Package ‘plotMCMC’

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Description

Markov chain Monte Carlo diagnostic plots. The purpose of the package is to combine existing tools from the *coda* and *lattice* packages, and make it easy to adjust graphical details.

Details

*Diagnostic plots:*

- `plotTrace`: trends
- `plotAuto`: thinning
- `plotCumu`: convergence
- `plotSplom`: confounding of parameters

*Posterior plots:*

- `plotDens`: posterior(s)
- `plotQuant`: multiple posteriors on a common y axis

Examples:

- `xpar`: model parameters
- `xrec`: recruitment
- `xbio`: biomass
- `xpro`: future projected biomass

Note

`browseVignettes()` shows a vignette with all the example plots.

The plot functions assume that MCMC results are stored either as a plain `numeric` vector (single chain) or in a `data.frame` (multiple chains). The `mcmc` class is also supported.

Author(s)

Arni Magnusson and Ian Stewart.

References


**See Also**

The [coda](#) package is a suite of diagnostic functions and plots for MCMC analysis, many of which are used in `plotMCMC`.

Many `plotMCMC` graphics are trellis plots, rendered with the [lattice](#) package.

The functions `Args` and `ll` (package `gdata`) can be useful for browsing unwieldy functions and objects.

---

**plotAuto**

*Plot MCMC Autocorrelation*

**Description**

Plot Markov chain Monte Carlo autocorrelation over a range of lag values. This is a diagnostic plot for deciding whether a chain needs further thinning.

**Usage**

```r
plotAuto(mcmc, thin=1, log=FALSE, base=10, main=NULL, xlab="Lag", ylab="Autocorrelation", lty=1, lwd=1, col="black", ...) 
```

**Arguments**

- `mcmc` MCMC chain(s) as a vector, data frame or `mcmc` object.
- `thin` interval to subsample chain(s), or 1 to keep chain intact.
- `log` whether values should be log-transformed.
- `base` logarithm base.
- `main` main title.
- `xlab` x-axis label.
- `ylab` y-axis label.
- `lty` line type.
- `lwd` line width.
- `col` line color.
- `...` passed to autocorr.plot, title, and axis.

**Value**

Null, but a plot is drawn on the current graphics device.
Note

The Args function from the gdata package is recommended for reviewing the arguments, instead of args.

See Also

autocorr.plot is the underlying plotting function, and window.mcmc is used to optionally thin the chain(s).
plotTrace, plotAuto, plotCumu, and plotSplom are diagnostic plots.
plotDens and plotQuant are posterior plots.
plotMCMC-package gives an overview of the package.

Examples

plotAuto(xpar$R0)
plotAuto(xpar$R0, thin=10)
plotAuto(xpar, lag.max=50, ann=FALSE, axes=FALSE)

---

**plotCumu**

*Plot MCMC Cumulative Quantiles*

Description

Plot Markov chain Monte Carlo cumulative quantiles. This is a diagnostic plot for deciding whether the chain has converged.

Usage

plotCumu(mcmc, probs=c(0.025, 0.975), div=1, log=FALSE, base=10,
main=NULL, xlab="Iterations", ylab="Value", lty.median=1,
lwd.median=2, col.median="black", lty.outer=2, lwd.outer=1,
col.outer="black", ...)

Arguments

- `mcmc` : MCMC chain(s) as a vector, data frame or mcmc object.
- `probs` : vector of outer quantiles to draw, besides the median.
- `div` : denominator to shorten values on the y axis.
- `log` : whether values should be log-transformed.
- `base` : logarithm base.
- `main` : main title.
- `xlab` : x-axis label.
- `ylab` : y-axis label.
- `lty.median` : line type of median.
**plotDens**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>lwd.median</td>
<td>line width of median.</td>
</tr>
<tr>
<td>col.median</td>
<td>color of median.</td>
</tr>
<tr>
<td>lty.outer</td>
<td>line type of outer quantiles.</td>
</tr>
<tr>
<td>lwd.outer</td>
<td>line width of outer quantiles.</td>
</tr>
<tr>
<td>col.outer</td>
<td>color of outer quantiles.</td>
</tr>
<tr>
<td>...</td>
<td>passed to cumplot, title, and axis.</td>
</tr>
</tbody>
</table>

**Value**

Null, but a plot is drawn on the current graphics device.

**Note**

The args function from the gdata package is recommended for reviewing the arguments, instead of args.

**See Also**

- cumplot is the underlying plotting function, and quantile is called iteratively to calculate the cumulative quantiles.
- plotTrace, plotAuto, plotCumu, and plotSplom are diagnostic plots.
- plotDens and plotQuant are posterior plots.
- plotMCMC-package gives an overview of the package.

**Examples**

```r
plotCumu(xpar$R0, main="R0")
plotCumu(xpar$cSfull, main="cSfull")
plotCumu(xpar, probs=c(0.25,0.75), ann=FALSE, axes=FALSE)
```

**Description**

Plot Markov chain Monte Carlo density. This is an approximation of the posterior probability density function.
Usage

```r
plotDens(mcmc, probs=c(0.025,0.975), points=FALSE, axes=TRUE,
          same.limits=FALSE, between=list(x=axes,y=axes), div=1,
          log=FALSE, base=10, main=NULL, xlab=NULL, ylab=NULL,
          cex.main=1.2, cex.lab=1, cex.axis=0.8, cex.strip=0.8,
          col.strip="gray95", las=0, tck=0.5, tick.number=5,
          lty.density=1, lwd.density=3, col.density="black",
          lty.median=2, lwd.median=1, col.median="darkgray", lty.outer=3,
          lwd.outer=1, col.outer="darkgray", pch="|", cex.points=1,
          col.points="black", plot=TRUE, ...)```

Arguments

- **mcmc**: MCMC chain(s) as a vector, data frame or `mcmc` object.
- **probs**: vector of outer quantiles to draw, besides the median.
- **points**: whether individual points should be plotted along the x axis.
- **axes**: whether axis values should be plotted.
- **same.limits**: whether panels should have same x-axis limits.
- **between**: list with x and y indicating panel spacing.
- **div**: denominator to shorten values on the x axis.
- **log**: whether values should be log-transformed.
- **base**: logarithm base.
- **main**: main title.
- **xlab**: x-axis label.
- **ylab**: y-axis label.
- **cex.main**: size of main title.
- **cex.lab**: size of axis labels.
- **cex.axis**: size of tick labels.
- **cex.strip**: size of strip labels.
- **col.strip**: color of strip labels.
- **las**: orientation of tick labels: 0=parallel, 1=horizontal, 2=perpendicular, 3=vertical.
- **tck**: tick mark length.
- **tick.number**: number of tick marks.
- **lty.density**: line type of density curve.
- **lwd.density**: line width of density curve.
- **col.density**: color of density curve.
- **lty.median**: line type of median.
- **lwd.median**: line width of median.
- **col.median**: color of median.
- **lty.outer**: line type of outer quantiles.
plotQuant

1wd.outer        line width of outer quantiles.
col.outer        color of outer quantiles.
pch              symbol for points.
cex.points       size of points.
col.points       color of points.
plot             whether to draw plot.
...              passed to densityplot and panel.densityplot.

Value

When plot=TRUE, a trellis plot is drawn and a data frame is returned, containing the data used for plotting. When plot=FALSE, a trellis object is returned.

Note

The Args function from the gdata package is recommended for reviewing the arguments, instead of args.

See Also

xyplot and panel.densityplot are the underlying drawing functions, and link[coda]{densplot} is a similar non-trellis plot.

plotTrace, plotAuto, plotCumu, and plotSplom are diagnostic plots.

plotDens and plotQuant are posterior plots.

plotMCMC-package gives an overview of the package.

Examples

plotDens(xbio$"2004", points=TRUE, div=1000, main="2004\n", xlab="Biomass age 4+ (kt)", tick.number=6, strip=FALSE)
plotDens(xpar, xlab="Parameter value", ylab="Posterior density\n")

plotQuant

Description

Plot quantiles of multiple Markov chain Monte Carlo chains, using bars, boxes, or lines.
plotQuant

Usage

plotQuant(mcmc, style="boxes", probs=c(0.025,0.975), axes=TRUE,
names=NULL, ylim=NULL, yaxs="i", div=1, log=FALSE, base=10,
main=NULL, xlab=NULL, ylab=NULL, cex.axis=0.8, las=1,
tck=-0.015, tick.number=8, lty.median=1*(style!="bars"),
lwd.median=1+l*(style!="boxes"), col.median="black",
lty.outer=1+2*(style=="lines"), lwd.outer=1,
col.outer="black", pch=16, cex=0.8, col="black",
boxfill="darkgray", boxwex=0.5, staplewex=0.5, sfrac=0.005,
mai=c(0.8,1,1,0.6),
mgp=list(bottom=c(2,0.4,0),left=c(3,0.6,0),top=c(0,0.6,0),
right=c(0,0.6,0)), ...)

Arguments

mcmc  MCMC chains as a data frame or mcmc object.
style  how quantiles should be drawn: "bars", "boxes", or "lines".
probs  vector of outer quantiles to draw, besides the median.
axes  numeric vector indicating which axis labels should be drawn: 1=bottom, 2=left, 3=top, 4=right, or TRUE to display all (default).
names  x-axis labels.
ylim  y-axis limits.
yaxs  y-axis style: "i" to truncate exactly at limits (default) or "r" to extend the axis slightly beyond the limits.
div  denominator to shorten values on the y axis.
log  whether values should be log-transformed.
base  logarithm base.
main  main title.
xlab  x-axis label.
ylab  y-axis label.
cex.axis  size of tick labels.
las  orientation of tick labels: 0=parallel, 1=horizontal, 2=perpendicular, 3=vertical.
tck  tick mark length.
tick.number  number of tick marks.
lty.median  line type of median.
lwd.median  line width of median.
col.median  color of median.
lty.outer  line type of outer quantiles.
lwd.outer  line width of outer quantiles.
col.outer  color of outer quantiles.
pch  symbol for points.
\textit{plotQuant}  

- \texttt{cex} size of points.  
- \texttt{col} color of points.  
- \texttt{boxfill} color of boxes.  
- \texttt{boxwex} width of boxes.  
- \texttt{staplewex} width of error bar staples when \texttt{style=\texttt{boxes}}, as a fraction of box width.  
- \texttt{sfrac} width of error bar staples when \texttt{style=\texttt{bars}}, as a fraction of plot region.  
- \texttt{mai} margins around plot as a vector of four numbers (bottom, left, top, right).  
- \texttt{mgp} margins around axis titles, labels, and lines as a list of four vectors (bottom, left, top, right).  

... passed to \texttt{plot, bxp, plotCI, lines, matplot, axis}, and \texttt{title}.  

\textbf{Value}  

List containing:  

- \texttt{x} midpoint coordinates on the x axis.  
- \texttt{y} quantile coordinates on the y axis.  

\textbf{Note}  

With \texttt{style=\texttt{boxes}}, the quartiles are shown as boxes.  

The \texttt{Args} function from the \texttt{gdata} package is recommended for reviewing the arguments, instead of \texttt{args}.  

\textbf{See Also}  

- \texttt{bxp, plotCI}, and \texttt{matplot} are the underlying drawing functions.  
- \texttt{plotTrace, plotAuto, plotCumu}, and \texttt{plotSplom} are diagnostic plots.  
- \texttt{plotDens} and \texttt{plotQuant} are posterior plots.  
- \texttt{plotMCMC-package} gives an overview of the package.  

\textbf{Examples}  

\begin{verbatim}
plotQuant(xrec, names=substring(names(xrec),3), div=1000, xlab="Year", ylab="Recruitment (million one-year-olds)")
plotQuant(xbio, div=1000, xlab="Year", ylab="Biomass age 4+ (kt)")
plotQuant(xbio, style="bars", div=1000, sfrac=0, xlab="Year", ylab="Biomass age 4+ (kt)")
plotQuant(xbio, style="lines", div=1000, xlab="Year", ylab="Biomass age 4+ (kt)")
plotQuant(xpro, axes=1:2, div=1000, xlab="Year", ylab="Biomass age 4+ (kt)"
\end{verbatim}
plotSplom

Plot MCMC Scatterplot Matrix

Description

Plot scatterplots of multiple Markov chain Monte Carlo chains. This is a diagnostic plot for deciding whether parameters are confounded. When parameter estimates are highly dependent on each other, it may undermine conclusions based on MCMC results of that model.

Usage

plotSplom(mcmc, axes=FALSE, between=0, div=1, log=FALSE, base=10, ...)

Arguments

- `mcmc`: MCMC chains as a data frame or `mcmc` object.
- `axes`: whether axis values should be plotted.
- `between`: space between panels.
- `div`: denominator to shorten values on the y axis.
- `log`: whether values should be log-transformed.
- `base`: logarithm base.
- `...`: passed to `pairs`.

Value

Null, but a plot is drawn on the current graphics device.

Note

The `Args` function from the `gdata` package is recommended for reviewing the arguments, instead of `args`.

See Also

- `pairs` is the underlying drawing function, and `splom` is a similar trellis plot.
- `plotTrace, plotAuto, plotCumu, and plotSplom` are diagnostic plots.
- `plotDens` and `plotQuant` are posterior plots.
- `plotMCMC-package` gives an overview of the package.

Examples

```r
plotSplom(xpar, pch=".")
plotSplom(xpro, axes=TRUE, between=1, div=1000, main="Future biomass",
          cex.labels=1.5, pch=".", cex=3)
```
plotTrace

Plot MCMC Traces

Description

Plot Markov chain Monte Carlo traces. This is a diagnostic plot for deciding whether a chain shows unwanted trends.

Usage

plotTrace(mcmc, axes=FALSE, same.limits=FALSE, 
  between=list(x=axes,y=axes), div=1, span=1/4, log=FALSE, 
  base=10, main=NULL, xlab=NULL, ylab=NULL, cex.main=1.2, 
  cex.lab=1, cex.axis=0.8, cex.strip=0.8, col.strip="gray95", 
  las=0, tck=0.5, tick.number=5, lty.trace=1, lwd.trace=1, 
  col.trace="gray", lty.median=1, lwd.median=1, 
  col.median="black", lty.loess=2, lwd.loess=1, 
  col.loess="black", plot=TRUE, ...)

Arguments

mcmc MCMC chain(s) as a vector, data frame or mcmc object.
axes whether axis values should be plotted.
same.limits whether panels should have same x-axis limits.
between list with x and y indicating panel spacing.
div denominator to shorten values on the y axis.
span smoothness parameter, passed to panel.loess
log whether values should be log-transformed.
base logarithm base.
main main title.
xlab x-axis title.
ylab y-axis title.
cex.main size of main title.
cex.lab size of axis labels.
cex.axis size of tick labels.
cex.strip size of strip labels.
col.strip color of strip labels.
las orientation of tick labels: 0=parallel, 1=horizontal, 2=perpendicular, 3=vertical.
tck tick mark length.
tick.number number of tick marks.
lty.trace line type of trace.
lwd.trace  line width of trace.
col.trace  color of trace.
lty.median line type of median.
lwd.median line width of median.
col.median color of median.
lty.loess line type of loess.
lwd.loess line width of loess.
col.loess color of loess.
plot    whether to draw plot.
... passed to xyplot and panel.loess.

Value

When plot=TRUE, a trellis plot is drawn and a data frame is returned, containing the data used for plotting. When plot=FALSE, a trellis object is returned.

Note

The Args function from the gdata package is recommended for reviewing the arguments, instead of args.

See Also

xyplot and panel.loess are the underlying drawing functions, and traceplot is a similar non-trellis plot.
plotTrace, plotAuto, plotCumu, and plotSplom are diagnostic plots.
plotDens and plotQuant are posterior plots.
plotMCMC-package gives an overview of the package.

Examples

plotTrace(xpar, xlab="Iterations", ylab="Parameter value", layout=c(2,4))
plotTrace(xpar$R0, axes=TRUE, div=1000)
Description

Markov chain Monte Carlo results from stock assessment of cod (*Gadus morhua*) in Icelandic waters, showing estimated biomass by year in tonnes.

Usage

xbio

Format

Data frame containing 1000 rows and 34 columns (years 1971 to 2004).

Details

Each column contains the results of 1 million MCMC iterations, after thinning to every 1000th iteration.

The MCMC analysis started at the best fit, so no burn-in period was discarded.

Note

Biomass is the total weight of all individuals in a population, in this case ages 4 and older.

This data frame is a subset of the xmcmc list from the scape package, which contains further documentation about the data and model. More specifically, xbio <- xmcmc$B.

The MCMC analysis was run using the *AD Model Builder* software ([http://www.admb-project.org/](http://www.admb-project.org/)).

References


See Also

xpar (parameters), xrec (recruitment), xbio (biomass), and xpro (projected future biomass) are MCMC data frames to explore.

plotMCMC-package gives an overview of the package.
Examples

plotDens(robio$"2004", points=TRUE, div=1000, main="2004
", xlab="Biomass age 4+ (1000 t)", tick.number=6, strip=FALSE)

plotQuant(robio, div=1000, xlab="Year", ylab="Biomass age 4+ (kt)")
plotQuant(robio, style="bars", div=1000, sfrac=0, xlab="Year",
 ylab="Biomass age 4+ (kt)")
plotQuant(robio, style="lines", div=1000, xlab="Year",
 ylab="Biomass age 4+ (kt)")

xpar  

MCMC Results for Model Parameters

Description

Markov chain Monte Carlo results from stock assessment of cod (Gadus morhua) in Icelandic waters, showing estimated model parameters.

Usage

xpar

Format

Data frame containing 1000 rows and 8 columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>R0</td>
<td>average virgin recruitment</td>
</tr>
<tr>
<td>Rinit</td>
<td>initial recruitment scaler</td>
</tr>
<tr>
<td>uinit</td>
<td>initial harvest rate</td>
</tr>
<tr>
<td>cSleft</td>
<td>left-side slope of commercial selectivity curve</td>
</tr>
<tr>
<td>cSfull</td>
<td>age at full commercial selectivity</td>
</tr>
<tr>
<td>sSleft</td>
<td>left-side slope of survey selectivity curve</td>
</tr>
<tr>
<td>sSfull</td>
<td>age at full survey selectivity</td>
</tr>
<tr>
<td>logq</td>
<td>log-transformed survey catchability</td>
</tr>
</tbody>
</table>

Details

Each column contains the results of 1 million MCMC iterations, after thinning to every 1000th iteration.

The MCMC analysis started at the best fit, so no burn-in period was discarded.

Note

This data frame is a subset of the xmcmc list from the scape package, which contains further documentation about the data and model. More specifically, xpar <- xmcmc$P.

The MCMC analysis was run using the AD Model Builder software (http://www.admb-project.org/).
References


See Also

*xpar* (parameters), *xrec* (recruitment), *xbio* (biomass), and *xpro* (projected future biomass) are MCMC data frames to explore.

*plotMCMC-package* gives an overview of the package.

Examples

```r
plotTrace(xpar, xlab="Iterations", ylab="Parameter value",
          layout=c(2,4))
plotTrace(xpar$R0, axes=TRUE, div=1000)

plotAuto(xpar$R0)
plotAuto(xpar$R0, thin=10)
plotAuto(xpar, lag.max=50, ann=FALSE, axes=FALSE)

plotCumu(xpar$R0, main="R0")
plotCumu(xpar$cSfull, main="cSfull")
plotCumu(xpar, probs=c(0.25,0.75), ann=FALSE, axes=FALSE)

plotSplom(xpar, pch=".")
plotDens(xpar, xlab="Parameter value", ylab="Posterior density\n")
```

---

**xpro**

*MCMC Results for Future Projections*

Description

Markov chain Monte Carlo results from stock assessment of cod (*Gadus morhua*) in Icelandic waters, showing future projected biomass in tonnes.

Usage

*xpro*

Format

Data frame containing 1000 rows and 4 columns (years 2004 to 2007).
Details

Each column contains the results of 1 million MCMC iterations, after thinning to every 1000th iteration.
The MCMC analysis started at the best fit, so no burn-in period was discarded.

Note

The projections are based on a fixed harvest rate, where 25% of the biomass (ages 4 and older) is caught every year.

This data frame is a subset of the `xproj` list from the `scape` package, which contains further documentation about the data and model. More specifically, `xpro <- xproj$"0.25"`.

The MCMC analysis was run using the `AD Model Builder` software (http://www.admb-project.org/).

References


See Also

`xpar` (parameters), `xrec` (recruitment), `xbio` (biomass), and `xpro` (projected future biomass) are MCMC data frames to explore.

`plotMCMC-package` gives an overview of the package.

Examples

```r
plotQuant(xpro, axes=1:2, div=1000, xlab="Year", ylab="Biomass age 4+ (kt)")

plotSplom(xpro, axes=TRUE, between=1, div=1000, main="Future biomass", cex.labels=1.5, pch=".", cex=3)
```

---

**xrec**

*MCMC Results for Recruitment*

Description

Markov chain Monte Carlo results from stock assessment of cod (*Gadus morhua*) in Icelandic waters, showing estimated recruitment by year.
Usage

`xrec`

Format

Data frame containing 1000 rows and 33 columns (years 1970 to 2002).

Details

Each column contains the results of 1 million MCMC iterations, after thinning to every 1000th iteration.

The MCMC analysis started at the best fit, so no burn-in period was discarded.

Note

Recruitment is the size of a cohort (year class), in this case thousands of one-year-olds.

For example, `xrec$"1980"` is the estimated number of one-year-olds in 1981, the cohort that hatched in 1980.

This data frame is a subset of the `xmcmc` list from the `scape` package, which contains further documentation about the data and model. More specifically, `xrec <- xmcmc$R`.

The MCMC analysis was run using the AD Model Builder software (http://www.admb-project.org/).

References


See Also

`xpar` (parameters), `xrec` (recruitment), `xbio` (biomass), and `xpro` (projected future biomass) are MCMC data frames to explore.

`plotMCMC-package` gives an overview of the package.

Examples

```r
plotQuant(xrec, names=substring(names(xrec),3), div=1000, xlab="Year", ylab="Recruitment (million one-year-olds)")
```
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