Package 'basicMCMCplots'

February 2, 2020

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

Version 0.2.5

Description Provides methods 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

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

NeedsCompilation no

Author Daniel Turek [aut, cre]

Maintainer Daniel Turek <danielturek@gmail.com>

R topics documented:

`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

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

Arguments

samplesList	List of arrays of MCMC samples from different chains
var	Parameter names to plot
nrows	Number of rows in the resulting plot
scale	Logical, whether to normalize each posterior chain
width	Width of figure
height	Height of figure
legend	Logical, whether to include a legend of chain names
legend.location	Legend location
jitter	Scale factor for spreading out lines from each chain
buffer	Buffer margin on both sides. Overrides buffer.right and buffer.left
buffer.right	Additional buffer on left side of plot
buffer.left	Additional buffer on right side of plot
cex	Expansion coefficient for text
file	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	Logaical, 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)
```

Index