R documentation

of 'OUwie.contour.Rd'

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OUwie.contour   *Contour plot of likelihood surface*

Description

Plots likelihood surface for pairs of free parameters for generalized Ornstein-Uhlenbeck-based Hansen models of continuous characters evolving under discrete selective regimes.

Usage

```
OUwie.contour(phy, data, model=c("BM1","BMS","OU1","OUM","OUMV","OUMA","OUMVA"),
simmap.tree=FALSE, scaleHeight=FALSE,root.station=TRUE, lb=0.000001, ub=1000,
focal.param=NULL, clade=NULL, mserr="none", nrep=1000, sd.mult=3,
levels=c(0.5,1,1.5,2), likelihood.boundary=Inf, lwd=2, ...)
```

Arguments

phy	a phylogenetic tree, in ape "phylo" format and with internal nodes labeled denoting the ancestral selective regimes.
data	a data matrix containing species information (see Details).
model	models to fit to comparative data (see Details).
simmap.tree	a logical indicating whether the input tree is in SIMMAP format. The default is FALSE.
scaleHeight	a logical indicating whether the total tree height should be scaled to 1 (see Details). The default is FALSE.
root.station	a logical indicating whether the starting state, θ_0, should be estimated (see Details).
lb	lower bound for the likelihood search. The default is lb=0.000001. Note that this value must be greater than zero.
ub	upper bound for the likelihood search. The default is ub=1000.
focal.param	a character vector with the pair of parameters (sigma.sq and/or alpha) to plot (see Details).
clade	a list containing a pair of taxa whose MRCA is the clade of interest (see Details).

mserr	designates whether a fourth column in the data matrix contains measurement error for each species value ("known"). The measurement error is assumed to be the standard error of the species mean. The default is "none".
nrep	the number of points to use for the likelihood surface.
sd.mult	the sd for the normal distribution to pull random points from is sd.mult * se for each parameter.
levels	the levels at which to draw contour lines, measured as lnL units away from the best values.
likelihood.boundary	
	default = Inf
lwd	a graphical control for the width of the line
...	Additional arguments to be passed to the plot device

Details

This function creates a plot of the likelihood surface for a pair of parameters, letting the other parameters find their own optima. It can be very slow, as it involves optimization `nrep` times (though with two fewer parameters than with the chosen model, as the focal parameter values are fixed). It uses half its points to sample near the MLE and half to uniformly sample across a range. However, it is important to do as on some trees and with some models, certain parameters may correlate with each other.

The pair of parameters to examine is passed by focal.param. For example, to do a plot of sigma.sq from the first regime and alpha from the second regime, one would pass

`focal.param = c( "sigma.sq_1", "alpha_2")`.

This returns a data.frame with the first two columns being the values of the points examined and the third column the loglik of those points. The last row contains the MLE.

IMPORTANT: this currently written to only do sigma.sq and/or alpha, not theta. IMPORTANT II: this function requires the package akima.

Value

finalResults	the parameter values and loglik

Author(s)

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References

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