

Package ‘phylocurve’

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Type Package

Title Phylogenetic comparative methods for function-valued traits

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Description phylocurve offers a variety of phylogenetic comparative tools for studying the evolution of function-valued traits, including ancestral state reconstruction, estimating phylogenetic signal, and assessing correlated function-valued trait evolution.

License GPL (>= 2)

Imports ape, geiger, phytools, phylolm

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phylocurve-package	<i>phylocurve: Phylogenetic comparative methods for function-valued traits</i>
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Description

phylocurve offers a variety of phylogenetic comparative tools for studying the evolution of function-valued traits, including ancestral state reconstruction, estimating phylogenetic signal, and assessing correlated function-valued trait evolution.

Details

Package: phylocurve
 Type: Package
 Version: 1.0
 Date: 2015-02-26
 License: GPL (>= 2)

Author(s)

Eric W. Goolsby <eric.goolsby.evolution@gmail.com>

References

- Goolsby, E.W. 2015. "Phylogenetic comparative methods for evaluating the evolutionary history of function-valued traits." *Systematic Biology*. In press.
- Adams, D.C. 2014. A method for assessing phylogenetic least squares models for shape and other high-dimensional multivariate data. *Evolution*. 68:2675-2688.
- Adams, D.C. 2014. A generalized K statistic for estimating phylogenetic signal from shape and other high-dimensional multivariate data. *Systematic Biology*. 63:685-697.
- Ho, L. S. T. and Ane, C. 2014. "A linear-time algorithm for Gaussian and non-Gaussian trait evolution models". *Systematic Biology* 63(3):397-408.

Examples

```
require(phytools)

# simulate evolution of a function-valued trait (glm with logit link)
sim_data <- simcurves()

# ancestral curve reconstruction
anc_recon <- phylocurve(formula = y~x, tree = sim_data$tree, data = sim_data$data)

# estimate phylogenetic signal
phylocurve.signal(tip_coefficients = anc_recon$tip_coefficients, tree = sim_data$tree)

# assess correlated trait evolution with a univariate trait
X <- fastBM(sim_data$tree)
phylocurve.pglis(tip_coefficients = anc_recon$tip_coefficients,
  univariate_trait = X, tree = sim_data$tree)
```

get_tip_coefficients *Estimate regression coefficients for tip species curves*

Description

Estimates regression coefficients for tip species curves from raw data. May be useful if wanting to perform methods without first performing ancestral curve reconstruction via the phylocurve() function.

Usage

```
get_tip_coefficients(formula, tree, data, ymin = 0.01, ymax = 0.99,  
ylength = 30, species_identifier = "species", verbose = FALSE)
```

Arguments

formula	Formula for function-valued trait (currently only supports models of the form $Y \sim X$)
tree	A phylogenetic tree of class "phylo"
data	A data frame with data for tip curve estimation, where each row contains a single data point. A column named "species" has the species names corresponding to each data point, a predictor (X) variable and the response (Y) variable, which must be scaled between 0 and 1.
ymin	Because 0 and 1 are undefined for inverse logit functions, the minimum and maximum values are defaulted to .01 and .99. Can be adjusted as needed.
ymax	Because 0 and 1 are undefined for inverse logit functions, the minimum and maximum values are defaulted to .01 and .99. Can be adjusted as needed.
ylength	How many landmarks (points on the curve) to evaluate.
species_identifier	Default is "species". Can be changed if the column in data has a different species identifier name.
verbose	either to print progress during tip curve coefficient estimation.

Value

Estimated regression coefficients of tip curves.

Examples

```
require(phytools)  
  
# simulate evolution of a function-valued trait (glm with logit link)  
sim_data <- simcurves()  
  
tip_coefficients <- get_tip_coefficients(formula = y~x, tree = sim_data$tree, data = sim_data$data)  
  
# ancestral curve reconstruction  
anc_recon <- phylocurve(tree = sim_data$tree, tip_coefficients = tip_coefficients)  
  
# estimate phylogenetic signal  
phylocurve.signal(tip_coefficients = tip_coefficients, tree = sim_data$tree)  
  
# assess correlated trait evolution with a univariate trait  
X <- fastBM(sim_data$tree)  
phylocurve.pgls(tip_coefficients = tip_coefficients, univariate_trait = X, tree = sim_data$tree)
```

 phylocurve

Ancestral curve reconstruction

Description

This function performs ancestral reconstruction of function-valued traits. Currently only logistic regression (glm with logit link) is implemented.

Usage

```
phylocurve(formula, tree, data, ymin = 0.01, ymax = 0.99, ylength = 30,
tip_coefficients, species_identifier = "species", verbose = FALSE)
```

Arguments

formula	Formula for function-valued trait (currently only supports models of the form $Y \sim X$)
tree	An phylogenetic tree of class "phylo"
data	A data frame with data for tip curve estimation, where each row contains a single data point. A column named "species" has the species names corresponding to each data point, a predictor (X) variable and the response (Y) variable, which must be scaled between 0 and 1.
ymin	Because 0 and 1 are undefined for inverse logit functions, the minimum and maximum values are defaulted to .01 and .99. Can be adjusted as needed.
ymax	Because 0 and 1 are undefined for inverse logit functions, the minimum and maximum values are defaulted to .01 and .99. Can be adjusted as needed.
ylength	How many landmarks (points on the curve) to evaluate.
tip_coefficients	A matrix of regression coefficients can be provided instead of raw data. Row names should be species names, the first column should be the glm logit intercept parameter, and the second column should be the glm logit slope parameter.
species_identifier	Default is "species". Can be changed if the column in data has a different species identifier name.
verbose	Whether to print progress during ancestral curve reconstruction.

Details

This function uses a PGLS-based method described in Goolsby (2015) to perform ancestral curve reconstruction. This function uses a fast tree transversal method via the phylolm package (Ho and Ane, 2014)

Value

node_coefficients	Estimated regression coefficients of internal nodes
fitted_x	Reconstructed x-values for each internal node. Curve coordinates for internal node i are (fitted_x[i], y_vals)
lower_CI_x	Lower 95 percent confidence interval for fitted x-values for each internal node

upper_CI_x Upper 95 percent confidence interval for fitted x-values for each internal node

y_vals Vector of y-values used as inputs for inverse function evaluation. Curve coordinates for internal node *i* are (fitted_x[,i],y_vals)

tip_coefficients Estimated regression coefficients of tip curves.

Author(s)

Eric W. Goolsby

References

Goolsby, E.W. 2015. "Phylogenetic comparative methods for evaluating the evolutionary history of function-valued traits." *Systematic Biology*. In press.

Ho, L. S. T. and Ane, C. 2014. "A linear-time algorithm for Gaussian and non-Gaussian trait evolution models". *Systematic Biology* 63(3):397-408.

Examples

```
require(phytools)

# simulate evolution of a function-valued trait (glm with logit link)
sim_data <- simcurves()

# ancestral curve reconstruction
anc_recon <- phylocurve(formula = y~x, tree = sim_data$tree, data = sim_data$data)

# estimate phylogenetic signal
phylocurve.signal(tip_coefficients = anc_recon$tip_coefficients, tree = sim_data$tree)

# assess correlated trait evolution with a univariate trait
X <- fastBM(sim_data$tree)
phylocurve.pgls(tip_coefficients = anc_recon$tip_coefficients,
univariate_trait = X, tree = sim_data$tree)
```

phylocurve.pgls

Phylogenetic ANOVA/regression for function-valued data

Description

This function wraps `procD.pgls` from the `geomorph` package (Adams 2014) to assess the significance of correlated evolution between a function-valued and a univariate trait.

Usage

```
phylocurve.pgls(tip_coefficients, univariate_trait, tree, ymin = 0.01,
ymax = 0.99, ylength = 30, iter = 1000)
```

Arguments

<code>tip_coefficients</code>	A matrix of regression coefficients can be provided instead of raw data. Row names should be species names, the first column should be the glm logit intercept parameter, and the second column should be the glm logit slope parameter.
<code>univariate_trait</code>	A univariate trait (with species names) to assess for correlated evolution with a function-valued trait.
<code>tree</code>	A phylogenetic tree of class "phylo"
<code>ymin</code>	Because 0 and 1 are undefined for inverse logit functions, the minimum and maximum values are defaulted to .01 and .99. Can be adjusted as needed.
<code>ymax</code>	Because 0 and 1 are undefined for inverse logit functions, the minimum and maximum values are defaulted to .01 and .99. Can be adjusted as needed.
<code>ylength</code>	How many landmarks (points on the curve) to evaluate.
<code>iter</code>	Number of iterations for significance testing

Details

See [procD.pgls](#) for additional details.

Value

Function returns an ANOVA table of statistical results for all factors: df (for each factor), SS, MS, F ratio, Prand, and Rsquare.

References

Adams, D.C. 2014. A method for assessing phylogenetic least squares models for shape and other high-dimensional multivariate data. *Evolution*. 68:2675-2688.

Goolsby, E.W. 2015. "Phylogenetic comparative methods for evaluating the evolutionary history of function-valued traits." *Systematic Biology*. In press.

Examples

```
require(phytools)

# simulate evolution of a function-valued trait (glm with logit link)
sim_data <- simcurves()

# ancestral curve reconstruction
anc_recon <- phylocurve(formula = y~x, tree = sim_data$tree, data = sim_data$data)

# assess correlated trait evolution with a univariate trait
X <- fastBM(sim_data$tree)
phylocurve.pgls(tip_coefficients = anc_recon$tip_coefficients,
univariate_trait = X, tree = sim_data$tree)
```

phylocurve.signal *Phylogenetic signal of function-valued traits*

Description

This function wraps `physignal` from the `geomorph` package (Adams 2014) to calculate a multivariate version of Blomberg's K (`Kmult`).

Usage

```
phylocurve.signal(tip_coefficients, tree, ymin = 0.01, ymax = 0.99,  
ylength = 30, iter = 1000)
```

Arguments

<code>tip_coefficients</code>	A matrix of regression coefficients can be provided instead of raw data. Row names should be species names, the first column should be the glm logit intercept parameter, and the second column should be the glm logit slope parameter.
<code>tree</code>	An phylogenetic tree of class "phylo"
<code>ymin</code>	Because 0 and 1 are undefined for inverse logit functions, the minimum and maximum values are defaulted to .01 and .99. Can be adjusted as needed.
<code>ymax</code>	Because 0 and 1 are undefined for inverse logit functions, the minimum and maximum values are defaulted to .01 and .99. Can be adjusted as needed.
<code>ylength</code>	How many landmarks (points on the curve) to evaluate.
<code>iter</code>	Number of iterations for significance testing

Details

A multivariate generalization of Blomberg's K. See [physignal](#) for additional details.

Value

<code>phy.signal</code>	The estimate of phylogenetic signal
<code>pvalue</code>	The significance level of the observed signal

References

- Adams, D.C. 2014. A generalized K statistic for estimating phylogenetic signal from shape and other high-dimensional multivariate data. *Systematic Biology*. 63:685-697.
- Blomberg SP, Garland T, Ives AR. 2003. Testing for phylogenetic signal in comparative data: behavioral traits are more labile. *Evolution*, 57:717-745.
- Goolsby, E.W. 2015. "Phylogenetic comparative methods for evaluating the evolutionary history of function-valued traits." *Systematic Biology*. In press.

Examples

```

require(phytools)

# simulate evolution of a function-valued trait (glm with logit link)
sim_data <- simcurves()

# ancestral curve reconstruction
anc_recon <- phylocurve(formula = y~x, tree = sim_data$tree, data = sim_data$data)

# estimate phylogenetic signal
phylocurve.signal(tip_coefficients = anc_recon$tip_coefficients, tree = sim_data$tree)

```

simcurves

Simulate function-valued curve evolution

Description

This function simulates evolution of a function-valued trait (glm with logit link) under Brownian motion.

Usage

```
simcurves(nspecies = 30, x_length = 20, starttree = FALSE, lambda = 1, seed)
```

Arguments

nspecies	Number of species
x_length	Number of points on the curve to simulate
starttree	Simulate using a star tree
lambda	Pagel's lambda tree transformation parameter (lambda = 0 for star tree; lambda = 1 for original tree)
seed	Optional seed to set for reproducibility

Value

data	Data frame with simulated curves formatted appropriately for phylocurve()
tree	Phylogenetic tree of class "phylo"
true_coefs	True tip and ancestral coefficients for glm logit link

References

Pagel, M. 1999. "Inferring the historical patterns of biological evolution". *Nature* 401:877-884.

Examples

```
require(phytools)

# simulate evolution of a function-valued trait (glm with logit link)
sim_data <- simcurves()

# ancestral curve reconstruction
anc_recon <- phylocurve(formula = y~x, tree = sim_data$tree, data = sim_data$data)

# estimate phylogenetic signal
phylocurve.signal(tip_coefficients = anc_recon$tip_coefficients, tree = sim_data$tree)

# assess correlated trait evolution with a univariate trait
X <- fastBM(sim_data$tree)
phylocurve.pgls(tip_coefficients = anc_recon$tip_coefficients,
univariate_trait = X, tree = sim_data$tree)
```

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