Package 'plotMCMC'

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Title MCMC Diagnostic Plots

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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.

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Author Arni Magnusson [aut, cre],
Ian Stewart [aut]

Maintainer Arni Magnusson <`thisisarni@gmail.com`>

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R topics documented:

`plotMCMC-package` *MCMC Diagnostic Plots*

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

Fournier, D. A., Skaug, H. J., Ancheta, J., Ianelli, J., Magnusson, A., Maunder, M. N., Nielsen, A. and Sibert, J. (2012) AD Model Builder: using automatic differentiation for statistical inference of highly parameterized complex nonlinear models. *Optimization Methods and Software*, **27**, 233–249.

Magnusson, A., Punt, A. E. and Hilborn, R. (2013) Measuring uncertainty in fisheries stock assessment: the delta method, bootstrap, and MCMC. *Fish and Fisheries*, **14**, 325–342.

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

```
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.

`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.
`...`	passed to `cumuplot`, `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

`cumuplot` 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

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

`plotDens` *Plot MCMC Density*

Description

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

Usage

```
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.

`lwd.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` *Plot MCMC Quantiles*

Description

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

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+1*(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.

`cex`	size of points.
`col`	color of points.
`boxfill`	color of boxes.
`boxwex`	width of boxes.
`staplewex`	width of error bar staples when `style="boxes"`, as a fraction of box width.
`sfrac`	width of error bar staples when `style="bars"`, as a fraction of plot region.
`mai`	margins around plot as a vector of four numbers (bottom, left, top, right).
`mgp`	margins around axis titles, labels, and lines as a list of four vectors (bottom, left, top, right).
`...`	passed to `plot`, `bxp`, `plotCI`, `lines`, `matplot`, `axis`, and `title`.

Value

List containing:

`x`	midpoint coordinates on the x axis.
`y`	quantile coordinates on the y axis.

Note

With `style="boxes"`, the quartiles are shown as boxes.

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

See Also

`bxp`, `plotCI`, and `matplot` are the underlying drawing functions.

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

`plotDens` and `plotQuant` are posterior plots.

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

Examples

```
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)")
```

`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

```
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)
```

`xbio` *MCMC Results for Biomass*

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/`).

References

Fournier, D. A., Skaug, H. J., Ancheta, J., Ianelli, J., Magnusson, A., Maunder, M. N., Nielsen, A. and Sibert, J. (2012) AD Model Builder: using automatic differentiation for statistical inference of highly parameterized complex nonlinear models. *Optimization Methods and Software*, **27**, 233–249.

Magnusson, A., Punt, A. E. and Hilborn, R. (2013) Measuring uncertainty in fisheries stock assessment: the delta method, bootstrap, and MCMC. *Fish and Fisheries*, **14**, 325–342.

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

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)")
```

`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:

`R0`	average virgin recruitment
`Rinit`	initial recruitment scaler
`uinit`	initial harvest rate
`cSleft`	left-side slope of commercial selectivity curve
`cSfull`	age at full commercial selectivity
`sSleft`	left-side slope of survey selectivity curve
`sSfull`	age at full survey selectivity
`logq`	log-transformed survey catchability

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

Fournier, D. A., Skaug, H. J., Ancheta, J., Ianelli, J., Magnusson, A., Maunder, M. N., Nielsen, A. and Sibert, J. (2012) AD Model Builder: using automatic differentiation for statistical inference of highly parameterized complex nonlinear models. *Optimization Methods and Software*, **27**, 233–249.

Magnusson, A., Punt, A. E. and Hilborn, R. (2013) Measuring uncertainty in fisheries stock assessment: the delta method, bootstrap, and MCMC. *Fish and Fisheries*, **14**, 325–342.

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

```
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

Fournier, D. A., Skaug, H. J., Ancheta, J., Ianelli, J., Magnusson, A., Maunder, M. N., Nielsen, A. and Sibert, J. (2012) AD Model Builder: using automatic differentiation for statistical inference of highly parameterized complex nonlinear models. *Optimization Methods and Software*, **27**, 233–249.

Magnusson, A., Punt, A. E. and Hilborn, R. (2013) Measuring uncertainty in fisheries stock assessment: the delta method, bootstrap, and MCMC. *Fish and Fisheries*, **14**, 325–342.

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

```
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

Fournier, D. A., Skaug, H. J., Ancheta, J., Ianelli, J., Magnusson, A., Maunder, M. N., Nielsen, A. and Sibert, J. (2012) AD Model Builder: using automatic differentiation for statistical inference of highly parameterized complex nonlinear models. *Optimization Methods and Software*, **27**, 233–249.

Magnusson, A., Punt, A. E. and Hilborn, R. (2013) Measuring uncertainty in fisheries stock assessment: the delta method, bootstrap, and MCMC. *Fish and Fisheries*, **14**, 325–342.

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

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

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