

Package ‘HelpersMG’

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Type Package

Title Tools for Earth Meteorological Analysis

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Depends coda, R (>= 2.14.0)

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pbmccapply, parallel, visNetwork, igraph

Description Contains many 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 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

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LazyLoad yes

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Description

Contains 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.
 The lastest version of this package can always been installed using:
`install.packages("http://www.ese.u-psud.fr/epc/conservation/CRAN/HelpersMG.tar.gz", repos=NULL,
 type="source")`

Details

Helpers functions for several packages

Package: HelpersMG
 Type: Package
 Version: 3 build 109
 Date: 2017-11-25
 License: GPL (>= 2)
 LazyLoad: yes

Author(s)

Marc Girondot <marc.girondot@u-psud.fr>

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=10000, 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")

## End(Not run)

```

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

See Also

Other mcmcComposite functions: [MHalgoGen](#), [as.parameters](#), [merge.mcmcComposite](#), [plot.mcmcComposite](#), [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 likelihood has been observed. If index="last", the function will return the parameters for the last likelihood. index can also be a numeric value.

Usage

```
as.parameters(x, index = "best", chain = 1)
```

Arguments

x	A mcmcComposite obtained as a result of MHalgoGen() function
index	At which iteration the parameters must be taken
chain	The number of the chain in which to get parameters

Value

A vector with parameters at maximum likelihood or index position

Author(s)

Marc Girondot

See Also

Other mcmcComposite functions: [MHalgoGen](#), [as.mcmc.mcmcComposite](#), [merge.mcmcComposite](#), [plot.mcmcComposite](#), [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)

```

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 UTF-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: [chr](#)

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 asymmetric. Use `y.plus` and `y.minus` to set absolute 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

<code>...</code>	Parameters for <code>barplot()</code> such as <code>main=</code> or <code>ylim=</code>
<code>errbar.y</code>	The length of error bars for y. Recycled if necessary.
<code>errbar.y.plus</code>	The length of positive error bars for y. Recycled if necessary.
<code>errbar.y.minus</code>	The length of negative error bars for y. Recycled if necessary.
<code>y.plus</code>	The absolute position of the positive error bar for y. Recycled if necessary.
<code>y.minus</code>	The absolute position of the negative error bar for y. Recycled if necessary.
<code>errbar.tick</code>	Size of small ticks at the end of error bars defined as a proportion of total width or height graph size.

<code>errbar.lwd</code>	Error bar line width, see <code>par("lwd")</code>
<code>errbar.lty</code>	Error bar line type, see <code>par("lwd")</code>
<code>errbar.col</code>	Error bar line color, see <code>par("col")</code>
<code>add</code>	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

See Also

`plot_errorbar`

Other plot and barplot functions: [ScalePreviousPlot](#), [plot_add](#), [plot_errbar](#)

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)
```

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

Examples

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

chr

Return the characters defined by the codes

Description

Return a string with characters defined by the codes.

Usage

```
chr(n)
```

Arguments

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

Details

chr 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](#)

Examples

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

clean.knitr

Delete temporary files created during knitr compile

Description

Delete temporary files created during knitr compile in working directory.
This function works only in UNIX system (LINUX or MacOSX).

Usage

```
clean.knitr()
```

Details

clean.knitr deletes temporary files created during knitr compile

Value

Nothing

Author(s)

Marc Girondot

Examples

```
## Not run:
clean.knitr()

## End(Not run)
```

`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

See Also

Other AIC: [ExtractAIC.glm](#), [compare_AICc](#), [compare_AIC](#), [compare_BIC](#)

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 $-\log(\text{likelihood})$, then factor.value must be 1 and if \$value is $\log(\text{likelihood})$, 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 fitted with its own set of parameters.

Take a look at `ICtab` in package `bbmlc` which is similar.

Usage

```
compare_AIC(..., factor.value = 1)
```

Arguments

... Successive results to be compared as lists.
factor.value The \$value of the list object is multiplied by factor.value to calculate AIC.

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

See Also

Other AIC: [ExtractAIC.glm](#), [compare_AICc](#), [compare_BIC](#), [compare](#)

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 $2 * \text{factor.value} * \text{logLik}(x) + (2 * \text{attributes}(\text{logLik}(x))\$df * (\text{attributes}(\text{logLik}(x))\$nobs - \text{attributes}(\text{logLik}(x))\$df)) / (\text{attributes}(\text{logLik}(x))\$nobs - \text{attributes}(\text{logLik}(x))\$df - 2)$.

Usage

```
compare_AICc(..., factor.value = -1)
```

Arguments

`...` Successive results to be compared as lists.
`factor.value` The `$value` of the list object is multiplied by `factor.value` to calculate BIC.

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

See Also

Other AIC: [ExtractAIC.glm](#), [compare_AIC](#), [compare_BIC](#), [compare](#)

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 $2 * \text{factor.value} * \text{sum}(\text{logLik}(x)) + \text{sum}(\text{attributes}(\text{logLik}(x))\$df) * \log(\text{attributes}(\text{logLik}(x))\$nobs)$

When several data (i..n) are included, the global BIC is calculated as:

$2 * \text{factor.value} * \text{sum}(\text{logLik}(x))$ for `i..n` + $\text{sum}(\text{attributes}(\text{logLik}(x))\$df)$ for `i..n` * $\log(\text{attributes}(\text{logLik}(x))\$nobs)$

Usage

```
compare_BIC(..., factor.value = -1)
```


Arguments

... Successive results to be compared as lists.
factor.value The \$value of the list object is multiplied by factor.value to calculate BIC.

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

See Also

Other AIC: [ExtractAIC.glm](#), [compare_AICc](#), [compare_AIC](#), [compare](#)

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

<code>table</code>	A matrix or a data.frame with series in rows and number of each category in column
<code>criterion</code>	Which criterion is used for model selection
<code>probs</code>	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

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

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")
```

Dlx

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

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 maximum 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

```
Dlx(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

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)
```

```

12 <- c(0.2, 0.2, 0.2, 0.2, 0.2)
DIx(11, 12)

11 <- c(0.3333, 0.3333, 0.3333)
12 <- c(0.3333, 0.3333, 0.3333)
DIx(11, 12)

## End(Not run)

```

dSnbinom	<i>Density for the sum of random variable with negative binomial distributions.</i>
----------	---

Description

Density for the sum of random variable with negative binomial distributions.
If all prob values are the same, infinite is automatically set to 0.

Usage

```
dSnbinom(x = stop("You must provide a x value"), size = NULL, prob = NULL,
mu = NULL, log = FALSE, infinite = 100)
```

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. $0 < \text{prob} \leq 1$.
mu	alternative parametrization via mean.
log	logical; if TRUE, probabilities p are given as $\log(p)$.
infinite	Number of maximal iterations; check different values to determine the error in estimation.

Details

dSnbinom returns the density for the sum of random variable with negative binomial distributions

Value

dSnbinom gives the density

Author(s)

Marc Girondot

References

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

See Also

Other Distribution of sum of random variable with negative binomial distributions: [pSnbinom](#), [qSnbinom](#), [rSnbinom](#)

Examples

```
## Not run:
alpha <- c(1, 2, 5, 1, 2)
p <- c(0.1, 0.12, 0.13, 0.14, 0.14)
# Test with lower iterations: 2 or 50 rather than 10 [default]; precision is very good still with 10
dSnbinom(20, size=alpha, prob=p, infinite=50)
dSnbinom(20, size=alpha, prob=p, infinite=10)
dSnbinom(20, size=alpha, prob=p, infinite=2)
# However it is not always the case; It depends on the parametrization (see Furman 2007)
dSnbinom(20, size=2, mu=c(0.01, 0.02, 0.03), infinite=1000)
dSnbinom(20, size=2, mu=c(0.01, 0.02, 0.03), infinite=100)
dSnbinom(20, size=2, mu=c(0.01, 0.02, 0.03), infinite=50)
dSnbinom(20, size=2, mu=c(0.01, 0.02, 0.03), infinite=10)
dSnbinom(20, size=2, mu=c(0.01, 0.02, 0.03), infinite=2)
# 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))
# The function is vectorized:
plot(0:200, dSnbinom(0:200, size=alpha, prob=p), bty="n", type="h", xlab="x", ylab="Density")
# 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, infinite=1000), 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")

# Example with the approximation mu=mean(mu)
plot(0:300, dSnbinom(0:300, size=alpha, mu=mu, infinite=0), 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")

# example to fit the distribution
data <- rnbino(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)

dSnbinox <- function(x, par) {
  -sum(dSnbino(x=x[,2], mu=rep(par["mu"], 10), size=par["size"], log=TRUE,
    infinite = 1000))
}

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

## End(Not run)

```

ellipse

Plot an ellipse

Description

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

- alpha is 1 - confidence interval
- method must be one of these "wilson", "exact", "asymptotic"

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(alpha = 0.05, method = "wilson"), 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

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

Details

ellipse plots an ellipse

Value

Nothing

Author(s)

marc.girondot@u-psud.fr

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))

```

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

<code>fit</code>	fitted model, the result of a fitter glm.
<code>scale</code>	unused for glm.
<code>k</code>	numeric specifying the 'weight' of the equivalent degrees of freedom (=: edf) part in the AIC formula.
<code>...</code>	further arguments (currently unused because some functions using this function do not use 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: [compare_AICc](#), [compare_AIC](#), [compare_BIC](#), [compare](#)

Examples

```
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)
```

growlnotify	<i>Send growl notification for MacOS X system.</i>
-------------	--

Description

This function is used to send a notification to MacOS user.

Usage

```
growlnotify(textinfo = "")
```

Arguments

textinfo	Text to display in the growlnotify window
----------	---

Details

growlnotify send growl notification for MacOS X systems.

Value

None

Author(s)

Marc Girondot

Examples

```
## Not run:
# If growlnotify is used on a non-mac system, it just quits.
growlnotify("It works if you are on a Mac with GrowlNotify installed!")

## 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_corr%C3%A9lations

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

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")
es <- matrix(c("e1", "52", "12", "12", "5",
"e2", "59", "12.5", "9", "5",
"e3", "55", "13", "15", "9",
"e4", "58", "14.5", "5", "5",
"e5", "66", "15.5", "11", "13.5",
"e6", "62", "16", "15", "18",
"e7", "63", "17", "12", "18",
"e8", "69", "18", "9", "18"), ncol=5, byrow = TRUE)
colnames(es) <- c("Élève", "Poids", "Âge", "Assiduité", "Note")
es <- as.data.frame(es, stringsasFactor=FALSE)
es[, 2] <- as.numeric(as.character(es[, 2]))
es[, 3] <- as.numeric(as.character(es[, 3]))
es[, 4] <- as.numeric(as.character(es[, 4]))
es[, 5] <- as.numeric(as.character(es[, 5]))

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_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

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 <- matrix(c("e1", "52", "12", "12", "5",
"e2", "59", "12.5", "9", "5",
"e3", "55", "13", "15", "9",
"e4", "58", "14.5", "5", "5",
"e5", "66", "15.5", "11", "13.5",
"e6", "62", "16", "15", "18",
"e7", "63", "17", "12", "18",
"e8", "69", "18", "9", "18"), ncol=5, byrow = TRUE)
colnames(es) <- c("Élève", "Poids", "Âge", "Assiduité", "Note")
es <- as.data.frame(es, stringsasFactor=FALSE)
es[, 2] <- as.numeric(as.character(es[, 2]))
```



```

es[, 3] <- as.numeric(as.character(es[, 3]))
es[, 4] <- as.numeric(as.character(es[, 4]))
es[, 5] <- as.numeric(as.character(es[, 5]))

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: a correlation is retained if it is higher than the threshold and if all partial correlations of the two variables and any third one are all lower than the threshold. 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 pbmccapply 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_corr%C3%A9lations

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"), 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).
progress	show a progress bar
debug	display information about progression of computing

Details

IC_threshold_matrix calculates correlation matrix thresholded by partial correlation

Value

A list

Author(s)

Marc Girondot

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 <- matrix(c("e1", "52", "12", "12", "5",
"e2", "59", "12.5", "9", "5",
"e3", "55", "13", "15", "9",
"e4", "58", "14.5", "5", "5",
"e5", "66", "15.5", "11", "13.5",
"e6", "62", "16", "15", "18",
"e7", "63", "17", "12", "18",
"e8", "69", "18", "9", "18"), ncol=5, byrow = TRUE)
colnames(es) <- c("Élève", "Poids", "Âge", "Assiduité", "Note")
es <- as.data.frame(es, stringsAsFactor=FALSE)
es[, 2] <- as.numeric(as.character(es[, 2]))
es[, 3] <- as.numeric(as.character(es[, 3]))
es[, 4] <- as.numeric(as.character(es[, 4]))
es[, 5] <- as.numeric(as.character(es[, 5]))
```

```

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=cor_matrix, 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)

# Using the model All at a time

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

## End(Not run)

```

index.periodic	<i>Estimate indices in periodic timeseries based on anchored minimum and maximum</i>
----------------	--

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@u-psud.fr>

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	<i>Return or the index in ncdf object from lat/longitude or inverse</i>
--------------	---

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, name.lon = "lon",
  name.lat = "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
name.lon	Name of argument for longitude, default is lon
name.lat	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

Examples

```
## Not run:
url <- "ftp://ftp.cdc.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

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

```

Arguments

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.
text	Text to search in files

Details

inside.search Search a string within files of a folder

Value

Return an invisible vector with filenames in which the pattern occurs

Author(s)

Marc Girondot

Examples

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

invlogit	<i>Return the inverse logit</i>
----------	---------------------------------

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

See Also

Other logit: [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= $1/(1+\exp(P+d*S))$

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 constant incubation doses used to fit sex ratio
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" 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@u-psud.fr>

See Also

Other LD50 functions: [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)
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)

## End(Not run)
```

local.search	<i>Return path of file searched for in local disk based on its file name</i>
--------------	--

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 searched 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	<i>Return the logit</i>
-------	-------------------------

Description

Return the logit.

Usage

```
logit(p)
```

Arguments

p The probability

Details

logit returns the logit

Value

A value

Author(s)

Marc Girondot

See Also

Other logit: [invlogit](#)

Examples

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

`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

<code>object</code>	A result file generated by fitRMU
<code>...</code>	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

See Also

Other LD50 functions: [LD50](#), [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

See Also

Other mcmcComposite functions: [MHalgoGen](#), [as.mcmc.mcmcComposite](#), [as.parameters](#), [plot.mcmcComposite](#), [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
- Prior1. The first parameter to send to the Density function
- Prior2. The second 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 take a parameter named x.

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"), ..., n.iter = 10000,
  n.chains = 1, n.adapt = 100, thin = 30, trace = FALSE,
  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

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
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
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

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

See Also

Other mcmcComposite functions: [as.mcmc.mcmcComposite](#), [as.parameters](#), [merge.mcmcComposite](#), [plot.mcmcComposite](#), [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'))
mcmc_run <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, data=val,
  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")
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)$statistics[,"Time-series SE"]
summary(mcmc_run)
as.parameters(mcmc_run)
lastp <- as.parameters(mcmc_run, index="last")
parameters_mcmc[,"Init"] <- lastp
# The n.adapt set to 1 is used to not record the first set of parameters
# then it is not duplicated (as it is also the last one for
# the object mcmc_run)
mcmc_run2 <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, x=x,
likelihood=dnormx, n.chains=1, n.adapt=1, thin=1, trace=1)
mcmc_run3 <- merge(mcmc_run, mcmc_run2)
##### no adaptation, n.adapt must be 0
parameters_mcmc[,"Init"] <- c(mean(x), sd(x))
mcmc_run3 <- MHalgoGen(n.iter=1000, parameters=parameters_mcmc, x=x,
likelihood=dnormx, n.chains=1, n.adapt=0, thin=1, trace=1)
# Here is how to use adaptive mcmc
mcmc_run <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, data=val, adaptive = FALSE,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=1)
1-rejectionRate(as.mcmc(mcmc_run))
mcmc_run <- MHalgoGen(n.iter=50000, parameters=parameters_mcmc, data=val, adaptive = TRUE,
likelihood=dnormx, n.chains=1, n.adapt=100, thin=1, trace=1)
1-rejectionRate(as.mcmc(mcmc_run))
# To see the dynamics :
var <- "mean"
par(mar=c(4, 4, 1, 1)+0.4)
plot(1:nrow(mcmc_run$resultMCMC[[1]]), mcmc_run$resultMCMC[[1]][, var], type="l",
      xlab="Iterations", ylab=var, bty="n", las=1)

## End(Not run)

```

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

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

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

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)
```

Arguments

x	A named vector.
val	A named vector with components to replace corresponding components in x.

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))
```

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 quarter

Author(s)

Marc Girondot <marc.girondot@u-psud.fr>

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)
```

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 compassRose sp

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 map.scale maps

Examples

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

## 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 visI-graph from package visNetwork. https://fr.wikipedia.org/wiki/Iconographie_des_corr%C3%A9lations

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", plot = TRUE)
```


Arguments

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

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 <- matrix(c("e1", "52", "12", "12", "5",
"e2", "59", "12.5", "9", "5",
"e3", "55", "13", "15", "9",
"e4", "58", "14.5", "5", "5",
"e5", "66", "15.5", "11", "13.5",
"e6", "62", "16", "15", "18",
"e7", "63", "17", "12", "18",
"e8", "69", "18", "9", "18"), ncol=5, byrow = TRUE)
colnames(es) <- c("Élève", "Poids", "Âge", "Assiduité", "Note")
```

```

es <- as.data.frame(es, stringsasFactor=FALSE)
es[, 2] <- as.numeric(as.character(es[, 2]))
es[, 3] <- as.numeric(as.character(es[, 3]))
es[, 4] <- as.numeric(as.character(es[, 4]))
es[, 5] <- as.numeric(as.character(es[, 5]))

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)

## End(Not run)

```

plot.LD50

Plot results of LD50() that best describe LD50

Description

Plot the estimates that best describe lethality of exposures.

Usage

```

## S3 method for class 'LD50'
plot(x, ..., las.x = 1, las.y = 1, lab.PT = "LD50",
     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 IC50()
...	Parameters for plot()
las.x	las parameter for x axis
las.y	las parameter for y axis
lab.PT	Label to describe pivotal temperature
lab.TRD	Label to describe transitional range of temperature
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 IC50() that best describe IC50

Value

Nothing

Author(s)

Marc Girondot

References

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.

Girondot M., Submitted. On the concept of embryological thermosensitive period for sex determination in reptiles.

See Also

Other LD50 functions: [LD50](#), [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)

## End(Not run)
```

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

Description

Plot the results within a mcmcComposite object.

The parameters to use can be called by:

```
parameters="all"
```

```
parameters=1:4
```

```
parameters=c("PAR1", "PAR2", "PAR5")
```

```
parameters=c(TRUE, TRUE, FALSE, TRUE)
```

If scale.prior is TRUE, another scale is shown at right.

Usage

```
## S3 method for class 'mcmcComposite'
plot(x, ..., chain = 1, parameters = 1,
     scale.prior = TRUE, legend = TRUE, ylab = "Posterior density",
     las = 1, col.prior = "red", lty.prior = 1, lwd.prior = 1,
     col.posterior = "white", lty.posterior = 1, lwd.posterior = 1,
     ylab.prior = "Prior density")
```

Arguments

x	A mcmcComposite object
...	Graphical parameters to be send to hist()
chain	The chain to use
parameters	Name of parameters or their number (see description)
scale.prior	If TRUE, the prior is scaled at the same size as posterior
legend	If FALSE, the legend is not shown
ylab	y-label for posterior
las	las parameter (orientation of y-axis graduation)
col.prior	Color for prior curve
lty.prior	Type of line for prior curve
lwd.prior	Width of line for prior curve
col.posterior	Color for posterior histogram
lty.posterior	Type of line for posterior histogram
lwd.posterior	Width of line for posterior histogram
ylab.prior	y-label for prior

Details

plot.mcmcComposite plots the result of a MCMC search

Value

None

Author(s)

Marc Girondot

See Also

Other mcmcComposite functions: [MHalgoGen](#), [as.mcmc.mcmcComposite](#), [as.parameters](#), [merge.mcmcComposite](#), [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=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=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)

## 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

See Also

Other plot and barplot functions: [ScalePreviousPlot](#), [barplot_errbar](#), [plot_errbar](#)

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 asymmetric and `errbar.y.minus`, `errbar.y.plus` if bars for y axis are asymmetric. Use `x.plus`, `x.minus`, `y.plus` and `y.minus` to set absolute 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 envelop 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), add = FALSE)
```

Arguments

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

Nothing

Author(s)

Marc Girondot

See Also

barplot_errorbar

Other plot and barplot functions: [ScalePreviousPlot](#), [barplot_errbar](#), [plot_add](#)

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)
```

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

See Also

Other LD50 functions: [LD50](#), [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)
```

pSnbinom	<i>Distribution function for the sum of random variable with negative binomial distributions.</i>
----------	---

Description

Distribution function for the sum of random variable with negative binomial distributions.

Usage

```
pSnbinom(q = stop("At least one quantile must be provided"), size = NULL,
         prob = NULL, mu = NULL, lower.tail = TRUE, log.p = FALSE,
         infinite = 100)
```

Arguments

q	vector of 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. $0 < \text{prob} \leq 1$.
mu	alternative parametrization via mean.
lower.tail	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.
log.p	logical; if TRUE, probabilities p are given as $\log(p)$.
infinite	Number of maximal iterations; check different values to determine the error in estimation.

Details

pSnbinom returns the distribution function for the sum of random variable with negative binomial distributions

Value

pSnbinom returns distribution function

Author(s)

Marc Girondot

See Also

Other Distribution of sum of random variable with negative binomial distributions: [dSnbinom](#), [qSnbinom](#), [rSnbinom](#)

Examples

```
## Not run:
alpha <- c(2.1, 2.05, 2)
mu <- c(10, 30, 20)
p <- pSnbinom(q=10, size=alpha, mu=mu, lower.tail = TRUE)

## End(Not run)
```

qSnbinom	<i>Quantile function for the sum of random variable with negative binomial distributions.</i>
----------	---

Description

Quantile function for the sum of random variable with negative binomial distributions.

Usage

```
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, infinite = 100)
```

Arguments

p	vector of probabilities.
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. $0 < \text{prob} \leq 1$.
mu	alternative parametrization via mean.
lower.tail	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.
log.p	logical; if TRUE, probabilities p are given as $\log(p)$.
infinite	Number of maximal iterations; check different values to determine the error in estimation.

Details

qSnbinom returns the quantile function for the sum of random variable with negative binomial distributions

Value

qSnbinom returns quantile function

Author(s)

Marc Girondot

See Also

Other Distribution of sum of random variable with negative binomial distributions: [dSnbinom](#), [pSnbinom](#), [rSnbinom](#)

Examples

```
## Not run:
alpha <- c(2.1, 2.05, 2)
mu <- c(10, 30, 20)
q <- qSnbinom(p=0.1, size=alpha, mu=mu, lower.tail = TRUE)

## End(Not run)
```

r2norm	<i>Random generation for Gaussian distributions different at left and right</i>
--------	---

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

Examples

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

hist(n)

## End(Not run)
```

read_folder	<i>Read files present in a folder and creates a list with the content of these files</i>
-------------	--

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

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)

## End(Not run)
```

rSnbinom

Random generation for the sum of random variable with negative binomial distributions.

Description

Random numbers for the sum of random variable with negative binomial distributions.

Usage

```
rSnbinom(n = 1, size = NULL, prob = NULL, mu = 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. $0 < \text{prob} \leq 1$.
mu	alternative parametrization via mean.

Details

rSnbinom returns random numbers for the sum of random variable with negative binomial distributions

Value

rSnbinom returns random number

Author(s)

Marc Girondot

See Also

Other Distribution of sum of random variable with negative binomial distributions: [dSnbinom](#), [pSnbinom](#), [qSnbinom](#)

Examples

```
## Not run:
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(distribEmpirique))] <- table(distribEmpirique)/rep

plot(0:300, dSnbinom(0:300, size=alpha, mu=mu, infinite=1000), 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")

## 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()
```

Details

ScalePreviousPlot returns the scale of the previous plot

Value

A list with xlim and ylim

Author(s)

Marc Girondot

See Also

Other plot and barplot functions: [barplot_errbar](#), [plot_add](#), [plot_errbar](#)

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)

## 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 will be used to generate the Cholesky matrix.

Usage

```
SEfromHessian(a, hessian = FALSE)
```

Arguments

a	An Hessian matrix
hessian	If TRUE, return a list with the hessian and SE

Details

SEfromHessian returns standard error of parameters based on Hessian matrix

Value

SEfromHessian returns a vector with standard errors

Author(s)

Marc Girondot

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

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)

```

similar	<i>Test if two vectors contains the same elements independently of their order</i>
---------	--

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 string elements
y	A vector with numeric or string 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

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)
```

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

See Also

Other mcmcComposite functions: [MHALgoGen](#), [as.mcmc.mcmcComposite](#), [as.parameters](#), [merge.mcmcComposite](#), [plot.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)
```

sun.info	<i>Estimate the time of sunrise and sunset according to longitude, latitude and date</i>
----------	--

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@u-psud.fr>

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

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

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. <ul style="list-style-type: none">• "max" For each position, $m_{i,j}$, use the maximum 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

The script extracts tide information from `http://tides.mobilegeographics.com/` into a `data.frame`. The presence of XLM package is required for this function.

Usage

```
tide.info(file = NULL, year = as.POSIXlt(Sys.time())$year + 1900,  
         location = 0, latitude = NA, longitude = NA, tz = "")
```

Arguments

<code>file</code>	An html file from the site <code>http://tides.mobilegeographics.com/</code>
<code>year</code>	Year to get the calendar
<code>location</code>	Code based on <code>http://tides.mobilegeographics.com/</code>
<code>latitude</code>	The latitude of the tide information
<code>longitude</code>	The longitude of the tide information
<code>tz</code>	Timezone

Details

`tide.info` gets the annual tide calendar for one particular location.

Value

Return a `data.frame` with tide calendar:
Level is the tide level, Tide is the High or Low Tide information and Date.Time is the date/time in POSIXlt format.

Author(s)

Marc Girondot <marc.girondot@u-psud.fr>

See Also

Other Periodic patterns of indices: [index.periodic](#), [minmax.periodic](#), [moon.info](#), [sun.info](#)

Examples

```
## Not run:
library("HelpersMG")
lat <- 5.74
long <- -54
Awala2004 <- tide.info(year=2004, longitude=long, latitude=lat, tz="America/Cayenne")
with(Awala2004, plot(Date.Time, Level, bty="n", las=1, type="l",
xlab=paste("Year", as.POSIXlt(Date.Time[1])$year+1900),
ylab="Tide level in m"))

## 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.

Usage

```
wget(url = stop("At least one internet address is required"), ...)
```

Arguments

<code>url</code>	The url where to download file
<code>...</code>	The parameters send to <code>download.file()</code>

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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