

Package ‘basicMCMCplots’

May 7, 2026

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

Version 0.2.7

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](https://doi.org/10.1080/10618600.2016.1172487)>.

Depends R (>= 3.4.0)

License GPL-3

Encoding UTF-8

RoxygenNote 7.1.1

NeedsCompilation no

Author Daniel Turek [aut, cre]

Maintainer Daniel Turek <danielturek@gmail.com>

Repository CRAN

Date/Publication 2021-11-04 19:00:02 UTC

Contents

chainsPlot	2
chainsSummary	3
samplesPlot	4
Index	6

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,
  line = NULL,
  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>line</code>	Numeric vector of true parameter values for adding lines to plots
<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,
  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,
  line = NULL,
  width = 7,
  height = 4,
  legend = TRUE,
  legend.location = "topright",
  traceplot = TRUE,
  densityplot = TRUE,
  file = NULL
)

```

Arguments

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

Examples

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

Index

chainsPlot, 2
chainsSummary, 3
samplesPlot, 4