

Package ‘upset.hp’

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Title Generate UpSet Plots of VP and HP Based on the ASV Concept

Version 0.0.3

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Description Using matrix layout to visualize the unique, common, or individual contribution of each predictor (or matrix of predictors) towards explained variation on different models. These contributions were derived from variation partitioning (VP) and hierarchical partitioning (HP), applying the algorithm of ``Lai et al. (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>".

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

Depends R (>= 3.6.0)

Imports MuMIn, vegan, glmm.hp, ggplot2, patchwork, grDevices

License GPL (>= 2)

Encoding UTF-8

RoxygenNote 7.3.1

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NeedsCompilation no

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upset.hp

*Visualization of VP and HP Using UpSet Diagram***Description**

Visualization of variation partitioning (VP) and hierarchical partitioning (HP) with unlimited number of predictor variables (or matrices of predictors) using UpSet matrix layout.

Usage

```
upset.hp(
  vp,
  hp,
  plot.hp = TRUE,
  order.part = "effect",
  decreasing.part = TRUE,
  order.var = TRUE,
  decreasing.var = TRUE,
  cutoff = -1,
  nVar = 30,
  col.width = 0.6,
  pch.size = 3,
  line.lwd = 0.5,
  show.effect = TRUE,
  effect.cex = 2.7,
  title.cex = 10,
  axis.cex = 8,
  height.ratio = c(2, 1),
  width.ratio = c(1, 3),
  col = "nature"
)
```

Arguments

vp	A matrix, which contains the output of variation partitioning (i.e. commonality analysis) from <code>rdacca.hp</code> , <code>glmm.hp</code> , <code>gam.hp</code> , and <code>phylolm.hp</code> .
hp	A matrix, which contains the output of hierarchical partitioning from <code>rdacca.hp</code> , <code>glmm.hp</code> , <code>gam.hp</code> , and <code>phylolm.hp</code> .
plot.hp	The default is TRUE, which plots the individual effect for each predictor on left column diagram. If FALSE, compute and plot the sum of unique effect and common effect for each predictor.
order.part	How the VP components in matrix layout should be ordered. Options include "effect" (order the intersections by their effects) or "degree" (sort by the number of predictors involved in the intersection), default is "effect".

decreasing.part	How the intersections in order .part should be ordered. Default is TRUE, "effect" is decreasing (from greatest to least) or "degree" is increasing (from least to greatest).
order.var	The predictors in the matrix layout should be ordered by. Default is TRUE, which orders the predictors by their effects. IF FALSE, sort by the order of predictors in input data.
decreasing.var	If order.var=TRUE, how the predictors should be ordered. Default is TRUE, from greatest to least.
cutoff	Effects below cutoff will not be displayed, default is -1. Note: Negative effects due to adjustment of R-squared mean negligible contributions, but they are included in the computation of the total contribution of each predictor category.
nVar	Number of components in VP to plot, default is 30.
col.width	Width of bars in column diagram, default is 0.6.
pch.size	Size of points in matrix diagram, default is 3.
line.lwd	Width of lines in matrix diagram, default is 0.5.
show.effect	Show the relative importance of predictors (unique, common, or individual effects) above bars, default is TRUE.
effect.cex	Font size of the effects, default is 2.7.
title.cex	Font size of axis titles, default is 10.
axis.cex	Font size of axis labels, default is 8.
height.ratio	Ratio between matrix and top column diagram, default is c(2, 1).
width.ratio	Ratio between matrix and left column diagram, default is c(1, 3).
col	Character. Color palette name: "nature" (default), "science", "cell", "bw" (black-white), or "cvd" (color-blind friendly).

Details

upset.hp diagram is an extension of UpSet technique to and is used to visualize the object of `rdacca.hp`, `glmm.hp`, `gam.hp`, and `phylo1m.hp` (Lai et al. 2022a, 2022b, 2023, 2024; Liu et al. 2023). The matrix layout enables the effective representation of relative importance of predictors, such as the unique effects and common effects in VP, as well as additional summary statistics or individual effects in HP. upset.hp diagram could, in principle, allow visualization of any number of predictor variables or groups of predictor variables. But considering the interpretability of data, we would like to recommend that the number of predictors (or groups of predictors) no more than 7.

Value

Returns a `ggplot2`.

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*, 13:782-788.

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.,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>

Liu Y., Yu X., Yu Y., et al. (2023) Application of "rdacca. hp" R package in ecological data analysis: case and progress. Chinese Journal of Plant Ecology, 27:134-144.

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>

Examples

```
library(glmm.hp)
#upset for glmm.hp() in lm()
m2<-lm(mpg~wt+carb+cyl,mtcars)
vp <- glmm.hp(m2,commonality=TRUE)$commonality.analysis
hp <- glmm.hp(m2)$hierarchical.partitioning
upset.hp(vp, hp, col = "cvd")
```

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