Package ‘MCMCvis’

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Type Package

Title Tools to Visualize, Manipulate, and Summarize MCMC Output

Version 0.13.5

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Description Performs key functions for MCMC analysis using minimal code - visualizes, manipulates, and summarizes MCMC output. Functions support simple and straightforward subsetting of model parameters within the calls, and produce presentable and 'publication-ready' output. MCMC output may be derived from Bayesian model output fit with JAGS, Stan, or other MCMC samplers.

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URL http://github.com/caseyyoungflesh/MCMCvis

BugReports http://github.com/caseyyoungflesh/MCMCvis/issues

LazyData TRUE

Imports coda, rstan, methods, overlapping

Depends R (>= 3.3.0)

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Description

Extract posterior chains from MCMC output for specific parameters of interest.

Usage

```r
MCMCchains(object, params = "all", excl = NULL, ISB = TRUE,
mcmc.list = FALSE, chain_num = NULL)
```

Arguments

- `object` Object containing MCMC output. See DETAILS below.
- `params` Character string (or vector of character strings) denoting parameters of interest. Default 'all' returns chains for all parameters.
- `excl` Character string (or vector of character strings) denoting parameters to exclude. Used in conjunction with `params` argument to select parameters of interest.
- `ISB` Ignore Square Brackets (ISB). Logical specifying whether square brackets should be ignored in the `params` and `excl` arguments. If TRUE, square brackets are ignored - input from `params` and `excl` are otherwise matched exactly. If FALSE, square brackets are not ignored - input from `params` and `excl` are matched using regular expression format. This allows partial names to be used when specifying parameters of interest.
- `mcmc.list` Logical specifying whether to return an `mcmc.list`. If TRUE, an `mcmc.list` object is returned, rather than a matrix.
- `chain_num` Numeric - specifies posterior chain number. When a value is specified, posterior for only that chain is output. Useful for determining the last iteration for each parameter, to be used as initial values in a subsequent model, to effectively 'continue' a model run.
Details

Function returns matrix with one parameter per column (for specified parameters). Each iteration is represented as a row. Multiple chains for each parameter are combined to one posterior chain (unless chain_num is specified, in which case only the specified chain will be returned). Parameters are arranged in columns alphabetically.

object argument can be a stanfit object (rstan package), a stanreg object (rstanarm package), a brmsfit object (brms package), an mcmc.list object (coda package), an R2jags model object (R2jags package), a jagsUI model object (jagsUI package), or a matrix containing MCMC chains (each column representing MCMC output for a single parameter, rows representing iterations in the chain). The function automatically detects the object type and proceeds accordingly.

Examples

#Load data
data(MCMC_data)

#Extract MCMC chains
ex <- MCMCchains(MCMC_data)
apply(ex, 2, mean)

#Extract MCMC chains for just 'beta' parameters
ex2 <- MCMCchains(MCMC_data, params = 'beta')
apply(ex2, 2, mean)

#Just 'beta[1]', 'beta[4]', and 'alpha[3]'
#params takes regular expressions when ISB = FALSE, square brackets must be escaped with '\'
ex3 <- MCMCchains(MCMC_data, params = c('beta[1]\', 'beta[4]\', 'alpha[3]\'), ISB = FALSE)
apply(ex3, 2, sd)

MCMCplot

Caterpillar plots of posterior distributions from MCMC output

Description

Visualize posterior distributions from MCMC output for specific parameters of interest using caterpillar plots. Color of median dot represents the overlap of the posterior distribution with 0 (or other specified value).

Usage

MCMCplot(object, object2 = NULL, params = "all", excl = NULL, ISB = TRUE, ref = 0, ref_ovl = FALSE, col = "black",
col2 = "red", offset = 0.1, rank = FALSE, horiz = TRUE, xlim, ylim, xlab, ylab, main, labels, guide_lines = FALSE,
guide_axis = TRUE, sz_labels = 1.2, sz_med = 1.5, sz_thick = 5,
sz_thin = 2, sz_ax = 3, sz_ax_txt = 1.3, sz_tick_txt = 1.2,
sz_main_txt = 1.2, pos_tick, mar = c(5.1, 4.1, 4.1, 2.1))
Arguments

object
Object containing MCMC output. See DETAILS below.

object2
Optional second object containing MCMC output. If specified, parameter estimates from each model will be displayed in a paired manner. Parameter names for `object` and `object2` must be identical. See DETAILS below.

params
Character string (or vector of character strings) denoting parameters to be plotted.
Default 'all' plots posteriors for all parameters. See VALUE below.

excl
Character string (or vector of character strings) denoting parameters to exclude. Used in conjunction with params argument to select parameters of interest.

ISB
Ignore Square Brackets (ISB). Logical specifying whether square brackets should be ignored in the params and excl arguments. If TRUE, square brackets are ignored - input from params and excl are otherwise matched exactly. If FALSE, square brackets are not ignored - input from params and excl are matched using grep, which can take arguments in regular expression format. This allows partial names to be used when specifying parameters of interest.

ref
Value indicating where vertical reference line should be created and what value to use a reference for caterpillar median coloration. Default is ref = 0.
Argument NULL will plot no reference line.

ref_ovl
Logical specifying whether the style/color of plotted median dots and CI should be changed based on whether the 50% and 95% credible intervals overlap the reference line. See DETAILS for more information.

col
Character string (or vector of character strings) specifying which color to render estimates on plot. When ref_ovl = TRUE, this argument has no effect and colors plotted will be based on the credible intervals and reference line. Number of specified colors must equal the number of specified parameters or one.

col2
Character string (or vector of character strings) specifying which color to render estimates on plot for object2 (if specified). Number of specified colors must equal the number of specified parameters or one. Red by default.

offset
Value indicating how much to offset plotted posteriors when object2 is specified (i.e., control the amount of space between the two plotted posteriors for each parameter). The distance from one set of parameters to another corresponds to a value of 1.

rank
Logical specifying whether output should be ranked. If TRUE posteriors will be ranked in decreasing order (based on specified measure of centrality) from top down.

horiz
Logical specifying orientation of plot. If TRUE posteriors will be plotted running horizontally (parallel to the x-axis). If FALSE posteriors will be plotted running vertically (perpendicular to the x-axis).

xlim
Numerical vector of length 2, indicating range of x-axis. Only applicable if horiz = TRUE.

ylim
Numerical vector of length 2, indicating range of y-axis. Only applicable if horiz = FALSE.
MCMCplot

- **xlab**: Character string labeling x-axis. Only applicable if horiz = TRUE. Default label is 'Parameter Estimate'. Option NULL will return plot with no label on x-axis.

- **ylab**: Character string labeling y-axis. Only applicable if horiz = FALSE. Default label is 'Parameter Estimate'. Option NULL will return plot with no label on y-axis.

- **main**: Character string indicating title of plot.

- **labels**: Character string (or vector of character strings if plotting > 1 parameter) labeling parameter estimates along y-axis (if horiz = FALSE) or x-axis (if horiz = TRUE). Default option will use parameter names from object. Option NULL will return plot with no labels on axis.

- **guide_lines**: Logical specifying whether to plot reference lines for each parameter in order to better visualize which parameter names correspond to each posterior.

- **guide_axis**: Logical specifying whether a second axis should be plotted (x-axis if HORIZ = TRUE, y-axis if HORIZ = FALSE) to help interpret values on plot.

- **sz_labels**: Number specifying size of text for parameter labels on axis.

- **sz_med**: Number specifying size of points represents posterior medians.

- **sz_thick**: Number specifying thickness of 50 percent CI line (thicker line).

- **sz_thin**: Number specifying thickness of 95 percent CI line (thinner line).

- **sz_ax**: Number specifying thickness of axis and ticks.

- **sz_ax_txt**: Number specifying size of text for axis label.

- **sz_tick_txt**: Number specifying size of text for tick labels on axis.

- **sz_main_txt**: Number specifying size of text for main title.

- **pos_tick**: Numeric vector specifying where ticks on axis should be placed.

- **mar**: Numerical vector of length 4 specifying plot margins - (BOTTOM, LEFT, TOP, RIGHT). Changes to the margin should be made within the function rather than using the par call. Default is c(5.1, 4.1, 4.1, 2.1) - the R plot default.

**Details**

Points represent posterior medians. Parameters where 50% credible intervals overlap 0 (or other specified value) are indicated by 'open' circles. Parameters where 50 percent credible intervals DO NOT overlap 0 AND 95 percent credible intervals DO overlap 0 (or other specified value) are indicated by 'closed' gray circles. Parameters where 95 percent credible intervals DO NOT overlap 0 (or other specified value) are indicated by 'closed' black circles. Thick lines represent 50 percent credible intervals while thin lines represent 95% credible intervals. ref_ovl = TRUE can be used to enable this feature.

When object2 is specified, paired caterpillar plots of each parameter are produced. For this reason, parameter names of object and object2 specified with the params argument must be identical (to be used for comparing posterior estimates of similar models). col and col2 arguments can be specified to change the color of output from object and object2, respectively. By default, output
from object is plotted in black and object2 is plotted in red. The ref_ovl argument can also be specified.

object argument can be a stanfit object (rstan package), a stanreg object (rstanarm package), a brmsfit object (brms package), an mcmc.list object (coda package), an R2jags model object (R2jags package), a jagsUI model object (jagsUI package), or a matrix containing MCMC chains (each column representing MCMC output for a single parameter, rows representing iterations in the chain). The function automatically detects the object type and proceeds accordingly.

Notes

When specifying rank = TRUE and specifying labels for labels, labels will be applied to parameters before they are ranked.

Thanks to Cinner et al. 2016, whose Fig. 1 inspired this plot.

References


Examples

#Load data
data(MCMC_data)

#Plot MCMC output
MCMCplot(MCMC_data, labels = NULL)

#Just 'beta' parameters
MCMCplot(MCMC_data, params = 'beta')

#Just 'beta[1]', 'beta[4]', and 'alpha[3]' # params' takes regular expressions when ISB = FALSE, square brackets must be escaped with '
MCMCplot(MCMC_data, params = c('beta[1]\]', 'beta[4]\]', 'alpha[3]\]'), ISB = FALSE)

#Rank parameters by posterior mean
MCMCplot(MCMC_data, params = 'beta', rank = TRUE)

#Create vertical plot
MCMCplot(MCMC_data, params = 'beta', horiz = FALSE)
MCMCpstr

Summarize and extract posterior chains from MCMC output while preserving parameter structure.

Description

Extract summary information and posterior chains from MCMC output (specific function specified) for specific parameters of interest while preserving original parameter structure (i.e., scalar, vector, matrix, array). Function outputs a list with calculated values or posterior chains for each specified parameter.

Usage

MCMCpstr(object, params = "all", excl = NULL, ISB = TRUE, func = mean, type = "summary")

Arguments

object Object containing MCMC output. See DETAILS below.
params Character string (or vector of character strings) denoting parameters to be returned in output. Default 'all' returns all parameters in output.
excl Character string (or vector of character strings) denoting parameters to exclude. Used in conjunction with params argument to select parameters of interest.ISB Ignore Square Brackets (ISB). Logical specifying whether square brackets should be ignored in the params and excl arguments. If TRUE, square brackets are ignored - input from params and excl are otherwise matched exactly. If FALSE, square brackets are not ignored - input from params and excl are matched using grep, which can take arguments in regular expression format. This allows partial names to be used when specifying parameters of interest.
func Function to be performed on MCMC output. When output of specified function is greater than length 1, an extra dimension is added. For instance, output of length 3 for a parameter with dimensions 2x2 results in a 2x2x3 output. Functions that produce output with dimensionality greater than 1 are not permitted. func is ignored when type = 'chains'.
type Character string specifying whether to return summary information (calculated based on func argument) or posterior chains. Valid options are 'summary' and 'chains'. When type = 'chains', the 'func' argument is ignored. When type = 'chains', posterior chains are concatenated and stored in the last dimension in the array for each element (parameter) of the list.

Details

object argument can be a stanfit object (rstan package), a stanreg object (rstanarm package), a brmsfit object (brms package), an mcmc.list object (coda package), an R2jags model object...
(R2jags package), a jagsUI model object (jagsUI package), or a matrix containing MCMC chains (each column representing MCMC output for a single parameter, rows representing iterations in the chain). The function automatically detects the object type and proceeds accordingly.

Examples

```r
# Load data
data(MCMC_data)
MCMCpstr(MCMC_data, func = function(x) quantile(x, probs = c(0.01, 0.99)))
```

---

**MCMCsummary**  
Summarize MCMC output

**Description**

Extract summary information from MCMC output (mean, median, quantiles, Gelman-Rubin convergence statistic, number of effective samples, and specified custom metrics) for specific parameters of interest.

**Usage**

```r
MCMCsummary(object, params = "all", excl = NULL, ISB = TRUE,
              probs = c(0.025, 0.5, 0.975), hpd_prob = 0.95, HPD = FALSE,
              digits = NULL, round = NULL, Rhat = TRUE, n.eff = TRUE,
              func = NULL, func_name = NULL)
```

**Arguments**

- `object`: Object containing MCMC output. See DETAILS below.
- `params`: Character string (or vector of character strings) denoting parameters to be returned in summary output. Default 'all' returns all parameters in summary output.
- `excl`: Character string (or vector of character strings) denoting parameters to exclude. Used in conjunction with `params` argument to select parameters of interest.
- `ISB`: Ignore Square Brackets (ISB). Logical specifying whether square brackets should be ignored in the `params` and `excl` arguments. If `TRUE`, square brackets are ignored - input from `params` and `excl` are otherwise matched exactly. If `FALSE`, square brackets are not ignored - input from `params` and `excl` are matched using `grep`, which can take arguments in regular expression format. This allows partial names to be used when specifying parameters of interest.
- `probs`: Numeric vector where each element in (0,1) representing probabilities used to calculate posterior sample quantiles for the selected parameters. Default is `c(0.025, 0.5, 0.975)`. 

---

**Notes**

- The function automatically detects the object type and proceeds accordingly.
- Examples show how to use the function, including loading data and summarizing MCMC output.
- The `MCMCpstr` function is an example of how to return quantiles for specific parameters.

---

**Details**

The `MCMCsummary` function is designed to extract summary information from MCMC output, providing a comprehensive overview of the parameters under study. It supports various output formats, including objects from the R2jags and jagsUI packages, as well as matrices containing MCMC chains. The function automatically identifies the input object type and processes accordingly, ensuring flexibility and ease of use for researchers and analysts working with MCMC output.
MCMCsummary

hpdp

Scalar in (0,1) representing probability used to calculate highest posterior density intervals for the selected parameters. Default is 0.95.

HPD

Logical specifying whether to calculate equal-tailed credible intervals (HPD = FALSE) or highest posterior density intervals (HPD = TRUE) for the selected parameters. Default is HPD = FALSE.

digits

Number of significant digits to include for posterior summary. All computed digits will be included by default. Note that Rhat is always rounded to 2 decimal places.

round

Number of decimal places to round to for posterior summary. Cannot be used in conjunction with digits argument. Note that Rhat is always rounded to 2 decimal places.

Rhat

Logical specifying whether to calculate and display the potential scale reduction statistic (Rhat). Values near 1 suggest convergence (Brooks and Gelman 1998). Rhat = FALSE will prevent display of this column in summary output. Specifying Rhat = FALSE, may increase function speed for very large mcmc.list objects.

n.eff

Logical specifying whether to calculate and display the number of effective samples for each parameter. n.eff = FALSE will prevent display of this column in summary output. Specifying n.eff = FALSE, may increase function speed for very large mcmc.list objects. Default is n.eff = TRUE.

func

Function to be performed on MCMC output. If a function is specified, it will be evaluated on posteriors for each specified parameter and returned as a column in the summary output (or multiple columns if the function returns more than one value).

func_name

Character string (or vector of character strings) specifying labels for output from func argument. If func_name is not specified, columns with func argument will be labeled 'func'.

Value

Function returns summary information (including parameter posterior mean, posterior sd, quantiles, potential scale reduction statistic (Rhat), number of effective samples, and other specified metrics) for specified parameters.

Details

object argument can be a stanfit object (rstan package), a stanreg object (rstanarm package), a brmsfit object (brms package), an mcmc.list object (coda package), an R2jags model object (R2jags package), a jagsUI model object (jagsUI package), or a matrix containing MCMC chains (each column representing MCMC output for a single parameter, rows representing iterations in the chain). The function automatically detects the object type and proceeds accordingly.

Notes

For mcmc.list objects, the potential scale reduction statistic statistic (Rhat) is calculated using the gelman.diag function in the coda package (what is typically displayed in the summary output from models fit with JAGS). For stanfit objects (as well as stanreg and brmsfit objects), Rhat
is calculated using the rstan package which computes a 'split chain' Rhat, which is thought to be a more conservative diagnostic (Stan Development Team 2018).

For mcmc.list objects, the number of effective samples is calculated using the effectiveSize function in the coda package. For stanfit objects (as well as stanreg and brmsfit objects), n.eff is calculated using the rstan package which (in a similar way to the Rhat computation noted above) employs a slightly different (and more conservative) method of computation for the number of effective samples (Stan Development Team 2018).

References


Examples

#Load data
data(MCMC_data)

#Summary information for MCMC output - display 2 significant digits
MCMCsummary(MCMC_data, digits = 2)

#Just 'beta' parameters - round to 2 decimal places
MCMCsummary(MCMC_data, params = 'beta', round = 2)

#Just 'beta[1]', 'beta[4]', and 'alpha[3]'
#'params' takes regular expressions when ISB = FALSE, square brackets must be escaped with '\' MCMCsummary(MCMC_data, params = c('beta\[1\]', 'beta\[4\]', 'alpha\[3\]'), ISB = FALSE)

MCMCtrace

Trace and density plots from MCMC output

Description

Trace and density plots of MCMC chains for specific parameters of interest. Print plots to pdf by default.

Usage

MCMCtrace(object, params = "all", excl = NULL, ISB = TRUE,
iter = 5000, gvals = NULL, priors = NULL, post_zm = TRUE,
PPO_out = FALSE, Rhat = FALSE, n.eff = FALSE, ind = FALSE,
pdf = TRUE, plot = TRUE, open_pdf = TRUE, filename, wd = getwd(),
type = "both", ylim = NULL, xlim = NULL, xlab_tr, ylab_tr,
xlab_den, ylab_den, main_den = NULL, main_tr = NULL, lwd_den = 1,
lwd_pr = 1, lty_den = 1, lty_pr = 1, col_den, col_pr, col_txt,
sz_txt = 1.2, sz_ax = 1, sz_ax_txt = 1, sz_tick_txt = 1,
    sz_main_txt = 1.2, pos_tick_x_tr = NULL, pos_tick_y_tr = NULL,
pos_tick_x_den = NULL, pos_tick_y_den = NULL)

Arguments

object Object containing MCMC output. See DETAILS below.

params Character string (or vector of character strings) denoting parameters of interest.
 Default 'all' returns chains for all parameters.

excl Character string (or vector of character strings) denoting parameters to exclude.
 Used in conjunction with params argument to select parameters of interest.

ISB Ignore Square Brackets (ISB). Logical specifying whether square brackets should
 be ignored in the params and excl arguments. If TRUE, square brackets are ignored
 - input from params and excl are otherwise matched exactly. If FALSE, square
 brackets are not ignored - input from params and excl are matched using
 grep, which can take arguments in regular expression format. This allows partial
 names to be used when specifying parameters of interest.

iter Number of iterations to plot for trace and density plots. The default value is
 5000, meaning the last 5000 iterations of the chain will be plotted.

gvals Vector containing generating values if simulated data was used to fit model.
 These values will be plotted as vertical lines on the density plots to compare
 posterior distributions with the true parameter values used to generate the data.
 No line will be apparent if the generating value is outside the plotted range of
 the posterior distribution.

priors Matrix containing random draws from prior distributions corresponding to pa-
 rameters of interest. If specified, priors are plotted along with posterior density
 plots. Percent overlap between prior and posterior (PPO) is also calculated and
 displayed on each plot. Each column of the matrix represents a prior for a dif-
 ferent parameter. Parameters are plotted alphabetically - priors should be sorted
 accordingly. If priors contains only one prior and more than one parameter is
 specified for the params argument, this prior will be used for all parameters. The
 number of draws for each prior should equal the number of iterations specified
 by iter (or total draws if less than iter) times the number of chains, though
 the function will automatically adjust if more or fewer iterations are specified.
 See DETAILS below.

post_zm Logical - if post_zm = FALSE x- and y-limits of density plots are scaled so that
 both the prior and posterior can be visualized on a single density plot (rather
 than zoomed on the posterior).

PPO_out Logical - if PPO_out = TRUE percent overlap between prior and posterior (PPO)
 will be output to a dataframe.

Rhat Logical - if Rhat = TRUE potential scale reduction factor (Rhat) for each param-
 eter is plotted on the trace plots.

n.eff Logical - if n.eff = TRUE number of effective samples for each parameter is
 plotted on the trace plots.

ind Logical - if ind = TRUE, separate density lines will be plotted for each chain. If
 ind= FALSE, one density line will be plotted for all chains.
pdf Logical - if pdf = TRUE plots will be exported to a pdf.
plot Logical - if plot = FALSE no plot will be output. Designed to be used in conjunction with PPO_out = TRUE, to calculate PPO without displaying plot output.
open_pdf Logical - if open_pdf = TRUE pdf will open in viewer after being generated.
filename Name of pdf file to be printed. Default is 'MCMCtrace'.
wd Working directory for pdf output. Default is current directory.
type Type of plot to be output. 'both' outputs both trace and density plots, 'trace' outputs only trace plots, and 'density' outputs only density plots.
ylim Vector of length two specifying limits for y-axis on density plots only. If specified, overrides argument post_zm.
xlim Vector of length two specifying limits for x-axis on density plots only. If specified, overrides argument post_zm.
xlab_tr Character string specifying label for x-axis on trace plots.
ylab_tr Character string specifying label for x-axis on trace plots.
xlab_den Character string specifying label for x-axis on density plots.
ylab_den Character string specifying label for x-axis on density plots.
main_den Character string (or vector of character strings if plotting > 1 parameter) specifying title(s) of density plot(s).
main_tr Character string (or vector of character strings if plotting > 1 parameter) specifying title(s) of trace plot(s).
lwd_den Number specifying thickness of density line on density plots.
lwd_pr Number specifying thickness of prior line on density plots.
lty_den Number specifying the line type for the density line on density plots.
lty_pr Number specifying the line type for the prior line on density plots.
col_den Character string specifying color of density line on density plots. Does not specify color if ind = TRUE.
col_pr Character string specifying color of prior line on density plots.
col_txt Character string specifying color of text (denoting PPO) on plot when value specified for priors. If NULL is specified, no text will be plot.
sz_txt Number specifying size of text (denoting PPO) when value specified for priors. If NULL is specified, no text will be plot.
sz_ax Number specifying thickness of axes and ticks.
sz_ax_txt Number specifying size of text for axes labels.
sz_tick_txt Number specifying size of text for tick labels on axis.
sz_main_txt Number specifying size of text for main title.
pos_tick_x_tr Numeric vector specifying where ticks on x-axis should be placed for trace plots.
pos_tick_y_tr Numeric vector specifying where ticks on y-axis should be placed for trace plots.
pos_tick_x_den Numeric vector specifying where ticks on x-axis should be placed for density plots.
pos_tick_y_den Numeric vector specifying where ticks on y-axis should be placed for density plots.
**Details**

The `MCMCvis` package

Details

object argument can be a `stanfit` object (rstan package), a `stanreg` object (rstanarm package), a `brmsfit` object (brms package), an `mcmc.list` object (coda package), an `R2jags` model object (R2jags package), a `jagsUI` model object (jagsUI package), or a matrix containing MCMC chains (each column representing MCMC output for a single parameter, rows representing iterations in the chain). The function automatically detects the object type and proceeds accordingly.

Matrices for the `priors` argument can be generated using commands such as `rnorm`, `rgamma`, `runif`, etc. Distributions not supported by base R can be generated by using the appropriate packages. It is important to note that some discrepancies between MCMC samplers and R may exist regarding the parameterization of distributions - one example of this is the use of precision in JAGS but standard deviation in R for the 'second parameter' of the normal distribution. If the number of draws for each prior distribution is greater than the total number used for the density plot (iter times the number of chains), the function will use a subset of the prior draws. If the number of draws for each prior distribution is less than the total number used for the density plot, the function will resample (with replacement) from the prior to obtain the appropriate number of draws.

**Examples**

```r
#Load data
data(MCMC_data)

#Traceplots for all 'beta' parameters - pdf is generated by default
MCMCtrace(MCMC_data, params = 'beta', pdf = FALSE)

#Traceplots (individual density lines for each chain) just for 'beta[1]'
#'params' takes regular expressions when ISB = FALSE, square brackets
#must be escaped with '\\'
MCMCtrace(MCMC_data, params = 'beta[1]',
          ISB = FALSE, ind = TRUE, pdf = FALSE)

#Plot prior on top of posterior, calculate prior/posterior overlap (PPO)
#just for 'beta[1]'
#Add Rhat and n.eff values to density plots
#'params' takes regular expressions when ISB = FALSE, square brackets must
#be escaped with '\\'
PR <- rnorm(15000, 0, 32)
MCMCtrace(MCMC_data, params = 'beta[1]', ISB = FALSE, priors = PR,
          pdf = FALSE, Rhat = TRUE, n.eff = TRUE)

#Output PPO to R object without plotting trace plots
PR <- rnorm(15000, 0, 32)
PPO <- MCMCtrace(MCMC_data, params = 'beta[1]', ISB = FALSE,
                priors = PR, plot = FALSE, PPO_out = TRUE)
```
MCMC_data

Description

'MCMCvis' is an R package used to visualize, manipulate, and summarize MCMC output. MCMC output may be derived from Bayesian model output fit with JAGS, Stan, or other MCMC samplers.

Details

The following functions are currently available:
- `MCMCsummary` - summarize MCMC output for particular parameters of interest
- `MCMCpstr` - summarize MCMC output for particular parameters of interest while preserving original parameter structure
- `MCMCtrace` - create trace and density plots of MCMC chains for particular parameters of interest
- `MCMCchains` - easily extract posterior chains from MCMC output for particular parameters of interest
- `MCMCplot` - create caterpillar plots from MCMC output for particular parameters of interest

Example data can be loaded using `data(MCMC_data)`.

'MCMCvis' was designed to perform key functions for MCMC analysis using minimal code, in order to free up time/brainpower for interpretation of analysis results. Functions support simple and straightforward subsetting of model parameters within the calls, and produce presentable, 'publication-ready' output.

The vignette can be run using `vignette('MCMCvis')` if vignette is built when installing package.

Author(s)

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MCMC_data  Simulated MCMC output data

Description

Sample MCMC output containing 12 parameters - alpha[1], ... , alpha[6], beta[1], ... , beta[6].

Usage

MCMC_data

Format

mcmc.list object with 3 chains for each parameter, 6000 iterations for each chain.
MCMC_data2

Simulated MCMC output data - #2

Description

Sample MCMC output containing 12 parameters - alpha[1], ... , alpha[6], beta[1], ... , beta[6].

Usage

MCMC_data2

Format

mcmc.list object with 3 chains for each parameter, 6000 iterations for each chain.
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