

# Package: glmm.hp (via r-universe)

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**Type** Package

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

**Version** 0.1-5

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**Depends** R (>= 3.4.0),MuMIn,ggplot2,vegan

**Imports** lme4

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**Description** Conducts hierarchical partitioning to calculate individual contributions of each predictor (fixed effects) towards marginal R2 for generalized linear mixed-effect model (including lm, glm and glmm) based on output of r.squaredGLMM() in 'MuMIn', applying the algorithm of 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>.

**License** GPL

**Encoding** UTF-8

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

**RoxygenNote** 7.3.1

**Repository** <https://laijiangshan.r-universe.dev>

**RemoteUrl** <https://github.com/laijiangshan/glmm.hp>

**RemoteRef** HEAD

**RemoteSha** 88a7180392a2a9a3117dd9536de1cc2abe565ad1

## Contents

glmm.hp . . . . .	2
plot.glmmhp . . . . .	3

<b>Index</b>	<b>5</b>
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glmm.hp	<i>Hierarchical Partitioning of Marginal R2 for Generalized Mixed-Effect Models</i>
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**Description**

Hierarchical Partitioning of Marginal R2 for Generalized Mixed-Effect Models

**Usage**

```
glmm.hp(mod, type = "adjR2", commonality = FALSE)
```

**Arguments**

mod	Fitted lme4, nlme, glmmTMB, glm or lm model objects.
type	The type of R-square of lm, either "R2" or "adjR2", in which "R2" is unadjusted R-square and "adjR2" is adjusted R-square, the default is "adjR2". The adjusted R-square is calculated using Ezekiel's formula (Ezekiel 1930) for lm.
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 (marginal) R2 for Generalized Linear Mixed-effect Model (including lm, glm and glmm). The marginal R2 is the output of r.squaredGLMM in MuMIn package for glm and glmm.

**Value**

r.squaredGLMM	The R2 for the full model.
hierarchical.partitioning	A matrix containing individual effects and percentage of individual effects towards total (marginal) R2 for 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.
- Nakagawa, S., & Schielzeth, H. (2013). A general and simple method for obtaining R<sup>2</sup> from generalized linear mixed-effects models. *Methods in Ecology and Evolution*, 4(2), 133-142.
- Nakagawa, S., Johnson, P. C., & Schielzeth, H. (2017). The coefficient of determination R<sup>2</sup> and intra-class correlation coefficient from generalized linear mixed-effects models revisited and expanded. *Journal of the Royal Society Interface*, 14(134), 20170213.
- Ezekiel, M. (1930) *Methods of Correlational Analysis*. Wiley, New York.

## Examples

```
library(MuMIn)
library(lme4)
mod1 <- lmer(Sepal.Length ~ Petal.Length + Petal.Width+(1|Species), data = iris)
r.squaredGLMM(mod1)
glmm.hp(mod1)
a <- glmm.hp(mod1)
plot(a)
mod2 <- glm(Sepal.Length ~ Petal.Length + Petal.Width, data = iris)
r.squaredGLMM(mod2)
glmm.hp(mod2)
b <- glmm.hp(mod2)
plot(b)
plot(glmm.hp(mod2))
mod3 <- lm(Sepal.Length ~ Petal.Length + Petal.Width + Petal.Length:Petal.Width, data = iris)
glmm.hp(mod3, type="R2")
glmm.hp(mod3, commonality=TRUE)
```

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plot.glmhnp

*Plot for a [glmm.hp](#) object*

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## Description

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

## Usage

```
## S3 method for class 'glmhnp'
plot(x, plot.perc = FALSE, color = NULL, n = 1, dig = 4, ...)
```

**Arguments**

<code>x</code>	A <code>glmh</code> object.
<code>plot.perc</code>	Logical;if TRUE, the bar plot (based on <code>ggplot2</code> 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>color</code>	Color of variables.
<code>n</code>	Integer; which marginal R2 in output of <code>r.squaredGLMM</code> to plot.
<code>dig</code>	Integer; number of decimal places in Venn diagram.
<code>...</code>	unused

**Value**

a `ggplot` object

**Author(s)**

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**Examples**

```
library(MuMIn)
library(lme4)
mod1 <- lmer(Sepal.Length ~ Petal.Length + Petal.Width +(1 | Species), data = iris)
a <- glmh.hp(mod1)
plot(a)
mod3 <- lm(Sepal.Length ~ Petal.Length+Petal.Width,data = iris)
plot(glmh.hp(mod3,type="R2"))
plot(glmh.hp(mod3,commonality=TRUE),color = c("#8DD3C7", "#FFFB3"))
```

# Index

`glm.hp`, [2](#), [3](#), [4](#)

`plot.glmhp`, [3](#)