

Package ‘gam.hp’

December 16, 2024

Type Package

Title Hierarchical Partitioning of Adjusted R2 and Explained Deviance for Generalized Additive Models

Version 0.0-3

Date 2024-12-15

Depends R (>= 3.4.0),mgcv,ggplot2

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Description Conducts hierarchical partitioning to calculate individual contributions of each predictor towards adjusted R2 and explained deviance for generalized additive models based on output of gam()in 'mgcv' package, applying the algorithm in this paper: Lai(2024) <doi:10.1016/j.pld.2024.06.002>.

License GPL

Encoding UTF-8

URL <https://github.com/laijiangshan/gam.hp>

RoxygenNote 7.3.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-12-16 03:40:02 UTC

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Description

Hierarchical Partitioning of Adjusted R2 and Explained Deviance for Generalized Additive Models

Usage

```
gam.hp(mod, iv = NULL, type = "dev", commonality = FALSE)
```

Arguments

mod	Fitted "gam" model objects.
iv	optional The relative importance of predictor groups will be assessed. The input for iv should be a list, where each element contains the names of variables belonging to a specific group. These variable names must correspond to the predictor variables defined in the model (mod).
type	The type of R-square of gam, either "dev" or "adjR2", in which "dev" is explained deviance and "adjR2" is adjusted R-square, the default is "dev".
commonality	Logical; If TRUE, the result of commonality analysis (2^{N-1} fractions for N predictors) is shown, the default is FALSE.

Details

This function conducts hierarchical partitioning to calculate the individual contributions of each predictor towards total adjusted R2 and explained deviance for Generalized Additive Models. The adjusted R2 and explained deviance are is the output of `summary.gam()` in `mgcv` package.

Value

dev	The R2 for the full model.
hierarchical.partitioning	A matrix containing individual effects and percentage of individual effects towards total adjusted R2 and explained deviance for each predictor.

Author(s)

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References

- Lai J.,Tang J., Li T., Zhang A.,Mao L.(2024)Evaluating the relative importance of predictors in Generalized Additive Models using the gam.hp R package.Plant Diversity,46(4):542-546<DOI:10.1016/j.pld.2024.06.002>

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- 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>
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- 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.

Examples

```
library(mgcv)
mod1 <- gam(Sepal.Length ~ s(Petal.Length) + s(Petal.Width) + Sepal.Width,data = iris)
summary(mod1)
gam.hp(mod1)
gam.hp(mod1,type="adjR2")
gam.hp(mod1,commonality=TRUE)
iv <- list(env1=c("s(Petal.Length)","s(Petal.Width)"),env2="Sepal.Width")
gam.hp(mod1,iv,type="adjR2")
gam.hp(mod1,iv,commonality=TRUE)
```

permu.gamhp

Permutation Test of Hierarchical Partitioning for GAM Analysis

Description

Permutation Test of Hierarchical Partitioning for GAM Analysis

Usage

```
permu.gamhp(mod = NULL, iv = NULL, type = "dev", permutations = 10)
```

Arguments

mod	gam model generated by mgcv::gam()
iv	optional The relative importance of predictor groups will be assessed. The input for iv should be a list, where each element contains the names of variables belonging to a specific group. These variable names must correspond to the predictor variables defined in the model (mod).
type	The type of total explained variation, either "dev" or "adjR2", in which "dev" is deviance explained and "adjR2" is adjusted R-square, the default is "adjR2".
permutations	An integer; Number of permutations for computing p value of individual contribution for the randomized dataset.

Details

This function is a permutation test of hierarchical partitioning for gam analysis. It returns a matrix of I values (the individual contribution towards total explained variation) for all values from permutations randomizations. For each permutation, the values in each variable (i.e each column of iv) are randomized independently, and gam.hp is run on the randomized iv. As well as the randomized I matrix, the function returns a summary table listing the observed I values, the p value of I for the randomized dataset.

Value

a data.frame containing a summary table listing the observed individual contribution, the p value of individual contribution for the randomized dataset

Author(s)

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Examples

```
library(mgcv)
mod1 <- gam(Sepal.Length ~ s(Petal.Length) + s(Petal.Width) + Sepal.Width, data = iris)
permu.gamhp(mod=mod1, type="dev", permutations=10)
iv <- list(env1=c("s(Petal.Length)", "s(Petal.Width)"), env2="Sepal.Width")
permu.gamhp(mod=mod1, iv, type="dev", permutations=10)
```

plot.gamhp

Plot for a [gam.hp](#) object

Description

Plot for a [gam.hp](#) object

Usage

```
## S3 method for class 'gamhp'
plot(x, plot.perc = FALSE, ...)
```

Arguments

x	A gam.hp object.
plot.perc	Logical; if TRUE, the bar plot (based on ggplot2 package) of the percentage to individual effects of variables towards total explained variation, the default is FALSE to show plot with original individual effects.
...	unused

Value

a ggplot object

Author(s)

Jiangshan Lai <lai@njfu.edu.cn>

Examples

```
library(mgcv)
mod1 <- gam(Sepal.Length ~ s(Petal.Length) + s(Petal.Width) + Sepal.Width, data = iris)
plot(gam.hp(mod1))
```

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