ecology Research, 1, 479-486.
Godfrey, M.H., Delmas, V., Girondot, M., 2003. Assessment of patterns of temperature-dependent sex determination using maximum likelihood model selection. Ecoscience 10, 265-272.
Hulin, V., Delmas, V., Girondot, M., Godfrey, M.H., Guillon, J.-M., 2009. Temperature-dependent sex determination and global change: are some species at greater risk? Oecologia 160, 493-506.
The flexit equation is not still published :

$$if dose < Pthen(1 + (2^K1 - 1) * exp(4 * S1 * (P - x)))^(- 1/K1)$$

$$if dose > Pthen1 - ((1 + (2^K2 - 1) * exp(4 * S2 * (x - P)))^(- 1/K2)$$

with:

$$S1 = S/((4/K1) * (2^(- K1))^(1/K1 + 1) * (2^K1 - 1))$$

$$S2 = S/((4/K2) * (2^(- K2))^(1/K2 + 1) * (2^K2 - 1))$$

Usage

```
LD50(
  df = NULL,
  alive = NULL,
  dead = NULL,
  N = NULL,
  doses = NULL,
  l = 0.05,
  parameters.initial = NULL,
  fixed.parameters = NULL,
  SE = NULL,
  equation = "logistic",
  replicates = 1000,
  range.CI = 0.95,
  limit.low.TRD.minimum = 5,
  limit.high.TRD.maximum = 1000,
  print = TRUE,
  doses.plot = seq(from = 0, to = 1000, by = 0.1)
)
```

Arguments

df	A dataframe with at least two columns named alive, dead or N and doses columns
alive	A vector with alive individuals at the end of experiment
dead	A vector with dead individuals at the end of experiment
N	A vector with total numbers of tested individuals
doses	The doses
l	The limit to define TRD (see Girondot, 1999)
parameters.initial	Initial values for P, S or K search as a vector, ex. c(P=29, S=-0.3)
fixed.parameters	Parameters that will not be changed during fit
SE	Standard errors for parameters
equation	Could be "logistic", "logit", "probit", Hill", "Richards", "Hulin", "flexit" or "Double-Richards"
replicates	Number of replicates to estimate confidence intervals
range.CI	The range of confidence interval for estimation, default=0.95
limit.low.TRD.minimum	Minimum lower limit for TRD
limit.high.TRD.maximum	Maximum higher limit for TRD
print	Do the results must be printed at screen? TRUE (default) or FALSE
doses.plot	Sequences of doses that will be used for plotting. If NULL, does not estimate them

Details

LD50 estimates the parameters that best describe LD50

Value

A list with the LD50, Transitional Range of Doses and their SE

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other LD50 functions: LD50_MHmcmc(), LD50_MHmcmc_p(), logLik.LD50(), plot.LD50(), predict.LD50()

Examples

```
## Not run:
library("HelpersMG")
data <- data.frame(Doses=c(80, 120, 150, 150, 180, 200),
Alive=c(10, 12, 8, 6, 2, 1),
Dead=c(0, 1, 5, 6, 9, 15))
LD50_logistic <- LD50(data, equation="logistic")
predict(LD50_logistic, doses=c(140, 170))
plot(LD50_logistic, xlim=c(0, 300), at=seq(from=0, to=300, by=50))
LD50_probit <- LD50(data, equation="probit")
predict(LD50_probit, doses=c(140, 170))
plot(LD50_probit)
LD50_logit <- LD50(data, equation="logit")
predict(LD50_logit, doses=c(140, 170))
plot(LD50_logit)
LD50_hill <- LD50(data, equation="hill")
predict(LD50_hill, doses=c(140, 170))
plot(LD50_hill)
LD50_Richards <- LD50(data, equation="Richards")
predict(LD50_Richards, doses=c(140, 170))
plot(LD50_Richards)
LD50_Hulin <- LD50(data, equation="Hulin")
predict(LD50_Hulin, doses=c(140, 170))
plot(LD50_Hulin)
LD50_DoubleRichards <- LD50(data, equation="Double-Richards")
predict(LD50_DoubleRichards, doses=c(140, 170))
plot(LD50_DoubleRichards)
LD50_flexit <- LD50(data, equation="flexit")
predict(LD50_flexit, doses=c(140, 170))
plot(LD50_flexit)

## End(Not run)
```

LD50_MHmcmc *Metropolis-Hastings algorithm for LD50*

Description

Run the Metropolis-Hastings algorithm for tsd.
Deeply modified from a MCMC script by Olivier Martin (INRA, Paris-Grignon).
The number of iterations is n.iter+n.adapt+1 because the initial likelihood is also displayed.
I recommend that thin=1 because the method to estimate SE uses resampling.
If initial point is maximum likelihood, n.adapt = 0 is a good solution.
To get the SE from result_mcmc <- tsd_MHmcmc(result=try), use:
result_mcmc$BatchSE or result_mcmc$TimeSeriesSE
The batch standard error procedure is usually thought to be not as accurate as the time series methods.
Based on Jones, Haran, Caffo and Neath (2005), the batch size should be equal to sqrt(n.iter).
Jones, G.L., Haran, M., Caffo, B.S. and Neath, R. (2006) Fixed Width Output Analysis for Markov chain Monte Carlo , Journal of the American Statistical Association, 101:1537-1547.
coda package is necessary for this function.
The parameters intermediate and filename are used to save intermediate results every 'intermediate' iterations (for example 1000). Results are saved in a file of name filename.
The parameter previous is used to indicate the list that has been save using the parameters intermediate and filename. It permits to continue a mcmc search.
These options are used to prevent the consequences of computer crash or if the run is very very long and processes at time limited.

Usage

```
LD50_MHmcmc(
  result = stop("A result of LD50() fit must be provided"),
  n.iter = 10000,
  parametersMCMC = NULL,
  n.chains = 1,
  n.adapt = 0,
  thin = 1,
  trace = FALSE,
  batchSize = sqrt(n.iter),
  adaptive = FALSE,
  adaptive.lag = 500,
  adaptive.fun = function(x) {
     ifelse(x > 0.234, 1.3, 0.7)
 },
  intermediate = NULL,
  filename = "intermediate.Rdata",
  previous = NULL
)
```

Arguments

result	An object obtained after a SearchR fit
n.iter	Number of iterations for each step
parametersMCMC	A set of parameters used as initial point for searching with information on priors
n.chains	Number of replicates
n.adapt	Number of iterations before to store outputs
thin	Number of iterations between each stored output
trace	True or False, shows progress
batchSize	Number of observations to include in each batch fo SE estimation
adaptive	Should an adaptive process for SDProp be used
adaptive.lag	Lag to analyze the SDProp value in an adaptive content
adaptive.fun	Function used to change the SDProp
intermediate	Period for saving intermediate result, NULL for no save
filename	If intermediate is not NULL, save intermediate result in this file
previous	Previous result to be continued. Can be the filename in which intermediate results are saved.

Details

LD50_MHmcmc runs the Metropolis-Hastings algorithm for LD50 (Bayesian MCMC)

Value

A list with resultMCMC being mcmc.list object, resultLnL being likelihoods and parametersMCMC being the parameters used

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other LD50 functions: LD50(), LD50_MHmcmc_p(), logLik.LD50(), plot.LD50(), predict.LD50()

Examples

```
## Not run:
library("HelpersMG")
data <- data.frame(Doses=c(80, 120, 150, 150, 180, 200),
Alive=c(10, 12, 8, 6, 2, 1),
Dead=c(0, 1, 5, 6, 9, 15))
LD50_logistic <- LD50(data, equation="logistic")
pMCMC <- LD50_MHmcmc_p(LD50_logistic, accept=TRUE)
# Take care, it can be very long
result_mcmc_LD50 <- LD50_MHmcmc(result=LD50_logistic,
  parametersMCMC=pMCMC, n.iter=10000, n.chains = 1,
```

```
  n.adapt = 0, thin=1, trace=1000, adaptive=TRUE, )
# summary() permits to get rapidly the standard errors for parameters
summary(result_mcmc_LD50)
plot(x=result_mcmc_LD50, parameters="S", scale.prior=TRUE, las=1)
plot(result_mcmc_LD50, parameters="S", scale.prior=TRUE, las=1, xlim=c(-20, 20))
plot(result_mcmc_LD50, parameters="P", scale.prior=TRUE, las=1)
1-rejectionRate(as.mcmc(result_mcmc_LD50))
raftery.diag(as.mcmc(result_mcmc_LD50))
heidel.diag(as.mcmc(result_mcmc_LD50))

#### Example with Uniforms priors

pMCMC <- structure(list(Density = c("dunif", "dunif"),
Prior1 = c(77.6216005852911, -31.0438095277258),
Prior2 = c(310.486402341165, 31.0438095277258),
SDProp = c(2, 0.5),
Min = c(77.6216005852911, -31.0438095277258),
Max = c(310.486402341165, 31.0438095277258),
Init = c(155.243201170582, -15.5219047638629)),
row.names = c("P", "S"), class = "data.frame")
result_mcmc_LD50 <- LD50_MHmcmc(result=LD50_logistic,
  parametersMCMC=pMCMC, n.iter=10000, n.chains = 1,
  n.adapt = 0, thin=1, trace=1000, adaptive=TRUE, )
# summary() permits to get rapidly the standard errors for parameters
summary(result_mcmc_LD50)
plot(x=result_mcmc_LD50, parameters="S", scale.prior=TRUE, las=1)
plot(result_mcmc_LD50, parameters="S", scale.prior=TRUE, las=1, xlim=c(-40, 40))
plot(result_mcmc_LD50, parameters="P", scale.prior=TRUE, las=1)
1-rejectionRate(as.mcmc(result_mcmc_LD50))
raftery.diag(as.mcmc(result_mcmc_LD50))
heidel.diag(as.mcmc(result_mcmc_LD50))


## End(Not run)
```

LD50_MHmcmc_p *Generates set of parameters to be used with LD50_MHmcmc()*

Description

Interactive script used to generate set of parameters to be used with LD50_MHmcmc().

Usage

```
LD50_MHmcmc_p(
  result = stop("An output from LD50() must be provided"),
  accept = FALSE
)
```

Arguments

result	An object obtained after a LD50 fit
accept	If TRUE, the script does not wait user information

Details

LD50_MHmcmc_p generates set of parameters to be used with LD50_MHmcmc()

Value

A matrix with the parameters

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other LD50 functions: LD50(), LD50_MHmcmc(), logLik.LD50(), plot.LD50(), predict.LD50()

Examples

```
## Not run:
library("HelpersMG")
data <- data.frame(Doses=c(80, 120, 150, 150, 180, 200),
Alive=c(10, 12, 8, 6, 2, 1),
Dead=c(0, 1, 5, 6, 9, 15))
LD50_logistic <- LD50(data, equation="logistic")
pmcmc <- LD50_MHmcmc_p(LD50_logistic, accept=TRUE)

## End(Not run)
```

---

list.packages *List the installed packages with their locations*

Description

List the installed packages with their locations and version.

Usage

```
list.packages()
```

Details

list.packages lists the installed packages with their locations

Value

A list with the installed packages and their version.

Author(s)

Marc Girondot

Examples

```
## Not run:
library(HelpersMG)
list.packages()

## End(Not run)
```

`local.search` *Return path of file searched for in local disk based on its file name*

Description

Return path of file searched for in local disk based on its file name.
It has been tested only with Windows XP and MacOSX. In MacOSX, you must have created the locate database first. Use OnyX utilities for this purpose.

Usage

```
local.search(
  pattern,
  directory = "",
  folder = "$HOME",
  intern = TRUE,
  ignore.stdout = FALSE,
  ignore.stderr = TRUE
)
```

Arguments

`pattern`	The name of file to be searched for. Can use wildcards *
`directory`	The path of directory to be explored in for Windows
`folder`	The path of folder to be explored in for Unix based systems
`intern`	A logical (not NA) which indicates whether to capture the output of the command as an R character vector (see system()).
`ignore.stdout`	a logical (not NA) indicating whether messages written to 'stdout' should be ignored (see system()).
`ignore.stderr`	a logical (not NA) indicating whether messages written to 'stderr' should be ignored (see system()).

Details

local.search() returns path of file serached in local disk based on its file name

Value

A vector with paths

Author(s)

Marc Girondot

Examples

```
## Not run:
RnwFiles <- local.search("*.Rnw")
nc.files <- local.search("*.nc", folder=paste0("'",getwd(),"'"))

## End(Not run)
```

---

logit *Return the logit*

Description

Return the logit.

Usage

```
logit(p)
```

Arguments

p	The probability

Details

logit returns the logit

Value

A value

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other logit: flexit(), invlogit()

Examples

```
n <- logit(0.5)
invlogit(n)
```

`logLik.compareAIC` *Return Log Likelihood generated by FormatCompareAIC*

Description

Return Log Likelihood generated by FormatCompareAIC

Usage

```
## S3 method for class 'compareAIC'
logLik(object, ...)
```

Arguments

`object`	A result generated by FormatCompareAIC
`...`	Not used

Details

logLik.compareAIC Return Log Likelihood of a fit

Value

The Log Likelihood value for the fitted model with data

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
## Not run:
ED <- FormatCompareAIC(logLik=-140, nobs=100, df=3)
logLik(ED)

## End(Not run)
```

logLik.cutter *Return log likelihood of a cutter fitted model*

Description

Return log likelihood of a cutter fitted model.

Usage

```
## S3 method for class 'cutter'
logLik(object, ...)
```

Arguments

object	A result file generated by cutter
...	Not used

Details

logLik.cutter return log likelihood of a cutter fitted model

Value

Nothing

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Distributions: cutter(), dSnbinom(), dbeta_new(), dcutter(), dggamma(), dnbinom_new(), plot.cutter(), print.cutter(), r2norm(), rcutter(), rmnorm(), rnbinom_new()

Examples

```
## Not run:
# ____________________________________________________________________
# Test for similarity in gamma left censored distribution between two
# datasets
# ____________________________________________________________________
obc1 <- rgamma(100, scale=20, shape=2)
# Detection limit for sample 1 to 50
LDL <- 10
# remove the data below the detection limit
obc1[obc1<LDL] <- -Inf
obc2 <- rgamma(100, scale=10, shape=2)
# remove the data below the detection limit
obc2[obc2<LDL] <- -Inf
```

```
# search for the parameters the best fit these censored data
result1 <- cutter(observations=obc1,
                          lower_detection_limit=LDL,
                          cut_method="censored")
logLik(result1)
result2 <- cutter(observations=obc2,
                          lower_detection_limit=LDL,
                          cut_method="censored")
logLik(result2)
result_totl <- cutter(observations=c(obc1, obc2),
                          lower_detection_limit=LDL,
                          cut_method="censored")
logLik(result_totl)
compare_AICc(Separate=list(result1, result2),
            Common=result_totl, factor.value=1)
compare_BIC(Separate=list(result1, result2),
            Common=result_totl, factor.value=1)

## End(Not run)
```

`logLik.LD50` *Return Log Likelihood of a fit generated by LD50*

Description

Return Log Likelihood of a fit generated by LD50

Usage

```
## S3 method for class 'LD50'
logLik(object, ...)
```

Arguments

`object`	A result file generated by fitRMU
`...`	Not used

Details

logLik.LD50 Return Log Likelihood of a fit for LD50

Value

The Log Likelihood value for the fitted model with data

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other LD50 functions: `LD50()`, `LD50_MHmcmc()`, `LD50_MHmcmc_p()`, `plot.LD50()`, `predict.LD50()`

Examples

```
## Not run:
data <- data.frame(Doses=c(80, 120, 150, 150, 180, 200),
Alive=c(10, 12, 8, 6, 2, 1),
Dead=c(0, 1, 5, 6, 9, 15))
LD50_logistic <- LD50(data, equation="logistic")
logLik(LD50_logistic)
AIC(LD50_logistic)

## End(Not run)
```

`merge.mcmcComposite` *Merge two mcmcComposite results*

Description

Merge two mcmcComposite results and produced a new one mcmcComposite object.
Note that the initial value for the second run must use the last value of the first one as shown in example.

Usage

```
## S3 method for class 'mcmcComposite'
merge(x, y, ...)
```

Arguments

`x`	A mcmcComposite obtained as a result of `MHalgoGen()` function
`y`	A mcmcComposite obtained as a result of `MHalgoGen()` function
`...`	not used

Details

merge.mcmcComposite Merge two mcmcComposite results

Value

A mcmcComposite result

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other mcmcComposite functions: +.PriorsmcmcComposite(), MHalgoGen(), PPD(), as.mcmc.mcmcComposite(), as.parameters(), plot.PriorsmcmcComposite(), plot.mcmcComposite(), setPriors(), setPriors1(), summary.mcmcComposite()

Examples

```
## Not run:
library(HelpersMG)
require(coda)
x <- rnorm(30, 10, 2)
dnormx <- function(data, x) {
 data <- unlist(data)
 return(-sum(dnorm(data, mean=x['mean'], sd=x['sd'], log=TRUE)))
}
parameters_mcmc <- data.frame(Density=c('dnorm', 'dlnorm'),
Prior1=c(10, 0.5), Prior2=c(2, 0.5), SDProp=c(1, 1),
Min=c(-3, 0), Max=c(100, 10), Init=c(10, 2), stringsAsFactors = FALSE,
row.names=c('mean', 'sd'))
mcmc_run <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, data=x,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=1)
plot(mcmc_run, xlim=c(0, 20))
plot(mcmc_run, xlim=c(0, 10), parameters="sd")
mcmcforcoda <- as.mcmc(mcmc_run)
#' heidel.diag(mcmcforcoda)
raftery.diag(mcmcforcoda)
autocorr.diag(mcmcforcoda)
acf(mcmcforcoda[[1]][,"mean"], lag.max=20, bty="n", las=1)
acf(mcmcforcoda[[1]][,"sd"], lag.max=20, bty="n", las=1)
batchSE(mcmcforcoda, batchSize=100)
# The batch standard error procedure is usually thought to
# be not as accurate as the time series methods used in summary
summary(mcmcforcoda)$statistics[,"Time-series SE"]
summary(mcmc_run)
as.parameters(mcmc_run)
lastp <- as.parameters(mcmc_run, index="last")
parameters_mcmc[,"Init"] <- lastp
# The n.adapt set to 1 is used to not record the first set of parameters
# then it is not duplicated (as it is also the last one for
# the object mcmc_run)
mcmc_run2 <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, data=x,
likelihood=dnormx, n.chains=1, n.adapt=1, thin=1, trace=1)
mcmc_run3 <- merge(mcmc_run, mcmc_run2)
####### no adaptation, n.adapt must be 0
parameters_mcmc[,"Init"] <- c(mean(x), sd(x))
mcmc_run3 <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, data=x,
likelihood=dnormx, n.chains=1, n.adapt=0, thin=1, trace=1)

## End(Not run)
```

MHalgoGen *Monte-Carlo Markov-chain with Metropolis-Hastings algorithm*

Description

The parameters must be stored in a data.frame with named rows for each parameter with the following columns:

- Density. The density function name, example `dnorm`, `dlnorm`, `dunif`, `dbeta`
- Prior1. The first parameter to send to the `Density` function
- Prior2. The second parameter to send to the `Density` function
- Prior3. The third parameter to send to the `Density` function
- SDProp. The standard error from new proposition value of this parameter
- Min. The minimum value for this parameter
- Max. The maximum value for this parameter
- Init. The initial value for this parameter

This script has been deeply modified from a MCMC script provided by Olivier Martin (INRA, Paris-Grignon).
The likelihood function must use a parameter named parameters_name for the named parameters.
For adaptive mcmc, see:
Rosenthal, J. S. 2011. Optimal Proposal Distributions and Adaptive MCMC. Pages 93-112 in S. Brooks, A. Gelman, G. Jones, and X.-L. Meng, editors. MCMC Handbook. Chapman and Hall/CRC.

Usage

```
MHalgoGen(
  likelihood = stop("A likelihood function must be supplied"),
  parameters = stop("Priors must be supplied"),
  ...,
  parameters_name = "x",
  n.iter = 10000,
  n.chains = 1,
  n.adapt = 100,
  thin = 30,
  trace = FALSE,
  traceML = FALSE,
  progress.bar.ini = NULL,
  progress.bar = NULL,
  adaptive = FALSE,
  adaptive.lag = 500,
  adaptive.fun = function(x) {
```

```
    ifelse(x > 0.234, 1.3, 0.7)
 },
  intermediate = NULL,
  filename = "intermediate.Rdata",
  previous = NULL,
  session = NULL,
  warn = FALSE,
  WAIC.out = FALSE,
  n.datapoints = NULL
)
```

Arguments

likelihood	The function that returns -ln likelihood using data and parameters
parameters	A data.frame with priors; see description and examples
...	Parameters to be transmitted to likelihood function
parameters_name	The name of the parameters in the likelihood function, default is "x".
n.iter	Number of iterations for each chain
n.chains	Number of chains
n.adapt	Number of iteration to stabilize likelihood
thin	Interval for thinning likelihoods
trace	Or FALSE or period to show progress
traceML	TRUE or FALSE to show ML
progress.bar.ini	The command to initialize progress bar
progress.bar	The command to run the progress bar
adaptive	Should an adaptive process for SDProp be used
adaptive.lag	Lag to analyze the SDProp value in an adaptive context
adaptive.fun	Function used to change the SDProp
intermediate	Or NULL of period to save intermediate result
filename	Name of file in which intermediate results are saved
previous	The content of the file in which intermediate results are saved
session	The shiny session
warn	If TRUE, show information for debug.
WAIC.out	If TRUE matrix or array are stored to be used with loo or waic.
n.datapoints	Number of datapoints when WAIC.out is TRUE.

Details

MHalgoGen is a function to use mcmc with Metropolis-Hastings algorithm

Value

A mcmcComposite object with all characteristics of the model and mcmc run

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other mcmcComposite functions: +.PriorsmcmcComposite(), PPD(), as.mcmc.mcmcComposite(), as.parameters(), merge.mcmcComposite(), plot.PriorsmcmcComposite(), plot.mcmcComposite(), setPriors(), setPriors1(), summary.mcmcComposite()

Examples

```
## Not run:
library(HelpersMG)
require(coda)
val <- rnorm(30, 10, 2)
dnormx <- function(data, x) {
 data <- unlist(data)
 return(-sum(dnorm(data, mean=x['mean'], sd=x['sd'], log=TRUE)))
}
parameters_mcmc <- data.frame(Density=c('dnorm', 'dlnorm'),
Prior1=c(10, 0.5), Prior2=c(2, 0.5), SDProp=c(0.35, 0.2),
Min=c(-3, 0), Max=c(100, 10), Init=c(10, 2), stringsAsFactors = FALSE,
row.names=c('mean', 'sd'))
# Or simpler
parameters_mcmc <- setPriors1(Name="mean", Density="dnorm", Parameters=c(mean=10, sd=2),
                              SDProp=0.35, Min=-3, Max=100, Init=10)
parameters_mcmc <- parameters_mcmc + setPriors1(Name="sd", Density="dlnorm",
                              Parameters=c(meanlog=0.5, sdlog=0.5),
                              SDProp=0.2, Min=0, Max=10, Init=2)
# Use of trace and traceML parameters
# trace=1 : Only one likelihood is printed
mcmc_run <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, data=val,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=1)
# trace=10 : 10 likelihoods are printed
mcmc_run <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, data=val,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=10)
# trace=TRUE : all likelihoods are printed
mcmc_run <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, data=val,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=TRUE)
# traceML=TRUE : values when likelihood is better are shown
mcmc_run <- MHalgoGen(n.iter=100, parameters=parameters_mcmc, data=val,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=TRUE, traceML=TRUE)
mcmc_run <- MHalgoGen(n.iter=100, parameters=parameters_mcmc, data=val,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=FALSE, traceML=TRUE)
# trace=FALSE : No likelihood is printed
mcmc_run <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, data=val,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=FALSE)
```

```
plot(mcmc_run, xlim=c(0, 20))
plot(mcmc_run, xlim=c(0, 10), parameters="sd")
library(graphics)
library(fields)
# show a scatter plot of the result
x <- mcmc_run$resultMCMC[[1]][, 1]
y <- mcmc_run$resultMCMC[[1]][, 2]
marpre <- par(mar=c(4, 4, 2, 6)+0.4)
smoothScatter(x, y)
# show a scale
n <- matrix(0, ncol=128, nrow=128)
xrange <- range(x)
yrange <- range(y)
for (i in 1:length(x)) {
  posx <- 1+floor(127*(x[i]-xrange[1])/(xrange[2]-xrange[1]))
  posy <- 1+floor(127*(y[i]-yrange[1])/(yrange[2]-yrange[1]))
  n[posx, posy] <- n[posx, posy]+1
}
image.plot(legend.only=TRUE, zlim= c(0, max(n)), nlevel=128,
 col=colorRampPalette(c("white", blues9))(128))
# Compare with a heatmap
x <- seq(from=8, to=12, by=0.2)
y <- seq(from=1, to=4, by=0.2)
df <- expand.grid(mean=x, sd=y)
df <- cbind(df, L=rep(0, length(nrow(df))))
for (i in 1:nrow(df)) df[i, "L"] <- -sum(dnorm(val, df[i, 1], df[i, 2], log = TRUE))
hm <- matrix(df[, "L"], nrow=length(x))
par(mar = marpre)
image.plot(x=x, y=y, z=hm, las=1)
# Diagnostic function from coda library
mcmcforcoda <- as.mcmc(mcmc_run)
#' heidel.diag(mcmcforcoda)
raftery.diag(mcmcforcoda)
autocorr.diag(mcmcforcoda)
acf(mcmcforcoda[[1]][,"mean"], lag.max=20, bty="n", las=1)
acf(mcmcforcoda[[1]][,"sd"], lag.max=20, bty="n", las=1)
batchSE(mcmcforcoda, batchSize=100)
# The batch standard error procedure is usually thought to
# be not as accurate as the time series methods used in summary
summary(mcmcforcoda)$statistics[,"Time-series SE"]
summary(mcmc_run)
as.parameters(mcmc_run)
lastp <- as.parameters(mcmc_run, index="last")
parameters_mcmc[,"Init"] <- lastp
# The n.adapt set to 1 is used to not record the first set of parameters
# then it is not duplicated (as it is also the last one for
# the object mcmc_run)
mcmc_run2 <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, x=x, data=val,
likelihood=dnormx, n.chains=1, n.adapt=1, thin=1, trace=1)
mcmc_run3 <- merge(mcmc_run, mcmc_run2)
####### no adaptation, n.adapt must be 0
parameters_mcmc[,"Init"] <- c(mean(x), sd(x))
mcmc_run3 <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, x=x, data=val,
```

```
likelihood=dnormx, n.chains=1, n.adapt=0, thin=1, trace=1)
# Here is how to use adaptive mcmc
mcmc_run <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, data=val, adaptive = FALSE,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=1)
1-rejectionRate(as.mcmc(mcmc_run))
mcmc_run <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, data=val, adaptive = TRUE,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=1)
1-rejectionRate(as.mcmc(mcmc_run))
# To see the dynamics :
var <- "mean"
par(mar=c(4, 4, 1, 1)+0.4)
plot(1:nrow(mcmc_run$resultMCMC[[1]]), mcmc_run$resultMCMC[[1]][, var], type="l",
       xlab="Iterations", ylab=var, bty="n", las=1)
plot(mcmc_run, what="Posterior", parameters="mean")
plot(mcmc_run, what="MarkovChain", parameters="mean", ylim=c(0, 20), legend="topleft")
plot(mcmc_run, what="MarkovChain", parameters="mean", legend="topleft")
# Exemple with a progress bar

val <- rnorm(30, 10, 2)
dnormx <- function(data, x) {
 data <- unlist(data)
 return(-sum(dnorm(data, mean=x['mean'], sd=x['sd'], log=TRUE)))
}
parameters_mcmc <- setPriors1(Name="mean", Density="dnorm", Parameters=c(mean=10, sd=2),
                              SDProp=0.35, Min=-3, Max=100, Init=10)
parameters_mcmc <- parameters_mcmc + setPriors1(Name="sd", Density="dlnorm",
                              Parameters=c(meanlog=0.5, sdlog=0.5),
                              SDProp=0.2, Min=0, Max=10, Init=2)
# Set up the progress bar
mcmc_run <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, data=val,
                      likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=FALSE,
                       progress.bar.ini=function(n.iter) {
                                assign("pb", txtProgressBar(min=0, max=n.iter, style=3),
                                        env = parent.frame())},
     progress.bar=function(iter) {setTxtProgressBar(get("pb", envir = parent.frame()), iter)})

## End(Not run)
```

`minmax.periodic` *Search for minimum and maximum indices in periodic timeseries*

Description

Search for minimum and maximum for periodic timeseries when only intermediate values are known.

For each couple of value with an increasing or decreasing segment of the sinusoid function, it is possible to estimate a minimum and maximum values using analytical algebra.

Then the average and standard deviations of all minima and maxima are evaluated.

It should be noted that any extremum can be estimated at least twice, one by increasing segment and one by decreasing segment. Both are used here to produce SD.

time.minmax.daily should be used when the time at which maximum and minimum indices are regular and time.minmax permits to define this time day by day.

Usage

```
minmax.periodic(
  time.minmax.daily = NULL,
  time.minmax = NULL,
  progressbar = FALSE,
  observed = stop("data.frame with observed indices"),
  period = 24,
  colname.time = "time",
  colname.index = "index",
  colname.SD = "SD",
  plot = FALSE
)
```

Arguments

time.minmax.daily	A named vector with Min and Max being the time in the day with minimum and maximum indices (temperature or level)
time.minmax	A named vector daily with time in the day at which minimum and maximum indices are observed
progressbar	Tell if a progression bar must be shown
observed	A dataframe with at least two columns: time and temperatures. A third column SD can indicate the know error in index
period	The unit of day period (24 for hours, 24*60 for minutes)
colname.time	The name of the column for time in observed
colname.index	The name of the column for indices in observed
colname.SD	The name of the column for SD in observed
plot	If TRUE, show a plot with the different estimates

Details

minmax.periodic search for minimum and maximum indices (temperatures or levels) in periodic timeseries

Value

A data.frame with a column time, a column index and a column SD

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Periodic patterns of indices: index.periodic(), moon.info(), sun.info(), tide.info()

Examples

```
## Not run:
library("HelpersMG")
# Generate a timeserie of time
time.obs <- NULL
for (i in 0:9) time.obs <- c(time.obs, c(0, 6, 12, 18)+i*24)
# For these time, generate a timeseries of temperatures
temp.obs <- rep(NA, length(time.obs))
temp.obs[3+(0:9)*4] <- rnorm(10, 25, 3)
temp.obs[1+(0:9)*4] <- rnorm(10, 10, 3)
for (i in 1:(length(time.obs)-1))
  if (is.na(temp.obs[i]))
  temp.obs[i] <- mean(c(temp.obs[i-1], temp.obs[i+1]))
  if (is.na(temp.obs[length(time.obs)]))
  temp.obs[length(time.obs)] <- temp.obs[length(time.obs)-1]/2
observed <- data.frame(time=time.obs, temperature=temp.obs)
# Search for the minimum and maximum values
r <- minmax.periodic(time.minmax.daily=c(Min=2, Max=15),
observed=observed, period=24, colname.index="temperature")

# Estimate all the temperatures for these values
t <- index.periodic(minmax=r)

plot_errbar(x=t[,"time"], y=t[,"index"],
errbar.y=ifelse(is.na(t[,"sd"]), 0, 2*t[,"sd"]),
type="l", las=1, bty="n", errbar.y.polygon = TRUE,
xlab="hours", ylab="Temperatures", ylim=c(0, 35),
errbar.y.polygon.list = list(col="grey"))

plot_add(x=t[,"time"], y=t[,"index"], type="l")

plot_add(observed$time, observed$temperature, pch=19, cex=0.5)

## End(Not run)
```

---

modeled.hist *Return the theoretical value for the histogram bar*

Description

Return the theoretical value for the histogram bar based on a model of distribution.

Usage

```
modeled.hist(breaks, FUN, ..., sum = 1)
```

Arguments

breaks	Vector with the breaks; it can be obtained directly from hist()
FUN	Function to be used to integrate the density, ex. pnorm
...	Parameters to be used by FUN
sum	Total numbers in the histogram; 1 for emperical frequencies

Details

modeled.hist returns the theoretical value for the histogram bar based on a model of distribution.

Value

A list with x (the center of the bar) and y components

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
## Not run:
n <- rnorm(100, mean=10, sd=2)
breaks <- 0:20
hist(n, breaks=breaks)

s <- modeled.hist(breaks=breaks, FUN=pnorm, mean=10, sd=2, sum=100)

points(s$x, s$y, pch=19)
lines(s$x, s$y)

n <- rlnorm(100, meanlog=2, sdlog=0.4)
b <- hist(n, ylim=c(0, 70))

s <- modeled.hist(breaks=b$breaks, FUN=plnorm, meanlog=2, sdlog=0.4, sum=100)

points(s$x, s$y, pch=19)
lines(s$x, s$y)

## End(Not run)
```

---

modifyVector *Modifies Elements of a Vector*

Description

Modifies a vector by changing a subset of elements to match a second vector.

Usage

```
modifyVector(x, val, add = TRUE)
```

Arguments

x	A named vector.
val	A named vector with components to replace corresponding components in x.
add	If FALSE, only existing elements of x are returned.

Details

modifyVector modifies elements of a vector

Value

A modified version of x, with the elements of val replacing the elements of x

Author(s)

Marc Girondot

Examples

```
library("HelpersMG")
e <- c(M=10, L=20, J=30)
modifyVector(e, c(U=10, M=30))
modifyVector(e, c(U=10, M=30), add=FALSE)
```

---

moon.info *Moon phase based on a date*

Description

The script gives an index (base 100) that represents moon phase.
If the return value (from 0 to 100) is between:
0 and 1.6931595 or 98.3068405 and 100, it is full moon,
23.3068405 and 26.6931595, last quarter,
48.3068405 and 51.6931595, new moon,
73.3068405 and 76.6931595, first quarter
When phase is set to TRUE, a character representing the moon phase is returned.

Usage

```
moon.info(date = Sys.Date(), phase = FALSE)
```

Arguments

date	A date in class Date. By default, it will use today date
phase	If TRUE, a vector of characters with NM, FQ, FL LQ will be returned

Details

moon.info calculates the moon phase based on a date.

Value

Return a value describing the moon phase:
0 and 100 are full moon, 50 is new moon, 25 last quarter and 75 first quater

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Periodic patterns of indices: index.periodic(), minmax.periodic(), sun.info(), tide.info()

Examples

```
## Not run:
library("HelpersMG")
moon.info(as.Date("2001-12-31"))
moon.info(as.Date("14/04/2010", "%d/%m/%Y"))
moon.info(as.Date("22/06/07", "%d/%m/%y"))
moon.info(seq(from=as.Date("2012-03-01"),
 to=as.Date("2012-04-15"), by="days"))
moon.info(seq(from=as.Date("2012-03-01"),
  to=as.Date("2012-04-15"), by="days"), phase=TRUE)

## End(Not run)
```

MovingWindow *Return a moving average of a vector.*

Description

Return a moving average of a vector.
hole parameter can be "none", "bothL", "bothR", "both", "begin", or "end".

Usage

```
MovingWindow(x, window, hole = "begin", fill = TRUE, FUN = mean)
```

Arguments

x	The vector to analyze
window	The window size
hole	Should the returned vector have the same length than x
fill	TRUE or FALSE, should the vector return NA
FUN	Function to apply to the window

Details

MovingWindow returns a moving average of a vector.

Value

A vector

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
MovingWindow(1:10, window = 4, fill = TRUE, hole="bothL")
MovingWindow(1:10, window = 4, fill = TRUE, hole="bothR")
MovingWindow(1:10, window = 4, fill = TRUE, hole="both")
MovingWindow(1:10, window = 4, fill = TRUE, hole="none")
MovingWindow(1:10, window = 4, fill = TRUE, hole="begin")
MovingWindow(1:10, window = 4, fill = TRUE, hole="end")
MovingWindow(1:10, window = 4, fill = TRUE, hole="end", FUN=sd)
```

NagelkerkeScaledR2 *Return the scaled R2 defined by Nagelkerke (1991)*

Description

Return the scaled R2 of a binomial model based on:
Nagelkerke NJD (1991) A note on a general definition of the coefficient of determination. Biometrika 78:691-192.
This definition of scaled R2 by Nagelkerke (1991) has the following properties:
(i) It is consistent with classical R2, that is the general definition applied to e.g. linear regression yields the classical R2.
(ii) It is consistent with maximum likelihood as an estimation method, i.e. the maximum likelihood estimates of the model parameters maximize R2.
(iii) It is asymptotically independent of the sample size n.
(iv) 1-R2 has the interpretation of the proportion of unexplained 'variation'.
(v) It is dimensionless, i.e. it does not depend on the units used.
The reported value is similar to the value estimated with nagelkerke() function from rcompanion package but not from the NagelkerkeR2() function from fmsb package. I don't know why.

Usage

```
NagelkerkeScaledR2(x, size, prediction, scaled = TRUE)
```

Arguments

x	The number of observations
size	Number of trials
prediction	Prediction of x/size
scaled	If TRUE, return the scaled R2

Details

NagelkerkeScaledR2 returns the scaled R2 defined by Nagelkerke (1991)

Value

The scaled R2 value

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
x <- c(10, 9, 6, 4, 3, 1, 0)
size <- c(10, 10, 10, 10, 10, 10, 10)
prediction <- c(0.9, 0.8, 0.7, 0.5, 0.4, 0.3, 0.2)
NagelkerkeScaledR2(x, size, prediction)

# Using the example in fmsb::NagelkerkeR2
res <- glm(cbind(ncases,ncontrols) ~ agegp+alcgp+tobgp, data=esoph, family=binomial())
NagelkerkeScaledR2(x=esoph$ncases, size = esoph$ncases+esoph$ncontrols,
                   prediction = res$fitted.values)
```

---

newcompassRose *Display a compass rose*

Description

Displays a basic compass rose, usually to orient a map.
newcompassRose displays a conventional compass rose at the position requested.
The size of the compass rose is determined by the character expansion, as the central "rose" is calculated relative to the character size.
Rotation is in degrees counterclockwise.

Usage

```
newcompassRose(
  x,
  y,
  rot = 0,
  cex = 1,
  col = "black",
  col.arrows.light = "white",
  col.arrows.dark = "black"
)
```

Arguments

x	The position of the center of the compass rose in user units.
y	The position of the center of the compass rose in user units.
rot	Rotation for the compass rose in degrees. See Details.
cex	The character expansion to use in the display.
col	The color of text
col.arrows.light	The color of lighter lines
col.arrows.dark	The color of darker lines

Details

newcompassRose Display a compass rose

Value

none

Author(s)

modified from Jim Lemon; See sp::compassRose()

Examples

```
## Not run:
library(HelpersMG)
require("maps")
map("world", "China")
newcompassRose(x=110, y=35, col.arrows.light="grey")

## End(Not run)
```

`newmap.scale` *Add Scale to Existing Unprojected Map*

Description

Adds a scale to an existing map, both as a ratio and a distance gauge. If x or y are not specified, this will be taken to be near the lower left corner of the map.

Usage

```
newmap.scale(
  x,
  y,
  relwidth = 0.15,
  metric = TRUE,
  ratio = TRUE,
  col.line = "black",
  ...
)
```

Arguments

`x`	Location of left end of distance gauge.
`y`	Location of left end of distance gauge.
`relwidth`	Proportion of width of display to be used for the scale. The default is 0.15.
`metric`	If TRUE, the distance gauge will be in km, otherwise miles.
`ratio`	If FALSE, the scale ratio of the map is not displayed.
`col.line`	The color of lines for the gauge.
`...`	Further plotting parameters may be specified as for the command text().

Details

newmap.scale Add Scale to Existing Unprojected Map

Value

The exact calculated scale is returned.

Author(s)

See `maps::map.scale()`.

Examples

```
## Not run:
library("maps")
library("HelpersMG")
map("world", "China")
newmap.scale(col.line = "red", col="blue")

## End(Not run)
```

---

openwd *Open a finder window with current working directory in MacOS X and windows*

Description

This function opens a finder window with directory files in MacOS X. It has not been fully tested in Windows. In linux, it just returns the list of files in directory.
By defaut, it uses the current working directory.

Usage

```
openwd(directory = getwd())
```

Arguments

directory	The directory you want to open

Details

openwd will open a finder window with current working directory

Value

A vector with the list of files.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
## Not run:
openwd()

## End(Not run)
```

plot.cutter *Plot results of cutter that best describe distribution*

Description

Plot the estimates of cut distribution.

Usage

```
## S3 method for class 'cutter'
plot(
  x,
  col.hist = "grey",
  col.DL = "blue",
  col.dist = "black",
  col.unobserved = "green",
  col.mcmc = rgb(red = 0.6, green = 0, blue = 0, alpha = 0.01),
  legend = TRUE,
  show.DL = TRUE,
  show.plot = TRUE,
  set = NULL,
  ...
)
```

Arguments

x	A result file generated by cutter
col.hist	The color of histogram
col.DL	The color of below of above samples
col.dist	The color of distribution
col.unobserved	The color of unobserved states
col.mcmc	The color of mcmc outputs
legend	If TRUE, a legend is shown
show.DL	If TRUE, the limits of DL are shown
show.plot	If FALSE, no plot is shown
set	In case of mixture, will show and return only this set
...	Parameters for plot

Details

plot.cutter plot result of cutter

Value

The matrix of all the mcmc curves with invisible state.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Distributions: cutter(), dSnbinom(), dbeta_new(), dcutter(), dggamma(), dnbinom_new(), logLik.cutter(), print.cutter(), r2norm(), rcutter(), rmnorm(), rnbinom_new()

Examples

```
## Not run:
library(HelpersMG)
# ____________________________________________________________________
# right censored distribution with gamma distribution
# ____________________________________________________________________
# Detection limit
DL <- 100
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# remove the data below the detection limit
obc[obc>DL] <- +Inf
# search for the parameters the best fit these censored data
result <- cutter(observations=obc, upper_detection_limit=DL,
                           cut_method="censored")
result
plot(result, xlim=c(0, 150), breaks=seq(from=0, to=150, by=10))
# ____________________________________________________________________
# The same data seen as truncated data with gamma distribution
# ____________________________________________________________________
obc <- obc[is.finite(obc)]
# search for the parameters the best fit these truncated data
result <- cutter(observations=obc, upper_detection_limit=DL,
                           cut_method="truncated")
result
plot(result, xlim=c(0, 150), breaks=seq(from=0, to=150, by=10))
# ____________________________________________________________________
# left censored distribution with gamma distribution
# ____________________________________________________________________
# Detection limit
DL <- 10
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# remove the data below the detection limit
obc[obc<DL] <- -Inf
# search for the parameters the best fit these truncated data
result <- cutter(observations=obc, lower_detection_limit=DL,
                          cut_method="censored")
result
plot(result)
plot(result, xlim=c(0, 200), breaks=seq(from=0, to=200, by=10))
# ____________________________________________________________________
# left and right censored distribution
```

```
# ____________________________________________________________________
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# Detection limit
LDL <- 10
# remove the data below the detection limit
obc[obc<LDL] <- -Inf
# Detection limit
UDL <- 100
# remove the data below the detection limit
obc[obc>UDL] <- +Inf
# search for the parameters the best fit these censored data
result <- cutter(observations=obc, lower_detection_limit=LDL,
                           upper_detection_limit=UDL,
                          cut_method="censored")
result
plot(result, xlim=c(0, 150), col.DL=c("black", "grey"),
                             col.unobserved=c("green", "blue"),
     breaks=seq(from=0, to=150, by=10))
# ____________________________________________________________________
# Example with two values for lower detection limits
# corresponding at two different methods of detection for example
# with gamma distribution
# ____________________________________________________________________
obc <- rgamma(50, scale=20, shape=2)
# Detection limit for sample 1 to 50
LDL1 <- 10
# remove the data below the detection limit
obc[obc<LDL1] <- -Inf
obc2 <- rgamma(50, scale=20, shape=2)
# Detection limit for sample 1 to 50
LDL2 <- 20
# remove the data below the detection limit
obc2[obc2<LDL2] <- -Inf
obc <- c(obc, obc2)
# search for the parameters the best fit these censored data
result <- cutter(observations=obc,
                           lower_detection_limit=c(rep(LDL1, 50), rep(LDL2, 50)),
                          cut_method="censored")
result
# It is difficult to choose the best set of colors
plot(result, xlim=c(0, 150), col.dist="red",
     col.unobserved=c(rgb(red=1, green=0, blue=0, alpha=0.1),
                      rgb(red=1, green=0, blue=0, alpha=0.2)),
     col.DL=c(rgb(red=0, green=0, blue=1, alpha=0.5),
                      rgb(red=0, green=0, blue=1, alpha=0.9)),
     breaks=seq(from=0, to=200, by=10))
# ____________________________________________________________________
# left censored distribution comparison of normal, lognormal and gamma
# ____________________________________________________________________
# Detection limit
DL <- 10
# Generate 100 random data from a gamma distribution
```

```
obc <- rgamma(100, scale=20, shape=2)
# remove the data below the detection limit
obc[obc<DL] <- -Inf
# search for the parameters the best fit these truncated data
result_gamma <- cutter(observations=obc, lower_detection_limit=DL,
                           cut_method="censored", distribution="gamma")
result_gamma
plot(result_gamma, xlim=c(0, 250), breaks=seq(from=0, to=250, by=10))

result_lognormal <- cutter(observations=obc, lower_detection_limit=DL,
                           cut_method="censored", distribution="lognormal")
result_lognormal
plot(result_lognormal, xlim=c(0, 250), breaks=seq(from=0, to=250, by=10))

result_normal <- cutter(observations=obc, lower_detection_limit=DL,
                           cut_method="censored", distribution="normal")
result_normal
plot(result_normal, xlim=c(0, 250), breaks=seq(from=0, to=250, by=10))

compare_AICc(gamma=result_gamma,
            lognormal=result_lognormal,
            normal=result_normal)
# ____________________________________________________________________
# Test for similarity in gamma left censored distribution between two
# datasets
# ____________________________________________________________________
obc1 <- rgamma(100, scale=20, shape=2)
# Detection limit for sample 1 to 50
LDL <- 10
# remove the data below the detection limit
obc1[obc1<LDL] <- -Inf
obc2 <- rgamma(100, scale=10, shape=2)
# remove the data below the detection limit
obc2[obc2<LDL] <- -Inf
# search for the parameters the best fit these censored data
result1 <- cutter(observations=obc1,
                  distribution="gamma",
                  lower_detection_limit=LDL,
                  cut_method="censored")
logLik(result1)
plot(result1, xlim=c(0, 200),
     breaks=seq(from=0, to=200, by=10))
result2 <- cutter(observations=obc2,
                  distribution="gamma",
                  lower_detection_limit=LDL,
                  cut_method="censored")
logLik(result2)
plot(result2, xlim=c(0, 200),
     breaks=seq(from=0, to=200, by=10))
result_totl <- cutter(observations=c(obc1, obc2),
                      distribution="gamma",
                      lower_detection_limit=LDL,
                      cut_method="censored")
```

```
logLik(result_totl)
plot(result_totl, xlim=c(0, 200),
     breaks=seq(from=0, to=200, by=10))

compare_AICc(Separate=list(result1, result2),
            Common=result_totl, factor.value=1)
compare_BIC(Separate=list(result1, result2),
            Common=result_totl, factor.value=1)

## End(Not run)
```

`plot.IconoCorel` *Clean the dataframe before to be used with IC_threshold_matrix*

Description

This function plots the data as a network. It returns an invisible object that can be used with visIgraph from package visNetwork. `https://fr.wikipedia.org/wiki/Iconographie_des_corrélations`

Usage

```
## S3 method for class 'IconoCorel'
plot(
  x,
  ...,
  show.legend.direction = "bottomright",
  show.legend.strength = "topleft",
  title = "Correlation iconography",
  vertex.label.color = "black",
  vertex.label = NULL,
  vertex.color = "white",
  vertex.label.cex = 1,
  plot = TRUE
)
```

Arguments

`x`	The correlation matrix to show
`...`	other options of plot.igraph()
`show.legend.direction`	the position of the legend of direction; FALSE to not show it
`show.legend.strength`	the position of the legend with intensity of correlation; FALSE to not show it
`title`	the title of the plot
`vertex.label.color`	a vector with the colors of labels

vertex.label	a vector with the labels
vertex.color	a vector of colors
vertex.label.cex	a vector of cex
plot	if TRUE, the plot is shown

Details

plot.IconoCorel checks and corrects the dataframe to be used with IC_threshold_matrix

Value

A igraph object

Author(s)

Marc Girondot <marc.girondot@gmail.com>

References

Lesty, M., 1999. Une nouvelle approche dans le choix des régresseurs de la régression multiple en présence d'interactions et de colinéarités. Revue de Modulad 22, 41-77.

See Also

Other Iconography of correlations: IC_clean_data(), IC_correlation_simplify(), IC_threshold_matrix()

Examples

```
## Not run:
library("HelpersMG")
es <- structure(list(Student = c("e1", "e2", "e3", "e4", "e5", "e6", "e7", "e8"),
                Mass = c(52, 59, 55, 58, 66, 62, 63, 69),
                Age = c(12, 12.5, 13, 14.5, 15.5, 16, 17, 18),
                Assiduity = c(12, 9, 15, 5, 11, 15, 12, 9),
                Note = c(5, 5, 9, 5, 13.5, 18, 18, 18)),
                row.names = c(NA, -8L), class = "data.frame")

es

df <- IC_clean_data(es, debug = TRUE)
cor_matrix <- IC_threshold_matrix(data=df, threshold = NULL, progress=FALSE)
cor_threshold <- IC_threshold_matrix(data=df, threshold = 0.3)
par(mar=c(1,1,1,1))
set.seed(4)
library("igraph")
library("visNetwork")
kk <- plot(cor_threshold, vertex.color="red")
# it can be shown also with the visNetwork package
visIgraph(kk)
cor_threshold_Note <- IC_correlation_simplify(matrix=cor_threshold, variable="Note")
```

```
plot(cor_threshold_Note)

# You can record the position of elements and use them later
ly <- layout_nicely(kk)
plot(cor_threshold, vertex.color="red", layout=ly)

## End(Not run)
```

`plot.LD50` *Plot results of LD50() that best describe LD50*

Description

Plot the estimates that best describe lethality of doses.

Usage

```
## S3 method for class 'LD50'
plot(
  x,
  ...,
  las.x = 1,
  las.y = 1,
  lab.PT = "LD50",
  at = NULL,
  lab.TRD = paste0("Transitional range of doses l=", l * 100, "%"),
  col.TRD = "gray",
  col.TRD.CI = rgb(0.8, 0.8, 0.8, 0.5),
  col.PT.CI = rgb(0.8, 0.8, 0.8, 0.5),
  show.CI = TRUE
)
```

Arguments

`x`	A result file generated by LD50()
`...`	Parameters for plot()
`las.x`	las parameter for x axis
`las.y`	las parameter for y axis
`lab.PT`	Label to describe pivotal dose
`at`	Position of ticks in x-axis
`lab.TRD`	Label to describe transitional range of dose
`col.TRD`	The color of TRD
`col.TRD.CI`	The color of CI of TRD based on range.CI
`col.PT.CI`	The color of CI of PT based on range.CI
`show.CI`	Do the CI for the curve should be shown

Details

plot.LD50 plot result of LD50() that best describe LD50

Value

Nothing

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other LD50 functions: LD50(), LD50_MHmcmc(), LD50_MHmcmc_p(), logLik.LD50(), predict.LD50()

Examples

```
## Not run:
data <- data.frame(Doses=c(80, 120, 150, 150, 180, 200),
Alive=c(10, 12, 8, 6, 2, 1),
Dead=c(0, 1, 5, 6, 9, 15))
LD50_logistic <- LD50(data, equation="logistic")
predict(LD50_logistic, doses=c(140, 170))
plot(LD50_logistic, xlim=c(0, 300))

## End(Not run)
```

---

plot.mcmcComposite *Plot the result of a mcmcComposite object*

Description

Plot the results within a mcmcComposite object.
If scale.prior is TRUE, another scale is shown at right.
legend can take these values:
FALSE, TRUE, topleft, topright, bottomleft, bottomright, c(x=, y=)

Usage

```
## S3 method for class 'mcmcComposite'
plot(
  x,
  ...,
  chains = "all",
  parameters = 1,
  transform = NULL,
  scale.prior = TRUE,
  legend = "topright",
```

```
  ylab.posterior = "Posterior density",
  las = 1,
  bty = "n",
  show.prior = TRUE,
  show.posterior.density = TRUE,
  col.prior = "red",
  lty.prior = 1,
  lwd.prior = 1,
  what = "Posterior",
  col.posterior = colorRampPalette(c("blue", "grey"), alpha = 0.001),
  lty.posterior = 1,
  lwd.posterior = 1,
  show.yaxis.prior = TRUE,
  ylab.prior = "Prior density"
)
```

Arguments

x	A mcmcComposite object
...	Graphical parameters to be sent to hist() or plot()
chains	The chains to use
parameters	Name of parameters or "all"
transform	Function to be used to transform the variable
scale.prior	If TRUE, the prior is scaled at the same size as posterior
legend	If FALSE, the legend is not shown; see description
ylab.posterior	y-label for posterior
las	las parameter (orientation of y-axis graduation)
bty	Design of box for Markov Chain plot
show.prior	Should the prior be shown?
show.posterior.density	Should the posterior density be shown?
col.prior	Color for prior curve
lty.prior	Type of line for prior curve
lwd.prior	Width of line for prior curve
what	can be Posterior, MarkovChain or LnL
col.posterior	Color for posterior histogram
lty.posterior	Type of line for posterior histogram
lwd.posterior	Width of line for posterior histogram
show.yaxis.prior	Should the y-axis for prior be shown
ylab.prior	y-label for prior

Details

plot.mcmcComposite plots the result of a MCMC search

Value

None

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other mcmcComposite functions: +.PriorsmcmcComposite(), MHalgoGen(), PPD(), as.mcmc.mcmcComposite(), as.parameters(), merge.mcmcComposite(), plot.PriorsmcmcComposite(), setPriors(), setPriors1(), summary.mcmcComposite()

Examples

```
## Not run:
library(HelpersMG)
require(coda)
x <- rnorm(30, 10, 2)
dnormx <- function(data, x) {
 data <- unlist(data)
 return(-sum(dnorm(data, mean=x['mean'], sd=x['sd'], log=TRUE)))
}
parameters_mcmc <- data.frame(Density=c('dnorm', 'dlnorm'),
                              Prior1=c(10, 0.5), Prior2=c(2, 0.5),
                              SDProp=c(1, 1),
                              Min=c(-3, 0), Max=c(100, 10),
                              Init=c(10, 2), stringsAsFactors = FALSE,
                              row.names=c('mean', 'sd'))

mcmc_run <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, data=x,
                      adaptive = TRUE,
                      likelihood=dnormx, n.chains=4,
                      n.adapt=100, thin=1, trace=1)
plot(mcmc_run, xlim=c(0, 20), parameters="mean")
plot(mcmc_run, xlim=c(0, 10), parameters="sd")
plot(x=mcmc_run, what="MarkovChain", ylim=c(0, 15), parameters="mean",
     col.posterior = colorRampPalette(c("blue", "grey"), alpha = 0.001)
                     (mcmc_run$parametersMCMC$n.chains))
plot(mcmc_run, what="MarkovChain", ylim=c(0, 10), parameters="sd",
     col.posterior = colorRampPalette(c("blue", "grey"), alpha = 0.001)
                     (mcmc_run$parametersMCMC$n.chains))
plot(mcmc_run, what="LnL",
     col.posterior = colorRampPalette(c("blue", "grey"), alpha = 0.001)
                     (mcmc_run$parametersMCMC$n.chains))
mcmcforcoda <- as.mcmc(mcmc_run)
heidel.diag(mcmcforcoda)
raftery.diag(mcmcforcoda)
```

```
autocorr.diag(mcmcforcoda)
acf(mcmcforcoda[[1]][,"mean"], lag.max=20, bty="n", las=1)
acf(mcmcforcoda[[1]][,"sd"], lag.max=20, bty="n", las=1)
batchSE(mcmcforcoda, batchSize=100)
# The batch standard error procedure is usually thought to
# be not as accurate as the time series methods used in summary
summary(mcmcforcoda)$statistics[,"Time-series SE"]
summary(mcmc_run)
as.parameters(mcmc_run)
lastp <- as.parameters(mcmc_run, index="last")
parameters_mcmc[,"Init"] <- lastp
# The n.adapt set to 1 is used to not record the first set of parameters
# then it is not duplicated (as it is also the last one for
# the object mcmc_run)
mcmc_run2 <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, data=x,
adaptive = TRUE,
likelihood=dnormx, n.chains=1, n.adapt=1, thin=1, trace=1)
mcmc_run3 <- merge(mcmc_run, mcmc_run2)
####### no adaptation, n.adapt must be 0
parameters_mcmc[,"Init"] <- c(mean(x), sd(x))
mcmc_run3 <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, data=x,
adaptive = TRUE,
likelihood=dnormx, n.chains=1, n.adapt=0, thin=1, trace=1)

#########################
## Example with transform
#########################

x.1<-rnorm(6000, 2.4, 0.6)
x.2<-rlnorm(10000, 1.3,0.1)

X<-c(x.1, x.2)
hist(X,100,freq=FALSE, ylim=c(0,1.5))
Lnormlnorm <- function(par, val) {
  p <- invlogit(par["p"])
  return(-sum(log(p*dnorm(val, par["m1"], abs(par["s1"]), log = FALSE)+
                    (1-p)*dlnorm(val, par["m2"], abs(par["s2"]), log = FALSE))))
}
# Mean 1
m1=2.3; s1=0.5
# Mean 2
m2=1.3; s2=0.1
# proportion of category 1 - logit transform
p=0

par<-c(m1=m1, s1=s1, m2=m2, s2=s2, p=p)

result2<-optim(par, Lnormlnorm, method="BFGS", val=X,
              hessian=FALSE, control=list(trace=1))

lines(seq(from=0, to=5, length=100),
dnorm(seq(from=0, to=5, length=100),
      result2$par["m1"], abs(result2$par["s1"])), col="red")
```

```
lines(seq(from=0, to=5, length=100),
      dlnorm(seq(from=0, to=5, length=100),
             result2$par["m2"], abs(result2$par["s2"])), col="green")

p <- invlogit(result2$par["p"])

paste("Proportion of Gaussian data",  p)

lines(seq(from=0, to=5, length=100),
      p*dnorm(seq(from=0, to=5, length=100),
              result2$par["m1"], result2$par["s1"])+
        (1-p)*dlnorm(seq(from=0, to=5, length=100),
                     result2$par["m2"], result2$par["s2"]), col="blue")

parameters_mcmc <- data.frame(Density=c('dunif', 'dunif', 'dunif', 'dunif', 'dunif'),
                                        Prior1=c(0, 0.001, 0, 0.001, -3),
                                        Prior2=c(10, 10, 10, 10, 3),
                                        SDProp=c(1, 1, 1, 1, 1),
                                        Min=c(0, 0.001, 0, 0.001, -3),
                                        Max=c(10, 10, 10, 10, 3),
                                        Init=result2$par, stringsAsFactors = FALSE,
                                        row.names=c('m1', 's1', 'm2', 's2', 'p'))

mcmc_run <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, val=X,
                      parameters_name = "par",
                      adaptive = TRUE,
                      likelihood=Lnormlnorm, n.chains=1,
                      n.adapt=100, thin=1, trace=100)
plot(mcmc_run, parameters="m1", breaks=seq(from=0, to =10, by=0.1),
     legend=c(x=6, y=3.10))
plot(mcmc_run, parameters="p", transform=invlogit, xlim=c(0,1),
     breaks=seq(from=0, to=1, by=0.01), legend=c(x=0.6, y=10))
plot(mcmc_run, parameters="p", xlim=c(-3,3),
     breaks=seq(from=-3, to =3, by=0.05), legend=c(x=1, y= 3.10))
plot(mcmc_run, parameters="p", what="MarkovChain")
plot(mcmc_run, parameters="p", transform=invlogit, what="MarkovChain",
     ylim=c(0, 1))
plot(mcmc_run, what="lnl", col.posterior = "black")

parameters_mcmc <- data.frame(Density=c('dunif', 'dunif', 'dunif', 'dunif', 'dnorm'),
                                        Prior1=c(0, 0.001, 0, 0.001, 0.5),
                                        Prior2=c(10, 10, 10, 10, 1),
                                        SDProp=c(1, 1, 1, 1, 1),
                                        Min=c(0, 0.001, 0, 0.001, -3),
                                        Max=c(10, 10, 10, 10, 3),
                                        Init=result2$par, stringsAsFactors = FALSE,
                                        row.names=c('m1', 's1', 'm2', 's2', 'p'))

mcmc_run_pnorm <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, val=X,
                      parameters_name = "par",
                      adaptive = TRUE,
                      likelihood=Lnormlnorm, n.chains=1,
```

```
                      n.adapt=100, thin=1, trace=100)
plot(mcmc_run_pnorm, parameters="m1", breaks=seq(from=0, to =10, by=0.1),
     legend=c(x=6, y=0.10))
plot(mcmc_run_pnorm, parameters="p", transform=invlogit, xlim=c(0,1),
     breaks=seq(from=0, to=1, by=0.01), legend=c(x=0.6, y=0.10))
plot(x=mcmc_run_pnorm, parameters="p", xlim=c(-3,3),
     breaks=seq(from=-3, to =3, by=0.05), legend=c(x=1, y= 0.10))


# Note that it is more logic to use beta distribution for p as a
# proportion. However p value must be checked to be used in optim
# The use of logit transform can be a problem because it can stuck
# the p value to 1 or 0 during fit.

Lnormlnorm <- function(par, val) {
  p <- par["p"]
  return(-sum(log(p*dnorm(val, par["m1"], abs(par["s1"]), log = FALSE)+
                    (1-p)*dlnorm(val, par["m2"], abs(par["s2"]), log = FALSE))))
}

# Example of beta distribution

# Mean is alpha/(alpha+beta)
# Variance is (alpha*beta)/((alpha+beta)^2*(alpha+beta+1))
alpha = 5
beta = 9
plot(x = seq(0.0001, 1, by = .0001),
    y = dbeta(seq(0.0001, 1, by = .0001), alpha, beta),
    type = "l", ylab="Density", xlab="p", bty="n")
points(x=alpha/(alpha+beta), y=0, pch=4)
segments(x0=alpha/(alpha+beta)-sqrt((alpha*beta)/((alpha+beta)^2*(alpha+beta+1))),
        x1=alpha/(alpha+beta)+sqrt((alpha*beta)/((alpha+beta)^2*(alpha+beta+1))),
        y0=0, y1=0)

# Use of optim with L-BFGS-B to limit p between 0 and 1 and s > 0

# Mean 1
m1=2.3; s1=0.5
# Mean 2
m2=1.3; s2=0.1
# proportion of category 1 - logit transform
p=0.5

par <- c(m1=m1, s1=s1, m2=m2, s2=s2, p=p)

result2 <- optim(par, Lnormlnorm, method="L-BFGS-B", val=X,
              lower = c(-Inf, 0, -Inf, 0, 0),
              upper = c(Inf, Inf, Inf, Inf, 1),
              hessian=FALSE, control=list(trace=1))

parameters_mcmc <- data.frame(Density=c('dunif', 'dunif', 'dunif', 'dunif', 'dbeta'),
                                      Prior1=c(0, 0.001, 0, 0.001, 5),
                                      Prior2=c(10, 10, 10, 10, 9),
```

```
                                        SDProp=c(1, 1, 1, 1, 1),
                                        Min=c(0, 0.001, 0, 0.001, 0),
                                        Max=c(10, 10, 10, 10, 1),
                                        Init=c('m1' = 2.4,
                                               's1' = 0.6,
                                               'm2' = 1.3,
                                               's2' = 0.1,
                                               'p' = 0.5), stringsAsFactors = FALSE,
                                        row.names=c('m1', 's1', 'm2', 's2', 'p'))

mcmc_run_pbeta <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, val=X,
                      parameters_name = "par",
                      adaptive = TRUE,
                      likelihood=Lnormlnorm, n.chains=1,
                      n.adapt=100, thin=1, trace=100)
plot(mcmc_run_pbeta, parameters="m1", breaks=seq(from=0, to =10, by=0.1),
     legend=c(x=6, y=2.10))
plot(mcmc_run_pbeta, parameters="p", xlim=c(0,1),
     breaks=seq(from=0, to=1, by=0.01), legend=c(x=0.6, y=6))



## End(Not run)
```

`plot.PriorsmcmcComposite` *Plot a prior defined with setPriors function*

Description

Create a ggplot graph with prior.
The function makes minimal effort to decorate the plot.

Usage

```
## S3 method for class 'PriorsmcmcComposite'
plot(x, parameter = 1, ...)
```

Arguments

`x`	The priors to show
`parameter`	The name or rank of prior to show
`...`	Not used

Details

plot.PriorsmcmcComposite plot a prior

Value

A ggplot object

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other mcmcComposite functions: +.PriorsmcmcComposite(), MHalgoGen(), PPD(), as.mcmc.mcmcComposite(), as.parameters(), merge.mcmcComposite(), plot.mcmcComposite(), setPriors(), setPriors1(), summary.mcmcComposite()

Examples

```
## Not run:
library("HelpersMG")
par <- c(a0=10, a1=2, b2=20, b1=-1)
rules <- rbind(data.frame(Name="^a", Min=0, Max="x*2"),
               data.frame(Name="^b", Min=0, Max=100))
p <- setPriors(par=par, se=NULL, density="dgamma", rules=rules)
plot(p, parameter="a0")
q <- plot(p, parameter="b1")
q + geom_line(color = "red") + theme_bw() +
theme(plot.margin=unit(c(2,1,1,1), 'cm'),
      panel.border = element_blank(),
      axis.line.x.bottom = element_line(colour = "black"),
      axis.line.y.left = element_line(colour = "black")) +
labs(title="Parameter: b1") + theme(plot.title = element_text(hjust = 0.5))

## End(Not run)
```

---

plot_add *Add a plot to a previous one*

Description

To plot data, just add use it as a normal plot. It will plot the new data without axes, or labels for axes.
This function is complementary to matlines() and matpoints() from package graphics.

Usage

```
plot_add(...)
```

Arguments

...	Parameters for plot()

Details

plot_add adds a plot to a previous one

Value

Nothing

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other plot and barplot functions: ScalePreviousPlot(), barplot_errbar(), plot_errbar(), show_name()

Examples

```
## Not run:
plot(x=1:100, y=sin(1:100), type="l", bty="n", xlim=c(1,200), xlab="x", ylab="y")
plot_add(x=1:200, y=cos(1:200), type="l", bty="n", col="red")

## End(Not run)
```

---

plot_errbar *Plot a xy graph with error bar on x and/or y*

Description

To plot data, just use it as a normal plot but add the errbar.x and errbar.y values or errbar.x.minus, errbar.x.plus if bars for x axis are asymetric and errbar.y.minus, errbar.y.plus if bars for y axis are asymetric. Use x.plus, x.minus, y.plus and y.minus to set absolut limits for error bars. Note that x.plus and x.minus have priority over errbar.x, errbar.x.minus and errbar.x.plus and that y.plus and y.minus have priority over errbar.y, errbar.y.minus and errbar.y.plus.
The parameter errbar.y.polygon=TRUE permits to define error as an envolop for y axis.

Usage

```
plot_errbar(
  ...,
  errbar.x = NULL,
  errbar.y = NULL,
  errbar.x.plus = NULL,
  errbar.x.minus = NULL,
  errbar.y.plus = NULL,
  errbar.y.minus = NULL,
  x.plus = NULL,
  x.minus = NULL,
```

```
  y.plus = NULL,
  y.minus = NULL,
  errbar.tick = 1/50,
  errbar.lwd = par("lwd"),
  errbar.lty = par("lty"),
  errbar.col = par("fg"),
  errbar.y.polygon = FALSE,
  errbar.y.polygon.list = list(NULL),
  names = NULL,
  add = FALSE
)
```

Arguments

...	Parameters for plot() such as main= or ylim=
errbar.x	The length of error bars for x. Recycled if necessary.
errbar.y	The length of error bars for y. Recycled if necessary.
errbar.x.plus	The length of positive error bars for x. Recycled if necessary.
errbar.x.minus	The length of negative error bars for x. Recycled if necessary.
errbar.y.plus	The length of positive error bars for y. Recycled if necessary.
errbar.y.minus	The length of negative error bars for y. Recycled if necessary.
x.plus	The absolut position of the positive error bar for x. Recycled if necessary.
x.minus	The absolut position of the negative error bar for x. Recycled if necessary.
y.plus	The absolut position of the positive error bar for y. Recycled if necessary.
y.minus	The absolut position of the nagative error bar for y. Recycled if necessary.
errbar.tick	Size of small ticks at the end of error bars defined as a proportion of total width or height graph size.
errbar.lwd	Error bar line width, see par("lwd")
errbar.lty	Error bar line type, see par("lwd")
errbar.col	Error bar line color, see par("col")
errbar.y.polygon	If true, the errors are shown as a filed polygon.
errbar.y.polygon.list	List of parameters to be used for polygon.
names	The names of the points to be used with show_name().
add	If true, add the graph to the previous one.

Details

plot_errbar plot a xy graph with error bar on x and/or y

Value

A list with x, y and names for points

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

barplot_errorbar

Other plot and barplot functions: ScalePreviousPlot(), barplot_errbar(), plot_add(), show_name()

Examples

```
## Not run:
plot_errbar(1:100, rnorm(100, 1, 2),
 xlab="axe x", ylab="axe y", bty="n", xlim=c(1,100),
  errbar.x=2, errbar.y=rnorm(100, 1, 0.1))
x <- 1:100
plot_errbar(x=1:100, rnorm(100, 1, 2),
                xlab="axe x", ylab="axe y", bty="n", xlim=c(1,100),
              x.minus=x-2, x.plus=x+2)
x <- 1:100
plot_errbar(x=1:100, rnorm(100, 1, 2),
                xlab="axe x", ylab="axe y", bty="n",
                pch=21, bg="white",
              x.minus=x-10, x.plus=x+10)
x <- (1:200)/10
y <- sin(x)
plot_errbar(x=x, y=y, xlab="axe x", ylab="axe y", bty="n", xlim=c(1,20),
     y.minus=y-1, y.plus=y+1, ylim=c(-3, 3), type="l",
  errbar.y.polygon=TRUE,
  errbar.y.polygon.list=list(border=NA, col=rgb(0, 0, 0, 0.5)))

## End(Not run)
```

PPD *Posterior Predictive Distribution from mcmcComposite object*

Description

Extract quantile distributions from mcmcComposite object. If FUN is used, it keeps the correlations between parameters.

Usage

```
PPD(
  x,
  chain = "all",
  FUN = NULL,
  probs = c(0.025, 0.975),
  xlim = NULL,
```

```
  nameparxlim = NULL,
  namepar = NULL
)
```

Arguments

x	A mcmcComposite obtained as a result of MHalgoGen() function
chain	The number of the chain in which to get parameters or "all"
FUN	The function to apply the parameters. It must be text.
probs	The probability to get quantiles
xlim	The values to apply in fun if required
nameparxlim	The name of the parameter for xlim
namepar	The name of parameters from mcmc object to be used in fun

Value

A data.frame with quantiles

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other mcmcComposite functions: +.PriorsmcmcComposite(), MHalgoGen(), as.mcmc.mcmcComposite(), as.parameters(), merge.mcmcComposite(), plot.PriorsmcmcComposite(), plot.mcmcComposite(), setPriors(), setPriors1(), summary.mcmcComposite()

Examples

```
## Not run:
library(HelpersMG)
require(coda)
x <- rnorm(30, 10, 2)
dnormx <- function(data, x) {
 data <- unlist(data)
 return(-sum(dnorm(data, mean=x['mean'], sd=x['sd'], log=TRUE)))
}

parameters_mcmc <- setPriors1(Name = "mean",
                              Density = "dnorm", Prior1 = 10, Prior2 = 2,
                              SDProp = 1, Min = -3, Max = 100, Init = 10)
parameters_mcmc <- parameters_mcmc + setPriors1(Name = "sd",
                              Density = "dlnorm", Prior1 = 0.5, Prior2 = 0.5,
                              SDProp = 1, Min = 0, Max = 10, Init = 2)

mcmc_run <- MHalgoGen(n.iter=10000, parameters=parameters_mcmc, data=x,
                      likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=1)
```

```
# Return the 2.5% and 97.5% quantiles of the mean parameter
k <- PPD(x=mcmc_run, namepar="mean")
k <- PPD(x=mcmc_run, namepar=NULL)
k <- PPD(x=mcmc_run, namepar=c("mean", "sd"))

# Here I return the distribution of coefficient of variation as a posterior predictive distribution
k <- PPD(x=mcmc_run            ,
                FUN="sd/mean" )

# I can generate an output based on a x variable
k <- PPD(x=mcmc_run                  ,
                 xlim=c(1, 2)        ,
                 nameparxlim="mult"  ,
                 FUN="mult*mean"     )

## End(Not run)
```

`predict.LD50` *Estimate survival according to doses*

Description

Estimate survival according to doses.
The returned data.frame has the following components:
doses, SE, survival, CI.minus.sexratio, CI.plus.sexratio, range.CI

Usage

```
## S3 method for class 'LD50'
predict(
  object,
  doses = NULL,
  SE = NULL,
  range.CI = 0.95,
  replicates = 1000,
  progressbar = FALSE,
  ...
)
```

Arguments

`object`	A result file generated by LD50
`doses`	A vector of temperatures
`SE`	The standard error for doses, optional
`range.CI`	The range of confidence interval for estimation, default=0.95
`replicates`	Number of replicates to estimate CI
`progressbar`	Logical. Does a progression bar must be shown
`...`	Not used

Details

predict.LD50 Estimate survival according to doses

Value

A data.frame with informations about survival

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other LD50 functions: LD50(), LD50_MHmcmc(), LD50_MHmcmc_p(), logLik.LD50(), plot.LD50()

Examples

```
## Not run:
#' data <- data.frame(Doses=c(80, 120, 150, 150, 180, 200),
Alive=c(10, 12, 8, 6, 2, 1),
Dead=c(0, 1, 5, 6, 9, 15))
LD50_logistic <- LD50(data, equation="logistic")
predict(LD50_logistic, doses=c(140, 170))
plot(LD50_logistic

## End(Not run)
```

---

print.cutter *Print results of cutter that best describe distribution*

Description

Print the estimates of cut distribution.

Usage

```
## S3 method for class 'cutter'
print(x, silent = FALSE, ...)
```

Arguments

x	A result file generated by cutter
silent	If TRUE does not show the outpout
...	Not used

Details

print.cutter plot result of cutter

Value

Nothing

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Distributions: cutter(), dSnbinom(), dbeta_new(), dcutter(), dggamma(), dnbinom_new(), logLik.cutter(), plot.cutter(), r2norm(), rcutter(), rmnorm(), rnbinom_new()

Examples

```
## Not run:
library(HelpersMG)
# ____________________________________________________________________
# right censored distribution with gamma distribution
# ____________________________________________________________________
# Detection limit
DL <- 100
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# remove the data below the detection limit
obc[obc>DL] <- +Inf
# search for the parameters the best fit these censored data
result <- cutter(observations=obc, upper_detection_limit=DL,
                           cut_method="censored")
result
plot(result, xlim=c(0, 150), breaks=seq(from=0, to=150, by=10))
# ____________________________________________________________________
# The same data seen as truncated data with gamma distribution
# ____________________________________________________________________
obc <- obc[is.finite(obc)]
# search for the parameters the best fit these truncated data
result <- cutter(observations=obc, upper_detection_limit=DL,
                           cut_method="truncated")
result
plot(result, xlim=c(0, 150), breaks=seq(from=0, to=150, by=10))
# ____________________________________________________________________
# left censored distribution with gamma distribution
# ____________________________________________________________________
# Detection limit
DL <- 10
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# remove the data below the detection limit
obc[obc<DL] <- -Inf
# search for the parameters the best fit these truncated data
result <- cutter(observations=obc, lower_detection_limit=DL,
                          cut_method="censored")
result
```

```
plot(result, xlim=c(0, 200), breaks=seq(from=0, to=200, by=10))
# ____________________________________________________________________
# left and right censored distribution
# ____________________________________________________________________
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# Detection limit
LDL <- 10
# remove the data below the detection limit
obc[obc<LDL] <- -Inf
# Detection limit
UDL <- 100
# remove the data below the detection limit
obc[obc>UDL] <- +Inf
# search for the parameters the best fit these censored data
result <- cutter(observations=obc, lower_detection_limit=LDL,
                           upper_detection_limit=UDL,
                          cut_method="censored")
result
plot(result, xlim=c(0, 150), col.DL=c("black", "grey"),
                             col.unobserved=c("green", "blue"),
     breaks=seq(from=0, to=150, by=10))
# ____________________________________________________________________
# Example with two values for lower detection limits
# corresponding at two different methods of detection for example
# with gamma distribution
# ____________________________________________________________________
obc <- rgamma(50, scale=20, shape=2)
# Detection limit for sample 1 to 50
LDL1 <- 10
# remove the data below the detection limit
obc[obc<LDL1] <- -Inf
obc2 <- rgamma(50, scale=20, shape=2)
# Detection limit for sample 1 to 50
LDL2 <- 20
# remove the data below the detection limit
obc2[obc2<LDL2] <- -Inf
obc <- c(obc, obc2)
# search for the parameters the best fit these censored data
result <- cutter(observations=obc,
                            lower_detection_limit=c(rep(LDL1, 50), rep(LDL2, 50)),
                           cut_method="censored")
result
# It is difficult to choose the best set of colors
plot(result, xlim=c(0, 150), col.dist="red",
     col.unobserved=c(rgb(red=1, green=0, blue=0, alpha=0.1),
                      rgb(red=1, green=0, blue=0, alpha=0.2)),
     col.DL=c(rgb(red=0, green=0, blue=1, alpha=0.5),
                      rgb(red=0, green=0, blue=1, alpha=0.9)),
     breaks=seq(from=0, to=200, by=10))
# ____________________________________________________________________
# left censored distribution comparison of normal, lognormal and gamma
# ____________________________________________________________________
```

```
# Detection limit
DL <- 10
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# remove the data below the detection limit
obc[obc<DL] <- -Inf
# search for the parameters the best fit these truncated data
result_gamma <- cutter(observations=obc, lower_detection_limit=DL,
                         cut_method="censored", distribution="gamma")
result_gamma
plot(result_gamma, xlim=c(0, 250), breaks=seq(from=0, to=250, by=10))

result_lognormal <- cutter(observations=obc, lower_detection_limit=DL,
                         cut_method="censored", distribution="lognormal")
result_lognormal
plot(result_lognormal, xlim=c(0, 250), breaks=seq(from=0, to=250, by=10))

result_normal <- cutter(observations=obc, lower_detection_limit=DL,
                         cut_method="censored", distribution="normal")
result_normal
plot(result_normal, xlim=c(0, 250), breaks=seq(from=0, to=250, by=10))

compare_AICc(gamma=result_gamma,
            lognormal=result_lognormal,
            normal=result_normal)
# ____________________________________________________________________
# Test for similarity in gamma left censored distribution between two
# datasets
# ____________________________________________________________________
obc1 <- rgamma(100, scale=20, shape=2)
# Detection limit for sample 1 to 50
LDL <- 10
# remove the data below the detection limit
obc1[obc1<LDL] <- -Inf
obc2 <- rgamma(100, scale=10, shape=2)
# remove the data below the detection limit
obc2[obc2<LDL] <- -Inf
# search for the parameters the best fit these censored data
result1 <- cutter(observations=obc1,
                  distribution="gamma",
                  lower_detection_limit=LDL,
                  cut_method="censored")
logLik(result1)
plot(result1, xlim=c(0, 200),
     breaks=seq(from=0, to=200, by=10))
result2 <- cutter(observations=obc2,
                  distribution="gamma",
                  lower_detection_limit=LDL,
                  cut_method="censored")
logLik(result2)
plot(result2, xlim=c(0, 200),
     breaks=seq(from=0, to=200, by=10))
result_totl <- cutter(observations=c(obc1, obc2),
```

```
                      distribution="gamma",
                      lower_detection_limit=LDL,
                      cut_method="censored")
logLik(result_totl)
plot(result_totl, xlim=c(0, 200),
     breaks=seq(from=0, to=200, by=10))

compare_AICc(Separate=list(result1, result2),
            Common=result_totl, factor.value=1)
compare_BIC(Separate=list(result1, result2),
            Common=result_totl, factor.value=1)

## End(Not run)
```

---

qvlmer *Quasi Variances for lmer Model Coefficients*

Description

Computes a set of quasi variances (and corresponding quasi standard errors) for estimated model coefficients relating to the levels of a categorical (i.e., factor) explanatory variable. For details of the method see Firth (2000), Firth (2003) or Firth and de Menezes (2004). Quasi variances generalize and improve the accuracy of "floating absolute risk" (Easton et al., 1991). This device for economical model summary was first suggested by Ridout (1989).
Modified from qvcalc.lm() of packages qvcalc by David Firth, d.firth@warwick.ac.uk

Usage

```
qvlmer(object, factorname = NULL, coef.indices = NULL, dispersion = NULL, ...)
```

Arguments

object	A object obtained using lmer from package lme4
factorname	Either NULL, or a character vector of length 1
coef.indices	Either NULL, or a numeric vector of length at least 3
dispersion	An optional scalar multiplier for the covariance matrix, to cope with overdispersion for example
...	Other arguments to pass to qvcalc.default

Details

qvlmer is Quasi Variances for lmer Model Coefficients

Value

A list of class qv.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

References

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McCullagh, P. and Nelder, J. A. (1989) Generalized Linear Models. London: Chapman and Hall.

Menezes, R. X. de (1999) More useful standard errors for group and factor effects in generalized linear models. D.Phil. Thesis, Department of Statistics, University of Oxford.

Ridout, M.S. (1989). Summarizing the results of fitting generalized linear models to data from designed experiments. In: Statistical Modelling: Proceedings of GLIM89 and the 4th International Workshop on Statistical Modelling held in Trento, Italy, July 17–21, 1989 (A. Decarli et al., eds.), pp 262–269. New York: Springer.

Examples

```
## Not run:
x <- rnorm(100)
y <- rnorm(100)
G <- as.factor(sample(c("A", "B", "C", "D"), 100, replace = TRUE))
R <- as.factor(rep(1:25, 4))
library(lme4)
m <- lmer(y ~ x + G + (1 | R))
qvlmer(m, factorname="G")

## End(Not run)
```

---

r2norm — *Random generation for Gaussian distributions different at left and right*

Description

Random generation for Gaussian distributions different at left and right

Usage

```
r2norm(n, mean = 0, sd_low = 1, sd_high = 1)
```

Arguments

n	number of observations.
mean	vector of means
sd_low	vector of standard deviations below the mean.
sd_high	vector of standard deviations above the mean.

Details

r2norm returns random numbers for Gaussian distributions different at left and right

Value

r2norm returns random numbers

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Distributions: cutter(), dSnbinom(), dbeta_new(), dcutter(), dggamma(), dnbinom_new(), logLik.cutter(), plot.cutter(), print.cutter(), rcutter(), rmnorm(), rnbinom_new()

Examples

```
## Not run:
n <- r2norm(1000, mean=25, sd_low=2, sd_high=10)

hist(n)

## End(Not run)
```

RandomFromHessianOrMCMC

Random numbers based on Hessian matrix or MCMC

Description

If it is very long, use silent parameter to check if something goes wrong.
If replicates is NULL or is 0, or if method is NULL, parameters are just copied into data.frame.
If method is NULL, replicate.CI is set to 0.
If method is hessian, it will generate replicate.CI random numbers using Hessian matrix with covariance.
If method is se, it will generate replicate.CI random numbers using SE values then without covariance.
If method is mcmc, it will generate replicate.CI random numbers using random samples of the MCMC or the regularThin number if it is a number.

Usage

```
RandomFromHessianOrMCMC(
  se = NULL,
  Hessian = NULL,
  mcmc = NULL,
  chain = "all",
  regularThin = TRUE,
  MinMax = NULL,
  fitted.parameters = NULL,
  fixed.parameters = NULL,
  method = NULL,
  probs = c(0.025, 0.5, 0.975),
  replicates = 10000,
  fn = NULL,
  silent = FALSE,
  ParTofn = "par",
  ...
)
```

Arguments

se	A named vector with SE of parameters
Hessian	An Hessian matrix
mcmc	A result from MHalgogen()
chain	MCMC chain to be used or "all"
regularThin	If TRUE, use regular thin for MCMC or use a number
MinMax	A data.frame with at least two columns: Min and Max and rownames being the variable names
fitted.parameters	The fitted parameters
fixed.parameters	The fixed parameters
method	Can be NULL, "SE", "Hessian", "MCMC", or "PseudoHessianFromMCMC"
probs	Probability for quantiles
replicates	Number of replicates to generate the randoms
fn	The function to apply to each replicate
silent	Should the function display some information
ParTofn	Name of the parameter to send random values to fn
...	Parameters send to fn function

Details

RandomFromHessianOrMCMC returns random numbers based on Hessian matrix or MCMC

Value

Returns a list with three data.frames named random, fn, and quantiles

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
## Not run:
library(HelpersMG)
val <- rnorm(100, mean=20, sd=5)+(1:100)/10
# Return -ln L of values in val in Gaussian distribution with mean and sd in par
fitnorm <- function(par, data) {
  -sum(dnorm(data, par["mean"], abs(par["sd"]), log = TRUE))
}
# Initial values for search
p<-c(mean=20, sd=5)
# fit the model
result <- optim(par=p, fn=fitnorm, data=val, method="BFGS", hessian=TRUE)
# Using Hessian
df <- RandomFromHessianOrMCMC(Hessian=result$hessian,
                              fitted.parameters=result$par,
                              method="Hessian")$random
hist(df[, 1], main="mean")
hist(df[, 2], main="sd")
plot(df[, 1], df[, 2], xlab="mean", ylab="sd", las=1, bty="n")

# Using MCMC
parameters_mcmc <- data.frame(Density=c('dnorm', 'dlnorm'),
Prior1=c(10, 0.5), Prior2=c(2, 0.5), SDProp=c(0.35, 0.2),
Min=c(-3, 0), Max=c(100, 10), Init=c(10, 2), stringsAsFactors = FALSE,
row.names=c('mean', 'sd'))
# Use of trace and traceML parameters
# trace=1 : Only one likelihood is printed
mcmc_run <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, data=val,
parameters_name = "par",
likelihood=fitnorm, n.chains=1, n.adapt=100, thin=1, trace=1)
df <- RandomFromHessianOrMCMC(mcmc=mcmc_run, fitted.parameters=NULL,
                              method="MCMC")$random
hist(df[, 1], main="mean")
hist(df[, 2], main="sd")
plot(df[, 1], df[, 2], xlab="mean", ylab="sd", las=1, bty="n")

# Return the two first elements of the MCMC
df <- RandomFromHessianOrMCMC(mcmc=mcmc_run, fitted.parameters=NULL,
               method="MCMC", replicates = 2, regularThin = c(1, 2))$random

# Using a function fn
fitnorm <- function(par, data, x) {
  y=par["a"]*(x)+par["b"]
  -sum(dnorm(data, y, abs(par["sd"]), log = TRUE))
```

```
}
p<-c(a=0.1, b=20, sd=5)
# fit the model
x <- 1:100
result <- optim(par=p, fn=fitnorm, data=val, x=x, method="BFGS", hessian=TRUE)
# Using Hessian
df <- RandomFromHessianOrMCMC(Hessian=result$hessian, fitted.parameters=result$par,
                              method="Hessian",
                              fn=function(par) (par["a"]*(x)+par["b"]))
plot(1:100, val)
lines(1:100, df$quantiles["50%", ])
lines(1:100, df$quantiles["2.5%", ], lty=2)
lines(1:100, df$quantiles["97.5%", ], lty=2)

## End(Not run)
```

`rcutter` *Random values of unobserved values of cut distribution.*

Description

Return n random numbers.
It can be used to get the posterior predictive distribution; see example.
If random_method is "ML", the parameter values obtained using maximum likelihood are used.
If random_method is "medianMCMC", the parameter values obtained using median of posterior distribution are used.
If random_method is "MCMC", the parameter values are one sample of the MCMC posterior distribution.
if observed_detection_limit is set to TRUE, the number of random number is equal to the number of observations; n is not used.
rcutter is the abbreviation for random-cutter.

Usage

```
rcutter(
  cutter = stop("A result of cutter() must be provided"),
  n = 1,
  lower_detection_limit = NULL,
  upper_detection_limit = NULL,
  method_cut = c("censored", "truncated"),
  observed_detection_limit = FALSE,
  random_method = c("medianMCMC", "MCMC", "ML"),
  index_mcmc = NULL
)
```

Arguments

`cutter`	The fitted model obtained with cutter()

n	number of random numbers
lower_detection_limit	The lower detection limit
upper_detection_limit	The upper detection limit
method_cut	What method is used to cut the distribution: "censored", "truncated"?
observed_detection_limit	If TRUE, will use the pattern of detection limit as in observations
random_method	How to get parameters; it can be "ML", "medianMCMC", or "MCMC"
index_mcmc	For MCMC random_method, the index of data to be used.

Details

rcutter returns random values based on fitted distribution with cut.

Value

A vector with the random numbers.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Distributions: cutter(), dSnbinom(), dbeta_new(), dcutter(), dggamma(), dnbinom_new(), logLik.cutter(), plot.cutter(), print.cutter(), r2norm(), rmnorm(), rnbinom_new()

Examples

```
## Not run:
library(HelpersMG)
# ------------------------------------------------------------------
# right censored distribution with gamma distribution
# ------------------------------------------------------------------
# Detection limit
DL <- 100
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# remove the data below the detection limit
obc[obc>DL] <- +Inf
# search for the parameters the best fit these censored data
result <- cutter(observations=obc, upper_detection_limit=DL,
                           cut_method="censored")
result
# Posterior predictive distribution
r <- rcutter(cutter=result, upper_detection_limit=DL, n=100)
hist(r)
# ------------------------------------------------------------------
# left censored distribution with gamma distribution
```

```
# ____________________________________________________________________
# Detection limit
DL <- 10
# Generate 100 random data from a gamma distribution
obc <- rgamma(100, scale=20, shape=2)
# remove the data below the detection limit
obc[obc<DL] <- -Inf
# search for the parameters the best fit these truncated data
result <- cutter(observations=obc, lower_detection_limit=DL,
                          cut_method="censored")
result
plot(result, breaks=seq(from=0, to=200, by=10))
r <- rcutter(cutter=result, n=100)
hist(r, breaks=seq(from=0, to=200, by=10))
r <- rcutter(cutter=result, lower_detection_limit=DL, n=100)
hist(r, breaks=seq(from=0, to=250, by=10))
# With censored method, some values are replaced with +Inf or -Inf
any(is.infinite(r))
r <- rcutter(cutter=result, upper_detection_limit=DL, n=100,
             method_cut="truncated")
# With truncated method, the values below LDL or upper UDL are not present
any(is.infinite(r))
hist(r, breaks=seq(from=0, to=10, by=0.25))
r <- rcutter(cutter=result, observed_detection_limit=TRUE)
hist(r, breaks=seq(from=0, to=300, by=10))

## End(Not run)
```

`read_folder` *Read files present in a folder and creates a list with the content of these files*

Description

To create a list, the syntax is:
datalist <- read_folder(folder=".", read=read.delim, header=FALSE)
It returns an error if the folder does not exist.
The names of the elements of the list are the filenames.
The parameter file can be used to predefine a list of file. If file is NULL, all the files of the folder/directory are used.

Usage

```
read_folder(
  folder = try(file.choose(), silent = TRUE),
  file = NULL,
  wildcard = "*.*",
  read = read.delim,
  ...
)
```

Arguments

folder	Where to search for files; can be or a file path or a folder path
file	list of files
wildcard	Define which files are to be read (examples: ".", "*.xls", "essai*.txt"). It can be also a vector with all filenames.
read	Function used to read file. Ex: read.delim or read.xls from gdata package
...	Parameters send to the read function

Details

read_folder reads all files present in a folder

Value

Return a list with the data in the files of the folder (directory for windows users)

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
## Not run:
library(HelpersMG)
# Read all the .csv files from the current folder/directory
contentaslist <- read_folder(folder=".", wildcard="*.csv", read=read.csv2)
# Read all the files from the current folder/directory
contentaslist <- read_folder(folder=".", wildcard="*.*", read=read.csv2)
# Read two files from the current folder/directory
files <- c("filename1.csv", "filename2.csv")
contentaslist <- read_folder(folder=".", wildcard=files, read=read.csv2)
# To concvert the list into a single dataframe:
mydf <- do.call("rbind", contentaslist)

## End(Not run)
```

RectangleRegression *Return parameters of rectangle regression*

Description

Fit a line using least rectangle method.

Usage

```
RectangleRegression(
  x1,
  x2,
  replicate = 1000,
  x1new = seq(from = min(x1), to = max(x1), length.out = 100)
)
```

Arguments

x1	The first series of data
x2	The second series of data
replicate	Number of replicates for bootstrap
x1new	Values for x1 to generate x2

Details

RectangleRegression performs rectangle regression

Value

A list with parameters of rectangle regression

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
x1 <- runif(100, min=10, max=20)
x2 <- runif(100, min=10, max=20)+x1

rectreg <- RectangleRegression(x1, x2)

plot(x=x1, y=x2, bty="n", las=1, xlim=c(10, 20), ylim=c(20, 40))
abline(a=rectreg$par["Intercept"], b=rectreg$par["Slope"], lwd=2)
par(xpd=FALSE)
lines(rectreg$x2new["x1new", ], rectreg$x2new["50%", ])
lines(rectreg$x2new["x1new", ], rectreg$x2new["2.5%", ], lty=2)
lines(rectreg$x2new["x1new", ], rectreg$x2new["97.5%", ], lty=2)

abline(a=rectreg$Intercept[1], b=rectreg$Slope[3], col="red")
abline(a=rectreg$Intercept[3], b=rectreg$Slope[1], col="red")
```

rmnorm *Generate random numbers from the multivariate normal distribution*

Description

rmnorm generate random numbers from a multivariate normal distribution.

Usage

```
rmnorm(n = 1, mean = rep(0, d), varcov)
```

Arguments

n	the number of random vectors to be generated.
mean	a vector with means of length d.
varcov	a variance-covariance matrix with dimentions d * d.

Details

rmnorm Generate random numbers from the multivariate normal distribution

Value

For n > 1 rmnorm returns a matrix of n rows of random vectors, while for n = 1 rmnorm returns a named random vector.

Author(s)

Based on lmf package

See Also

Other Distributions: cutter(), dSnbinom(), dbeta_new(), dcutter(), dggamma(), dnbinom_new(), logLik.cutter(), plot.cutter(), print.cutter(), r2norm(), rcutter(), rnbinom_new()

Examples

```
## Not run:
#Variance-covariance matrix
varcov <- matrix(c(2.047737e-03, 3.540039e-05, 0.0075178920, 3.540039e-05,
6.122832e-07, 0.0001299661, 7.517892e-03, 1.299661e-04, 0.0276005740), ncol = 3)
#Set names
nam <- c("a", "b", "c")
dimnames(varcov) <- list(nam, nam)
#Check positive definiteness (all positive eigenvalues = positive definite)
eigen(varcov) $values
#Mean
mean <- c(1, 0.3, 0.5)
```

```
#Generate n = 1 random vector
rmnorm(n = 1, mean = mean, varcov = varcov)
#Generate n = 10 random vectors
rmnorm(n = 10, mean = mean, varcov = varcov)
#Generate n = 1 random vectors when varcov is non-positive definite
#Non-positive definite varcov matrix
varcov2 <- matrix(c(2.04e-03, 3.54e-05, 7.52e-03, 3.54e-05, 6.15e-07,
  1.30e-04, 7.52e-03, 1.30e-04, 2.76e-02), ncol = 3)
  dimnames(varcov2) <- dimnames(varcov)
eigen(varcov2)
#Random vector
rmnorm(n = 1, mean = mean, varcov = varcov2)

## End(Not run)
```

RM_add *Create a results managment or add a value in a results managment to an object*

Description

Return original object with a new value or a new results managment.

Usage

```
RM_add(
  x = stop("An object with results managment must be provided"),
  RM = "RM",
  RMname = stop("A results managment name must be provided"),
  valuename = NULL,
  value = NULL
)
```

Arguments

x	The object to add a results managment or a result in a results managment
RM	The name of results managment stored
RMname	The name of the results managment to be modified or created
valuename	The name of the new value to be added
value	The value to be added

Details

RM_add adds a results managment or a value in results managment to an object

Value

The original object with a new value in a results managment object or a new results managment

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Results Managment: RM_delete(), RM_duplicate(), RM_get(), RM_list()

Examples

```
## Not run:
library("HelpersMG")
# Let an object of class objclass being created
obj <- list(A=100, name="My object")
class(obj) <- "objclass"
# And now I create a RM to this object
obj <- RM_add(x=obj, RMname="NewAnalysis1")
RM_list(obj)
obj <- RM_add(x=obj, RMname="NewAnalysis2")
RM_list(obj)
obj <- RM_add(x=obj, RMname="NewAnalysis2", valuename="V1", value=100)
RM_get(x=obj, RMname="NewAnalysis2", valuename="V1")
obj <- RM_add(x=obj, RMname="NewAnalysis2", valuename="V1", value=200)
RM_get(x=obj, RMname="NewAnalysis2", valuename="V1")
obj <- RM_add(x=obj, RMname="NewAnalysis2", valuename="V2", value=300)
RM_get(x=obj, RMname="NewAnalysis2", valuename="V2")
RM_list(obj)

## End(Not run)
```

RM_delete *Delete a results managment or a result within a results managment from an object*

Description

Return the original object with the deleted results managment or result.

Usage

```
RM_delete(
  x = stop("An object with results managment must be provided"),
  RM = "RM",
  RMname = stop("A name must be provided"),
  valuename = NULL
)
```

Arguments

x	The object to delete a results managment
RM	The name of results managment stored
RMname	The name of the result that will be deleted or its rank
valuename	The name of the result that will be deleted

Details

RM_delete deletes a results managment or a result within a results managment from an object

Value

The original object with the deleted results managment

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Results Managment: RM_add(), RM_duplicate(), RM_get(), RM_list()

Examples

```
## Not run:
library("HelpersMG")
# Let an object of class objclass being created
obj <- list(A=100, name="My object")
class(obj) <- "objclass"
# And now I create a RM to this object
obj <- RM_add(x=obj, RMname="NewAnalysis1")
obj <- RM_add(x=obj, RMname="NewAnalysis2")
RM_list(obj)
obj <- RM_delete(x=obj, RMname="NewAnalysis1")
RM_list(obj)
obj <- RM_delete(x=obj, RMname=1)
RM_list(obj)
obj <- RM_add(x=obj, RMname="NewAnalysis1", valuename="V1", value=100)
RM_list(obj)
RM_get(x=obj, RMname="NewAnalysis1", valuename="V1")
obj <- RM_add(x=obj, RMname="NewAnalysis1", valuename="V2", value=200)
RM_get(x=obj, RMname="NewAnalysis1", valuename="V2")
obj <- RM_delete(x=obj, RMname="NewAnalysis1", valuename="V1")
RM_get(x=obj, RMname="NewAnalysis1", valuename="V1")
RM_get(x=obj, RMname="NewAnalysis1", valuename="V2")

## End(Not run)
```

RM_duplicate *Duplicate a results managment within an object.*

Description

RM_duplicate duplicates a results managment within an object.

Usage

```
RM_duplicate(
  x = stop("An object with results managment must be provided"),
  RM = "RM",
  RMnamefrom = 1,
  RMnameto = 2
)
```

Arguments

x	The object to duplicate a results managment
RM	The name of results managment stored
RMnamefrom	The name of the results managment to be duplicated
RMnameto	The new name of the results managment

Details

RM_duplicate duplicates a results managment within an object

Value

The original object with a duplicated results managment.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Results Managment: RM_add(), RM_delete(), RM_get(), RM_list()

Examples

```
## Not run:
library("HelpersMG")
# Let an object of class objclass being created
obj <- list(A=100, name="My object")
class(obj) <- "objclass"
# And now I create a RM to this object
obj <- RM_add(x=obj, RMname="NewAnalysis1")
```

```
RM_list(obj)
obj <- RM_duplicate(x=obj, RMnamefrom="NewAnalysis1", RMnameto="NewAnalysis2")
RM_list(obj)

## End(Not run)
```

RM_get *Get a value in a results managment to an object*

Description

Return the value valuename of the results managment RMname.

Usage

```
RM_get(
  x = stop("An object with results managment must be provided"),
  RM = "RM",
  RMname = NULL,
  valuename = NULL
)
```

Arguments

x	The object in which to get a result in a results managment
RM	The name of results managment stored
RMname	The name of the results managment to be read
valuename	The name of the value to be read

Details

RM_get gets a value in results managment to an object

Value

Return a value in a results managment object

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Results Managment: RM_add(), RM_delete(), RM_duplicate(), RM_list()

Examples

```
## Not run:
library("HelpersMG")
# Let an object of class objclass being created
obj <- list(A=100, name="My object")
class(obj) <- "objclass"
# And now I create a RM to this object
obj <- RM_add(x=obj, RMname="NewAnalysis1")
RM_list(obj)
obj <- RM_add(x=obj, RMname="NewAnalysis2")
RM_list(obj)
obj <- RM_add(x=obj, RMname="NewAnalysis2", valuename="V1", value=100)
RM_get(x=obj, RMname="NewAnalysis2", valuename="V1")

## End(Not run)
```

RM_list *Return the list of results managment of an object.*

Description

RM_list returns the list of results managment of an object.

Usage

```
RM_list(
  x = stop("An object with results managment must be provided"),
  RM = "RM",
  silent = FALSE,
  max.level = FALSE
)
```

Arguments

x	The object to add a results managment
RM	The name of results managment stored
silent	Should the results be shown ?
max.level	If TRUE, will return all list element of the objects

Details

RM_list returns the list of results managment of an object

Value

A list with the names of results stored in an object

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Results Managment: RM_add(), RM_delete(), RM_duplicate(), RM_get()

Examples

```
## Not run:
library("HelpersMG")
# Let an object of class objclass being created
obj <- list(A=100, name="My object")
class(obj) <- "objclass"
# And now I create a RM to this object
obj <- RM_add(x=obj, RMname="NewAnalysis1")
RM_list(obj)
obj <- RM_add(x=obj, RMname="NewAnalysis2")
RM_list(obj)
obj <- RM_add(x=obj, RMname="NewAnalysis2", valuename="V1", value=100)
RM_get(x=obj, RMname="NewAnalysis2", valuename="V1")
obj <- RM_add(x=obj, RMname="NewAnalysis2", valuename="V1", value=200)
RM_get(x=obj, RMname="NewAnalysis2", valuename="V1")
obj <- RM_add(x=obj, RMname="NewAnalysis2", valuename="V2", value=300)
RM_get(x=obj, RMname="NewAnalysis2", valuename="V2")
RM_list(obj)
rmlist <- RM_list(obj, max.level=TRUE)
rmlist

## End(Not run)
```

---

rnbinom_new *Random numbers for the negative binomial distribution.*

Description

See rnbinom.

Usage

```
rnbinom_new(n, size = NULL, prob = NULL, mu = NULL, sd = NULL, var = NULL)
```

Arguments

n	number of observations.
size	target for number of successful trials, or dispersion parameter (the shape parameter of the gamma mixing distribution). Must be strictly positive, need not be integer.

prob	probability of success in each trial. 0 < prob <= 1.
mu	alternative parametrization via mean.
sd	alternative parametrization via standard deviation.
var	alternative parametrization via variance.

Details

rnbinom_new returns random numbers for the negative binomial distribution

Value

Random numbers for the negative binomial distribution

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Distributions: cutter(), dSnbinom(), dbeta_new(), dcutter(), dggamma(), dnbinom_new(), logLik.cutter(), plot.cutter(), print.cutter(), r2norm(), rcutter(), rmnorm()

Examples

```
## Not run:
library("HelpersMG")
set.seed(1)
x <- rnbinom_new(n=1000, prob=6.25/(5+6.25), size=6.25)
mean(x)
sd(x)
set.seed(1)
x <- rnbinom_new(n=1000, mu=5, sd=3)
mean(x)
sd(x)
set.seed(1)
x <- rnbinom_new(n=1000, mu=5, var=3^2)
mean(x)
sd(x)
set.seed(1)
x <- rnbinom_new(n=1000, mu=5, size=6.25)
mean(x)
sd(x)
set.seed(1)
x <- rnbinom_new(n=1000, size=6.25, var=3^2)
mean(x)
sd(x)
set.seed(1)
x <- rnbinom_new(n=1000, prob=6.25/(5+6.25), var=3^2)
mean(x)
sd(x)
# Example of wrong parametrization
```

```
set.seed(1)
x <- rnbinom_new(n=1000, sd=3, var=3^2)
set.seed(1)
x <- rnbinom_new(n=1000, mu=10, var=3^2)

## End(Not run)
```

ScalePreviousPlot *Return the scale of the previous plot*

Description

Return a list with the limits of the previous plot, the center, the range, and the position of label on this axe.

Usage

```
ScalePreviousPlot(x = NULL, y = NULL)
```

Arguments

x	The position in x as relative position
y	The position in y as relative position

Details

ScalePreviousPlot returns the scale of the previous plot

Value

A list with xlim and ylim

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other plot and barplot functions: barplot_errbar(), plot_add(), plot_errbar(), show_name()

Examples

```
## Not run:
par(xaxs="i", yaxs="i")
plot(x=1:100, y=sin(1:100), type="l", bty="n", xlim=c(1,200), xlab="x", ylab="y")
xlim= ScalePreviousPlot()$xlim[1:2]
ylim= ScalePreviousPlot()$ylim[1:2]
par(xaxs="r", yaxs="i")
plot(x=1:100, y=sin(1:100), type="l", bty="n", xlim=c(1,200), xlab="x", ylab="y")
```

```
xlim= ScalePreviousPlot()$xlim[1:2]
ylim= ScalePreviousPlot()$ylim[1:2]
# Here is an example of the use of the label output
plot(x=1:100, y=sin(1:100), type="l", bty="n", xlim=c(1,200), xlab="", ylab="")
text(x=ScalePreviousPlot()$xlim["label"], y=ScalePreviousPlot()$ylim["center"],
  xpd=TRUE, "Legend for Y axes", pos=3, srt=90)
text(x=ScalePreviousPlot()$xlim["center"], y=ScalePreviousPlot()$ylim["label"],
  xpd=TRUE, "Legend for X axes", pos=1)
Example to plot legend always in the same place
layout(1:2)
plot(x=1:100, y=sin(1:100), type="l", bty="n", xlim=c(1,200), xlab="", ylab="")
text(x=ScalePreviousPlot(x=0.95, y=0.05)$x,
     y=ScalePreviousPlot(x=0.95, y=0.05)$y,
     labels="A", cex=2)
plot(x=0:1, y=0:1, type="p", bty="n")
text(x=ScalePreviousPlot(x=0.95, y=0.05)$x,
     y=ScalePreviousPlot(x=0.95, y=0.05)$y,
     labels="B", cex=2)

## End(Not run)
```

`SEfromHessian` *Standard error of parameters based on Hessian matrix*

Description

Standard error of parameters based on Hessian matrix.
The strategy is as follow:
First it tries to inverse the Hessian matrix. If it fails, it uses the near positive definite matrix of the Hessian.
So now the inverse of the Hessian matrix can be computed.
The diagonal of the inverse of the Hessian matrix is calculated. If all values are positive, the SEs are the square root of the inverse of the Hessian.
If not all values are positive, it will estimate the pseudo-variance matrix based on Gill & King (2004). It necessitates a Cholesky matrix.
If from some reason it fails (for example all SE are 0 in output), then the strategy of Rebonato and Jackel (2000) will be used to generate the Cholesky matrix.

Usage

```
SEfromHessian(a, hessian = FALSE, silent = FALSE)
```

Arguments

`a`	An Hessian matrix
`hessian`	If TRUE, return a list with the hessian and SE
`silent`	If TRUE, report some problems

Details

SEfromHessian returns standard error of parameters based on Hessian matrix

Value

SEfromHessian returns a vector with standard errors

Author(s)

Marc Girondot <marc.girondot@gmail.com>

References

Gill J. and G. King 2004. What to do when your Hessian is not invertible: Alternatives to model respecification in nonlinear estimation. Sociological Methods & Research 33: 54-87.

Rebonato and Jackel, "The most general methodology for creating a valid correlation matrix for risk management and option pricing purposes", Journal of Risk, Vol 2, No 2, 2000.

Examples

```
## Not run:
val=rnorm(100, mean=20, sd=5)
# Return -ln L of values in val in Gaussian distribution with mean and sd in par
fitnorm<-function(par, val) {
  -sum(dnorm(val, par["mean"], par["sd"], log = TRUE))
}
# Initial values for search
p<-c(mean=20, sd=5)
# fit the model
result <- optim(par=p, fn=fitnorm, val=val, method="BFGS", hessian=TRUE)
SE <- SEfromHessian(result$hessian)
library(MASS)
fitdistr(val, densfun = "normal")

## End(Not run)
```

---

series.compare *Data series comparison using Akaike weight*

Description

This function is used as a replacement of t.test() to not use p-value.

Usage

```
series.compare(..., criterion = c("BIC", "AIC", "AICc"), var.equal = TRUE)
```

Arguments

...	Series of data (at least two or data are in a table with series in different rows)
criterion	Which criterion is used for model selection. can be AIC, AICc or BIC
var.equal	Should the variances of all series being equal? Default TRUE

Details

series.compare compares series of data using Akaike weight.

Value

The probability that a single proportion model is sufficient to explain the data

Author(s)

Marc Girondot <marc.girondot@gmail.com>

References

Girondot, M., Guillon, J.-M., 2018. The w-value: An alternative to t- and X2 tests. Journal of Biostatistics & Biometrics 1, 1-4.

See Also

Other w-value functions: compare(), contingencyTable.compare()

Examples

```
## Not run:
library("HelpersMG")
A <- rnorm(100, 10, 2)
B <- rnorm(100, 11.1, 2)
series.compare(A, B, criterion = "BIC", var.equal=TRUE)
B <- B[1:10]
series.compare(A, B, criterion = "BIC", var.equal=TRUE)
A <- rnorm(100, 10, 2)
B <- rnorm(100, 10.1, 2)
C <- rnorm(100, 10.5, 2)
series.compare(A, B, C, criterion = "BIC", var.equal=TRUE)
B <- B[1:10]
series.compare(A, B, criterion = "BIC", var.equal=TRUE)
t.test(A, B, var.equal=TRUE)
# Example with a data.frame
series.compare(t(data.frame(A=c(10, 27, 19, 20, NA), B=c(10, 20, NA, NA, NA))))
# Test in the context of big data
A <- rnorm(10000, 10, 2)
B <- rnorm(10000, 10.1, 2)
series.compare(A, B, criterion = "BIC", var.equal=TRUE)
t.test(A, B, var.equal=TRUE)
############################
w <- NULL
```

```
p <- NULL

for (i in 1:1000) {

  A <- rnorm(50000, 10, 2)
  B <- rnorm(50000, 10.01, 2)
  w <- c(w, unname(series.compare(A, B, criterion = "BIC", var.equal=TRUE)[1]))
  p <- c(p, t.test(A, B, var.equal=TRUE)$p.value)

}

layout(mat = 1:2)
par(mar=c(4, 4, 1, 1)+0.4)
hist(p, main="", xlim=c(0, 1), las=1, breaks = (0:20)/20,
     freq=FALSE, xlab = expression(italic("p")*"-value"))
hist(w, main="", xlim=c(0, 1), las=1, breaks = (0:20)/20,
    freq=FALSE, xlab = expression(italic("w")*"-value"))
############################

x <- seq(from=8, to=13, by=0.1)

pv <- NULL
aw <- NULL
A <- rnorm(100, mean=10, sd=2)
B <- A-2

for (meanB in x) {
  pv <- c(pv, t.test(A, B, var.equal = FALSE)$p.value)
  aw <- c(aw, series.compare(A, B, criterion="BIC", var.equal = FALSE)[1])
  B <- B + 0.1
}

par(mar=c(4, 4, 2, 1)+0.4)
y <- pv
plot(x=x, y=y, type="l", lwd=2,
     bty="n", las=1, xlab="Mean B value (SD = 4)", ylab="Probability", ylim=c(0,1),
     main="")
y2 <- aw
lines(x=x, y=y2, type="l", col="red", lwd=2)

l1 <- which(aw>0.05)[1]
l2 <- max(which(aw>0.05))

aw[l1]
pv[l1]

aw[l2]
pv[l2]

l1 <- which(pv>0.05)[1]
l2 <- max(which(pv>0.05))

aw[l1]
```

```
pv[l1]

aw[l2]
pv[l2]

par(xpd=TRUE)
segments(x0=10-1.96*2/10, x1=10+1.96*2/10, y0=1.1, y1=1.1, lwd=2)
segments(x0=10, x1=10, y0=1.15, y1=1.05, lwd=2)
par(xpd=TRUE)
text(x=10.5, y=1.1, labels = "Mean A = 10, SD = 2", pos=4)

v1 <- c(expression(italic("p")*"-value"), expression("based on "*italic("t")*"-test"))
v2 <- c(expression(italic("w")*"-value for A"), expression("and B identical models"))
legend("topright", legend=c(v1, v2),
       y.intersp = 1,
       col=c("black", "black", "red", "red"), bty="n", lty=c(1, 0, 1, 0))

segments(x0=min(x), x1=max(x), y0=0.05, y1=0.05, lty=2)
par(xpd = TRUE)
text(x=13.05, y=0.05, labels = "0.05", pos=4)

## End(Not run)
```

`setPriors` *Set priors for MHalgoGen()*

Description

Set priors for MHalgoGen()

Usage

```
setPriors(
  par = stop("A vector with init values is necessary."),
  se = NULL,
  density = "dunif",
  rules = NULL,
  silent = FALSE
)
```

Arguments

`par`	Named vector with init value of parameters
`se`	Named vector with standard error of parameters
`density`	Named vector with density or single value
`rules`	List of rules to define priors
`silent`	If TRUE, do not show warning.

Details

setPriors is a general function to set priors for MHalgoGen()

Value

Return a data.frame with priors

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other mcmcComposite functions: +.PriorsmcmcComposite(), MHalgoGen(), PPD(), as.mcmc.mcmcComposite(), as.parameters(), merge.mcmcComposite(), plot.PriorsmcmcComposite(), plot.mcmcComposite(), setPriors1(), summary.mcmcComposite()

Examples

```
## Not run:
library(HelpersMG)
rules <- rbind(data.frame(Name="^a", Min=0, Max="x*2"),
               data.frame(Name="^b", Min=0, Max=100))
par <- c(a0=10, a1=2, b2=20)
(p <- setPriors(par=par, se=NULL, density="dgamma", rules=rules))
(p <- setPriors(par=par, se=NULL, density="dnorm", rules=rules))
(p <- setPriors(par=par, se=NULL, density="dunif", rules=rules))
par <- c(a0=10, a1=2, b2=20, b1=-1)
(p <- setPriors(par=par, se=NULL, density="dgamma", rules=rules))

## End(Not run)
```

---

setPriors1 *Set priors for MHalgoGen()*

Description

Set priors for MHalgoGen()
A check is done to verify that the Init value is well between the Min and Max range.
The order of Prior1, 2, and 3 must be similar to the order in the Density function. For this reason, it is safer to use Parameters.
As a rule of thumb, SDProp can be 1/10th of the range of posterior. For example if the posterior is thought to be from 0.1 to 0.2, you can use SDProp being (0.2-0.1)/10=0.01.

Usage

```
setPriors1(
  Name = stop("A name of parameter is required."),
  Prior1 = NULL,
  Prior2 = NULL,
  Prior3 = NULL,
  Parameters = NULL,
  Density = stop("A density is required."),
  SDProp = stop("A SD of proposal is required."),
  Min = -Inf,
  Max = +Inf,
  Init = stop("An initial value is required.")
)
```

Arguments

Name	Name of the parameter.
Prior1	The value for the first parameter of the prior distribution.
Prior2	The value for the second parameter of the prior distribution.
Prior3	The value for the third parameter of the prior distribution.
Parameters	A vector with parameters of the prior distribution
Density	The density function of the prior (ex. "dunif", "dnorm", "dbeta").
SDProp	The SD of the propositions for the Markov chain.
Min	The minimum value to truncate the prior distribution.
Max	The maximum value to truncate the prior distribution.
Init	The value at the first iteration.

Details

setPriors1 is a general function to set priors for MHalgoGen()

Value

Return a data.frame with the formatted prior

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other mcmcComposite functions: `+.PriorsmcmcComposite()`, `MHalgoGen()`, `PPD()`, `as.mcmc.mcmcComposite()`, `as.parameters()`, `merge.mcmcComposite()`, `plot.PriorsmcmcComposite()`, `plot.mcmcComposite()`, `setPriors()`, `summary.mcmcComposite()`

Examples

```
## Not run:
library(HelpersMG)
Priors <- setPriors1(Name="a0", Prior1=0, Prior2=1, Density="dunif",
                     SDProp=0.1, Min=0, Max=1, Init=0.5)
Priors <- Priors + setPriors1(Name="a1", Prior1=0.5, Prior2=0.1, Density="dnorm",
                     SDProp=0.05, Min=0, Max=1, Init=0.5)
# Using Parameters
Priors <- setPriors1(Name="a0", Parameters=c(min=0, max=1), Density="dunif",
                     SDProp=0.1, Min=0, Max=1, Init=0.5)
Priors <- Priors + setPriors1(Name="a1", Parameters=c(mean=0.5, sd=0.1), Density="dnorm",
                     SDProp=0.05, Min=0, Max=1, Init=0.5)

## End(Not run)
```

---

show_name *Show the name of a point*

Description

Click on a point in plot region and it will tell you what is the point.

Usage

```
show_name(
  points = NULL,
  x = NULL,
  y = NULL,
  names = NULL,
  col = "red",
  silent = FALSE
)
```

Arguments

points	A list with x, y and names elements
x	The x coordinates
y	The y coordinates.
names	The names of the points
col	Color of the legend.
silent	TRUE or FALSE

Details

Show the name of a point

Value

Name of the point

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

plot_errorbar

Other plot and barplot functions: ScalePreviousPlot(), barplot_errbar(), plot_add(), plot_errbar()

Examples

```
## Not run:
k <- plot_errbar(1:100, rnorm(100, 1, 2),
 xlab="axe x", ylab="axe y", bty="n", xlim=c(1,100),
  errbar.x=2, errbar.y=rnorm(100, 1, 0.1))
show_name(k)
k <- plot_errbar(1:10, rnorm(10, 1, 2),
 xlab="axe x", ylab="axe y", bty="n", xlim=c(1,10),
  errbar.x=2, errbar.y=rnorm(10, 1, 0.1),
  names=LETTERS[1:10])
show_name(k)
k <- plot_errbar(1:10, rnorm(10, 1, 2),
 xlab="axe x", ylab="axe y", bty="n", xlim=c(1,10),
  errbar.x=2, errbar.y=rnorm(10, 1, 0.1))
show_name(k, names=LETTERS[1:10])

## End(Not run)
```

---

similar *Test if two vectors contains the same elements independently of their order*

Description

Return TRUE only if all elements of x are present and only once in y.

Usage

```
similar(x, y, test.names = FALSE)
```

Arguments

x	A vector with numeric or character elements
y	A vector with numeric or character elements
test.names	Logical. If TRUE, the names of the vector elements must be also identical and unique

Value

A logical TRUE or FALSE

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
## Not run:
A <- c("A", "B", "C", "D")
B <- c("A", "B", "C", "D")
similar(A, B)
similar(B, A)
A <- c(x="A", y="B", z="C", k="D")
B <- c(x="A", y="B", z="C", l="D")
similar(B, A)
similar(A, B, test.names=TRUE)
A <- c(x="A", y="B", z="C", k="D")
B <- c(x="A", z="C", k="D", y="B")
similar(B, A)
similar(A, B, test.names=TRUE)

## End(Not run)
```

---

specify_decimal *Return a number as character with specified number of decimals*

Description

Return a number as character with specified number of decimals. If a is a matrix, it will return a matrix of the same size and the same attributes.

Usage

```
specify_decimal(x, decimals = NULL, decimal.point = ".")
```

Arguments

x	The numbers to be formated
decimals	Number of decimals to print
decimal.point	Character to be used as decimal point

Details

specify_decimals format a number with specified number of decimals

Value

A character

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
specify_decimal(x=pi, decimal.point=".")
specify_decimal(x=pi, decimals=4, decimal.point=".")
specify_decimal(x=c(pi, exp(1)), decimals=3, decimal.point=",")
specify_decimal(x=c(pi, exp(1)), decimal.point=",")
specify_decimal(x=c(pi*10, pi, pi/10, pi/100, pi/1000))
specify_decimal(x=c(pi=pi), decimal.point=".")
specify_decimal(x=matrix(pi*1:4, ncol=2), decimal.point=".")
m <- matrix(pi*1:4, ncol=2)
rownames(m) <- c("A", "B")
colnames(m) <- c("C", "D")
specify_decimal(x=m, decimal.point=".")
```

---

summary.mcmcComposite *Summarize the result of a mcmcComposite object*

Description

Summary for the result of a mcmcComposite object.

Usage

```
## S3 method for class 'mcmcComposite'
summary(object, chain = NULL, ...)
```

Arguments

object	A mcmcComposite object
chain	The chain to use
...	Not used

Details

summary.mcmcComposite get info on the result of a mcmcComposite object

Value

A summary of the result

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other mcmcComposite functions: +.PriorsmcmcComposite(), MHalgoGen(), PPD(), as.mcmc.mcmcComposite(), as.parameters(), merge.mcmcComposite(), plot.PriorsmcmcComposite(), plot.mcmcComposite(), setPriors(), setPriors1()

Examples

```
## Not run:
library(HelpersMG)
require(coda)
x <- rnorm(30, 10, 2)
dnormx <- function(data, x) {
 data <- unlist(data)
 return(-sum(dnorm(data, mean=x['mean'], sd=x['sd'], log=TRUE)))
}
parameters_mcmc <- data.frame(Density=c('dnorm', 'dlnorm'),
Prior1=c(10, 0.5), Prior2=c(2, 0.5), SDProp=c(1, 1),
Min=c(-3, 0), Max=c(100, 10), Init=c(10, 2), stringsAsFactors = FALSE,
row.names=c('mean', 'sd'))
mcmc_run <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, data=x,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=1)
plot(mcmc_run, xlim=c(0, 20))
plot(mcmc_run, xlim=c(0, 10), parameters="sd")
mcmcforcoda <- as.mcmc(mcmc_run)
#' heidel.diag(mcmcforcoda)
raftery.diag(mcmcforcoda)
autocorr.diag(mcmcforcoda)
acf(mcmcforcoda[[1]][,"mean"], lag.max=20, bty="n", las=1)
acf(mcmcforcoda[[1]][,"sd"], lag.max=20, bty="n", las=1)
batchSE(mcmcforcoda, batchSize=100)
# The batch standard error procedure is usually thought to
# be not as accurate as the time series methods used in summary
summary(mcmcforcoda)$statistics[,"Time-series SE"]
summary(mcmc_run)
as.parameters(mcmc_run)
lastp <- as.parameters(mcmc_run, index="last")
parameters_mcmc[,"Init"] <- lastp
# The n.adapt set to 1 is used to not record the first set of parameters
# then it is not duplicated (as it is also the last one for
# the object mcmc_run)
mcmc_run2 <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, data=x,
likelihood=dnormx, n.chains=1, n.adapt=1, thin=1, trace=1)
mcmc_run3 <- merge(mcmc_run, mcmc_run2)
####### no adaptation, n.adapt must be 0
parameters_mcmc[,"Init"] <- c(mean(x), sd(x))
mcmc_run3 <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, data=x,
likelihood=dnormx, n.chains=1, n.adapt=0, thin=1, trace=1)
```

```
## End(Not run)
```

`sun.info` *Estimate the time of sunrise and sunset according to longitude, latitude and date*

Description

Estimate the sun fates according to latitude and date.
Can be compared with the function `sunrise.set()` of package `StreamMetabolism`.

Usage

```
sun.info(date, latitude, longitude)
```

Arguments

`date`	A vector with the time at which sun fates are needed
`latitude`	The latitude at which estimate the sun fates
`longitude`	The longitude at which estimate the sun fates

Details

sun.info estimate the time of sunrise and sunset according to longitude, latitude and date

Value

A data.frame with information about daily sun

Author(s)

Marc Girondot <marc.girondot@gmail.com>

References

Teets, D.A. 2003. Predicting sunrise and sunset times. The College Mathematics Journal 34(4):317-321.

See Also

Other Periodic patterns of indices: `index.periodic()`, `minmax.periodic()`, `moon.info()`, `tide.info()`

Examples

```
## Not run:
# Generate a timeserie of time
date <- seq(from=as.Date("2000-01-01"), to=as.Date("2000-12-31"), by="1 day")
plot(date, sun.info(date, latitude=23, longitude=0)$day.length, bty="n",
 las=1, type="l", xlab="Ordinal days", ylab="Day length in hours")
plot(date, sun.info(date, latitude=23, longitude=0)$sunrise, bty="n",
 las=1, type="l", xlab="Ordinal days", ylab="Sun rise in hours")

## End(Not run)
```

`symbol.Female` *Plot a female symbol in the plotting region*

Description

Plot a female symbol in the plotting region.

Usage

```
symbol.Female(centerx, centery, rayonx, lwd = 2, col = "black")
```

Arguments

`centerx`	The x position of the center of the circle
`centery`	The y position of the center of the circle
`rayonx`	The size of the rayon in the scale of the x axis
`lwd`	The width of the line of the symbol
`col`	The color of the symbol

Details

symbol.Female plot a female symbol in the plotting region

Value

Nothing

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Symbol: `symbol.Male()`

Examples

```
## Not run:
plot(x=1:2, y=c(10,20), type="n", bty="n", xlab="", ylab="")

rayonx <- 0.01
centerx <- 1.2
centery <- 15

symbol.Male(centerx=centerx, centery = centery, rayonx=rayonx)
symbol.Female(centerx=centerx+0.5, centery = centery, rayonx=rayonx)

rayonx <- 0.03
centerx <- 1.2
centery <- 18

symbol.Male(centerx=centerx, centery = centery, rayonx=rayonx, lwd=3)
symbol.Female(centerx=centerx+0.5, centery = centery, rayonx=rayonx, lwd=3, col="red")

rayonx <- 0.05
centerx <- 1.4
centery <- 13

symbol.Male(centerx=centerx, centery = centery, rayonx=rayonx, lwd=4, col="blue")
symbol.Female(centerx=centerx+0.5, centery = centery, rayonx=rayonx, lwd=4, col="red")

## End(Not run)
```

---

symbol.Male *Plot a male symbol in the plotting region*

Description

Plot a male symbol in the plotting region.

Usage

```
symbol.Male(centerx, centery, rayonx, lwd = 2, col = "black")
```

Arguments

centerx	The x position of the center of the circle
centery	The y position of the center of the circle
rayonx	The size of the rayon in the scale of the x axis
lwd	The width of the line of the symbol
col	The color of the symbol

Details

symbol.Male plot a male symbol in the plotting region

Value

Nothing

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Symbol: symbol.Female()

Examples

```
## Not run:
plot(x=1:2, y=c(10,20), type="n", bty="n", xlab="", ylab="")

rayonx <- 0.01
centerx <- 1.2
centery <- 15

symbol.Male(centerx=centerx, centery = centery, rayonx=rayonx)
symbol.Female(centerx=centerx+0.5, centery = centery, rayonx=rayonx)

rayonx <- 0.03
centerx <- 1.2
centery <- 18

symbol.Male(centerx=centerx, centery = centery, rayonx=rayonx, lwd=3)
symbol.Female(centerx=centerx+0.5, centery = centery, rayonx=rayonx, lwd=3, col="red")

rayonx <- 0.05
centerx <- 1.4
centery <- 13

symbol.Male(centerx=centerx, centery = centery, rayonx=rayonx, lwd=4, col="blue")
symbol.Female(centerx=centerx+0.5, centery = centery, rayonx=rayonx, lwd=4, col="red")

## End(Not run)
```

---

symmetricize *Make a matrix symmetric*

Description

This function was part of the package ENA. This package is no more available and it cannot be installed from archive because some dependencies are no more available.

Usage

```
symmetricize(
  matrix,
  method = c("max", "min", "avg", "ld", "ud"),
  adjacencyList = FALSE
)
```

Arguments

matrix	The matrix to make symmetric
method	The method to use to make the matrix symmetric. Default is to take the maximum. **"max"** For each position, $m_{i,j}$, use the maxiumum of $(m_{i,j}, m_{j,i})$ **"min"** For each position, $m_{i,j}$, use the minimum of $(m_{i,j}, m_{j,i})$ **"avg"** For each position, $m_{i,j}$, use the mean: $(m_{i,j} + m_{j,i})/2$ **"ld"** Copy the lower triangular portion of the matrix to the upper triangular portion. **"ud"** Copy the upper triangular portion of the matrix to the lower triangular portion.
adjacencyList	Logical. If false, returns the symmetric matrix (the same format as the input). If true, returns an adjacency list representing the upper triangular portion of the adjacency matrix with addressing based on the row.names of the matrix provided.

Details

Make the matrix symmetric by making all "mirrored" positions consistent. A variety of methods are provided to make the matrix symmetrical.

Value

The symmetric matrix

Author(s)

Jeffrey D. Allen <Jeffrey.Allen@UTSouthwestern.edu>

Examples

```
#Create a sample 3x3 matrix
mat <- matrix(1:9, ncol=3)

#Copy the upper diagonal portion to the lower
symmetricize(mat, "ud")

#Take the average of each symmetric location
symmetricize(mat, "avg")
```

`tide.info` *Annual tide calendar for one particular location*

Description

Annual tide information.
The columns are: Location, Longitude, Latitude, Phase, DateTime.local, DateTime.UTC, Tide.meter
This function uses an API linking xtide software (https://flaterco.com/xtide/) with tide.info() function.
You must have a working internet connection for this function.

Usage

```
tide.info(
  location = NULL,
  year = 2021,
  longitude = NULL,
  latitude = NULL,
  force.tide.height = TRUE
)
```

Arguments

`location`	Textual information about location name
`year`	Year to get the calendar
`longitude`	Longitude to search for
`latitude`	Latitude to search for
`force.tide.height`	If FALSE, can return a current speed rather than tide height

Details

tide.info gets the annual tide calendar for one particular location.

Value

Return a data.frame with annual tide calendar.

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Periodic patterns of indices: `index.periodic()`, `minmax.periodic()`, `moon.info()`, `sun.info()`

Examples

```
## Not run:
library("HelpersMG")
Location <- "Les Hattes"
Year <- 2010
tide <- tide.info(Location, Year)
plot(tide[, "DateTime.local"], tide[, "Tide.meter"],
     type="l", bty="n", las=1,
     main=tide[1, "Location"],
     xlab=as.character(Year), ylab="Tide level in meter")

Location <- "Hawaii"
Year <- 2010
tide <- tide.info(Location, Year)

Location <- "Hanamaulu Bay, Kauai Island, Hawaii"
Year <- 2010
tide <- tide.info(Location, Year)
plot(tide[, "DateTime.local"], tide[, "Tide.meter"],
     type="l", bty="n", las=1,
     main=tide[1, "Location"],
     xlab=as.character(Year), ylab="Tide level in meter")

tide <- tide.info(year=2010, longitude=-32, latitude=-4)
library(maps)
map(database = "world", regions = "Brazil", asp=1,
    xlim=c(-80, -30), ylim=c(-33, 5))
points(tide[1, "Longitude"], tide[1, "Latitude"], col="red", pch=19)
points(-32, -4, col="blue", pch=19)
axis(1)
axis(2, las=1)

# Show the locations with data
library(maps)
map(xlim=c(-180, 180), ylim=c(-90, 90))
title("Locations with harmonics data")
axis(1, at=seq(from=-180, to=180, by=45))
axis(2, las=1, at=seq(from=-90, to=90, by=15))
points(getFromNamespace(x="tide_location", ns="HelpersMG")[, c("longitude")],
       getFromNamespace(x="tide_location", ns="HelpersMG")[, c("latitude")],
       pch=".", col="red", cex=2)
# Another example
tikei_lon  <- (-144.5465183)
tikei_lat <- -14.9505897
Year <- 2021
tikei_tide <- tide.info(year=Year, longitude=tikei_lon, latitude=tikei_lat)
plot(tikei_tide[, "DateTime.local"], tikei_tide[, "Tide.meter"],
     type="l", bty="n", las=1,
     main=tikei_tide[1, "Location"],
     xlab=as.character(Year), ylab="Tide level in meter")
## Another one
tikei_lon <- (-75.56861111)
```

```
tikei_lat <- 39.50083333
Year <- 2012
tikei_tide <- tide.info(year=Year, longitude=tikei_lon, latitude=tikei_lat)

library(mapdata)
map('worldHires', xlim=c(-77, -74), ylim=c(37, 40))
points(x=tikei_lon, y=tikei_lat, pch=19, col="red", cex=1)
points(x=tikei_tide$Longitude[1], y=tikei_tide$Latitude[2],
       pch=19, col="blue", cex=1)

par(mar=c(4, 4, 2, 2))
plot(tikei_tide$DateTime.local, tikei_tide$Tide.meter, type="l")

## End(Not run)
```

`tnirp` *Read an ASCII text representation of a named or not vector object*

Description

Read an ASCII text representation of a named or not vector object.
Note that paste0(rev(c("p", "r", "i", "n", "t")), collapse="") = "tnirp"

Usage

```
tnirp(x, named = TRUE)
```

Arguments

`x`	A string or a vector of strings with value and possibly names.
`named`	TRUE if names are included.

Details

tnirp reads an ASCII text representation of a named or not vector object

Value

A vector

Author(s)

Marc Girondot <marc.girondot@gmail.com>

See Also

Other Characters: `asc()`, `char()`, `d()`

Examples

```
A <- structure(runif(26), names=letters)
text <- capture.output(A)
tnirp(text)

tnirp("         mu   mu_season         OTN       p1.09       p1.10       p1.11
 4.63215947 10.78627511  0.36108497  0.08292101 -0.52558196 -0.76430859
       p1.12       p1.13       p1.14       p1.15       p1.16       p1.17
       -0.75186542 -0.57632291 -0.58017174 -0.57048696 -0.56234135 -0.80645122
       p1.18       p1.19       p1.20       p1.21       p1.22       p1.23
       -0.77752524 -0.80909494 -0.56920540 -0.55317302  0.45757298 -0.64155368
       p1.24       p1.25       p1.26       p1.27       p1.28       p1.29
       -0.59119637 -0.66006794 -0.66582399 -0.66772684 -0.67351412 -0.66941992
       p1.30       p1.31       p1.32       p1.33       p1.34       p1.35
       -0.67038245 -0.68938726 -0.68889078 -0.68779016 -0.68604629 -0.68361820
       p1.36       p1.37       p2.09       p2.10       p2.11       p2.12
       -0.67045238 -0.66115613  2.55403149  2.31060620  2.31348160  2.20958757
       p2.13       p2.14       p2.15       p2.16       p2.17       p2.18
       2.14304918  2.19699719  2.30705457  2.18740019  2.32305811  2.31668302
       p2.19       p2.20       p2.21       p2.22       p2.23       p2.24
       1.99424288  2.06613445  2.38092301  2.40551276  2.31987342  2.30344402
       p2.25       p2.26       p2.27       p2.28       p2.29       p2.30
       2.26869058  2.25008836  2.23385204  2.22768782  2.25341904  1.77043360
       p2.31       p2.32       p2.33       p2.34       p2.35       p2.36
       2.21606813  2.21581431  2.21153872  2.21118013  2.21375660  2.21182196
       p2.37
       1.86137833 ")
tnirp("   27.89 289.99
      90.56", named=FALSE)
```

`universalmclapply` *Run the function FUN on X using parallel computing*

Description

Return the results of the function FUN applied to X. It uses forking in unix system and not in windows system.
By default, it will send all the content of environment.

Usage

```
universalmclapply(
  X,
  FUN,
  ...,
  mc.cores = getOption("mc.cores", parallel::detectCores()),
  mc.preschedule = TRUE,
  clusterExport = list(),
  clusterEvalQ = list(),
```

```
  forking = ifelse(.Platform$OS.type == "windows", FALSE, TRUE),
  progressbar = FALSE
)
```

Arguments

X	A vector (atomic or list) or an expressions vector. Other objects (including classed objects) will be coerced by as.list.
FUN	The function to be applied to each element of X
...	Optional arguments to FUN
mc.cores	The number of cores to use, i.e. at most how many child processes will be run simultaneously.
mc.preschedule	if set to TRUE then the computation is first divided to (at most) as many jobs are there are cores and then the jobs are started, each job possibly covering more than one value. If set to FALSE then one job is forked for each value of X. The former is better for short computations or large number of values in X, the latter is better for jobs that have high variance of completion time and not too many values of X compared to mc.cores.
clusterExport	List of clusterExport parameters as list
clusterEvalQ	List of clusterEvalQ parameters as list
forking	If TRUE will use forking
progressbar	If pbapply package is installed, show a progressbar

Details

universalmclapply runs the function FUN on X using parallel computing

Value

The results of the function FUN applied to X

Author(s)

Marc Girondot <marc.girondot@gmail.com>

Examples

```
## Not run:
library(HelpersMG)
x <- 1:1000
funx <- function(y) {
  mint <- rep(NA, length(y))
  for (i in seq_along(y)) {
    k <- rnorm(runif(n = 1, 50, 50), mean=10, sd=2)
    mint[i] <- mean(k)
  }
  mint
}
```

```
# Note that parallel computing is not always the best solution !
(tp <- system.time({
   m <- lapply(X=x, FUN=funx)
}))
(tp <- system.time({
   m <- universalmclapply(X=x, FUN=funx, forking=FALSE)
}))
(tp <- system.time({
   m <- universalmclapply(X=x, FUN=funx, forking=TRUE)
}))

### An example using clusterExport
# Here no error is generated because environment was exported
# However forking is not possible in windows and non parallel code is ran
pp <- runif(100)
x <- 1:100
funx1 <- function(y) {pp[y]*10}
u <- universalmclapply(x, FUN=funx1, forking=TRUE)

# Here an error is generated because environment was not exported when parLapplyLB is used
pp <- runif(100)
x <- 1:100
u <- universalmclapply(x, FUN=funx1, forking=FALSE)
u <- universalmclapply(x, FUN=funx1, forking=FALSE,
                       clusterExport=list())

# here no error is generated because the variable pp is exported
pp <- runif(100)
x <- 1:100
u <- universalmclapply(x, FUN=funx1, forking=FALSE,
                       clusterExport=list(varlist=c("pp"), envir=environment()))

# here no error is generated because all the environment is exported
pp <- runif(100)
x <- 1:100
u <- universalmclapply(x, FUN=funx1, forking=FALSE,
                       clusterExport=list(varlist=c(ls()), envir=environment()))

### An example using clusterEvalQ
asc("a") # asc() is a function from packages HelpersMG
funx2 <- function(y) {asc("a")*10}
# In unix, the loaded packages are visible from all cores
x <- 1:100
u <- universalmclapply(x, FUN=funx2, forking=TRUE)
# In windows, the loaded packages are not visible from all cores
x <- 1:100
u <- universalmclapply(x, FUN=funx2, forking=FALSE)
# In windows, the loaded packages are not visible from all cores
x <- 1:100
u <- universalmclapply(x, FUN=funx2, forking=FALSE,
clusterEvalQ=list(expr=expression(library(HelpersMG)))
)
```

```
### If package pbapply is available, progress bar can be shown
m <- universalmclapply(X=x, FUN=funx, forking=FALSE, progressbar=TRUE)
m <- universalmclapply(X=x, FUN=funx, forking=TRUE, progressbar=TRUE)

## You can manage the number of cores used using:
options(mc.cores=1)

## End(Not run)
```

---

wget *Download a file from internet and save it locally*

Description

Download a file from internet and save it locally. This function is a wrapper for download.files() that keep the name identical and can get several files at once. It was written to simplify downloading of file. It doest not use the true wget function (https://www.gnu.org/software/wget/) which is much more complex but also powerful.

Usage

```
wget(url = stop("At least one internet adress is required"), ...)
```

Arguments

url	The url where to download file
...	The parameters send to download.file()

Details

wget download a file from internet and save it locally

Value

Nothing

Author(s)

Marc Girondot

Examples

```
## Not run:
library(HelpersMG)
# Save locally the files send in the parameter url
wget(c("https://cran.r-project.org/web/packages/HelpersMG/HelpersMG.pdf",
         "https://cran.r-project.org/web/packages/embryogrowth/embryogrowth.pdf"))

## End(Not run)
```

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