Package 'phylolm.hp'

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Type Package

Title Hierarchical Partitioning of R2 for Phylogenetic Linear
Regression

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Depends R (>= 3.4.0),rr2,phylolm,ggplot2,vegan

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Description Conducts hierarchical partitioning to calculate individual contributions of phylogenetic tree and predictors (groups) towards total R2 for phylogenetic linear regression models.

License GPL

Encoding UTF-8

RoxygenNote 7.3.1

NeedsCompilation no

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Repository CRAN

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phyloglm.hp	*Hierarchical Partitioning of R2 for Phylogenetic Generalized Linear Regression*

Description

Hierarchical Partitioning of R2 for Phylogenetic Generalized Linear Regression

Usage

```
phyloglm.hp(mod, iv = NULL, commonality = FALSE)
```

Arguments

mod	Fitted phylolm or phyloglm model objects.
iv	optional the relative importance of predicotr groups will be evaluated. The input for iv should be a list containing the names of each group of variables. The variable names must be the names of the predictor variables in mod.
commonality	Logical; If TRUE, the result of commonality analysis is shown, the default is FALSE.

Details

This function conducts hierarchical partitioning to calculate the individual contributions of phylogenetic signal and each predictor towards total R2 from rr2 package for phylogenetic linear regression.

Value

Total.R2	The R2 for the full model.
commonality.analysis	
	If commonality=TRUE, a matrix containing the value and percentage of all commonality (2^N-1 for N predictors or matrices).
Individual.R2	A matrix containing individual effects and percentage of individual effects for phylogenetic tree and each predictor

Author(s)

Jiangshan Lai <lai@njfu.edu.cn>

References

- Lai J.,Zhu W., Cui D.,Mao L.(2023)Extension of the glmm.hp package to Zero-Inflated generalized linear mixed models and multiple regression.Journal of Plant Ecology,16(6):rtad038<DOI:10.1093/jpe/rtad038>

- Lai J.,Zou Y., Zhang S.,Zhang X.,Mao L.(2022)glmm.hp: an R package for computing individual effect of predictors in generalized linear mixed models.Journal of Plant Ecology,15(6):1302-1307<DOI:10.1093/jpe/rtac096>

- Lai J.,Zou Y., Zhang J.,Peres-Neto P.(2022) Generalizing hierarchical and variation partitioning in multiple regression and canonical analyses using the rdacca.hp R package.Methods in Ecology and Evolution,13(4):782-788<DOI:10.1111/2041-210X.13800>

- Chevan, A. & Sutherland, M. (1991). Hierarchical partitioning. American Statistician, 45, 90-96. doi:10.1080/00031305.1991.10475776

- Nimon, K., Oswald, F.L. & Roberts, J.K. (2013). Yhat: Interpreting regression effects. R package version 2.0.0.

- Nimon, 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

```
library(phylolm)
library(rr2)
set.seed(231)
tre <- rcoal(60)
taxa <- sort(tre$tip.label)
b0 <- 0
b1 <- 0.3
b2 <- 0.5
b3 <- 0.4
x <- rTrait(n=1, phy=tre, model="lambda", parameters=list(ancestral.state=0, sigma2=15, lambda=0.9))
x2 <- rTrait(n=1, phy=tre, model="lambda",
parameters=list(ancestral.state=0, sigma2=10, lambda=0.9))
x3 <- rTrait(n=1, phy=tre, model="lambda",
parameters=list(ancestral.state=0, sigma2=13, lambda=0.9))
y <- b0 + b1 * x + b2 * x2 + b3*x3+ rTrait(n=1, phy=tre, model="lambda",
parameters=list(ancestral.state=0, sigma2=5, lambda=0.9))
dat <- data.frame(trait=y[taxa], pred=x[taxa], pred2=x2[taxa],pred3=x3[taxa])
fit <- phylolm(trait ~ pred + pred2 + pred3, data=dat, phy=tre, model="lambda")
phyloglm.hp(fit,commonality=TRUE)
iv=list(env1="pred",env2=c("pred2","pred3"))
phyloglm.hp(fit,iv)
set.seed(123456)
tre <- rtree(50)
x1 <- rTrait(n=1, phy=tre)
x2 <- rTrait(n=1, phy=tre)
x3 <- rTrait(n=1, phy=tre)
X <- cbind(rep(1, 50), x1, x2, x3)
y <- rbinTrait(n=1, phy=tre, beta=c(-1, 0.9, 0.9, 0.5), alpha=1, X=X)
dat <- data.frame(trait01=y, predictor1=x1, predictor2=x2, predictor3=x3)
fit <- phyloglm(trait01 ~ predictor1 + predictor2 + predictor3, phy=tre, data=dat)
phyloglm.hp(fit)
iv=list(env1="predictor1",env2=c("predictor2","predictor3"))
phyloglm.hp(fit,iv)
```

phylolm.hp   *Hierarchical Partitioning of R2 for Phylogenetic Linear Regression*

Description

Hierarchical Partitioning of R2 for Phylogenetic Linear Regression

Usage

```
phylolm.hp(mod, iv = NULL, commonality = FALSE)
```

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`commonality`	Logical; If TRUE, the result of commonality analysis is shown, the default is FALSE.

Details

This function conducts hierarchical partitioning to calculate the individual contributions of phylogenetic signal and each predictor towards total R2 from rr2 package for phylogenetic linear regression.

Value

`Total.R2`	The R2 for the full model.
`commonality.analysis`	
	If commonality=TRUE, a matrix containing the value and percentage of all commonality (2^N-1 for N predictors or matrices).
`Individual.R2`	A matrix containing individual effects and percentage of individual effects for phylogenetic tree and each predictor

Author(s)

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x2 <- rTrait(n=1, phy=tre, model="lambda",
parameters=list(ancestral.state=0, sigma2=10, lambda=0.9))
x3 <- rTrait(n=1, phy=tre, model="lambda",
parameters=list(ancestral.state=0, sigma2=13, lambda=0.9))
y <- b0 + b1 * x + b2 * x2 + b3*x3+ rTrait(n=1, phy=tre, model="lambda",
parameters=list(ancestral.state=0, sigma2=5, lambda=0.9))
dat <- data.frame(trait=y[taxa], pred=x[taxa], pred2=x2[taxa],pred3=x3[taxa])
fit <- phylolm(trait ~ pred + pred2 + pred3, data=dat, phy=tre, model="lambda")
phylolm.hp(fit,commonality=TRUE)
iv=list(env1="pred",env2=c("pred2","pred3"))
phylolm.hp(fit,iv)
set.seed(123456)
tre <- rtree(50)
x1 <- rTrait(n=1, phy=tre)
x2 <- rTrait(n=1, phy=tre)
x3 <- rTrait(n=1, phy=tre)
X <- cbind(rep(1, 50), x1, x2, x3)
y <- rbinTrait(n=1, phy=tre, beta=c(-1, 0.9, 0.9, 0.5), alpha=1, X=X)
dat <- data.frame(trait01=y, predictor1=x1, predictor2=x2, predictor3=x3)
fit <- phyloglm(trait01 ~ predictor1 + predictor2 + predictor3, phy=tre, data=dat)
phylolm.hp(fit)
iv=list(env1="predictor1",env2=c("predictor2","predictor3"))
phylolm.hp(fit,iv)
```

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plot.phyloglmhp   *Plot for a* phyloglm.hp *object*

Description

Plot for a phyloglm.hp object

Usage

```
## S3 method for class 'phyloglmhp'
plot(x, plot.perc = FALSE, commonality = FALSE, color = NULL, dig = 4, ...)
```

Arguments

x	A phyloglm.hp object.
plot.perc	Logical;if TRUE, the bar plot (based on ggplot2 package) of the percentage to individual effects of variables and phylogenetic signal towards total explained variation, the default is FALSE to show plot with original individual effects.
commonality	Logical; If TRUE, the result of commonality analysis is shown, the default is FALSE.
color	Color of variables.
dig	Integer; number of decimal places in Venn diagram.
...	unused

Value

a ggplot object

Author(s)

Jiangshan Lai <lai@njfu.edu.cn>

Examples

```
library(phylolm)
library(rr2)
set.seed(123456)
tre <- rtree(50)
x1 <- rTrait(n=1, phy=tre)
x2 <- rTrait(n=1, phy=tre)
X <- cbind(rep(1, 50), x1, x2)
y <- rbinTrait(n=1, phy=tre, beta=c(-1, 0.8, 0.9), alpha=1, X=X)
dat <- data.frame(trait01=y, predictor1=x1, predictor2=x2)
fit <- phyloglm(trait01 ~ predictor1 + predictor2, phy=tre, data=dat)
plot(phyloglm.hp(fit,commonality=TRUE))
plot(phyloglm.hp(fit,commonality=TRUE),commonality=TRUE)
```

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