Package 'MCMCtreeR'

October 12, 2022

Title Prepare MCMCtree Analyses and Plot Bayesian Divergence Time
Analyses Estimates on Trees

Version 1.1

Author Mark Puttick [aut,cre], Pascal Title [ctb]

Maintainer Mark Puttick <mark.puttick@bristol.ac.uk>

Description Provides functions to prepare time priors for 'MCMCtree' analyses in the 'PAML' software from Yang (2007)<doi:10.1093/molbev/msm088> and plot time-scaled phylogenies from any Bayesian divergence time analysis. Most time-calibrated node prior distributions require user-specified parameters. The package provides functions to refine these parameters, so that the resulting prior distributions accurately reflect confidence in known, usually fossil, time information. These functions also enable users to visualise distributions and write 'MCMCtree' ready input files. Additionally, the package supplies flexible functions to visualise age uncertainty on a plotted tree with using node bars, using branch widths proportional to the age uncertainty, or by plotting the full posterior distributions on nodes. Time-scaled phylogenetic plots can be visualised with absolute and geological timescales . All plotting functions are applicable with output from any Bayesian software, not just 'MCMCtree'.

Depends R (>= 3.3), ape (>= 3.0-7), sn, coda

Imports methods, utils, stats, grDevices, graphics

License GPL (>= 2)

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

Date/Publication 2019-05-21 22:20:31 UTC

R topics documented:

apeData	*ApeData Ape phylogeny in ape format, monophyletic clades, and maximum and minimum ages*

Description

ApeData Ape phylogeny in ape format, monophyletic clades, and maximum and minimum ages

Usage

```
data(apeData)
```

Format

An object of class list of length 4.

References

Yang 2014

Examples

```
data(apeData)
attach(apeData)
names(apeData)
```

---

estimateBound   *Estimate a Uniform Distribution for MCMCtree*

Description

Estimate the paramaters of a soft-bounded uniform distribution and output trees for MCMCtree input

Usage

```
estimateBound(minAge, maxAge, minProb = 0.025, rightTail = 0.025, phy,
  monoGroups, writeMCMCtree = FALSE, plot = TRUE,
  MCMCtreeName = "bound.tre", pdfOutput = "uniformPlot.pdf")
```

Arguments

minAge	vector of minimum age bounds for nodes matching order in monoGroups
maxAge	vector of maximum age bounds for nodes matching order in monoGroups
minProb	probability of left tail (minimum bound) - default to hard minimum (minProb=0)
rightTail	probability of right tail (maximum bound default = 0.975)
phy	fully resolved phylogeny in ape format
monoGroups	list with each element containing species that define a node of interest
writeMCMCtree	logical whether to write tree in format that is compatible with MCMCTree to file
plot	logical specifying whether to plot to PDF
MCMCtreeName	MCMCtree.output file name
pdfOutput	pdf output file name

Value

list containing node estimates for each distribution

- "parameters" estimated parameters for each node
- "apePhy" phylogeny in ape format with node labels showing node distributions
- "MCMCtree" phylogeny in MCMCtreeR format
- "nodeLabels" node labels in MCMCtreeR format

If plot=TRUE plot of distributions in file 'pdfOutput' written to current working directory

If writeMCMCtree=TRUE tree in MCMCtree format in file "MCMCtreeName" written to current working directory

Author(s)

Mark Puttick

Examples

```
data(apeData)
attach(apeData)
## extract taxon descending from calibrated nodes 8, 10, 11, 13
## these nodes can be visualised using plot.phylo
## and nodelabels from ape
monophyleticGroups <- tipDes(apeData$apeTree, c(8,10,11,13))
minimumTimes <- c("nodeOne"=15, "nodeTwo"=6,
"nodeThree"=8, "nodeFour"=13) / 10
maximumTimes <- c("nodeOne" = 30, "nodeTwo" = 12,
"nodeThree"=12, "nodeFour" = 20) / 10
estimateBound(minAge=minimumTimes, maxAge=maximumTimes,
monoGroups=monophyleticGroups, phy=apeTree, plot=FALSE)$MCMCtree
```

---

estimateCauchy   *Estimate Cauchy Distribution for MCMCtree*

Description

Estimate the offset and scale paramaters of a soft-tailed cauchy distribution and output trees for MCMCtree input

Usage

```
estimateCauchy(minAge, maxAge, phy, monoGroups, scale = 1.5,
  offset = 50, estimateScale = TRUE, minProb = 0, maxProb = 0.975,
  plot = FALSE, pdfOutput = "cauchyPlot.pdf", writeMCMCtree = FALSE,
  MCMCtreeName = "cauchyInput.tre")
```

Arguments

minAge	vector of minimum age bounds for nodes matching order in monoGroups
maxAge	vector of maximum age bounds for nodes matching order in monoGroups
phy	fully resolved phylogeny in ape format
monoGroups	list with each element containing species that define a node of interest
scale	scale value for cauchy distribution (default = 1.5) (c in PAML manual page 49)
offset	offset value for cauchy distribution (default = 50) (p in PAML manual page 49)
estimateScale	logical specifying whether to estimate scale with a given shape value (default = TRUE)
minProb	probability of left tail (minimum bound) - default to hard minimum (minProb=0)
maxProb	probability of right tail (maximum bound. default = 0.975)
plot	logical specifying whether to plot to PDF
pdfOutput	pdf output file name
writeMCMCtree	logical whether to write tree in format that is compatible with MCMCTree to file
MCMCtreeName	MCMCtree.output file name

Value

list containing node estimates for each distribution

- "parameters" estimated parameters for each node
- "apePhy" phylogeny in ape format with node labels showing node distributions
- "MCMCtree" phylogeny in MCMCtree format
- "nodeLabels" node labels in MCMCtreeR format

If plot=TRUE plot of distributions in file 'pdfOutput' written to current working directory

If writeMCMCtree=TRUE tree in MCMCtree format in file "MCMCtreeName" written to current working directory

Author(s)

Mark Puttick data(apeData) attach(apeData) ## extract taxon descending from calibrated nodes 8, 10, 11, 13 ## these nodes can be visualised using plot.phylo ## and nodelabels from ape monophyleticGroups <- tipDes(apeData$apeTree, c(8,10,11,13)) minimumTimes <- c("nodeOne"=15, "nodeTwo"=6, "nodeThree"=8, "nodeFour"=13) / 10 maximumTimes <- c("nodeOne" = 30, "nodeTwo" = 12, "nodeThree"=12, "nodeFour" = 20) / 10 estimateCauchy(minAge=minimumTimes, maxAge=maximumTimes, monoGroups=monophyleticGroups, offset=0.5, phy=apeTree, plot=FALSE)$MCMCtree

---

estimateFixed *Fixed Age for MCMCtree analysis input*

Description

Produce fixed age trees for MCMCtree analysis

Usage

```
estimateFixed(minAge, phy, monoGroups, writeMCMCtree = FALSE,
  MCMCtreeName = "estimateFixed.tre")
```

Arguments

minAge	vector of fixed age bounds for nodes matching order in monoGroups
phy	fully resolved phylogeny in ape format
monoGroups	list with each element containing species that define a node of interest
writeMCMCtree	logical whether to write tree in format that is compatible with MCMCTree to file
MCMCtreeName	MCMCtree.output file name

Value

list containing node estimates for each distribution

- "parameters" estimated parameters for each node
- "apePhy" phylogeny in ape format with node labels showing node distributions
- "MCMCtree" phylogeny in MCMCtreeR format
- "nodeLabels" node labels in MCMCtreeR format

If writeMCMCtree=TRUE tree in MCMCtree format in file "MCMCtreeName" written to current working directory

Author(s)

Mark Puttick

Examples

```
data(apeData)
attach(apeData)
## extract taxon descending from calibrated nodes 8, 10, 11, 13
## these nodes can be visualised using plot.phylo
## and nodelabels from ape
monophyleticGroups <- tipDes(apeData$apeTree, c(8,10,11,13))
minimumTimes <- c("nodeOne"=15, "nodeTwo"=6,
"nodeThree"=8, "nodeFour"=13) / 10
maximumTimes <- c("nodeOne" = 30, "nodeTwo" = 12,
"nodeThree"=12, "nodeFour" = 20) / 10
estimateFixed(minAge=minimumTimes[1],
monoGroups=monophyleticGroups[[1]], phy=apeTree)$MCMCtree
```

---

estimateGamma *Estimate Gamma Distribution for MCMCtree analysis*

Description

Estimate the shape and rate paramaters of Gamma distribution and output trees for MCMCtree input

Usage

```
estimateGamma(minAge, maxAge, phy, monoGroups, alpha = 188,
  beta = 2690, offset = 0.1, estimateAlpha = TRUE,
  estimateBeta = FALSE, plot = FALSE, pdfOutput = "gammaPlot.pdf",
  writeMCMCtree = FALSE, MCMCtreeName = "gammaInput.tre")
```

Arguments

`minAge`	vector of minimum age bounds for nodes matching order in monoGroups
`maxAge`	vector of maximum age bounds for nodes matching order in monoGroups
`phy`	fully resolved phylogeny in ape format
`monoGroups`	list with each element containing species that define a node of interest
`alpha`	alpha value for gamma distribution (default = 188)
`beta`	beta value for gamma distribution (default = 2690)
`offset`	distance of mean value from minimum bound
`estimateAlpha`	logical specifying whether to estimate alpha with a given beta value (default = TRUE)
`estimateBeta`	logical specifying whether to estimate beta with a given alpha value (default = FALSE)
`plot`	logical specifying whether to plot to PDF
`pdfOutput`	pdf output file name
`writeMCMCtree`	logical whether to write tree in format that is compatible with MCMCTree to file
`MCMCtreeName`	MCMCtree.output file name

Value

list containing node estimates for each distribution

- "parameters" estimated parameters for each node
- "apePhy" phylogeny in **APE** format with node labels showing node distributions
- "MCMCtree" phylogeny in MCMCtreeR format
- "nodeLabels" node labels in MCMCtreeR format

If plot=TRUE plot of distributions in file 'pdfOutput' written to current working directory

If writeMCMCtree=TRUE tree in MCMCtree format in file "MCMCtreeName" written to current working directory

Author(s)

Mark Puttick

Examples

```
data(apeData)
attach(apeData)
## extract taxon descending from calibrated nodes 8, 10, 11, 13
## these nodes can be visualised using plot.phylo
## and nodelabels from ape
monophyleticGroups <- tipDes(apeData$apeTree, c(8,10,11,13))
minimumTimes <- c("8"=15, "10"=6,
"11"=8, "13"=13) / 10
```

```
maximumTimes <- c("8" = 30, "10" = 12,
"11"=12, "13" = 20) / 10
gamma.nodes <- estimateGamma(minAge=minimumTimes, maxAge=maximumTimes,
monoGroups=monophyleticGroups, alpha=188, beta=2690,
offset=0.1, phy=apeTree, plot=FALSE)
gamma.nodes
```

---

estimateSkewNormal   *Estimate Skew Normal for MCMCtree analysis*

Description

Estimate the shape, scale, and location paramaters of a skew normal distribution and output trees
for MCMCtree input

Usage

```
estimateSkewNormal(minAge, maxAge, monoGroups, phy, shape = 50,
  scale = 1.5, addMode = 0, maxProb = 0.975, minProb = 0.003,
  estimateScale = TRUE, estimateShape = FALSE, estimateMode = FALSE,
  plot = FALSE, pdfOutput = "skewNormalPlot.pdf",
  writeMCMCtree = FALSE, MCMCtreeName = "skewNormalInput.tre")
```

Arguments

minAge	vector of minimum age bounds for nodes matching order in monoGroups
maxAge	vector of maximum age bounds for nodes matching order in monoGroups
monoGroups	list with each element containing species that define a node of interest
phy	fully resolved phylogeny in ape format
shape	shape value for skew normal distribution (default = 50)
scale	scale value for skew normal distribution (default = 1.5)
addMode	addition to the minimum age to give the location of the distribution
maxProb	probability of right tail (maximum bound default = 0.975)
minProb	probability of left tail (maximum bound default = 0.003)
estimateScale	logical specifying whether to estimate scale with a given shape value (default = TRUE)
estimateShape	logical specifying whether to estimate shape with a given scale value (default = FALSE)
estimateMode	logical speciftying whether to estimate the scale that produces probabilities of each tail that corresponds roughly to the values given by minProb (lower tail) and maxProb (upper tail)
plot	logical specifying whether to plot to PDF
pdfOutput	pdf output file name
writeMCMCtree	logical whether to write tree in format that is compatible with MCMCTree to file
MCMCtreeName	MCMCtree.output file name

Value

list containing node estimates for each distribution

- "parameters" estimated parameters for each node
- "apePhy" phylogeny in ape format with node labels showing node distributions
- "MCMCtree" phylogeny in MCMCtree format
- "nodeLabels" node labels in MCMCtreeR format

If plot=TRUE plot of distributions in file 'pdfOutput' written to current working directory

If writeMCMCtree=TRUE tree in MCMCtree format in file "MCMCtreeName" written to current working directory

Author(s)

Mark Puttick

See Also

[qst](#)

Examples

```
data(apeData)
attach(apeData)
monophyleticGroups <- list()
## extract taxon descending from calibrated nodes 8, 10, 11, 13
## these nodes can be visualised using plot.phylo
## and nodelabels from ape
monophyleticGroups <- tipDes(apeData$apeTree, c(8,10,11,13))
minimumTimes <- c("nodeOne"=15, "nodeTwo"=6,
"nodeThree"=8, "nodeFour"=13) / 10
maximumTimes <- c("nodeOne" = 30, "nodeTwo" = 12,
"nodeThree"=12, "nodeFour" = 20) / 10
estimateSkewNormal(minAge=minimumTimes, maxAge=maximumTimes,
monoGroups=monophyleticGroups, phy=apeTree, plot=FALSE)
```

---

estimateSkewT | *Estimate Skew-t Distribution for MCMCtree analysis*

Description

Estimate the shape, scale, and location paramaters of a Skew-t distribution and output trees for MCMCtree input

Usage

```
estimateSkewT(minAge, maxAge, monoGroups, phy, shape = 50, scale = 1.5,
  df = 1, addMode = 0, maxProb = 0.975, minProb = 0.003,
  estimateScale = TRUE, estimateShape = FALSE, estimateMode = FALSE,
  plot = FALSE, pdfOutput = "skewTPlot.pdf", writeMCMCtree = FALSE,
  MCMCtreeName = "skewTInput.tre")
```

Arguments

minAge	vector of minimum age bounds for nodes matching order in monoGroups
maxAge	vector of maximum age bounds for nodes matching order in monoGroups
monoGroups	list with each element containing species that define a node of interest
phy	fully resolved phylogeny in ape format
shape	shape value for skew-t distribution (default = 50)
scale	scale value for skew-t distribution (default = 1.5)
df	degrees of freedom for skew-t distribution (default = 1)
addMode	addition to the minimum age to give the location of the distribution
maxProb	probability of right tail (maximum bound default = 0.975)
minProb	probability of left tail (maximum bound default = 0.003)
estimateScale	logical specifying whether to estimate scale with a given shape value (default = TRUE)
estimateShape	logical specifying whether to estimate shape with a given scale value (default = FALSE)
estimateMode	logical speciftying whether to estimate the scale that produces probabilities of each tail that corresponds roughly to the values given by minProb (lower tail) and maxProb (upper tail)
plot	logical specifying whether to plot to PDF
pdfOutput	pdf output file name
writeMCMCtree	logical whether to write tree in format that is compatible with MCMCTree to file
MCMCtreeName	MCMCtree.output file name

Value

list containing node estimates for each distribution

- "parameters" estimated parameters for each node
- "apePhy" phylogeny in **APE** format with node labels showing node distributions
- "MCMCtree" phylogeny in MCMCtree format
- "nodeLabels" node labels in MCMCtreeR format

If plot=TRUE plot of distributions in file 'pdfOutput' written to current working directory

If writeMCMCtree=TRUE tree in MCMCtree format in file "MCMCtreeName" written to current working directory

Author(s)

Mark Puttick

See Also

[qst](#)

Examples

```
data(apeData)
attach(apeData)
## extract taxon descending from calibrated nodes 8, 10, 11, 13
## these nodes can be visualised using plot.phylo
## and nodelabels from ape
monophyleticGroups <- tipDes(apeData$apeTree, c(8,10,11,13))
minimumTimes <- c("nodeOne"=15, "nodeTwo"=6,
"nodeThree"=8, "nodeFour"=13) / 10
maximumTimes <- c("nodeOne" = 30, "nodeTwo" = 12,
"nodeThree"=12, "nodeFour" = 20) / 10
estimateSkewT(minAge=minimumTimes, maxAge=maximumTimes,
monoGroups=monophyleticGroups, phy=apeTree, plot=FALSE)$MCMCtree
```

---

estimateUpper   *Estimate Upper Age for MCMCtree analysis*

Description

Estimate the upper age distribution and output trees for MCMCtree input

Usage

```
estimateUpper(maxAge, rightTail = 0.025, phy, monoGroups,
  writeMCMCtree = FALSE, MCMCtreeName = "estimateUpper.tre")
```

Arguments

maxAge	vector of maximum age bounds for nodes matching order in monoGroups
rightTail	probability of right tail (maximum bound default = 0.025)
phy	fully resolved phylogeny in ape format
monoGroups	list with each element containing species that define a node of interest
writeMCMCtree	logical whether to write tree in format that is compatible with MCMCTree to file
MCMCtreeName	MCMCtree.output file name

Value

list containing node estimates for each distribution

- "parameters" estimated parameters for each node
- "apePhy" phylogeny in **APE** format with node labels showing node distributions
- "MCMCtree" phylogeny in MCMCtree format
- "nodeLabels" node labels in MCMCtreeR format

If plot=TRUE plot of distributions in file 'pdfOutput' written to current working directory

If writeMCMCtree=TRUE tree in MCMCtree format in file "MCMCtreeName" written to current working directory

Author(s)

Mark Puttick

Examples

```
data(apeData)
attach(apeData)
## extract taxon descending from calibrated nodes 8, 10, 11, 13
## these nodes can be visualised using plot.phylo
## and nodelabels from ape
monophyleticGroups <- tipDes(apeData$apeTree, c(8,10,11,13))
minimumTimes <- c("nodeOne"=15, "nodeTwo"=6,
"nodeThree"=8, "nodeFour"=13) / 10
maximumTimes <- c("nodeOne" = 30, "nodeTwo" = 12,
"nodeThree"=12, "nodeFour" = 20) / 10
estimateUpper(maxAge=maximumTimes, monoGroups=monophyleticGroups,
rightTail=0.025, phy=apeTree)
```

MCMC.tree.plot *Plot time-scaled phylogenies*

Description

Plot time-scaled phylogenies with node uncertainty and timescale

Usage

```
MCMC.tree.plot(phy = NULL, analysis.type = "MCMCtree",
  MCMC.chain = NULL, node.ages = NULL, directory.files = NULL,
  plot.type = "phylogram", build.tree = FALSE, node.method = "bar",
  all.nodes = NULL, add.time.scale = TRUE, add.abs.time = TRUE,
  scale.res = "Epoch", label.timescale.names = FALSE,
  time.correction = 1, col.age = "blue", tip.lengths = FALSE,
  density.col = "#00000050", density.border.col = "#00000080",
```

```
cex.tips = 1, show.tip.label = TRUE, col.tree = "black",
tip.color = "black", lwd.bar = 1, grey.bars = TRUE, cex.age = 1,
cex.labels = 1, cex.names = 1, relative.height = 0.08,
tip.bar.col = "#ff000050", burn.in = 0.25,
distribution.height = 0.8, abs.age.mgp = c(3, 0.35, 0),
abs.age.lwd.ticks = 0.7, abs.age.lwd = 0, tck.abs.age = -0.01,
abs.age.line = -0.4, pos.age = NULL, n.runs = 2,
ladderize.tree = TRUE, ...)
```

Arguments

phy	A timescaled phylogeny, unless analysis.type="MCMCtree" and build.tree=TRUE
analysis.type	The method used to generate the time-scale tree, one of MCMCtree, MrBayes, RevBayes, or User.
MCMC.chain	The full posterior of age estimates for all nodes (default NULL)
node.ages	List of user-supplied node ages applicable for analysis.type user. Either all nodes or a selection of nodes. Each list element must be named with its corresponding node label from the APE format.
directory.files	
	The directory for files to summarise for MrBayes and RevBayes analyses
plot.type	The plotting method for the phylogram corresponding to the APE definition. Phylogram is available for all analysis types, but cladogram is only avilable for MCMCtree analyses at present. Type distributions plots a phylogram with stats::density distributions on each of the nodes.
build.tree	Logical. Only applicable to MCMCtree analyses, whether to timescale the phylogeny based on the full MCMC chain
node.method	For plot.type phylogram the method to dispay age uncertainty on each node, either bar, node.length, or full.length. If 'none' is supplied plotting node uncertainty is suppressed.
all.nodes	If NULL (default) node uncertainty is plotted on all nodes. If node numbers are supplied, only these nodes will be labelled with uncertainty.
add.time.scale	Logical. Adds a timescale to the plotted phylogeny.
add.abs.time	Logical. Adds an absolute timescale alongside the geological timescale. Only applicable if add.time.scale is TRUE
scale.res	The geological age designation to add to the plot can be one or a combination of Eon, Period, Epoch, Age. The order of plot (from bottom to top) is the same as the supplied order. Subsequent arguments add.abs.time and grey.bars are based on the last supplied age designation.
label.timescale.names	
	Logical. Add names (Eon, Period, Epoch, Age, Ma) to axis if timescale used
time.correction	
	Number to place branch lengths and age estimates in absolute time, deafult to one.
col.age	The colouring of the node.method bars to summarise node age uncertainty

`tip.lengths`	Logical. If the tree contains non-present tip ages, the age uncertainty associated with them will be added to the plot
`density.col`	Colour of the node distributions (if analysis.type=distributions)
`density.border.col`	
	Colour of the node distributions (if analysis.type=distributions) borders
`cex.tips`	Size of the phylogeny tip labels
`show.tip.label`	Logical. Should the tree tip labels be displayed
`col.tree`	Colour of the phylogeny edges
`tip.color`	Colour of the phylogeny tip labels
`lwd.bar`	Width of the bar to summarise age uncertainty, applicable only if plot.type is phylogram and node.method is bar
`grey.bars`	Logical. Should grey bars be used to signify time bins, applicable only if add.time.scale is TRUE
`cex.age`	Size of the labels for the absolute timescale
`cex.labels`	Size of the labels for the geological timescale
`cex.names`	Logical. Add label.timescale.names, if applicable.
`relative.height`	
	the relative height of the timescale labels
`tip.bar.col`	The colour of uncertainty around non-contemporary tips
`burn.in`	The number of points in the chain to discard for MrBayes and RevBayes analyses
`distribution.height`	
	The relative height of node distributions when plot.type is distributions measured as the relative height of the descendent node
`abs.age.mgp`	mgp values for the absolute age axis, only applicable if add.abs.time is TRUE
`abs.age.lwd.ticks`	
	lwd values for the absolute age axis ticks, only applicable if add.abs.time is TRUE
`abs.age.lwd`	lwd values for the absolute age axis horizontal line, only applicable if add.abs.time is TRUE
`tck.abs.age`	tck values for the absolute age axis tick height, only applicable if add.abs.time is TRUE
`abs.age.line`	line correction for the absolute age axis tick, only applicable if add.abs.time is TRUE
`pos.age`	position position of absolute age axis
`n.runs`	For analysis.type mrbayes, the number of independent chains to summarise
`ladderize.tree`	Logical. Plot a ladderized tree (TRUE) or not (FALSE)
`...`	further arguments to be used in [`plot.phylo`](plot.phylo)

Details

The primary inputs for the 'method' options are outputs from analysis conducting using MCMCtree, MrBayes, RevBayes, or User.

For analyses under the 'MCMCtree' option (the default) the function only requires a 'FigTree' output from MCMCtree analysis or the full MCMCtree posterior. For option "MrBayes" and "RevBayes", the method argument takes the user-supplied directory address in which all the output files are stored.

For the option 'User' the function requires a full posterior distribution and time-scaled phylogeny. This function can take any posterior distribution, but it may require some manipulation. The argument node.ages in MCMC.tree.plot takes a named list containing the posterior ages for each node, with the name of each element corresponding to the node in the phylogeny.

Value

If plot=TRUE plot of distributions in file 'pdfOutput' written to current working directory

Author(s)

Mark Puttick

Examples

```
data(MCMCtree.output)
attach(MCMCtree.output)
## if it is necessary to read in file manually
## MCMCtree.posterior <- read.csv("mcmc.posterior.file.directory", sep="\t")
MCMCtree.file <- readMCMCtree(MCMCtree.phy, from.file=FALSE)$apePhy
MCMC.tree.plot(phy=MCMCtree.file,  analysis.type="MCMCtree",
MCMC.chain=MCMCtree.posterior, plot.type="distributions", cex.tips=0.5)
```

MCMCtree.output   *MCMCtree.output*

Description

Phylogeny output from MCMCtree, and posterior estimates from MCMCtree 'out' file from a re-analysis of data from Morris et al. 2018

Usage

```
data(MCMCtree.output)
```

Format

An object of class list of length 2.

References

Morris et al. 2018

Examples

```
data(MCMCtree.output)
attach(MCMCtree.output)
names(MCMCtree.output)
```

MCMCtreePhy   *MCMCtreePhy*

Description

Wrapper function to estimate node distributions and add them to tree and output MCMCtree format phylogeny file. If parameter values are in vectors shorter than the number of nodes they are recycled.

Usage

```
MCMCtreePhy(phy, minAges, maxAges, monoGroups, method = c("cauchy",
  "upper", "bound", "gamma", "skewNormal", "skewT", "fixed"),
  offset = 0.1, df = 1, shape = 50, scale = 1.5, minProb = 1e-08,
  addMode = 0, maxProb = 0.975, rightTail = 0.025, alpha = 188,
  beta = 100, estimateScale = TRUE, estimateShape = FALSE,
  estimateMode = FALSE, estimateAlpha = TRUE, estimateBeta = FALSE,
  plot = FALSE, pdfOutput = "nodeDistributions.pdf",
  writeMCMCtree = TRUE, MCMCtreeName = "output.tre")
```

Arguments

phy	fully resolved phylogeny in ape format
minAges	vector of minimum age bounds for nodes matching order in monoGroups
maxAges	vector of maximum age bounds for nodes matching order in monoGroups
monoGroups	list with each element containing species that define a node of interest
method	vector of the type of calibration distribution for each node
offset	offset value for distribution (default = 50)
df	degrees of freedom for skew-t distribution (default = 1)
shape	shape value for skew-t distribution (default = 50)
scale	scale value for distribution (default = 1.5)
minProb	probability of left tail (minimum bound) - default to hard minimum (minProb=0)
addMode	addition to the minimum age to give the location of the distribution
maxProb	probability of right tail (maximum bound. default = 0.975)
rightTail	probability of right tail (maximum bound default = 0.025)

alpha	alpha value for gamma distribution (default = 188)
beta	beta value for gamma distribution (default = 2690)
estimateScale	logical specifying whether to estimate scale with a given shape value (default = TRUE)
estimateShape	logical specifying whether to estimate shape with a given scale value
estimateMode	logical speciftying whether to estimate the scale that produces probabilities of each tail that corresponds roughly to the values given by minProb (lower tail) and maxProb (upper tail)
estimateAlpha	logical specifying whether to estimate alpha with a given beta value (default = TRUE)
estimateBeta	logical specifying whether to estimate beta with a given alpha value (default = FALSE)
plot	logical specifying whether to plot to PDF
pdfOutput	pdf output file name
writeMCMCtree	logical whether to write tree in format that is compatible with MCMCTree to file
MCMCtreeName	MCMCtree.output file name

Value

list containing node estimates for each distribution

- "parameters" estimated parameters for each node
- "apePhy" phylogeny in **APE** format with node labels showing node distributions
- "MCMCtree" phylogeny in MCMCtree format
- "nodeLabels" node labels in MCMCtreeR format

If plot=TRUE plot of distributions in file 'pdfOutput' written to current working directory

If writeMCMCtree=TRUE tree in MCMCtree format in file "MCMCtreeName" written to current working directory

Author(s)

Mark Puttick

Examples

```
data(apeData)
attach(apeData)
## extract taxon descending from calibrated nodes 8, 10, 11, 13
## these nodes can be visualised using plot.phylo
## and nodelabels from ape
monophyleticGroups <- tipDes(apeData$apeTree, c(8,10,11,13))
minimumTimes <- c("nodeOne"=15, "nodeTwo"=6,
"nodeThree"=8, "nodeFour"=13) / 10
maximumTimes <- c("nodeOne" = 30, "nodeTwo" = 12,
```

```
"nodeThree"=12, "nodeFour" = 20) / 10
# Cauchy, upper age, bound, and gamma applied individually to each node
MCMCtreePhy(phy=apeTree, minAge=minimumTimes, maxAge=maximumTimes,
monoGroups=monophyleticGroups, plot=FALSE,
method=c("cauchy", "upper", "bound", "gamma"), writeMCMCtree=FALSE)
```

---

nodeToPhy   *Add Node Constraints to Tree in MCMCtree Format*

Description

Produce tree with node labels in MCMCtree format

Usage

```
nodeToPhy(phy, monoGroups, nodeCon, returnPhy = TRUE)
```

Arguments

phy	fully resolved phylogeny in ape format
monoGroups	list with each element containing species that define a node of interest
nodeCon	node distributions in MCMCtreeR format
returnPhy	logical specifying whether to return phy to console or write MCMCtree for input (default = TRUE)

Value

If returnPhy=TRUE phylogeny with node labels in ape format

If returnPhy=FALSE phylogeny with node labels in MCMCtree format

Author(s)

Mark Puttick

---

plotMCMCtree   *Plot distribution from MCMCtree node estimations*

Description

Estimate the offset and scale paramaters of a soft-tailed cauchy distribution and output trees for MCMCtree input

Usage

```
plotMCMCtree(parameters, method = c("skewT", "skewNormal", "cauchy",
  "gamma", "bound"), title, upperTime, lowerTime = 0,
  plotMCMCtreeData = TRUE)
```

Arguments

`parameters`	output parameters from node estimation function
`method`	one of skewT, skewNormal, cauchy, gamma, or bound
`title`	title for the plot
`upperTime`	maxmimum age for x-axis plot
`lowerTime`	maxmimum age for x-axis plot (default = 0)
`plotMCMCtreeData`	
	If TRUE returns co-ordinates to plot distributions to allow greater flexibility (default = TRUE)

Value

plot of the specified prior applied for a node

If plotMCMCtreeData=TRUE x and y coordinates of distributions from 0 to upperTime on x axis

Author(s)

Mark Puttick

Examples

```
data(apeData)
attach(apeData)
# create monophyletic groups descending from nodes 8, 10, 11, and 13
monophyleticGroups <- tipDes(apeData$apeTree, c(8,10,11,13))
minimumTimes <- c("nodeOne"=15, "nodeTwo"=6,
"nodeThree"=8, "nodeFour"=13) / 10
maximumTimes <- c("nodeOne" = 30, "nodeTwo" = 12,
"nodeThree"=12, "nodeFour" = 20) / 10
cauchy <- estimateCauchy(minAge=minimumTimes[1], maxAge=maximumTimes[1],
monoGroups=monophyleticGroups[[1]], offset=0.5, phy=apeTree, plot=FALSE)
## un-comment to run
plotMCMCtree(parameters=cauchy$parameters, method="cauchy",
title="cauchyPlot", upperTime=maximumTimes[1]+1)
```

---

priorPosterior	*priorPosterior*

Description

Analyse prior and posterior node distributions from MCMCtree analysis

Usage

```
priorPosterior(MCMCPrior, MCMCPosterior = NULL, inputTree,
  return.density = FALSE, rootCalibration = NULL)
```

Arguments

`MCMCPrior`	prior of MCMC file from MCMCtree analysis using data=0
`MCMCPosterior`	posterior of MCMC file from MCMCtree analysis using data
`inputTree`	phylogeny in MCMCtree format used in MCMCtree analysis
`return.density`	Logical. Whether to return the density or original values for the effective prior and posterior.
`rootCalibration`	
	= NULL If NULL, then behaves as by default. Alternatively, if a user has specified a root prior in the MCMCtreeR control file it can be added here as a vector in the form it would appear tree.

Value

list containing node estimates for each distribution

- "prior" distribution of effective prior
- "posterior" distribution of posterior
- "specifiedPrior" distribution of specified prior

Author(s)

Mark Puttick, Pascal Title

Examples

```
data(MCMCtree.output)
# priorPosterior(MCMCPrior,
# MCMCPosterior=MCMCtree.output$MCMCtree.posterior,
# path.to.input.tree)
```

---

readMCMCtree	*Read MCMCtree output tree into R*

Description

Read MCMCtree output tree into R to produce time-scaled tree in APE format, and a table of the mean and 95

Usage

```
readMCMCtree(inputPhy, forceUltrametric = TRUE, from.file = TRUE)
```

Arguments

`inputPhy`	file directory of 'Figtree' output from MCMCtree
`forceUltrametric`	
	alters branch lengths at tips so tree is fully ultrametric (default = TRUE)
`from.file`	Logical. Read a tree from file or locally from within R?

Value

apePhy time-scaled output tree from MCMCtree in APE format

nodeAges mean and 95

Author(s)

Mark Puttick

Examples

```
data(MCMCtree.output)
attach(MCMCtree.output)
# tree and node ages
readMCMCtree(MCMCtree.phy, from.file=FALSE)
```

---

tipDes   *Find Descendent Tips From A Common Ancestor*

Description

This function finds tip descendants from a common ancestor

Usage

```
tipDes(phy, node)
```

Arguments

phy   user tree in ape format

node   one or more nodes from the ape format that designate the crown monophyletic
             group

Details

If a single node number is supplied the function returns a vector of tip labels. When more than one
node number is supplied the function returns a list with each element a vector of tip labels for that
node.

Author(s)

Mark Puttick

Examples

```
set.seed(1029)
# one node
phy <- rcoal(10)
node <- 13
tipDes(phy, node)
## multiple nodes
node <- c(13,14,15)
tipDes(phy, node)
```

Index