# Package ‘PVR’

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**Type**  Package  

**Title**  Computes phylogenetic eigenvectors regression (PVR) and phylogenetic signal-representation curve (PSR) (with null and Brownian expectations)  

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**Author**  Thiago Santos, Jose Alexandre Diniz-Filho, Thiago Rangel e Luis Mauricio Bini  

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**Suggests**  picante, geiger  

**Maintainer**  Thiago Santos <thiagobioufg@gmail.com>  

**Description**  Computes PVR and PSR.  

**License**  GPL (>= 2)  

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PVR-package

Computes Phylogenetic eigenVectors Regression and Phylogentic Signal-Representation curve (with null and neutral expectations).

Description

Computes PVR and PSR curve along with some plot utilities.

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Author(s)

Santos, T; Diniz-Filho, J.A.F.; Rangel, T.F.; Bini, L.M.
Maintainer: Thiago Santos <thiagobioufg@gmail.com>

References


See Also

PVR-class, PSR-class, PVR, PSR, PVRdecomp, PSRplot, VarPartplot

Examples

#Creating a 10 tips ultrametric random phylogeny
library(ape)
tree <- rcoal(10)
#Decomposing phylogenetic distance matrix derived from tree into a set of orthogonal vectors
PSR

x <- PVRdecomp(tree)
trait <- runif(10)
y <- PSR(x, trait)
plot(y)

PSR

Creates a phylogenetic signal-representation (PSR) curve for a given phylogeny and trait set and computes its area.

Description

Phylogenetic signal-representation (PSR) curve, built upon phylogenetic eigenvector regression (PVR). Sequential PVR models are fitted after successively increasing the number of eigenvectors and plotting their R² against the accumulated eigenvalues. The PSR area, expressing deviations from Brownian motion, is strongly correlated with Blomberg’s K-statistics, so nonlinear PSR curves reveal if traits are evolving at a slower or higher rate than expected. The PSR area is also correlated with phylogenetic half-life under an OU process, so both methods describe the relationship between interspecific variation and time since divergence among species shape.

Usage

PSR(x, trait = NULL, null.model = FALSE, Brownian.model = FALSE, times = 1000)

Arguments

x
A object of class PVR (created using PVRdecomp function).

trait
A vector, data frame or matrix that contains continuous or binary traits sets (for data frames and matrices, each column must represent a trait set). For now, only the first column will be used.

null.model
Logical. Should the function estimates the null expectation for the PSR area. Default is FALSE.

Brownian.model
Logical. Should the function estimates the Brownian (neutral) expectation for the PSR area. Default is FALSE.

times
Number of iterations used in null.model and Brownian.model.

Value

PSR function returns a object of (S4) class PSR that extends the (S4) class PVR, by adding: a PSR slot that contains the area (and p if null.model = TRUE) for each trait set, the cumulative eigenvalues and R² that determine the curve; a slot with the null and neutral expectations (if any).

Author(s)

Santos, T; Diniz-Filho, J.A.F.; Rangel, T.F.; Bini, L.M.
References


See Also

PVR, PVRdecomp, PSRplot, VarPartplot

Examples

library(splancs)
#Creating a 10 tips ultrametric random phylogeny
library(ape)
tree <- rcoal(10)
#Decomposing phylogenetic distance matrix derived from tree into a set of orthogonal vectors
x <- PVRdecomp(tree)
trait <- runif(10)
y <- PSR(x, trait)
plot(y)

---

PSR-class

Class "PSR"

Description

A S4 class that extends S4 PVR class in order to accommodate PSR analysis results.

Objects from the Class

Objects can be created by calls of the form new("PSR", ...).

Slots

PSRarea: Object of class "data.frame" that contains PSR curve area.
PSR: Object of class "data.frame" that contains accumulated r squared and eigenvalues.
Expect.area.values: Object of class "list" that contains the expected null and neutral area values.
nullPSR: Object of class "matrix" nested in the Expect.area.values slot that contains the expected null area values.
PSR-class

BrownianPSR: Object of class "matrix" nested in the Expect.area.values slot that contains the expected Brownian (neutral) area values.

Eigen: Object of class "list" that contains the eigenvalues and eigenvectors generated by phylogenetic distance matrix eigendecomposition. Inherited from PVR class.

phyDist: Object of class "matrix" that contains a phylogenetic distance matrix. Inherited from PVR class.

phylo: Object of class "phylo" that contains a phylogeny. Inherited from PVR class.

Selection: Object of class "list" that contains the selection method (along with its statistics) used to select the vectors, the selected vectors IDs and a matrix that contains the selected vectors. Inherited from PVR class.

PVR: Object of class "list" that contains the Phyllogenetic Eigenvectors Regression r squared and residuals. Inherited from PVR class.

VarPart: Object of class "list" that contains the variation partition components. Inherited from PVR class.

Extends

Class "PVR", directly.

Methods

plot signature(x = "PSR")

show signature(object = "PSR")

Author(s)

Santos, T; Diniz-Filho, J.A.F.; Rangel, T.F.; Bini, L.M.

References


See Also

PVR-class, PVR, PSR, PVRdecomp, PSRplot, VarPartplot

Examples

showClass("PSR")
PSRplot

Plot function for objects of class PSR

Description
Plot PSR curve along with null and neutral expectations curves.

Usage
PSRplot(x, info = c("area", "null", "Brownian", "both"), ...)

Arguments
x        An object of class PSR
info     Type of information to be plotted. It can be "area" (to plot only the PSR curve), "null" (to plot PSR curve and null PSR curve), "neutral" (to plot PSR curve and neutral PSR curve) and "both" (to plot PSR curve and both null and neutral PSR curve).
...      Parameters passed to the plot function.

Author(s)
Santos, T; Diniz-Filho, J.A.F.; Rangel, T.F.; Bini, L.M.

References

See Also
PSR, PVRdecomp, PVR, VarPartplot

Examples
library(splancs)
#Creating a 10 tips ultrametric random phylogeny
library(ape)
tree <- rcoal(10)
#Decomposing phylogenetic distance matrix derived from tree into a set of orthogonal vectors
x <- PVRdecomp(tree)
trait <- runif(10)
res <- PSR(x, trait = trait, null.model = TRUE, Brownian.model = TRUE, times = 10)
PSRplot(res, info = "both")

---

**PVR**  
*Phylogenetic eigenvectors regression.*

**Description**

The phylogenetic eigenvector regression (PVR) starts by performing an eigendecomposition of a pairwise double-centered phylogenetic distance matrix between species. The eigenvectors (representing the traits under analysis) estimated values express phylogenetic trends in data and residuals express independent evolution of each species.

**Usage**

PVR(x, phy = NULL, trait = NULL, envVar = NULL, method = "moran", weights = NULL, scaled = FALSE, significance = TRUE, alternative = "two.sided")

**Arguments**

- **x**
  An object of class PVR (created by the PVRdecomp function) or class PSR (required by the "PSR" method).

- **phy**
  An object of class phylo that contains an ultrametric phylogeny.

- **trait**
  A vector, data frame or matrix that contains traits sets (for data frames and matrices, each column must represent a trait set).

- **envVar**
  A vector, data frame or matrix that contains environmental variables. Used to estimate the variation of a trait set that is explained by phylogeny and by environment.

- **method**
  Character string. A name for the eigenvectors selection method. It can be "moran", "stepwise", "psr" or "sequential".

- **weights**
  Weighting matrix based on Phylogenetic distances used in the "moran" method. If no weights matrix is provided, weights will be set to max(D) - Dij, where D is the phylogenetic distance matrix.

- **scaled**
  Logical. Should the phylogenetic distances be scaled into the range of 0 to 1. Default is FALSE.

- **significance**
  Logical. Should the eigenvectors selected by the "moran" method be selected by the significance of residuals autocorrelation. If FALSE the eigenvectors will be selected by Moran’s I values.

- **alternative**
  The alternative hypothesis used to compute the significance level when selecting eigenvectors by the "moran" method.

- **mi.treshold**
  Minimum residuals Moran’s I value used to select eigenvectors when significance is FALSE.

- **sig.treshold**
  The significance threshold used to select eigenvectors by the "moran" method.
psr.treshold  The minimum accumulate R2 gain threshold used to select eigenvectors by the "PSR" method.

accvalue.treshold  Relative accumulated eigenvalue threshold used to select the eigenvectors by the "sequential" method.

Value

A PVR class object.

Author(s)

Santos, T; Diniz-Filho, J.A.F.; Rangel, T.F.; Bini, L.M.

References


See Also

PSR, PVRdecomp, PSRplot, VarPartplot

Examples

library(ape)
tree <- rcoal(10)
#Decomposing phylogenetic distance matrix derived from tree into a set of orthogonal vectors
x <- PVRdecomp(tree)
trait <- runif(10)
y <- PVR(x, trait = trait, method = "moran")
str(y)
**PVR-class**

**Class "PVR"**

---

**Description**

A S4 class that contains eigenvalues and eigenvectors from decomposition of a phylogenetic distance matrix and PVR r squared and residuals.

**Objects from the Class**

Objects can be created by calls of the form `new("PVR", ...).

**Slots**

- **Eigen**: Object of class "list" that contains the eigenvalues and eigenvectors generated by phylogenetic distance matrix eigendecomposition.
- **phyDist**: Object of class "matrix" that contains a phylogenetic distance matrix.
- **phylo**: Object of class "phylo" that contains a phylogeny.
- **Selection**: Object of class "list" that contains the selection method (along with its statistics) used to select the vectors, the selected vectors IDs and a matrix that contains the selected vectors.
- **PVR**: Object of class "list" that contains the **Philogenetic EigenVectors Regression r squared and residuals.**
- **VarPart**: Object of class "list" that contains the variation partition components.

**Methods**

- **show** signature(object = "PVR"): Always print the Eigen slot.

**Author(s)**

Santos, T; Diniz-Filho, J.A.F.; Rangel, T.F.; Bini, L.M.

**References**


See Also

PSR-class, PVR, PSR, PVRdecomp, PSRplot, VarPartplot

Examples

showClass("PVR")

PVRdecomp

Phylogenetic distances matrix (eigen)decomposition.

Description

The PVRdecomp function decomposes phylogenetic distance matrices (computed based on phylogenies) into a set of orthogonal eigenvectors.

Usage

PVRdecomp(phy, type = "newick", dist = NULL, scale = FALSE, ...)

Arguments

phy  An object of class phylo that contains an ultrametric phylogeny with branch lengths or a character string that represents a phylogeny file (must have full path) of type given by type.

type  A character string with the phylogeny file format. It can be "newick" or "nexus". Used only if phy is a character string, ignored otherwise.

dist  A phylogenetic distance matrix. Not used.

scale  Logical. Should the phylogenetic distances be scaled into the range of 0 to 1. Default is FALSE.

...  Not used.

Value

The PVRdecomp function returns an object of (S4) class PVR with an Eigen slot that contains eigenvalues and eigenvectors computed after the matrix decomposition.

Author(s)

Santos, T; Diniz-Filho, J.A.F.; Rangel, T.F.; Bini, L.M.
References


See Also

PVR, PSR

Examples

library(ape)

```
tree <- rcoal(10)
#Decomposing phylogenetic distance matrix derived from tree into a set of orthogonal vectors
x <- PVRdecomp(tree, scale = TRUE)
str(x)
```

---

### VarPartplot

Plot function for objects of class PVR to show variation partition components.

#### Description

Plot a, b, c and d components of traits variation partition between phylogeny and environment (as defined by Desdevises et al., 2003).

#### Usage

```
VarPartplot(x, ...)  
```

#### Arguments

- **x**: An object of class PVR with a non NULL slot VarPart.
- **...**: Parameters passed to the plot function.

#### Author(s)

Santos, T; Diniz-Filho, J.A.F.; Rangel, T.F.; Bini, L.M.
References


See Also

PSR, PVRdecomp, PVR, PSRplot

Examples

```r
library(ape)
tree <- rcoal(10)
# Decomposing phylogenetic distance matrix derived from tree into a set of orthogonal vectors
x <- PVRdecomp(tree)
trait <- runif(10)
envvar <- runif(10)
y <- PVR(x, trait = trait, envVar = envvar, method = "moran")
VarPartplot(y)
```
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