

# Package ‘rdacca.hp’

April 5, 2026

**Type** Package

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

**Version** 1.1-2

**Date** 2026-4-5

**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 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>.

**License** GPL

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

**Encoding** UTF-8

**RoxygenNote** 7.3.1

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2026-04-05 13:50:02 UTC

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permu.hp

*Permutation Test of Hierarchical Partitioning for Canonical Analysis***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".

<code>sqrtdist</code>	Logical, If the square root of dissimilarities should be taken. This often euclidifies dissimilarities. The argument has an effect only when <code>method="dbRDA"</code> (see <code>dbRDA</code> function in <code>vegan</code> for details).
<code>n.perm</code>	An integer; Number of permutations for computing the adjusted R-square for CCA. The argument has an effect only when <code>method="CCA"</code> .
<code>permutations</code>	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=10)
```

---

`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, color = NULL, ...)
```

**Arguments**

<code>x</code>	A <a href="#">rdacca.hp</a> 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>color</code>	Color of variables.
<code>...</code>	unused

**Value**

a ggplot object

**Author(s)**

Jiangshan Lai <lai@njfu.edu.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)
avc<-rdacca.hp(mite.hel,mite.env[,1:3],method="RDA",type="adjR2",var.part=TRUE)
plot(avc,color = c("#8DD3C7", "#FFFB3", "#BEBADA"))
```

---

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, matrix or data frame. If method="dbrDA", dv should be of class "dist".
iv	Predictors represented in 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 to be performed, 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. If response variable (dv) is of class "dist", "dbrDA" will be chosen automatically.
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; Specifies whether 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, Specifies whether 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	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) is 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.

**Value**

a list containing

Method_Type	The type of canonical analysis and whether the raw or adjusted R2 was used in the analysis.
Total_explained_variation	The explained variation for the full model (raw or adjusted R2).
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 effects towards total explained variation for each predictor or matrix.

**Author(s)**

Jiangshan Lai <lai@njfu.edu.cn>

**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 <DOI:10.1111/2041-210X.13800>
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- Nimon, K., Oswald, F.L. & Roberts, J.K. (2013). Yhat: Interpreting regression effects. R package version 2.0.0.
- Legendre, P. & Anderson, M. J. (1999). Distance-based redundancy analysis: testing multispecies responses in multifactorial ecological experiments. *Ecological Monographs*, 69, 1-24. <DOI:10.1890/0012-9615(1999)069[0001:dbratm]2.0.co;2>
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- Peres-Neto, P.R., Legendre, P., Dray, S. & Borcard, D. (2006) Variation partitioning of species data matrices: Estimation and comparison of fractions. *Ecology*, 87, 2614-2625. <DOI: doi.org/10.1890/0012-9658(2006)87[2614:VPOSDM]2.0.CO;2>
- 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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