Package 'UpSetVP'

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Title An Alternative Visualization of VPA and HP in Canonical Analysis

Version 1.0.0

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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 canonical analysis. These contributions were derived from variance partitioning analysis (VPA) and hierarchical partitioning (HP), 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>.

URL https://github.com/LiuXYh/UpSetVP

BugReports https://github.com/LiuXYh/UpSetVP/issues

Depends R (>= 3.6.0)

Imports rdacca.hp, ggplot2, patchwork, grDevices

Suggests adespatial

LazyData no

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Contents

`baima` *EcM Fungal Data with Environmental Variables*

Description

Ectomycorrhizal (EcM) fungal community and environmental data were excerpted from Gong et al. (2022). Sampling was conducted along the elevation gradient (2,900 m to 4,500 m) in the eastern slope of Baima Snow Mountain during both dry (November 2017) and wet (August 2018) seasons after studying community compositions of the host plants of EcM fungi.

Usage

```
data(baima.fun)

data(baima.env)
```

Format

263 samples from the root tips were excerpted. There are two linked data sets: `baima.fun`, a data frame containing 3,099 amplicon sequence variants (ASVs) of root associated EcM fungi; `baima.env`, a data frame containing 14 environmental variables.

The fields in the environmental data are:

environmental_medium Sample type

latitude Latitude

lontitude Lontitude

altitude Elevation (m)

season Season, a factor with levels `dry` and `wet`

em.GR Richness of EcM plant at genus level

em.abun The number of individuals of each EcM genus

sea.MT Dry-season and wet-season mean temperature

pH Soil pH

TP Total phosphorus (g/kg)

TK Total potassium (g/kg)

AN Alkaline-hydrolysable nitrogen (mg/kg)

AP Available phosphorus (mg/kg)

AK Available potassium (mg/kg)

References

Gong S, Feng B, Jian S P, et al. Elevation Matters More than Season in Shaping the Heterogeneity of Soil and Root Associated Ectomycorrhizal Fungal Community. Microbiology spectrum, 2022, 10(1): e01950-21.

Examples

```
data(baima.fun)
data(baima.env)
```

---

barplot_hp *Visualization of HP Using Column Diagram*

Description

Visualization of individual effects in hierarchical partitioning (HP) using column diagram.

Usage

```
barplot_hp(
  x,
  order.var = TRUE,
  decreasing.var = TRUE,
  cutoff = -1,
  col.fill = "valid",
  col.color = NULL,
  col.width = 0.6,
  show.effect = TRUE,
  effect.cex = 2.7,
  title.cex = 10,
  axis.cex = 8
)
```

Arguments

x	A rdacca.hp object, which contains the output of HP from canonical analysis.
order.var	The predictors in the matrix layout should be ordered by. Default is TRUE, which orders the predictors by their effect values. 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	Effect values below cutoff will not be displayed, default is -1. Note: Negative values due to adjustment of R-squared mean negligible contributions, but they are included in the computation of the total contribution of each predictor category.
col.fill	How the bars should be colored. Options include "valid" (according to the validity of effects) or "vars" (color by predictors), default is "valid".
col.color	Color of bars.
col.width	Width of bars, default is 0.6.
show.effect	Show the effect values above bars, default is TRUE.

effect.cex	Font size of the effect values, default is 2.7.
title.cex	Font size of axis titles, default is 10.
axis.cex	Font size of axis labels, default is 8.

Details

This function is used to visualize the object of rdacca.hp (Lai et al. 2022), which calculates the individual effects of predictor variables or groups of predictor variables in canonical analysis based on HP.

Value

Returns a ggplot2.

References

Lai J, Zou Y, Zhang J, et al. Generalizing hierarchical and variation partitioning in multiple regression and canonical analyses using the rdacca.hp R package. Methods in Ecology and Evolution, 2022.

Examples

```
library(rdacca.hp)

## A simple example of partial dbRDA
data(baima.fun)
data(baima.env)

# Bray-Curtis index was used to calculate community composition dissimilarity
baima.fun.bray <- vegdist(baima.fun, method = "bray")

# Quantify the individual effects of soil properties on EcM fungal community composition
soil <- baima.env[c("pH", "TP", "TK", "AN", "AP", "AK")]
baima.soil.vp <- rdacca.hp(baima.fun.bray, soil, method = "dbRDA", type = "adjR2")

# Plot individual effects
barplot_hp(baima.soil.vp, col.fill = "var",
 col.color = c("#8DD3C7", "#FFFFB3", "#BEBADA", "#FB8072", "#80B1D3", "#FDB462", "#B3DE69"))
```

---

upset_vp *Visualization of VPA and HP Using UpSetVP Diagram*

Description

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

Usage

```
upset_vp(
  x,
  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)
)
```

Arguments

x	A rdacca.hp object, which contains the output of VPA and HP from canonical analysis.
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 VPA 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 VPA 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).

Details

UpSetVP diagram is an extension of UpSet technique (Conway et al. 2017; Lex et al. 2014) to canonical analysis and is used to visualize the object of rdacca.hp (Lai et al. 2022). The matrix layout enables the effective representation of relative importance of predictors, such as the unique effects and common effects in VPA, as well as additional summary statistics or individual effects in HP. UpSetVP 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

Conway J R, Lex A, Gehlenborg N. UpSetR: an R package for the visualization of intersecting sets and their properties. Bioinformatics, 2017, 33(18): 2938-2940.

Gong S, Feng B, Jian S P, et al. Elevation Matters More than Season in Shaping the Heterogeneity of Soil and Root Associated Ectomycorrhizal Fungal Community. Microbiology spectrum, 2022, 10(1): e01950-21.

Lai J, Zou Y, Zhang J, et al. Generalizing hierarchical and variation partitioning in multiple regression and canonical analyses using the rdacca.hp R package. Methods in Ecology and Evolution, 2022.

Lex A, Gehlenborg N, Strobelt H, et al. UpSet: visualization of intersecting sets. IEEE transactions on visualization and computer graphics, 2014, 20(12): 1983-1992.

Examples

```
library(rdacca.hp)

## A simple example of partial dbRDA
data(baima.fun)
data(baima.env)

# Bray-Curtis index was used to calculate community composition dissimilarity
baima.fun.bray <- vegdist(baima.fun, method = "bray")
```

```
# The relative importance of individual soil properties on EcM fungal community compositionon
soil <- baima.env[c("pH", "TP", "TK", "AN", "AP", "AK")]
baima.soil.vp <- rdacca.hp(baima.fun.bray, soil,
  method = "dbRDA", var.part = TRUE, type = "adjR2")

# Plot unique, common, as well as individual effects
upset_vp(baima.soil.vp, plot.hp = TRUE)

## Example was referenced from Gong et al. (2022)
if(requireNamespace("adespatial", quietly = TRUE)) {

# Distance-based Moran's eigenvector maps (dbMEM) was used to extract spatial relationships
space.dbmem <- adespatial::dbmem(baima.env[c("latitude", "lontitude")])

 # The relative importance of groups of environmental factors on EcM fungal community composition
  env.list <- list(
    elevation = baima.env["altitude"],
    season = baima.env["season"],
    space = data.frame(space.dbmem)[1:2],
    host = baima.env[c("em.GR", "em.abun")],
    climate = baima.env["sea.MT"],
    soil = baima.env[c("pH", "TP", "TK", "AN", "AP", "AK")]
  )
  baima.env.vp <- rdacca.hp(baima.fun.bray, env.list,
    method = "dbRDA", var.part = TRUE, type = "adjR2")

  # Plot unique, common, as well as individual effects
  upset_vp(baima.env.vp, plot.hp = TRUE, order.part = "degree")
}
```

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