Package: bfw (via r-universe)

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Title Bayesian Framework for Computational Modeling

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Description Derived from the work of Kruschke (2015, <ISBN:9780124058880>), the present package aims to provide a framework for conducting Bayesian analysis using Markov chain Monte Carlo (MCMC) sampling utilizing the Just Another Gibbs Sampler ('JAGS', Plummer, 2003, <https://mcmc-jags.sourceforge.io>). The initial version includes several modules for conducting Bayesian equivalents of chi-squared tests, analysis of variance (ANOVA), multiple (hierarchical) regression, softmax regression, and for fitting data (e.g., structural equation modeling).

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BugReports https://github.com/oeysan/bfw/issues/

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`AddNames` *Add Names*

Description

Add names to columns from naming list

Usage

```
AddNames(
  par,
  job.names,
  job.group = NULL,
  keep.par = TRUE,
  names.only = FALSE,
  ...
)
```

Arguments

`par`	defined parameter to analyze (e.g., "cor[1,2]")
`job.names`	names of all parameters in analysis, Default: NULL
`job.group`	for some hierarchical models with several layers of parameter names (e.g., latent and observed parameters), Default: NULL

keep.par	logical, indicating whether or not to keep parameter name (e.g., "cor[1,2]"), Default: TRUE
names.only	logical, indicating whether or not to return vector (TRUE) or string with separator (e.g., "cor[1,2]: A vs. B"), Default: FALSE
...	further arguments passed to or from other methods

Examples

```
par <- "cor[1,2]"
job.names <- c("A","B")
AddNames(par, job.names, keep.par = TRUE)
# [1]  "cor[1,2]: A vs. B"
AddNames(par, job.names, keep.par = FALSE)
# [1]  "A vs. B"
AddNames(par, job.names, names.only = TRUE)
# [1]  "A" "B"
```

---

bfw *Settings*

Description

main settings for bfw

Usage

```
bfw(
  job.title = NULL,
  job.group = NULL,
  jags.model,
  jags.seed = NULL,
  jags.method = NULL,
  jags.chains = NULL,
  custom.function = NULL,
  custom.model = NULL,
  params = NULL,
  saved.steps = 10000,
  thinned.steps = 1,
  adapt.steps = NULL,
  burnin.steps = NULL,
  initial.list = list(),
  custom.name = NULL,
  project.name = "Project",
  project.dir = "Results/",
  project.data = NULL,
  time.stamp = TRUE,
  save.data = FALSE,
```

```
  data.set = "AllData",
  data.format = "csv",
  raw.data = FALSE,
  run.robust = FALSE,
  merge.MCMC = FALSE,
  run.diag = FALSE,
  sep = ",",
  silent = FALSE,
  ...
)
```

Arguments

job.title	title of analysis, Default: NULL
job.group	for some hierarchical models with several layers of parameter names (e.g., latent and observed parameters), Default: NULL
jags.model	specify which module to use
jags.seed	specify seed to replicate a analysis, Default: NULL
jags.method	specify method for JAGS (e.g., parallel or simple), Default: NULL
jags.chains	specify specify number of chains for JAGS, Default: NULL
custom.function	custom function to use (e.g., defined function, external R file or string with function), Default: NULL
custom.model	define a custom model to use (e.g., string or text file (.txt), Default: NULL
params	define parameters to observe, Default: NULL
saved.steps	define the number of iterations/steps/chains in the MCMC simulations, Default: 10000
thinned.steps	save every kth step of the original saved.steps, Default: 1
adapt.steps	the number of adaptive iterations to use at the start of each simulation, Default: NULL
burnin.steps	the number of burnin iterations, NOT including the adaptive iterations to use for the simulation, Default: NULL
initial.list	initial values for analysis, Default: list()
custom.name	custom name of project, Default: NULL
project.name	name of project, Default: 'Project'
project.dir	define where to save data, Default: 'Results/'
project.data	define data to use for analysis (e.g., csv, rda, custom data.frame or matrix, or data included in package, Default: NULL
time.stamp	logical, indicating whether or not to append unix time stamp to file name, Default: TRUE
save.data	logical, indicating whether or not to save data, Default: FALSE
data.set	define subset of data, Default: 'AllData'

data.format	define what data format is being used, Default: 'csv'
raw.data	logical, indicating whether or not to use unprocessed data, Default: FALSE
run.robust	logical, indicating whether or not robust analysis, Default: FALSE
merge.MCMC	logical, indicating whether or not to merge MCMC chains, Default: FALSE
run.diag	logical, indicating whether or not to run diagnostics, Default: FALSE
sep	symbol to separate data (e.g., comma-delimited), Default: ','
silent	logical, indicating whether or not to run analysis without output, Default: FALSE
...	further arguments passed to or from other methods

Details

Settings act like the main framework for bfw, connecting function, model and JAGS.

Value

data from MCMC RunMCMC

See Also

head,modifyList,capture.output

CapWords *Capitalize Words*

Description

capitalize the first letter in each words in a string

Usage

```
CapWords(s, strict = FALSE)
```

Arguments

s	string
strict	logical, indicating whether or not string it set to title case , Default: FALSE

Value

returns capitalized string

Examples

```
CapWords("example eXAMPLE", FALSE)
# [1] "Example EXAMPLE"
CapWords("example eXAMPLE", TRUE)
# [1] "Example Example"
```

Cats *Dataset with Cats*

Description

Shamelessly adapted from Field (2017).

Usage

```
Cats
```

Format

A data frame with 2000 rows and 4 variables:

`Reward` integer Food or Affection

`Dance` integer Yes or No

`Alignment` integer Good or Evil

`Ratings` double Cats rate their owners (average of multiple seven-point Likert-type scale (1 = Hate ... 7 = Love)

Details

Example data for BFW

ChangeNames *Change Names*

Description

Change names, colnames or rownames of single items or a list of items

Usage

```
ChangeNames(
  x,
  names,
  single.items = FALSE,
  row.names = FALSE,
  param = NULL,
  where = NULL,
  environment = NULL
)
```

Arguments

x	list, vector, matrix, dataframe or a list of such items
names	names to insert
single.items	logical, indicating whether or not to use names rather than colnames or rownames, Default: FALSE
row.names	logical, indicating whether or not to use rownames rather than colnames, Default: FALSE
param	Variable name, Default: NULL
where	select parents, Default: NULL
environment	select reference environment, Default: NULL

Value

returns Named items # ABC <- c("1","2","3") # "1" "2" "3" # ChangeNames(ABC, names = c("A","B","C") , single.items = TRUE) # A B C # "1" "2" "3"

ComputeHDI *Compute HDI*

Description

Compute highest density interval (HDI) from posterior output

Usage

```
ComputeHDI(data, credible.region)
```

Arguments

data	data to compute HDI from
credible.region	summarize uncertainty by defining a region of most credible values (e.g., 95 percent of the distribution), Default: 0.95

Details

values within the HDI have higher probability density than values outside the HDI, and the values inside the HDI have a total probability equal to the credible region (e.g., 95 percent).

Value

Return HDI

Examples

```
set.seed(1)
data <-rnorm(100,0,1)
credible.region <- 0.95
ComputeHDI(data,credible.region)
# HDIlo HDIhi
# -1.99 1.60
```

`ContrastNames` *Contrast Names*

Description

utilize the AddNames function to create contrast names

Usage

```
ContrastNames(items, job.names, col.names)
```

Arguments

`items`	items to create names for
`job.names`	names of all parameters in analysis, Default: NULL
`col.names`	columns in MCMC to create names from

`DiagMCMC` *Diagnose MCMC*

Description

MCMC convergence diagnostics

Usage

```
DiagMCMC(
  data.MCMC,
  par.name,
  job.names,
  job.group,
  credible.region = 0.95,
  monochrome = TRUE,
  plot.colors = c("#495054", "#e3e8ea")
)
```

Arguments

data.MCMC	MCMC chains to diagnose
par.name	parameter to analyze
job.names	names of all parameters in analysis, Default: NULL
job.group	for some hierarchical models with several layers of parameter names (e.g., latent and observed parameters), Default: NULL
credible.region	summarize uncertainty by defining a region of most credible values (e.g., 95 percent of the distribution), Default: 0.95
monochrome	logical, indicating whether or not to use monochrome colors, else use DistinctColors, Default: TRUE
plot.colors	range of color to use, Default: c("#495054", "#e3e8ea")

Value

list of diagnostic plots

See Also

dev.new,colorRampPalette,recordPlot,graphics.off,dev.list,dev.off par,layout,plot.new,matplot,abline,text
traceplot,gelman.plot,effectiveSize sd,acf,density

DistinctColors *Distinct Colors*

Description

create vector containing Hex color codes

Usage

```
DistinctColors(range, random = FALSE)
```

Arguments

range	number of colors as sequence
random	logical, indicating whether or not to provide random colors, Default: FALSE

Examples

```
DistinctColors(1:3)
# [1] "#FFFF00" "#1CE6FF" "#FF34FF"
set.seed(1)
DistinctColors(1:3, TRUE)
# [1] "#575329" "#CB7E98" "#D86A78"
```

ETA *ETA*

Description

Print estimated time for arrival (ETA)

Usage

```
ETA(start.time, i, total, results = NULL)
```

Arguments

start.time	start time (preset variable with Sys.time())
i	incremental steps towards total
total	total number of steps
results	message to display, Default: NULL

See Also

flush.console

FileName *File Name*

Description

simple function to construct a file name for data

Usage

```
FileName(
  project = "Project",
  subset = NULL,
  type = NULL,
  name = NULL,
  unix = TRUE,
  ...
)
```

Arguments

project	name of project, Default: 'Project'
subset	define subset of data, Default: NULL
type	type of data, Default: NULL
name	save name, Default: NULL
unix	logical, indicating whether or not to append unix timestamp, Default: TRUE
...	further arguments passed to or from other methods

Examples

```
FileName()
# [1] "Project-Name-1528834963"

FileName(project = "Project" ,
        subset = "subset" ,
        type = "longitudinal" ,
        name = "cheese",
        unix = FALSE)
# [1] "Projectsubset-longitudinal-cheese"
```

FindEnvironment *Find Environment*

Description

Find the environment of a selected variable.

Usage

```
FindEnvironment(x, where = NULL)
```

Arguments

x	any type of named object
where	select reference environment, Default: NULL

Value

returns Found environment, Default: R_GlobalEnv.

`FlattenList` *Flatten List*

Description

flatten a nested list into a single list

Usage

```
FlattenList(li, rm.duplicated = TRUE, unname.li = TRUE, rm.empty = TRUE)
```

Arguments

`li`	list to flatten
`rm.duplicated`	logical, indicating whether or not to remove duplicated lists, Default: TRUE
`unname.li`	logical, indicating whether or not to unname lists, Default: TRUE
`rm.empty`	logical, indicating whether or not to remove empty lists, Default: TRUE

Examples

```
li <- list(LETTERS[1:3],
           list(letters[1:3],
                list(LETTERS[4:6])),
           DEF = letters[4:6],
           LETTERS[1:3],
           list() # Emtpy list
)
print(li)
# [[1]]
# [1] "A" "B" "C"
#
# [[2]]
# [[2]][[1]]
# [1] "a" "b" "c"
#
# [[2]][[2]]
# [[2]][[2]][[1]]
# [1] "D" "E" "F"
#
#
#
# $DEF
# [1] "d" "e" "f"
#
# [[4]]
# [1] "A" "B" "C"
#
# [[5]]
# list()
```

```
FlattenList(li)
# [[1]]
# [1] "A" "B" "C"
#
# [[2]]
# [1] "a" "b" "c"
#
# [[3]]
# [1] "D" "E" "F"
#
# [[4]]
# [1] "d" "e" "f"
```

GammaDist *Gamma Distribution*

Description

compute gamma distribution (shape and rate) from mode and standard deviation

Usage

```
GammaDist(mode, sd)
```

Arguments

mode	mode from data
sd	standard deviation from data

Examples

```
GammaDist(1,0.5)
# $shape
# [1] 5.828427
# $rate
# [1] 4.828427
```

GetRange *Get Range*

Description

simple function to extract columns from data frame

Usage

```
GetRange(var, range = 1:8, df)
```

Arguments

var	variable of interest (e.g., V)
range	range of variables with same stem name (e.g., V1, V2, ..., V8) , Default: 1:8
df	data to extract from

Examples

```
data <- as.data.frame(matrix(1:80,ncol=8))
GetRange("V", c(1,4), data)
#    V1 V4
# 1   1 31
# 2   2 32
# 3   3 33
# 4   4 34
# 5   5 35
# 6   6 36
# 7   7 37
# 8   8 38
# 9   9 39
# 10 10 40
```

Interleave *Interleave*

Description

mix vectors by alternating between them

Usage

```
Interleave(a, b)
```

Arguments

a	first vector
b	second vector

Value

mixed vector

Examples

```
a <- 1:3
b <- LETTERS[1:3]
Interleave(a,b)
# [1] "1" "A" "2" "B" "3" "C"
```

`InverseHDI` *Compute Inverse HDI*

Description

Compute inverse cumulative density function of the distribution

Usage

```
InverseHDI(
  beta,
  shape1,
  shape2,
  credible.region = 0.95,
  tolerance = 0.00000001
)
```

Arguments

`beta`	density, distribution function, quantile function and random generation for the Beta distribution with parameters shape1 and shape2
`shape1`	non-negative parameter of the Beta distribution.
`shape2`	non-negative parameter of the Beta distribution.
`credible.region`	summarize uncertainty by defining a region of most credible values (e.g., 95 percent of the distribution), Default: 0.95
`tolerance`	the desired accuracy, Default: 1e-8

Details

values within the HDI have higher probability density than values outside the HDI, and the values inside the HDI have a total probability equal to the credible region (e.g., 95 percent).

Value

Return HDI

See Also

`Beta`,`optimize`

Examples

```
InverseHDI( qbeta , 554 , 149 )
# HDIlo HDIhi
# 0.758 0.818
```

Layout *Layout*

Description

collection of layout sizes

Usage

```
Layout(x = "a4", layout.inverse = FALSE)
```

Arguments

x	type of layout, Default: 'a4'
layout.inverse	logical, indicating whether or not to inverse layout (e.g., landscape) , Default: FALSE

Value

width and height of select medium

Examples

```
Layout()
# [1]  8.3 11.7
```

MatrixCombn *Matrix Combinations*

Description

Create matrices from combinations of columns

Usage

```
MatrixCombn(
  matrix,
  first.stem,
  last.stem = NULL,
  q.levels,
  rm.last = TRUE,
  row.means = TRUE
)
```

Arguments

matrix	matrix to combine
first.stem	first name of columns to use (e.g., "m" for mean)
last.stem	optional last name of columns to use (e.g., "p" for proportions) , Default: NONE
q.levels	number of levels per column
rm.last	logical, indicating whether or not to remove last combination (i.e., m1m2m3m4) , Default: TRUE
row.means	logical, indicating whether or not to compute row means from combined columns, else use row sums, Default: TRUE

MergeMCMC *Merge MCMC*

Description

Merge two or more MCMC simulations

Usage

```
MergeMCMC(pat, project.dir = "Results/", data.sets)
```

Arguments

pat	pattern to select MCMC chain from
project.dir	define where to save data, Default: 'Results/'
data.sets	data sets to combine

Value

Merged MCMC chains

See Also

head combine.mcmc

MultiGrep *Multi Grep*

Description

Use multiple patterns from vector to find element in another vector, with option to remove certain patterns

Usage

```
MultiGrep(find, from, remove = NULL, value = TRUE)
```

Arguments

find	vector to find
from	vector to find from
remove	variables to remove, Default: NULL
value	logical, if TRUE returns value, Default: TRUE

Normalize *Normalize*

Description

simple function to normalize data

Usage

```
Normalize(x)
```

Arguments

x	numeric vector to normalize

Examples

```
Normalize(1:10)
# [1] 0.0182 0.0364 0.0545 0.0727 0.0909
# 0.1091 0.1273 0.1455 0.1636 0.1818
```

PadVector *Pad Vector*

Description

Pad a numeric vector according to the highest value

Usage

```
PadVector(v)
```

Arguments

v	numeric vector to pad

Examples

```
PadVector(1:10)
# [1] "01" "02" "03" "04" "05" "06" "07" "08" "09" "10"
```

ParseNumber *Parse Numbers*

Description

simple function to extract numbers from string/vector

Usage

```
ParseNumber(x, digits = FALSE)
```

Arguments

x	string or vector
digits	logical, indicating whether or not to extract decimals, Default: FALSE

See Also

na.omit

Examples

```
ParseNumber("String1WithNumbers2")
# [1] 1 2
```

ParsePlot *Parse Plot*

Description

Display and/or save plots

Usage

```
ParsePlot(
  plot.data,
  project.dir = "Results/",
  project.name = FileName(name = "Print"),
  graphic.type = "pdf",
  plot.size = "15,10",
  scaling = 100,
  plot.aspect = NULL,
  save.data = FALSE,
  vector.graphic = FALSE,
  point.size = 12,
  font.type = "serif",
  one.file = TRUE,
  ppi = 300,
  units = "in",
  layout = "a4",
  layout.inverse = FALSE,
  return.files = FALSE,
  ...
)
```

Arguments

plot.data	a list of plots
project.dir	define where to save data, Default: 'Results/'
project.name	define name of project, Default: 'FileName(name="Print")'
graphic.type	type of graphics to use (e.g., pdf, png, ps), Default: 'pdf'
plot.size	size of plot, Default: '15,10'
scaling	scale size of plot, Default: 100
plot.aspect	aspect of plot, Default: NULL
save.data	logical, indicating whether or not to save data, Default: FALSE
vector.graphic	logical, indicating whether or not visualizations should be vector or raster graphics, Default: FALSE
point.size	point size used for visualizations, Default: 12
font.type	font type used for visualizations, Default: 'serif'

one.file	logical, indicating whether or not visualizations should be placed in one or several files, Default: TRUE
ppi	define pixel per inch used for visualizations, Default: 300
units	define unit of length used for visualizations, Default: 'in'
layout	define a layout size for visualizations, Default: 'a4'
layout.inverse	logical, indicating whether or not to inverse layout (e.g., landscape) , Default: FALSE
return.files	logical, indicating whether or not to return saved file names
...	further arguments passed to or from other methods

See Also

dev, png, ps.options, recordPlot head readPNG par, plot, rasterImage read_pptx, add_slide, ph_with dml

Examples

```
# Create three plots
plot.data <- lapply(1:3, function (i) {
  # Open new device
  grDevices::dev.new()
  # Print plot
  plot(1:i)
  # Record plot
  p <- grDevices::recordPlot()
  # Turn off graphics device drive
  grDevices::dev.off()
  return (p)
} )

# Print plots
ParsePlot(plot.data)
```

PlotCirclize *Circlize Plot*

Description

Create a circlize plot

Usage

```
PlotCirclize(
  data,
  category.spacing = 1.2,
  category.inset = c(-0.4, 0),
  monochrome = TRUE,
```

```
  plot.colors = c("#CCCCCC", "#DEDEDE"),
  font.type = "serif"
)
```

Arguments

data	data for circlize plot
category.spacing	spacing between category items , Default: 1.25
category.inset	inset of category items form plot , Default: c(-0.5, 0)
monochrome	logical, indicating whether or not to use monochrome colors, else use Distinct-Colors, Default: TRUE
plot.colors	range of color to use, Default: c("#CCCCCC", "#DEDEDE")
font.type	font type used for visualizations, Default: 'serif'

See Also

dev, recordPlot legend circos.par, chordDiagram, circos.trackPlotRegion, circos.clear

---

PlotData *Plot Data*

Description

Plot data as violin plot visualizing density, box plots to display HDI, whiskers to display standard deviation

Usage

```
PlotData(data, data.type = "Mean", ...)
```

Arguments

data	data to plot data from
data.type	define what kind of data is being used, Default: 'Mean'
...	further arguments passed to or from other methods

PlotMean *Plot Mean*

Description

Create a (repeated) mean plot

Usage

```
PlotMean(
  data,
  monochrome = TRUE,
  plot.colors = c("#495054", "#e3e8ea"),
  font.type = "serif",
  run.repeated = FALSE,
  run.split = FALSE,
  y.split = FALSE,
  ribbon.plot = TRUE,
  y.text = "Score",
  x.text = NULL,
  remove.x = FALSE
)
```

Arguments

data	MCMC data to plot
monochrome	logical, indicating whether or not to use monochrome colors, else use DistinctColors, Default: TRUE
plot.colors	range of color to use, Default: c("#495054", "#e3e8ea")
font.type	font type used for visualizations, Default: 'serif'
run.repeated	logical, indicating whether or not to use repeated measures plot, Default: FALSE
run.split	logical, indicating whether or not to use split violin plot and compare distribution between groups, Default: FALSE
y.split	logical, indicating whether or not to split within (TRUE) or between groups, Default: FALSE
ribbon.plot	logical, indicating whether or not to use ribbon plot for HDI, Default: TRUE
y.text	label on y axis, Default: 'Score'
x.text	label on x axis, Default: NULL
remove.x	logical, indicating whether or not to show x.axis information, Default: FALSE

See Also

ggproto, ggplot2-ggproto, aes, margin, geom_boxplot, geom_crossbar, geom_path, geom_ribbon, geom_violin, ggplot, scale_manual, scale_x_discrete, theme, layer, labs arrange, rbind.fill zero_range grid.grob, grobName, unit approxfun colorRamp

PlotNominal *Plot Nominal*

Description

Create a nominal plot

Usage

```
PlotNominal(
  data,
  monochrome = TRUE,
  plot.colors = c("#CCCCCC", "#DEDEDE"),
  font.type = "serif",
  bar.dodge = 0.6,
  bar.alpha = 0.7,
  bar.width = 0.4,
  bar.extras.dodge = 0,
  bar.border = "black",
  bar.label = FALSE,
  bar.error = TRUE,
  use.cutoff = FALSE,
  diff.cutoff = 1,
  q.items = NULL
)
```

Arguments

data	MCMC data to plot
monochrome	logical, indicating whether or not to use monochrome colors, else use Distinct-Colors, Default: TRUE
plot.colors	range of color to use, Default: c("#CCCCCC", "#DEDEDE")
font.type	font type used for visualizations, Default: 'serif'
bar.dodge	distance between within bar plots, Default: 0.6
bar.alpha	transparency for bar plot, Default: 0.7
bar.width	width of bar plot, Default: 0.4
bar.extras.dodge	dodge of error bar and label, Default: 0
bar.border	color of the bar border, Default: 'black'
bar.label	logical, indicating whether or not to show bar labels, Default: TRUE
bar.error	logical, indicating whether or not to show error bars, Default: TRUE
use.cutoff	logical, indicating whether or not to use a cutoff for keeping plots, Default: FALSE
diff.cutoff	if using a cutoff, determine the percentage that expected and observed values should differ, Default: 1
q.items	which variables should be used in the plot. Defaults to all , Default: NULL

See Also

aes,margin,geom_crossbar,ggplot,scale_manual,theme

PlotParam *Plot Param*

Description

Create a density plot with parameter values

Usage

```
PlotParam(
  data,
  param,
  ROPE = FALSE,
  monochrome = TRUE,
  plot.colors = c("#495054", "#e3e8ea"),
  font.type = "serif",
  font.size = 4.5,
  rope.line = -0.2,
  rope.tick = -0.1,
  rope.label = -0.35,
  line.size = 0.5,
  dens.zero.col = "black",
  dens.mean.col = "white",
  dens.median.col = "white",
  dens.mode.col = "black",
  dens.rope.col = "black",
  scale = FALSE,
  y.limits = NULL,
  y.breaks = NULL,
  x.limits = NULL,
  x.breaks = NULL,
  plot.title = NULL
)
```

Arguments

data	MCMC data to plot
param	parameter of interest
ROPE	plot ROPE values, Default: FALSE
monochrome	logical, indicating whether or not to use monochrome colors, else use Distinct-Colors, Default: TRUE
plot.colors	range of color to use, Default: c("#495054", "#e3e8ea")

font.type	font type used for visualizations, Default: 'serif'
font.size	font size, Default: 4.5
rope.line	size of ROPE lien, Default: -0.2
rope.tick	distance to ROPE tick, Default: -0.1
rope.label	distance to ROPE label, Default: -0.35
line.size	overall line size, Default: 0.5
dens.zero.col	colour of line indicating zero, Default: 'black'
dens.mean.col	colour of line indicating mean value, Default: 'white'
dens.median.col	colour of line indicating median value, Default: 'white'
dens.mode.col	colour of line indicating mode value, Default: 'black'
dens.rope.col	colour of line indicating ROPE value, Default: 'black'
scale	scale x and y axis, Default: FALSE
y.limits	vector of y limits, Default: NULL
y.breaks	vector of y breaks, Default: NULL
x.limits	= vector of x limits, Default: NULL
x.breaks	= vector of x breaks, Default: NULL
plot.title	= title of plot, Default: NULL

Value

Density plot of parameter values

See Also

mutate,group_by,join,select,slice,filter approxfun aes,margin,geom_density,geom_polygon,geom_segment,geom_

ReadFile *Read File*

Description

opens connection to a file

Usage

```
ReadFile(
  file = NULL,
  path = "models/",
  package = "bfw",
  type = "string",
  sep = ",",
  data.format = "txt",
  custom = FALSE
)
```

Arguments

file	name of file, Default: NULL
path	path to file, Default: 'models/'
package	choose package to open from, Default: 'bfw'
type	Type of file (i.e., text or data), Default: 'string'
sep	symbol to separate data (e.g., comma-delimited), Default: ','
data.format	define what data format is being used, Default: 'csv'
custom	logical, indicating whether or not to use custom file, , Default: FALSE

See Also

read.csv

Examples

```
# Print JAGS model for bernoulli trials
cat(ReadFile("stats_bernoulli"))
# model {
#   for (i in 1:n){
#     x[i] ~ dbern(theta)
#   }
#   theta ~ dunif(0,1)
# }
```

RemoveEmpty *Remove Empty*

Description

Remove empty elements in vector

Usage

```
RemoveEmpty(x)
```

Arguments

x	vector to eliminate NA and blanks

Examples

```
RemoveEmpty( c("",NA,"","Remains") )
# [1] "Remains"
```

RemoveGarbage *Remove Garbage*

Description

Remove variable(s) and remove garbage from memory

Usage

```
RemoveGarbage(v)
```

Arguments

v	variables to remove

RemoveSpaces *Remove Spaces*

Description

simple function to remove whitespace

Usage

```
RemoveSpaces(x)
```

Arguments

x	string

Examples

```
RemoveSpaces("  No More S p a c e s")
# [1] "NoMoreSpaces"
```

RunContrasts *Run Contrasts*

Description

Compute contrasts from mean and standard deviation (Cohen's d) or frequencies (odds ratio)

Usage

```
RunContrasts(contrast.type, q.levels, use.contrast, contrasts, data, job.names)
```

Arguments

contrast.type	type of contrast: "m" indicate means and standard deviations, "o" indicate frequency
q.levels	Number of levels of each variable/column
use.contrast	choose from "between", "within" and "mixed". Between compare groups at different conditions. Within compare a group at different conditions. Mixed compute all comparisons
contrasts	specified contrasts columns
data	data to compute contrasts from
job.names	names of all parameters in analysis, Default: NULL

See Also

combn

RunMCMC *Run MCMC*

Description

Conduct MCMC simulations using JAGS

Usage

```
RunMCMC(
  jags.model,
  params = NULL,
  name.list,
  data.list,
  initial.list = list(),
  run.contrasts = FALSE,
  use.contrast = "between",
```

```
  contrasts = NULL,
  custom.contrast = NULL,
  run.ppp = FALSE,
  k.ppp = 10,
  n.data,
  credible.region = 0.95,
  save.data = FALSE,
  ROPE = NULL,
  merge.MCMC = FALSE,
  run.diag = FALSE,
  param.diag = NULL,
  sep = ",",
  monochrome = TRUE,
  plot.colors = c("#495054", "#e3e8ea"),
  graphic.type = "pdf",
  plot.size = "15,10",
  scaling = 100,
  plot.aspect = NULL,
  vector.graphic = FALSE,
  point.size = 12,
  font.type = "serif",
  one.file = TRUE,
  ppi = 300,
  units = "in",
  layout = "a4",
  layout.inverse = FALSE,
  ...
)
```

Arguments

jags.model	specify which module to use
params	define parameters to observe, Default: NULL
name.list	list of names
data.list	list of data
initial.list	initial values for analysis, Default: list()
run.contrasts	logical, indicating whether or not to run contrasts, Default: FALSE
use.contrast	choose from "between", "within" and "mixed". Between compare groups at different conditions. Within compare a group at different conditions. Mixed compute all comparisons, Default: "between",
contrasts	define contrasts to use for analysis (defaults to all) , Default: NULL
custom.contrast	define contrasts for custom models , Default: NULL
run.ppp	logical, indicating whether or not to conduct ppp analysis, Default: FALSE
k.ppp	run ppp for every kth length of MCMC chains, Default: 10
n.data	sample size for each parameter

credible.region
: summarize uncertainty by defining a region of most credible values (e.g., 95 percent of the distribution), Default: 0.95

save.data
: logical, indicating whether or not to save data, Default: FALSE

ROPE
: define range for region of practical equivalence (e.g., c(-0.05 , 0.05), Default: NULL

merge.MCMC
: logical, indicating whether or not to merge MCMC chains, Default: FALSE

run.diag
: logical, indicating whether or not to run diagnostics, Default: FALSE

param.diag
: define parameters to use for diagnostics, default equals all parameters, Default: NULL

sep
: symbol to separate data (e.g., comma-delimited), Default: ','

monochrome
: logical, indicating whether or not to use monochrome colors, else use Distinct-Colors, Default: TRUE

plot.colors
: range of color to use, Default: c("#495054", "#e3e8ea")

graphic.type
: type of graphics to use (e.g., pdf, png, ps), Default: 'pdf'

plot.size
: size of plot, Default: '15,10'

scaling
: scale size of plot, Default: 100

plot.aspect
: aspect of plot, Default: NULL

vector.graphic
: logical, indicating whether or not visualizations should be vector or raster graphics, Default: FALSE

point.size
: point size used for visualizations, Default: 12

font.type
: font type used for visualizations, Default: 'serif'

one.file
: logical, indicating whether or not visualizations should be placed in one or several files, Default: TRUE

ppi
: define pixel per inch used for visualizations, Default: 300

units
: define unit of length used for visualizations, Default: 'in'

layout
: define a layout size for visualizations, Default: 'a4'

layout.inverse
: logical, indicating whether or not to inverse layout (e.g., landscape) , Default: FALSE

...
: further arguments passed to or from other methods

Value

list containing MCMC chains , MCMC chains as matrix , summary of MCMC, list of name used, list of data, the jags model, running time of analysis and names of saved files

See Also

runjags.options,run.jags detectCores as.mcmc.list,varnames rbind.fill cor,cov,sd mvrnorm write.table

SingleString *Single String*

Description

determine whether input is a single string

Usage

```
SingleString(x)
```

Arguments

x	string

Value

true or false

Examples

```
A <- "This is a single string"
SingleString(A)
# [1] TRUE
is.character(A)
# [1] TRUE
B <- c("This is a vector" , "containing two strings")
SingleString(B)
# [1] FALSE
is.character(B)
# [1] TRUE
```

StatsBernoulli *Bernoulli Trials*

Description

Conduct bernoulli trials

Usage

```
StatsBernoulli(
  x = NULL,
  x.names = NULL,
  DF,
  params = NULL,
  initial.list = list(),
  ...
)
```

Arguments

x	predictor variable(s), Default: NULL
x.names	optional names for predictor variable(s), Default: NULL
DF	data for analysis
params	define parameters to observe, Default: NULL
initial.list	initial values for analysis, Default: list()
...	further arguments passed to or from other methods

See Also

complete.cases

Examples

```
## Create coin toss data: heads = 50 and tails = 50
#fair.coin<- as.matrix(c(rep("Heads",50),rep("Tails",50)))
#colnames(fair.coin) <- "X"
#fair.coin <- bfw(project.data = fair.coin,
#                 x = "X",
#                 saved.steps = 50000,
#                 jags.model = "bernoulli",
#                 jags.seed = 100,
#                 ROPE = c(0.4,0.6),
#                 silent = TRUE)
#fair.coin.freq <- binom.test( 50000 * 0.5, 50000)

## Create coin toss data: heads = 20 and tails = 80
#biased.coin <- as.matrix(c(rep("Heads",20),rep("Tails",80)))
#colnames(biased.coin) <- "X"
#biased.coin <- bfw(project.data = biased.coin,
#                   x = "X",
#                   saved.steps = 50000,
#                   jags.model = "bernoulli",
#                   jags.seed = 101,
#                   initial.list = list(theta = 0.7),
#                   ROPE = c(0.4,0.6),
#                   silent = TRUE)
#biased.coin.freq <- binom.test( 50000 * 0.8, 50000)

## Print Bayesian and frequentist results of fair coin
#fair.coin$summary.MCMC[,c(3:6,9:12)]

## Mode       ESS     HDIlo     HDIhi    ROPElo    ROPEhi    ROPEin         n
## 0.505 50480.000     0.405     0.597     2.070     2.044    95.886   100.00

#sprintf("Frequentist: %.3f [%.3f , %.3f], p = %.3f" ,
#        fair.coin.freq$estimate ,
#        fair.coin.freq$conf.int[1] ,
#        fair.coin.freq$conf.int[2] ,
#        fair.coin.freq$p.value)
```

```
## [1] "Frequentist: 0.500 [0.496 , 0.504], p = 1.000"

## Print Bayesian and frequentist results of biased coin
#biased.coin$summary.MCMC[,c(3:6,9:12)]

## Mode       ESS     HDIlo     HDIhi    ROPElo    ROPEhi    ROPEin         n
## 0.803 50000.000     0.715     0.870     0.000    99.996     0.004   100.000

#sprintf("Frequentist: %.3f [%.3f , %.3f], p = %.3f" ,
#        biased.coin.freq$estimate ,
#        biased.coin.freq$conf.int[1] ,
#        biased.coin.freq$conf.int[2] ,
#        biased.coin.freq$p.value)

## [1] "Frequentist: 0.800 [0.796 , 0.803], p = 0.000"
```

StatsCovariate *Covariate*

Description

Covariate estimations (including correlation and Cronbach's alpha)

Usage

```
StatsCovariate(
  y = NULL,
  y.names = NULL,
  x = NULL,
  x.names = NULL,
  DF,
  params = NULL,
  job.group = NULL,
  initial.list = list(),
  jags.model,
  ...
)
```

Arguments

y	criterion variable(s), Default: NULL
y.names	optional names for criterion variable(s), Default: NULL
x	predictor variable(s), Default: NULL
x.names	optional names for predictor variable(s), Default: NULL
DF	data to analyze
params	define parameters to observe, Default: NULL

job.group	for some hierarchical models with several layers of parameter names (e.g., latent and observed parameters), Default: NULL
initial.list	initial values for analysis, Default: list()
jags.model	specify which module to use
...	further arguments passed to or from other methods

Value

covariate, correlation and (optional) Cronbach's alpha

See Also

complete.cases

Examples

```
## Create normal distributed data with mean = 0 and standard deviation = 1
### r = 0.5
#data <- MASS::mvrnorm(n=100,
#                      mu=c(0, 0),
#                      Sigma=matrix(c(1, 0.5, 0.5, 1), 2),
#                      empirical=TRUE)
## Add names
#colnames(data) <- c("X","Y")
## Create noise with mean = 10 / -10 and sd = 1
### r = -1.0
#noise <- MASS::mvrnorm(n=2,
#                       mu=c(10, -10),
#                       Sigma=matrix(c(1, -1, -1, 1), 2),
#                       empirical=TRUE)
## Combine noise and data
#biased.data <- rbind(data,noise)
#
#
## Run analysis on normal distributed data
#mcmc <- bfw(project.data = data,
#            y = "X,Y",
#            saved.steps = 50000,
#            jags.model = "covariate",
#            jags.seed = 100,
#            silent = TRUE)
## Run robust analysis on normal distributed data
#mcmc.robust <- bfw(project.data = data,
#                   y = "X,Y",
#                   saved.steps = 50000,
#                   jags.model = "covariate",
#                   run.robust = TRUE,
#                   jags.seed = 101,
#                   silent = TRUE)
## Run analysis on data with outliers
#biased.mcmc <- bfw(project.data = biased.data,
```

```
#                   y = "X,Y",
#                   saved.steps = 50000,
#                   jags.model = "covariate",
#                   jags.seed = 102,
#                   silent = TRUE)
## Run robust analysis on data with outliers
#biased.mcmc.robust <- bfw(project.data = biased.data,
#                          y = "X,Y",
#                          saved.steps = 50000,
#                          jags.model = "covariate",
#                          run.robust = TRUE,
#                          jags.seed = 103,
#                          silent = TRUE)
## Print frequentist results
#stats::cor(data)[2]
## [1] 0.5
#stats::cor(noise)[2]
## [1] -1
#stats::cor(biased.data)[2]
## [1] -0.498
## Print Bayesian results
#mcmc$summary.MCMC
##                    Mean Median  Mode   ESS HDIlo HDIhi   n
## cor[1,1]: X vs. X 1.000  1.000 0.999     0 1.000 1.000 100
## cor[2,1]: Y vs. X 0.488  0.491 0.496 19411 0.337 0.633 100
## cor[1,2]: X vs. Y 0.488  0.491 0.496 19411 0.337 0.633 100
## cor[2,2]: Y vs. Y 1.000  1.000 0.999     0 1.000 1.000 100
#mcmc.robust$summary.MCMC
##                    Mean Median  Mode   ESS HDIlo HDIhi   n
## cor[1,1]: X vs. X 1.00  1.000 0.999     0 1.000 1.000 100
## cor[2,1]: Y vs. X 0.47  0.474 0.491 18626 0.311 0.626 100
## cor[1,2]: X vs. Y 0.47  0.474 0.491 18626 0.311 0.626 100
## cor[2,2]: Y vs. Y 1.00  1.000 0.999     0 1.000 1.000 100
#biased.mcmc$summary.MCMC
##                     Mean Median   Mode   ESS  HDIlo  HDIhi   n
## cor[1,1]: X vs. X  1.000  1.000  0.999     0  1.000  1.000 102
## cor[2,1]: Y vs. X -0.486 -0.489 -0.505 19340 -0.627 -0.335 102
## cor[1,2]: X vs. Y -0.486 -0.489 -0.505 19340 -0.627 -0.335 102
## cor[2,2]: Y vs. Y  1.000  1.000  0.999     0  1.000  1.000 102
#biased.mcmc.robust$summary.MCMC
##                    Mean Median  Mode   ESS HDIlo HDIhi   n
## cor[1,1]: X vs. X 1.000  1.000 0.999     0 1.000 1.000 102
## cor[2,1]: Y vs. X 0.338  0.343 0.356 23450 0.125 0.538 102
## cor[1,2]: X vs. Y 0.338  0.343 0.356 23450 0.125 0.538 102
```

`StatsFit` *Fit Data*

Description

Apply latent or observed models to fit data (e.g., SEM, CFA, mediation)

Usage

```
StatsFit(
  latent = NULL,
  latent.names = NULL,
  observed = NULL,
  observed.names = NULL,
  additional = NULL,
  additional.names = NULL,
  DF,
  params = NULL,
  job.group = NULL,
  initial.list = list(),
  model.name,
  jags.model,
  custom.model = NULL,
  run.ppp = FALSE,
  run.robust = FALSE,
  ...
)
```

Arguments

latent	latenr variables, Default: NULL
latent.names	optional names for for latent variables, Default: NULL
observed	observed variable(s), Default: NULL
observed.names	optional names for for observed variable(s), Default: NULL
additional	supplemental parameters for fitted data (e.g., indirect pathways and total effect), Default: NULL
additional.names	optional names for supplemental parameters, Default: NULL
DF	data to analyze
params	define parameters to observe, Default: NULL
job.group	for some hierarchical models with several layers of parameter names (e.g., latent and observed parameters), Default: NULL
initial.list	initial values for analysis, Default: list()
model.name	name of model used
jags.model	specify which module to use
custom.model	define a custom model to use (e.g., string or text file (.txt), Default: NULL
run.ppp	logical, indicating whether or not to conduct ppp analysis, Default: FALSE
run.robust	logical, indicating whether or not robust analysis, Default: FALSE
...	further arguments passed to or from other methods

See Also

complete.cases

StatsKappa *Cohen's Kappa*

Description

Bayesian alternative to Cohen's kappa

Usage

```
StatsKappa(
  x = NULL,
  x.names = NULL,
  DF,
  params = NULL,
  initial.list = list(),
  ...
)
```

Arguments

x	predictor variable(s), Default: NULL
x.names	optional names for predictor variable(s), Default: NULL
DF	data to analyze
params	define parameters to observe, Default: NULL
initial.list	initial values for analysis, Default: list()
...	further arguments passed to or from other methods

See Also

complete.cases

Examples

```
## Simulate rater data
#Rater1 <- c(rep(0,20),rep(1,80))
#set.seed(100)
#Rater2 <- c(rbinom(20,1,0.1), rbinom(80,1,0.9))
#data <- data.frame(Rater1,Rater2)

#mcmc <- bfw(project.data = data,
#            x = "Rater1,Rater2",
#            saved.steps = 50000,
#            jags.model = "kappa",
#            jags.seed = 100,
#            silent = TRUE)

## Print frequentist and Bayesian kappa
```

```
#library(psych)
#psych::cohen.kappa(data)$confid[1,]
##  lower     estimate  upper
##  0.6137906 0.7593583 0.9049260
##' mcmc$summary.MCMC
##             Mean     Median    Mode      ESS   HDIlo    HDIhi    n
##  Kappa[1]:  0.739176 0.7472905 0.7634503 50657 0.578132 0.886647 100
```

`StatsMean` *Mean Data*

Description

Compute means and standard deviations.

Usage

```
StatsMean(
  y = NULL,
  y.names = NULL,
  x = NULL,
  x.names = NULL,
  DF,
  params = NULL,
  initial.list = list(),
  ...
)
```

Arguments

`y`	criterion variable(s), Default: NULL
`y.names`	optional names for criterion variable(s), Default: NULL
`x`	categorical variable(s), Default: NULL
`x.names`	optional names for categorical variable(s), Default: NULL
`DF`	User defined data frame, Default: NULL
`params`	define parameters to observe, Default: NULL
`initial.list`	Initial values for simulations, Default: list()
`...`	further arguments passed to or from other methods

Value

mean and standard deviation

`StatsMetric` *Predict Metric*

Description

Bayesian alternative to ANOVA

Usage

```
StatsMetric(
  y = NULL,
  y.names = NULL,
  x = NULL,
  x.names = NULL,
  DF,
  params = NULL,
  job.group = NULL,
  initial.list = list(),
  model.name,
  jags.model,
  custom.model = NULL,
  run.robust = FALSE,
  ...
)
```

Arguments

`y`	criterion variable(s), Default: NULL
`y.names`	optional names for criterion variable(s), Default: NULL
`x`	categorical variable(s), Default: NULL
`x.names`	optional names for categorical variable(s), Default: NULL
`DF`	data to analyze
`params`	define parameters to observe, Default: NULL
`job.group`	for some hierarchical models with several layers of parameter names (e.g., latent and observed parameters), Default: NULL
`initial.list`	initial values for analysis, Default: list()
`model.name`	name of model used
`jags.model`	specify which module to use
`custom.model`	define a custom model to use (e.g., string or text file (.txt), Default: NULL
`run.robust`	logical, indicating whether or not robust analysis, Default: FALSE
`...`	further arguments passed to or from other methods

See Also

`complete.cases`, `sd`, `aggregate`, `median` `head`

`StatsNominal` *Predict Nominal*

Description

Bayesian alternative to chi-square test

Usage

```
StatsNominal(
  x = NULL,
  x.names = NULL,
  DF,
  params = NULL,
  job.group = NULL,
  initial.list = list(),
  model.name,
  jags.model,
  custom.model = NULL,
  ...
)
```

Arguments

`x`	categorical variable(s), Default: NULL
`x.names`	optional names for categorical variable(s), Default: NULL
`DF`	data to analyze
`params`	define parameters to observe, Default: NULL
`job.group`	for some hierarchical models with several layers of parameter names (e.g., latent and observed parameters), Default: NULL
`initial.list`	initial values for analysis, Default: list()
`model.name`	name of model used
`jags.model`	specify which module to use
`custom.model`	define a custom model to use (e.g., string or text file (.txt), Default: NULL
`...`	further arguments passed to or from other methods

Examples

```
## Use cats data
# mcmc <- bfw(project.data = bfw::Cats,
#             x = "Reward,Dance,Alignment",
#             saved.steps = 50000,
#             jags.model = "nominal",
#             run.contrasts = TRUE,
#             jags.seed = 100)
```

```
## Print only odds-ratio and effect sizes
#    mcmc$summary.MCMC[ grep("Odds ratio|Effect",
#                        rownames(mcmc$summary.MCMC)) , c(3:7) ]
##                                                 Mode   ESS    HDIlo     HDIhi    n
## Effect size: Affection/Food vs. Evil/Good       0.12844 45222  0.00115   0.25510 2000
## Effect size: Affection/Food vs. No/Yes          1.05346 44304  0.90825   1.18519 2000
## Effect size: Affection/Food vs. No/Yes @ Evil   2.58578 30734  2.35471   2.85450 1299
## Effect size: Affection/Food vs. No/Yes @ Good  -0.51934 35316 -0.73443  -0.30726  701
## Effect size: Food/Affection vs. Evil/Good      -0.12844 45222 -0.25510  -0.00115 2000
## Effect size: Food/Affection vs. No/Yes         -1.05346 44304 -1.18519  -0.90825 2000
## Effect size: Food/Affection vs. No/Yes @ Evil  -2.58578 30734 -2.85450  -2.35471 1299
## Effect size: Food/Affection vs. No/Yes @ Good   0.51934 35316  0.30726   0.73443  701
## Effect size: No/Yes vs. Evil/Good               1.43361 43603  1.30715   1.55020 2000
## Effect size: Yes/No vs. Evil/Good              -1.43361 43603 -1.55020  -1.30715 2000
## Odds ratio: Affection/Food vs. Evil/Good        1.25432 45225  0.99311   1.57765 2000
## Odds ratio: Affection/Food vs. No/Yes           6.49442 44215  5.10392   8.46668 2000
## Odds ratio: Affection/Food vs. No/Yes @ Evil  104.20109 30523 66.55346 169.12331 1299
## Odds ratio: Affection/Food vs. No/Yes @ Good    0.36685 35417  0.25478   0.55982  701
## Odds ratio: Food/Affection vs. Evil/Good        0.77604 45245  0.62328   0.98904 2000
## Odds ratio: Food/Affection vs. No/Yes           0.14586 44452  0.11426   0.18982 2000
## Odds ratio: Food/Affection vs. No/Yes @ Evil    0.00848 31117  0.00527   0.01336 1299
## Odds ratio: Food/Affection vs. No/Yes @ Good    2.44193 35397  1.65204   3.63743  701
## Odds ratio: No/Yes vs. Evil/Good               13.12995 43500 10.58859  16.49207 2000
## Odds ratio: Yes/No vs. Evil/Good                0.07393 43739  0.05909   0.09221 2000
#
## The results indicate that evil cats are 13.13 times more likely than good cats to decline dancing
## Furthermore, when offered affection, evil cats are 104.20 times more likely to decline dancing,
## relative to evil cats that are offered food.
```

StatsRegression *Regression*

Description

Simple, multiple and hierarchical regression

Usage

```
StatsRegression(
  y = NULL,
  y.names = NULL,
  x = NULL,
  x.names = NULL,
  x.steps = NULL,
  x.blocks = NULL,
  DF,
  params = NULL,
  job.group = NULL,
  initial.list = list(),
```

```
  ...
)
```

Arguments

y	criterion variable(s), Default: NULL
y.names	optional names for criterion variable(s), Default: NULL
x	predictor variable(s), Default: NULL
x.names	optional names for predictor variable(s), Default: NULL
x.steps	define number of steps in hierarchical regression , Default: NULL
x.blocks	define which predictors are included in each step (e.g., for three steps "1,2,3") , Default: NULL
DF	data to analyze
params	define parameters to observe, Default: NULL
job.group	for some hierarchical models with several layers of parameter names (e.g., latent and observed parameters), Default: NULL
initial.list	initial values for analysis, Default: list()
...	further arguments passed to or from other methods

See Also

complete.cases

StatsSoftmax *Softmax Regression*

Description

Perform softmax regression (i.e., multinomial logistic regression)

Usage

```
StatsSoftmax(
  y = NULL,
  y.names = NULL,
  x = NULL,
  x.names = NULL,
  DF,
  params = NULL,
  job.group = NULL,
  initial.list = NULL,
  run.robust = FALSE,
  ...
)
```

Arguments

y	criterion variable(s), Default: NULL
y.names	optional names for criterion variable(s), Default: NULL
x	predictor variable(s), Default: NULL
x.names	optional names for predictor variable(s), Default: NULL
DF	data to analyze
params	define parameters to observe, Default: NULL
job.group	for some hierarchical models with several layers of parameter names (e.g., latent and observed parameters), Default: NULL
initial.list	initial values for analysis, Default: list()
run.robust	logical, indicating whether or not robust analysis, Default: FALSE
...	further arguments passed to or from other methods

See Also

complete.cases

Examples

```
## Conduct softmax regression on Cats data
### Reward is 0 = Food and 1 = Dance
### Sample 100 datapoints from Cats data
#mcmc <- bfw(project.data = bfw::Cats,
#            y = "Alignment",
#            x = "Ratings,Reward",
#            saved.steps = 50000,
#            jags.model = "softmax",
#            jags.seed = 100)
## Conduct binominal generalized linear model
#model <- glm(Alignment ~ Ratings + Reward, data=bfw::Cats, family = binomial(link="logit"))
## Print output from softmax
#mcmc$summary.MCMC
#
##                               Mean Median      Mode   ESS  HDIlo  HDIhi    n
##beta[1,1]: Evil vs. Ratings   0.000   0.00 -0.000607     0  0.000  0.000 2000
##beta[1,2]: Evil vs. Reward    0.000   0.00 -0.000607     0  0.000  0.000 2000
##beta[2,1]: Good vs. Ratings   1.289   1.29  1.283403 19614  1.187  1.387 2000
##beta[2,2]: Good vs. Reward    1.276   1.27  1.279209 20807  0.961  1.597 2000
##beta0[1]: Intercept: Evil     0.000   0.00 -0.000607     0  0.000  0.000 2000
##beta0[2]: Intercept: Good    -7.690  -7.68 -7.659198 17693 -8.472 -6.918 2000
##zbeta[1,1]: Evil vs. Ratings  0.000   0.00 -0.000607     0  0.000  0.000 2000
##zbeta[1,2]: Evil vs. Reward   0.000   0.00 -0.000607     0  0.000  0.000 2000
##zbeta[2,1]: Good vs. Ratings  2.476   2.47  2.464586 19614  2.280  2.664 2000
##zbeta[2,2]: Good vs. Reward   0.501   0.50  0.501960 20807  0.377  0.626 2000
##zbeta0[1]: Intercept: Evil    0.000   0.00 -0.000607     0  0.000  0.000 2000
##zbeta0[2]: Intercept: Good   -1.031  -1.03 -1.024178 22812 -1.185 -0.870 2000
#
## Print (truncated) output from GML
```

```
##                Estimate   Std. Error z value Pr(>|z|)
##(Intercept)     -6.39328    0.27255 -23.457  < 2e-16 ***
##Ratings          1.28480    0.05136  25.014  < 2e-16 ***
##RewardAffection  1.26975    0.16381   7.751  9.1e-15 ***
```

SumMCMC *Summarize MCMC*

Description

The function provide a summary of each parameter of interest (mean, median, mode, effective sample size (ESS), HDI and n)

Usage

```
SumMCMC(
  par,
  par.names,
  job.names = NULL,
  job.group = NULL,
  credible.region = 0.95,
  ROPE = NULL,
  n.data,
  ...
)
```

Arguments

par	defined parameter
par.names	parameter names
job.names	names of all parameters in analysis, Default: NULL
job.group	for some hierarchical models with several layers of parameter names (e.g., latent and observed parameters), Default: NULL
credible.region	summarize uncertainty by defining a region of most credible values (e.g., 95 percent of the distribution), Default: 0.95
ROPE	define range for region of practical equivalence (e.g., c(-0.05 , 0.05), Default: NULL
n.data	sample size for each parameter
...	further arguments passed to or from other methods

See Also

effectiveSize

SumToZero *Sum to Zero*

Description

Compute sum to zero values across all levels of a data matrix

Usage

```
SumToZero(q.levels, data, contrasts)
```

Arguments

q.levels	number of levels of each variable/column
data	data matrix to combine from
contrasts	specified contrasts columns

Examples

```
data <- matrix(c(1,2),ncol=2)
colnames(data) <- c("m1[1]","m1[2]")
SumToZero( 2 , data , contrasts = NULL )
#               b0[1] b1[1] b1[2]
#       m1[1]   1.5  -0.5   0.5
```

TidyCode *Tidy Code*

Description

Small function that clears up messy code

Usage

```
TidyCode(tidy.code, jags = TRUE)
```

Arguments

tidy.code	Messy code that needs cleaning
jags	logical, if TRUE run code as JAGS model, Default: TRUE

Value

(Somewhat) tidy code

Examples

```
messy <- "code <- function( x ) {
print (x ) }"
cat(messy)
code <- function( x ) {
print (x ) }
cat ( TidyCode(messy, jags = FALSE) )
code <- function(x) {
   print(x)
}
```

Trim *Trim*

Description

remove excess whitespace from string

Usage

```
Trim(s, multi = TRUE)
```

Arguments

s	string
multi	logical, indicating whether or not to remove excess whitespace between characters, Default: TRUE

Examples

```
Trim("             Trimmed      string")
# [1] "Trimmed string"
Trim("             Trimmed      string", FALSE)
# [1] "Trimmed      string"
```

TrimSplit *Trim Split*

Description

Extends strsplit by trimming and unlisting string

Usage

```
TrimSplit(
  x,
  sep = ",",
  fixed = FALSE,
  perl = FALSE,
  useBytes = FALSE,
  rm.empty = TRUE
)
```

Arguments

x	string
sep	symbol to separate data (e.g., comma-delimited), Default: ','
fixed	logical, if TRUE match split exactly, otherwise use regular expressions. Has priority over perl, Default: FALSE
perl	logical, indicating whether or not to use Perl-compatible regexps, Default: FALSE
useBytes	logical, if TRUE the matching is done byte-by-byte rather than character-by-character, Default: FALSE
rm.empty	logical. indicating whether or not to remove empty elements, Default: TRUE

Details

strsplit

Examples

```
TrimSplit("Data 1,     Data2, Data3")
# [1] "Data 1" "Data2"  "Data3"
```

VectorSub *Pattern Matching and Replacement From Vectors*

Description

extending gsub by matching pattern and replacement from two vectors

Usage

```
VectorSub(pattern, replacement, string)
```

Arguments

pattern	vector containing words to match
replacement	vector containing words to replace existing words.
string	string to replace from

Value

modified string with replaced values

Examples

```
pattern <- c("A","B","C")
replacement <- 1:3
string <- "A went to B went to C"
VectorSub(pattern,replacement,string)
# [1] "1 went to 2 went to 3"
```

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