

# Package ‘rdacca.hp’

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**Type** Package

**Title** Hierarchical and Variation Partitioning for Canonical Analysis

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

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**Description** This function conducts variation partitioning and hierarchical partitioning to calculate the unique, shared (referred as to “common”) and individual contributions of each predictor (or matrix) towards explained variation (R-square and adjusted R-square) on canonical analysis (RDA,CCA and db-RDA), applying the algorithm of Chevan, A. and Sutherland, M. 1991 Hierarchical Partitioning.The American Statistician, 90-96 <doi:10.1080/00031305.1991.10475776>.

**License** GPL

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

**Encoding** UTF-8

**RoxygenNote** 7.1.1

**NeedsCompilation** no

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**Description**

Permutation Test of Hierarchical Partitioning for Canonical Analysis

**Usage**

```
permu.hp(
  dv,
  iv,
  method = c("RDA", "dbrDA", "CCA"),
  type = c("adjR2", "R2"),
  scale = FALSE,
  add = FALSE,
  sqrt.dist = FALSE,
  n.perm = 1000,
  permutations = 1000
)
```

**Arguments**

dv	Response variable, either a numeric vector or a matrix. If method="dbrDA", dv should be a "dist" matrix.
iv	Predictors (explanatory variable), either a data frame or a list of data frames. If it is a data frame, the relative importance of each column of the data frame will be evaluated; if it is a list, the relative importance of each element (matrix) will be evaluated.
method	Type of canonical analysis used for variation partitioning, should be a character string, either "RDA", "dbrDA" or "CCA", the default is "RDA". If the response variable (dv) is a numerical vector and method="RDA", the hierarchical and variation partitioning for the classical multiple regression is implemented.
type	The type of total explained variation, 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 RDA and dbrDA, while permutation procedure is used for CCA (Peres-Neto et al. 2006).
scale	Logical; If the columns of dv should be standardized to unit variance when method="RDA" is applied.
add	Logical; If a constant should be added to the non-diagonal values to euclidify dissimilarities (see dbrda function in vegan for details). Choice "lingoes" (or TRUE) uses the recommended method of Legendre & Anderson (1999: "method 1") and "cailliez" uses their "method 2". The argument has an effect only when method="dbrDA".

sqrt.dist	Logical, If the square root of dissimilarities should be taken. This often euclidifies dissimilarities. The argument has an effect only when method="dbRDA"(see dbrda function in vegan for details).
n.perm	An integer; Number of permutations for computing the adjusted R-square for CCA. The argument has an effect only when method="CCA".
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 canonical 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 rdacca.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)

Jiangshan Lai <lai@ibcas.ac.cn>

### Examples

```
library(vegan)
data(mite)
data(mite.env)
#Hellinger-transform the species dataset for RDA
mite.hel <- decostand(mite, "hellinger")
permu.hp(mite.hel,mite.env,method="RDA",type="adjR2",permutations=9)
```

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plot.rdaccahp

*Plot for a rdacca.hp object*

---

### Description

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

### Usage

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

**Arguments**

x	A <a href="#">rdacca.hp</a> object.
plot.perc	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.
...	unused

**Value**

a ggplot object

**Author(s)**

Jiangshan Lai <lai@ibcas.ac.cn>

**Examples**

```
library(vegan)
data(mite)
data(mite.env)
mite.hel <- decostand(mite, "hellinger")
avc<-rdacca.hp(mite.hel,mite.env,method="RDA",type="adjR2")
plot(avc)
plot(avc, plot.perc=TRUE)
```

---

rdacca.hp

*Hierarchical and Variation Partitioning for Canonical Analysis Without Limiting the Number of Predictors (Matrices)*

---

**Description**

Hierarchical and Variation Partitioning for Canonical Analysis Without Limiting the Number of Predictors (Matrices)

**Usage**

```
rdacca.hp(
  dv,
  iv,
  method = c("RDA", "dbRDA", "CCA"),
  type = c("adjR2", "R2"),
  scale = FALSE,
  add = FALSE,
  sqrt.dist = FALSE,
  n.perm = 1000,
  var.part = FALSE
)
```

**Arguments**

dv	Response variable, either a numeric vector or a matrix. If method="dbRDA", dv should be a "dist" matrix.
iv	Predictors (explanatory variable), either a data frame or a list of data frames. If it is a data frame, the relative importance of each column of the data frame will be evaluated; if it is a list, the relative importance of each element (matrix) will be evaluated.
method	Type of canonical analysis used for variation partitioning, should be a character string, either "RDA", "dbRDA" or "CCA", the default is "RDA". If the response variable (dv) is a numerical vector and method="RDA", the hierarchical and variation partitioning for the classical multiple regression is implemented.
type	The type of total explained variation, 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 RDA and dbRDA, while permutation procedure is used for CCA (Peres-Neto et al. 2006).
scale	Logical; If the columns of dv should be standardized to unit variance when method="RDA" is applied.
add	Logical; If a constant should be added to the non-diagonal values to euclidify dissimilarities (see dbrda function in vegan for details). Choice "lingoes" (or TRUE) uses the recommended method of Legendre & Anderson (1999: "method 1") and "cailliez" uses their "method 2". The argument has an effect only when method="dbRDA".
sqrt.dist	Logical, If the square root of dissimilarities should be taken. This often euclidifies dissimilarities. The argument has an effect only when method="dbRDA"(see dbrda function in vegan for details).
n.perm	An integer; Number of permutations for computing the adjusted R-square for CCA. The argument has an effect only when method="CCA".
var.part	Logical; If TRUE, the result of variation partitioning ( $2^N-1$ fractions for N predictors or matrices) are shown, the default is FALSE.

**Details**

This function conducts variation partitioning and hierarchical partitioning to calculate the unique, average shared (referred as to "common") and individual contributions of each predictor (or matrix) towards explained variation (R-square) on canonical analysis (RDA,CCA and dbRDA). Variation partitioning should be conducted before hierarchical partitioning. The former emphasizes unique and common variation among predictors, the latter emphasizes the overall importance of each predictor (or group of predictors). This function simultaneously implements variation and hierarchical partitioning for single- and multiple-response models without limiting in the number of predictors / matrices of predictors. This package was inspired by Chevan & Sutherland (1991)'s paper, the "yhat" (Nimon, Oswald & Roberts 2013) and "hier.part"(Walsh & Mac Nally 2013) R packages.

**Value**

a list containing

Method_Type	Type of canonical analysis and the type of total explained variation.
Total_explained_variation	The explained variation for the full model.
Var.part	If var.part=TRUE, a matrix containing the value and percentage of all commonality ( $2^{N-1}$ for N predictors or matrices).
Hier.part	A matrix containing unique, average shared, individual effects and percentage of individual effect towards total explained variation for each predictor or matrix.

### Author(s)

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### References

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- Ezekiel, M. (1930) *Methods of Correlational Analysis*. Wiley, New York

### Examples

```
library(vegan)
data(mite)
data(mite.env)
data(mite.xy)
data(mite.pcnm)
#Hellinger-transform the species dataset for RDA
mite.hel <- decostand(mite, "hellinger")
rdacca.hp(mite.hel, mite.env, method="RDA", type="adjR2")
rdacca.hp(vegdist(mite), mite.env, method="dbRDA", type="adjR2")
rdacca.hp(mite, mite.env, method="CCA", type="adjR2")
iv <- list(env=mite.env, xy=mite.xy, pcnm=mite.pcnm)
rdacca.hp(mite.hel, iv, method="RDA", var.part = TRUE)
rdacca.hp(vegdist(mite), iv, method="dbRDA", var.part = TRUE)
rdacca.hp(mite, iv, method="CCA", var.part = TRUE)
```

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