

Package ‘MCMCvis’

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Type Package

Title Tools to Visualize, Manipulate, and Summarize MCMC Output

Version 0.6.3

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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 sub-setting 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 5.0.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

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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

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.

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)
```

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 relationship of parameter to reference line (default is 0; see DETAILS below).

Usage

```
MCMCplot(object, params = "all", excl = NULL, ref = 0, ref_ovl = TRUE,
  rank = FALSE, xlim, ylim, xlab, 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. Valid entries are jags_object, mcmc_list, and chains. See DETAILS 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	Numerical vector indicating where vertical reference line should be created. 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 DETAILS for more information.
rank	If TRUE posteriors will ranked in decreasing order (based on specified measure of centrality) from top down.
xlim	Numerical vector of length 2, indicating range of x-axis.
ylim	Numerical vector of length 2, indicating range of y-axis
xlab	Character string labeling x-axis. Option NULL will return plot with no labels on y-axis.

<code>main</code>	Character string indicating title of plot.
<code>labels</code>	Character string (or vector of character strings if plotting > 1 parameter) labeling parameter estimates along y-axis. Specifying labels in the argument will use these to label parameter estimates on y-axis. Default option will use parameter names from object. Option NULL will return plot with no labels on y-axis.
<code>labels_sz</code>	Number specifying size of text for parameter labels on y-axis.
<code>med_sz</code>	Number specifying size of points represents posterior medians.
<code>thick_sz</code>	Number specifying thickness of 50 percent CI line (thicker line).
<code>thin_sz</code>	Number specifying thickness of 95 percent CI line (thinner line).
<code>ax_sz</code>	Number specifying thickness of x-axis and ticks.
<code>x_axis_text_sz</code>	Number specifying size of text for x-axis label.
<code>x_tick_text_sz</code>	Number specifying size of text for tick labels on x-axis.
<code>main_text_sz</code>	Number specifying size of text for main title.
<code>tick_pos</code>	Numeric vector specifying where ticks on x-axis should be placed.
<code>mar</code>	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. For parameters where 50 circles. For parameters where 50 percent credible intervals DO NOT overlap 0 AND 95 percent credible intervals DO overlap 0 are indicated by 'closed' grey circles. For parameters where 95 percent credible intervals DO NOT overlap 0 are indicated by 'closed' black circles. Thick lines represent 50 percent credible intervals while thin lines represent 95 percent 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)
```

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.
params	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 value. 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 plots 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_st = 1, 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_st	Starting point in chain for trace and density plots. Default is 1, meaning the entire chain is 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 and '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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