

Package ‘glmm.hp’

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Type Package

Title Hierarchical Partitioning of Marginal R2 for Generalized Mixed-Effect Models

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Depends R (>= 3.4.0),MuMIn,ggplot2

Imports lme4

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Description Conducts hierarchical partitioning to calculate individual contributions of each fixed effects towards marginal R2 for generalized mixed-effect model based on output of `r.squaredGLMM()` in 'MuMIn', applying the algorithm of 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,13:782-788<[DOI:10.1111/2041-210X.13800](https://doi.org/10.1111/2041-210X.13800)>.

License GPL

Encoding UTF-8

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

RoxygenNote 7.1.1

NeedsCompilation no

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glmm.hp

*Hierarchical Partitioning of Marginal R2 for Generalized Mixed-Effect Models***Description**

Hierarchical Partitioning of Marginal R2 for Generalized Mixed-Effect Models

Usage

glmm.hp(mod)

Arguments

mod Fitted lme4 or nlme model objects.

Details

This function conducts hierarchical partitioning to calculate the individual contributions of each predictor towards marginal R2 for Generalized Mixed-effect Model. The marginal R2 is the output of r.squaredGLMM in MuMIn package.

Value

Total.Marginal.R2 The marginal R2 (fixed effect) for the full model.

Hier.part A matrix containing individual effects and percentage of individual effects towards total marginal R2 for each predictor.

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References

- 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>
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- Nakagawa, S., & Schielzeth, H. (2013). A general and simple method for obtaining R2 from generalized linear mixed-effects models. *Methods in Ecology and Evolution*, 4(2), 133-142.
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Examples

```
library(MuMIn)
library(lme4)
mod1 <- lmer(Sepal.Length ~ Petal.Length + Petal.Width +(1 | Species), data = iris)
r.squaredGLMM(mod1)
glmhnp(mod1)
plot(glmhnp(mod1))
```

`plot.glmhnp`*Plot for a `glmhnp` object*

Description

Plot for a `glmhnp` object

Usage

```
## S3 method for class 'glmhnp'
plot(x, plot.perc = FALSE, n = 1, ...)
```

Arguments

<code>x</code>	A <code>glmhnp</code> object.
<code>plot.perc</code>	Logical; if TRUE, the bar plot (based on ggplot2 package) of the percentage to individual effects of variables or groups towards total explained variation, the default is FALSE to show plot with original individual effects.
<code>n</code>	Integer; which marginal R2 in output of r.squaredGLMM to plot.
<code>...</code>	unused

Value

a ggplot object

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Examples

```
library(MuMIn)
library(lme4)
mod1 <- lmer(Sepal.Length ~ Petal.Length + Petal.Width +(1 | Species), data = iris)
plot(glmhnp(mod1))
```

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