Package: rdacca.hp (via r-universe)

August 24, 2024

Type Package

Title Hierarchical Partitioning for Canonical Analysis

Version 0.2.0

Date 2021-1-17

Depends R (>= 3.4.0),vegan,ggplot2

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Description This function calculates the independent contribution of
each explanatory variable to explained variation (R-squared) on
RDA,CCA and db-RDA, applying the hierarchy 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

LazyData true

RoxygenNote 7.1.1

Repository https://laijiangshan.r-universe.dev

RemoteUrl https://github.com/laijiangshan/rdacca.hp

RemoteRef HEAD

RemoteSha df6f0b66b87de70b0fd4012dac906b55ca7db30d

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creatbin   *Internal function for rdacca.hp()*

Description

Internal function for rdacca.hp()

Usage

```
creatbin(col, binmatrix)
```

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genList   *Internal function for rdacca.hp()*

Description

Internal function for rdacca.hp()

Usage

```
genList(ivlist, value)
```

GMI   *Internal function for rdacca.hp()*

Description

Internal function for rdacca.hp()

Usage

```
GMI(X, tol = 1e-06)
```

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odd	*Internal function for rdacca.hp( )*

Description

Internal function for rdacca.hp()

Usage

```
odd(val)
```

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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".
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=10)
```

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plot.rdaccahp   *plot output of rdacca.hp() based on ggplot2*

Description

plot output of rdacca.hp() based on ggplot2

Usage

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

Arguments

outputList	the output of rdacca.hp().
plot.perc	logical value, if TRUE, the bar plot (based on ggplot2) of the percentage ot independent effects of variables to total Rsquared, the default is FALSE to show plot with original independent effects.

Author(s)

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Pedro Peres-Neto <pedro.peres-neto@concordia.ca>

Examples

```
library(vegan)
data(mite)
data(mite.env)
#Hellinger-transform the species dataset for RDA to deal with the "double zero" problem
mite.hel <- decostand(mite, "hellinger")
rda.hp <- rdacca.hp(mite.hel,mite.env,method="RDA",type="adjR2")
plot(rda.hp)
plot(rda.hp,plot.perc=TRUE)
```

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rdacca.hp   *Hierarchical Partitioning for Canonical Analysis*

Description

Hierarchical Partitioning for Canonical Analysis

Usage

```
rdacca.hp(
  dv,
  iv,
  method = c("RDA", "dbRDA", "CCA"),
  type = c("adjR2", "R2"),
  trace = FALSE
)
```

Arguments

dv	Response variables. if method="dbRDA", dv is the "dist" matrix.
iv	Explanatory variables, typically of environmental variables.
method	The type of canonical analysis: RDA, dbRDA or CCA, the default is "RDA".
type	The type of total explained variation: "adjR2" is adjusted R-squared and "R2" for unadjusted R-squared, the default is "adjR2".
trace	logical value, if TRUE, the vaules of commonality (2^N-1for N explanatory variables) are outputed,the default is FALSE.

Details

This function calculates the independent contribution of each explanatory variable to explained variation (R-squared) on canonical analysis (RDA,CCA and dbRDA), applying the hierarchy algorithm of Chevan, A. and Sutherland, M. 1991 Hierarchical Partitioning.The American Statistician, 90–96. DOI: 10.1080/00031305.1991.10475776. Under the idea of hierarchy algorithm, the shared R2 can be divided into equal components by number of involved variables, and then allocated equally to these variables as joint effects. The independent contribution of each explanatory variable is the sum of all its allocated common R2 and its unique R2. The order of importance of explanatory variables are determined by their independent contributions.

Value

a list containing

Method_Type	The type of canonical analysis and the type of total explained variation.
R.squared	Total explained variation.
Commonality	If trace=TRUE,a mtrix listing tha value and percentage of all commonality (2^N-1 for N explanatory variables).
Var.part	A matrix listing independent effect and its percentage to total explained variation for each explanatory variable.

Author(s)

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Examples

```
library(vegan)
data(mite)
data(mite.env)
#Hellinger-transform the species dataset for RDA to deal with the "double zero" problem
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")
```

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rdacca.mhp   *Hierarchical Partitioning for Canonical Analysis by Explanatory Ma-*
                              trices

Description

Hierarchical Partitioning for Canonical Analysis by Explanatory Matrices

Usage

```
rdacca.mhp(
  dv,
  iv,
  method = c("RDA", "dbRDA", "CCA"),
  type = c("adjR2", "R2"),
  trace = FALSE,
  plot.perc = FALSE
)
```

Arguments

dv	Data frame or matrix containing the response data table or dissimilarity structure inheriting from dist. In community ecology, that table is often a site-by-species table or a dissimilarity object.
iv	A list containing N groups explanatory data frame or matrix.
method	The type of canonical analysis: RDA, dbRDA or CCA, the default is "RDA".
type	The type of total explained variation: "adjR2" is adjusted R-squared and "R2" for unadjusted R-squared, the default is "adjR2".
trace	logical value, if TRUE, the vaules of commonality (2^N-1 for N group of explanatory variables) are outputed,the default is FALSE.
plot.perc	logical value, if TRUE, the bar plot (based on ggplot2) of the percentage to independent effects of variables group to total Rsquared, the default is FALSE to show plot with original independent effects.

Details

This function calculates the independent contribution of each explanatory group to explained variation (R-squared) on canonical analysis (RDA,CCA and dbRDA), applying the hierarchy algorithm of Chevan and Sutherland (1991). The algorithm is that all joint R-squared will be decomposed into equal fractions by number of involved explanatory groups and average assigned to these group. Independent R-squared of each variable will be the sum of assigned R-squared from joint R-squared and unique R-squared.

Value

a list containing

Method_Type	The type of canonical analysis and the type of total explained variation.
R.squared	The explained variation for global model.
Commonality	If trace=TRUE,a mtrix listing tha value and percentage of all commonality (2^N-1 for N explanatory variables groups).
Var.part	A matrix listing independent effect and its percentage to total explained variation for each explanatory variable group.

Author(s)

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Examples

```
require(vegan)
data(mite)
data(mite.env)
data(mite.xy)
data(mite.pcnm)
mite.hel <- decostand(mite, "hellinger")
iv <- list(env=mite.env,xy=mite.xy,pcnm=mite.pcnm)
rdacca.mhp(mite.hel,iv,method="RDA",trace = TRUE,plot.perc = FALSE)
rdacca.mhp(vegdist(mite),iv,method="dbRDA",trace = TRUE,plot.perc = FALSE)
rdacca.mhp(mite,iv,method="CCA",trace = TRUE,plot.perc = FALSE)
```

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