

Canonical redundancy analysis (RDA)

Description

This function computes a simple or partial canonical redundancy analysis (RDA), with permutation tests, following the algorithm described in Legendre and Legendre (1998, Chapter 11).

Usage

```
rdaTest(  
  YY.mat, XX.mat, WW.mat=NULL, scale.Y=FALSE, testF=NULL,  
  nperm=NULL, print.results=TRUE, print.cum=FALSE)
```

Arguments

YY.mat	An ($n \times p$) response (e.g. site-by-species) data table.
XX.mat	An ($n \times m$) table of explanatory variables. The number of variables (m) is recomputed after eliminating collinear explanatory variables, if any.
WW.mat	An optional ($n \times q$) table of covariables.
scale.Y	A logical value (TRUE or FALSE) defining if YY.mat should be standardized (TRUE), or only centred on the column means (FALSE).
testF	If NULL (default), the program will ask if the user wishes to test the F-statistic. If testF is TRUE or FALSE, no question will be asked; the program will perform the test, or not, in accordance with that indication.
nperm	Number of permutations for the F-test. If NULL (default), a question will be asked by the program.
print.results	If TRUE, prints the basic rdaTest output to the screen. See the paragraph Value.
print.cum	If TRUE, prints the fractions of the response variable's (e.g. species) variances explained by canonical axes 1, 2, 3, ... and by the whole canonical analysis.

Details

Canonical redundancy analysis (RDA) of a data table producing scaling 1 and scaling 2 biplots. The response variables must be standardized (scale.Y=TRUE) if they are not all expressed in the same physical dimensions. The default is scale.Y=FALSE.

Scaling type 1 biplot uses matrices Z or F for objects and U for variables; notation as in Legendre and Legendre (1998, Section 9.1). This projection preserves the Euclidean distances among the objects.

Scaling type 2 biplot uses matrices ZSc2 or FSc2 for objects and USc2 for variables. This projection preserves the correlations among the variables.

Value

If `print.res=TRUE`, the function prints the following information to the R window:

- The variance inflation factors (VIF) for the explanatory variables. The value is 0 for entirely collinear variables. The covariables are not included in this calculation.
- The bimultivariate redundancy statistic (canonical R-square), as well as the adjusted R-square when there are no covariables in the analysis.
- Test of significance of the canonical relationship: the F-statistic and permutational probability, if the test of significance has been carried out.
- The number of objects, number of response variables, and number of explanatory variables after removing collinear variables; the number of canonical eigenvalues larger than 0.
- The total variance in matrix `YY.mat`, i.e., the $SS/(n-1)$.
- The eigenvalues, relative eigenvalues, and the cumulative % the variance of species data accounted for by the successive canonical eigenvalues.

Function `rdaTest` also returns a list containing the following results and matrices:

VIF	Variance inflation factors for the explanatory variables X; the value is 0 for entirely collinear variables. The covariables are not included in this calculation.
canEigval	Canonical eigenvalues.
U	Canonical eigenvectors normalized to 1 (scaling 1).
USc2	Canonical eigenvectors normalized to $\sqrt{\text{eigenvalue}}$ (scaling 2).
F	Matrix of object scores (scaling 1).
Z	Matrix of fitted object scores (scaling 1).
FSc2	Matrix of object scores (scaling 2).
ZSc2	Matrix of fitted object scores (scaling 2).
biplotScores1	Biplot scores of explanatory variables (scaling 1).
biplotScores2	Biplot scores of explanatory variables (scaling 2).
FitSpe	Table of cumulative fit per species (in %) as fraction of variance of species.
VarExpl	Vector of total % fit per species after all canonical axes.
ProbFrda	Probability associated with F test of the canonical relationship.
X.mat	Original X matrix (required by the plotting function).
Rsq	Canonical R-square.

Reference

Legendre, P. and Legendre, L. 1998. *Numerical Ecology*. 2nd English ed. Elsevier, Amsterdam.

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See Also

[graph.rdaTest](#)

Examples

```
## Example from Legendre and Legendre (1998), p. 590, Table 11.3
Table11.3 = read.table(file.choose())      # File "Table_11-3.txt"
Y = Table11.3[,1:6]
X = Table11.3[,7:10]
result = rdaTest(Y, X, testF=TRUE, nperm=999)
graph.rdaTest(result, graph.type="Z")

## Run rdaTest in such a way that it prints no output to the screen
results <- rdaTest(Y, X, testF=TRUE, nperm=999, print.results=FALSE, print.cum=FALSE)

## Reverse the orientation of the abscissa ('xax') in the plot
graph.rdaTest(result, xax=-1, yax=2, mul.spc=0.90, mul.env=0.70, mul.text=0.10, scaling=1,
graph.type="F", mai.perc=0.15, pos.sites=3)

## Draw confidence ellipses around groups of points, spider data
spiders.spe = read.table("Spiders_28x12_spe.txt")
spiders.hel = decostand(spiders.spe, "hellinger")
spiders.env = read.table("Spiders_28x4_env.txt")
result.spiders = rdaTest(spiders.hel, spiders.env)
# 'vec' divides the sites into three a priori group
vec = c(2,1,2,1,1,3,1,3,2,2,2,2,1,3,3,3,3,3,3,3,2,2,2,3,2,2,2)
graph.rdaTest(result.spiders, graph.type="Z", ell=vec, lty.ell=3, pos.sites=4, mar.perc=0.15)

## Plot the sites and environmental variables, but not the species
graph.rdaTest(result.spiders, graph.type="Z", plot.spc=FALSE, ell=vec, lty.ell=3, pos.sites=4,
mar.perc=0.15)
```