

Package ‘basicMCMCplots’

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Title Trace Plots, Density Plots and Chain Comparisons for MCMC Samples

Version 0.2.2

Description Provides a function for examining posterior MCMC samples from a single chain using trace plots and density plots, and from multiple chains by comparing posterior medians and credible intervals from each chain. These plotting functions have a variety of options, such as figure sizes, legends, parameters to plot, and saving plots to file. Functions interface with the NIMBLE software package, see de Valpine, Turek, Paciorek, Anderson-Bergman, Temple Lang and Bodik (2017) <doi:10.1080/10618600.2016.1172487>.

Depends R (>= 3.4.0)

License GPL-3

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chainsPlot

*Compare trace plots from multiple MCMC chains***Description**

Overlays trace plots from each MCMC chain, for each parameter

Usage

```
chainsPlot(samplesList, var = NULL, ind = NULL, burnin = NULL,
           scale = FALSE, ncols = NULL, width = 7, height = NULL,
           legend = !is.null(names(samplesList)), legend.location = "topright",
           cex = 1, traceplot = TRUE, densityplot = TRUE, file = NULL)
```

Arguments

<code>samplesList</code>	List of arrays of MCMC samples from different chains
<code>var</code>	Parameter names to plot
<code>ind</code>	Indices of MCMC samples to plot
<code>burnin</code>	Number of initial samples to discard from each MCMC chain (default: 0)
<code>scale</code>	Logical, whether to normalize each posterior chain (default: FALSE)
<code>ncols</code>	Number of columns in grid of parameter traceplots or densityplots
<code>width</code>	Width of the plot
<code>height</code>	Height of the plot
<code>legend</code>	Logical, whether to include a legend of chain names
<code>legend.location</code>	Legend location
<code>cex</code>	Expansion coefficient for text (default: 1)
<code>traceplot</code>	Logical, whether to generate posterior trace plots (default: TRUE)
<code>densityplot</code>	Logical, whether to generate posterior density plots (default: TRUE)
<code>file</code>	Filename for saving figure to a file

Examples

```
samples1 <- cbind(rnorm(1000, 1), rgamma(1000, 1), rpois(1000, 1))
colnames(samples1) <- c('alpha', 'beta', 'gamma')
samples2 <- cbind(rnorm(1000, 2), rgamma(1000, 2), rpois(1000, 2))
colnames(samples2) <- c('alpha', 'beta', 'gamma')
samplesList <- list(chain1 = samples1, chain2 = samples2)

chainsPlot(samplesList)

chainsPlot(samplesList, densityplot = FALSE, burnin = 500)

chainsPlot(samplesList, traceplot = FALSE, legend.location = 'topleft', cex = 0.7)
```

chainsSummary *Compare summary statistics from multiple MCMC chains*

Description

Plots median and 95

Usage

```
chainsSummary(samplesList, var = NULL, nrows = NULL, scale = FALSE,
              width = 7, height = NULL, legend = !is.null(names(samplesList)),
              legend.location = "topright", jitter = 1, buffer.right = 0,
              buffer.left = 0, cex = 1, file = NULL)
```

Arguments

<code>samplesList</code>	List of arrays of MCMC samples from different chains
<code>var</code>	Parameter names to plot
<code>nrows</code>	Number of rows in the resulting plot
<code>scale</code>	Logical, whether to normalize each posterior chain
<code>width</code>	Width of figure
<code>height</code>	Height of figure
<code>legend</code>	Logical, whether to include a legend of chain names
<code>legend.location</code>	Legend location
<code>jitter</code>	Scale factor for spreading out lines from each chain
<code>buffer.right</code>	Additional buffer on left side of plot
<code>buffer.left</code>	Additional buffer on right side of plot
<code>cex</code>	Expansion coefficient for text
<code>file</code>	Filename for saving figure to a file

Examples

```
samples1 <- cbind(rnorm(1000, 1), rgamma(1000, 1), rpois(1000, 1))
colnames(samples1) <- c('alpha', 'beta', 'gamma')
samples2 <- cbind(rnorm(1000, 2), rgamma(1000, 2), rpois(1000, 2))
colnames(samples2) <- c('alpha', 'beta', 'gamma')
samplesList <- list(chain1 = samples1, chain2 = samples2)
chainsSummary(samplesList, nrow = 1, jitter = .3, buffer.left = .5, buffer.right = .5)
```

 samplesPlot

Plot MCMC traceplots and density plots

Description

Plot MCMC traceplots and density plots

Usage

```
samplesPlot(samples, var = colnames(samples), ind = NULL,
  burnin = NULL, scale = FALSE, width = 7, height = 4,
  legend = TRUE, legend.location = "topright", traceplot = TRUE,
  densityplot = TRUE, file = NULL)
```

Arguments

samples	Array of MCMC samples, or a list of samples from multiple chains in which case the first chain is used
var	Parameter names to plot
ind	Indices of MCMC samples to plot
burnin	Number of initial MCMC samples to discard (default: 0)
scale	Logical, whether to normalize each posterior chain
width	Width of the plot
height	Height of the plot
legend	Logical, whether to include a legend of parameter names
legend.location	Location of legend
traceplot	Logical, whether to include traceplots (default: TRUE)
densityplot	Logical, whether to include density plots (default: TRUE)
file	Optional filename to save figure as a file

Examples

```
samples <- cbind(rnorm(1000), rgamma(1000, 1))
colnames(samples) <- c('alpha', 'beta')
samplesPlot(samples)
```