

Package ‘MCMCvis’

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Type Package

Title Tools to Visualize, Manipulate, and Summarize MCMC Output

Version 0.7.1

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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, grDevices, graphics, stats

Depends R (>= 3.2.3)

RoxygenNote 6.0.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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MCMCchains	<i>Extract posterior chains from MCMC output</i>
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Description

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

Usage

```
MCMCchains(object, params = "all", excl = NULL)
```

Arguments

<code>object</code>	Object containing MCMC output. See DETAILS below.
<code>params</code>	Character string (or vector of character strings) denoting parameters of interest. Partial names may be used to return all parameters containing that set of characters. Default 'all' returns chains for all parameters.
<code>excl</code>	Character string (or vector of character strings) denoting parameters to exclude. Partial names may be used to exclude all parameters containing that set of characters. Used in conjunction with <code>params</code> argument to select parameters of interest.

Details

Function returns matrix with one chain per column for specified parameters. Multiple input chains for each parameter are combined to one posterior chain.

`object` argument can be a `stanfit` object (`rstan` package), an `mcmc.list` object (`coda` package), an `R2jags` model object (`R2jags` 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)
```

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, params = "all", excl = NULL, ref = 0, ref_ovl = TRUE,
  rank = FALSE, horiz = TRUE, xlim, ylim, xlab, ylab, main, labels,
  labels_sz = 1.2, med_sz = 1.5, thick_sz = 5, thin_sz = 2, ax_sz = 3,
  x_axis_text_sz = 1.3, x_tick_text_sz = 1.2, main_text_sz = 1.2,
  tick_pos, mar = c(5.1, 4.1, 4.1, 2.1))
```

Arguments

object	Object containing MCMC output. See DETAILS below.
params	Character string (or vector of character strings) denoting parameters to be plotted. Partial names may be used to plot all parameters containing that set of characters. Default 'all' plots posteriors for all parameters. See VALUE below.
excl	Character string (or vector of character strings) denoting parameters to exclude. Partial names may be used to exclude all parameters containing that set of characters. Used in conjunction with params argument to select 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.
rank	If TRUE posteriors will be ranked in decreasing order (based on specified measure of centrality) from top down.
horiz	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.

xlab	Character string labeling x-axis. Only applicable if <code>horiz = TRUE</code> . Default label is 'Parameter Estimate'. Option <code>NULL</code> will return plot with no label on x-axis.
ylab	Character string labeling y-axis. Only applicable if <code>horiz = FALSE</code> . Default label is 'Parameter Estimate'. Option <code>NULL</code> 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 <code>horiz = FALSE</code>) or x-axis (if <code>horiz = TRUE</code>). Default option will use parameter names from object. Option <code>NULL</code> will return plot with no labels on axis.
labels_sz	Number specifying size of text for parameter labels on axis.
med_sz	Number specifying size of points represents posterior medians.
thick_sz	Number specifying thickness of 50 percent CI line (thicker line).
thin_sz	Number specifying thickness of 95 percent CI line (thinner line).
ax_sz	Number specifying thickness of axis and ticks.
x_axis_text_sz	Number specifying size of text for axis label.
x_tick_text_sz	Number specifying size of text for tick labels on axis.
main_text_sz	Number specifying size of text for main title.
tick_pos	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 <code>par</code> call. Default is <code>c(5.1, 4.1, 4.1, 2.1)</code> - 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' grey 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 = FALSE` can be used to disable this feature. All median dots will be represented as 'closed' black circles. `object` argument can be a `stanfit` object (`rstan` package), an `mcmc.list` object (`coda` package), an `R2jags` model object (`R2jags` 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

Cinner, J. E., C. Huchery, M. A. MacNeil, N. A. J. Graham, T. R. McClanahan, J. Maina, E. Maire, J. N. Kittinger, C. C. Hicks, C. Mora, E. H. Allison, S. D'Agata, A. Hoey, D. A. Feary, L. Crowder, I. D. Williams, M. Kulbicki, L. Vigliola, L. Wantiez, G. Edgar, R. D. Stuart-Smith, S. A. Sandin, A. L. Green, M. J. Hardt, M. Beger, A. Friedlander, S. J. Campbell, K. E. Holmes, S. K. Wilson, E. Brokovich, A. J. Brooks, J. J. Cruz-Motta, D. J. Booth, P. Chabanet, C. Gough, M. Tupper, S. C. A. Ferse, U. R. Sumaila, and D. Mouillot. 2016. Bright spots among the world's coral reefs. *Nature* 535:416-419.

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]', 'gamma[4]', and 'alpha[3]'
MCMCplot(MCMC_data, params = c('beta[1]', 'gamma[4]', 'alpha[3]'))

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

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

MCMCsummary

Summary function for MCMC output

Description

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

Usage

```
MCMCsummary(object, params = "all", excl = NULL, digits = 2,
  Rhat = TRUE)
```

Arguments

`object` Object containing MCMC output. See DETAILS below.

<code>params</code>	Character string (or vector of character strings) denoting parameters to be returned in summary output. Partial names may be used to return all parameters containing that set of characters. Default 'all' returns all parameters in summary output.
<code>excl</code>	Character string (or vector of character strings) denoting parameters to exclude. Partial names may be used to exclude all parameters containing that set of characters. Used in conjunction with <code>params</code> argument to select parameters of interest.
<code>digits</code>	Number of digits to include for posterior summary. Values will be rounded to the specified number of digits. Default is <code>digits = 2</code> .
<code>Rhat</code>	If TRUE, summary information contains Gelman-Rubin convergence statistic (Rhat) and if FALSE, Rhat output is masked.

Value

Function returns summary information (including parameter posterior mean, 2.5% quantile, median, 97.5% quantile, and Gelman-Rubin convergence statistic (Rhat)) for specified parameters.

Details

object argument can be a `stanfit` object (rstan package), an `mcmc.list` object (coda package), an `R2jags` model object (R2jags 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, Gelman-Rubin convergence statistic (Rhat) is calculated using the `gelman.diag` function in the coda package.

Examples

```
#Load data
data(MCMC_data)

#Summary information for MCMC output
MCMCsummary(MCMC_data)

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

#Just 'beta[1]', 'gamma[4]', and 'alpha[3]'
MCMCsummary(MCMC_data, params= c('beta[1]', 'gamma[4]', 'alpha[3]'))
```

MCMCtrace

Trace and density plots from MCMC output

Description

Trace and density plots of MCMC chains for specific parameters of interest. Option to print plots to pdf.

Usage

```
MCMCtrace(object, params = "all", excl = NULL, iter = 2000, pdf = FALSE,
          filename, wd = getwd(), type = "both", ind = FALSE)
```

Arguments

object	Object containing MCMC output. See DETAILS below.
params	Character string (or vector of character strings) denoting parameters of interest. Partial names may be used to return all parameters containing that set of characters. Default 'all' returns chains for all parameters.
excl	Character string (or vector of character strings) denoting parameters to exclude. Partial names may be used to exclude all parameters containing that set of characters. Used in conjunction with params argument to select parameters of interest.
iter	Number of iterations to plot for trace and density plots. The default value is 2000, meaning the last 2000 iterations of the chain will be plotted.
pdf	Logical - if pdf = TRUE plots will be exported to a pdf.
filename	Name of pdf file to be printed.
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.
ind	Logical - if ind = TRUE, different lines will be plotted for each chain. If ind= FALSE, one line will be plotted for all chains.

Details

object argument can be a stanfit object (rstan package), an mcmc.list object (coda package), or an R2jags model object (R2jags package). The function automatically detects the object type and proceeds accordingly.

Examples

```
#Load data
data(MCMC_data)

#Traceplot for all 'beta' parameters
MCMCtrace(MCMC_data, params='beta')

#Print traceplot output to pdf
MCMCtrace(MCMC_data, pdf= TRUE, filename = 'PDF_file.pdf')
```

MCMCvis

The 'MCMCvis' package

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)
- 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.

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`MCMC_data`*Simulated MCMC output data*

Description

Sample MCMC output containing 30 parameters - `alpha[1]`, ... , `alpha[10]`, `beta[1]`, ... , `beta[10]`, `gamma[1]`, ... , `gamma[10]`.

Usage

```
MCMC_data
```

Format

`mcmc.list` object with 3 chains for each parameter, 1000 iterations for each chain

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