

Package ‘gam.hp’

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Type Package

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

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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()' and 'bam()' in 'mgcv' package, applying the algorithm in this paper: Lai(2024) <[doi:10.1016/j.pld.2024.06.002](https://doi.org/10.1016/j.pld.2024.06.002)>.

License GPL

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

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gam.hp

Hierarchical Partitioning of Adjusted R² and Explained Deviance for Generalized Additive Models (GAM and BAM)

Description

This function conducts hierarchical partitioning to calculate the individual contributions of each predictor towards total adjusted R² and explained deviance for Generalized Additive Models fitted by either `gam` or `bam` in the **mgcv** package.

Usage

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

Arguments

<code>mod</code>	Fitted "gam" or "bam" model object from the mgcv package.
<code>iv</code>	Optional. A list specifying groups of predictor variables for assessing group-wise relative importance. Each element of the list should contain the names of variables belonging to a specific group, corresponding to the predictor names defined in the model (<code>mod</code>).
<code>type</code>	Character. The type of R-square for GAM/BAM models, either "dev" or "adjR2". "dev" represents the explained deviance, and "adjR2" represents the adjusted R-square. The default is "dev".
<code>commonality</code>	Logical; if TRUE, the function returns the results of commonality analysis (i.e., 2 ^N - 1 fractions for N predictors). Default is FALSE.
<code>data</code>	Optional. The dataset used to fit the model. If not provided, the function will attempt to extract the data directly from the fitted <code>mod</code> object. This argument is mainly useful for <code>bam</code> models, where the model object may not always store the full dataset (especially when using large datasets or parallel fitting options).

Details

The function supports both `gam` and `bam` model objects. It decomposes the total explained deviance or adjusted R² into unique and shared contributions of individual predictors or groups of predictors using hierarchical partitioning. The adjusted R² and explained deviance values are extracted from `summary.gam()` or `summary.bam()`.

Value

<code>dev</code>	The R ² (either explained deviance or adjusted R ²) for the full model.
<code>hierarchical.partitioning</code>	A matrix containing the individual effects and the percentage contribution of each predictor to total explained deviance or adjusted R ² .

Author(s)

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References

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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. **The 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)

## Example 1: Using gam()
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)

## Example 2: Using bam()
mod2 <- bam(Sepal.Length ~ s(Petal.Length) + s(Petal.Width) + Sepal.Width,
            data = iris)
summary(mod2)
gam.hp(mod2)
gam.hp(mod2, type = "adjR2")
gam.hp(mod2, commonality = TRUE)
## Explicitly specifying data (useful for bam)
gam.hp(mod2, data = iris)
```

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	<i>Plot for a gam.hp object</i>
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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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