The NCAP package for R

Initializing NCAP

The NCAP function definitions are contained in file `NCAP.R`. These definitions can be loaded into your R session using the code

```
source(file.choose())
```

and using the browser window to select `NCAP.R`.

NOTE: The NCAP package now includes an option to maximize a redundancy statistic (Legendre and Anderson, 1999) rather than the canonical correlation. The redundancy statistic provides a down-weighting of less important principal co-ordinates. The canonical correlation is more appropriate if the researcher is looking for any effect of the covariate, whereas the redundancy statistic is more appropriate if one is more concerned with the covariates ability to explain community pattern.

References

Legendre, P. and Anderson, M. J. 1999. Distance-based redundancy analysis: testing multi-species responses in multi-factorial ecological experiments. *Ecological Monographs* 69: 1-24.

McArdle, B.H. and Anderson, M.J. 2001. Fitting multivariate models to community data: a comment on distance-based redundancy analysis. *Ecology* 82: 290-297.

Millar, R. B, M. J. Anderson, and G. Zunun. 2005. Fitting nonlinear environmental gradients to community data: A general distance-based approach. *Ecology* 86: 2245-2251.

`distance` *Function for calculating a dissimilarity matrix from abundance data*

Description

`distance` calculates a dissimilarity matrix from a matrix of species abundance data.

Usage

```
distance(N,measure="BC",trans="none")
```

Arguments

`N`	Matrix containing the abundance data with rows corresponding to sites and columns to species.
`measure`	Distance measure to be use. Options include none, Bray-Curtis (`BC`), square-root Bray-Curtis (`sqrtBC`), Canberra (`Can`), square-root Canberra (`sqrtCan`), Horn-Morisita (`HornM`) and Euclidean (`Eucl`).

`trans` Transformation to be applied to abundance data before application of the distance measure. Options include none, square-root (`sqrt`), fourth-root (`fourthroot`), presence-absence (`pa`) and row proportions (`rowpropns`).

Value

Distance matrix.

`gradient.choice` *Function for specifying the type of nonlinear gradient*

Description

`gradient.choice` is used to specify the type of nonlinear gradient to be fitted.

Usage

```
gradient.choice(type=”vonB”)
```

Arguments

`type` Character value specifying the gradient type. Must be one of “`vonB`”, “`hyperbolic`” or “`logistic`”.

Value

A function corresponding to the desired gradient.

`LinCCor` *Function to determine best fit of a linear gradient*

Description

`LinCCor` returns the value of `stat` from the best linear gradient fit.

Usage

```
LinCCor=function(X,pcoD,m,stat="Rsquare”)
```

Arguments

`X` Design matrix.

`pcoD` List containing the principal co-ordinates and eigenvalues.

`m` The number of principal co-ordinates to use.

`stat` Character string specifying the statistic to be calculated. If the value is "`Rsquare`" then the nonlinear canonical correlation is returned. If the value is "`RDA`" then the redundancy statistic is returned. The RDA choice can be regarded as a weighted Rsquare whereby the principal co-ordinates are weighted proportional to their eigenvalue.

Value

Numeric, the maximized value of `stat`.

`model` *Function to create design matrix for specified covariates*

Description

`model` is used to construct the design matrix, `X`, in the linear portion the NCAP model.

Usage

```
model(formula.spec,fixed.intercept=T)
```

Arguments

`Formula.spec` Formula.

`Fixed.intercept` Logical value. If `True`, then the intercept term is omitted from the model. If the intercept term corresponds to a scale parameter in the nonlinear gradient then it can not be used, due to parameter confounding.

Value

The design matrix, `X`.

`NLCCor` *Function to return nonlinear R-square or redundancy statistic*

Description

`NLCCor` is used to return the statistic to be maximized.

Usage

```
NLCCor(b,X,pcoD,gradient,m,stat="Rsquare",
                blow=NULL,bhigh=NULL,pwgt=0.001)
```

Arguments

`b`	Numeric value or vector, containing the value of the `b` parameter(s).
`X`	Design matrix.
`pcoD`	List containing the principal co-ordinates and eigenvalues.
`gradient`	The gradient function to use.
`m`	The number of principal co-ordinates to use.
`stat`	Character string specifying the statistic to be calculated. If the value is "`Rsquare`" then the nonlinear canonical correlation is returned. If the value is "`RDA`" then the redundancy statistic is returned. The RDA choice can be regarded as a weighted Rsquare whereby the principal co-ordinates are weighted proportional to their eigenvalue.
`blow`	Numeric, of same dimension as `b`, specifying lower bounds.

Value

Numeric, the statistic to be maximized.

`NLCCorSeq` *Function to fit and plot NCAP for a varying number of principal co-ordinate dimensions*

Description

`NLCCorSeq` calls function `NLCCor` to fit NCAP for increasing number of dimensions, to facilitate choice of the appropriate number of dimensions to use.

Usage

```
NLCCorSeq(b0,X,pcoD,grad,m=NULL,stat="Rsquare",
          plots=T,...)
```

Arguments

`b0`	Numeric value or vector, containing the starting value of the `b` parameter(s).
`X`	Design matrix.
`pcoD`	List containing the principal co-ordinates and eigenvalues.
`grad`	The gradient function to use.
`m`	The maximum number of principal co-ordinates to use.
`stat`	Character string specifying the statistic to be calculated. If the value is "`Rsquare`" then the nonlinear canonical correlation is returned. If the value is "`RDA`" then the redundancy statistic is returned. The RDA choice can be regarded as a weighted Rsquare whereby the principal co-ordinates are weighted proportional to their eigenvalue.

`plots`	Logical. Setting to `False` suppresses the plots.
`...`	Additional arguments to be passed to `NLCCor`.

Value

Matrix, containing fitted statistics.

`pco` *Function to calculate principal co-ordinates and their eigenvalues*

Description

`pco` performs an eigen-decomposition of the matrix obtained from centering $-0.5D^2$, where D is a dissimilarity matrix. It also plots variation explained against number principal co-ordinate dimensions. Variation explained is the cumulative sum of eigenvalues divided by the sum of all eigenvalues (McArdle and Anderson, 2001). Negative eigenvalues will occur for non-metric dissimilarity matrices, and the variation explained will then reach 100% for fewer dimensions then the total number of dimensions.

Usage

```
pco(D,varplot=T)
```

Arguments

`D`	Dissimilarity matrix.
`varplot`	Logical value. Set to `F` to suppress variation plot.

Value

A list with components `values` and `vectors`.

Additional functions (unsupported)

See function definitions for arguments required by these functions.

`BootNLCor`	*Function to calculate bootstrap confidence interval for* b.
`centre.matrix`	*Function to centre a matrix to have row and column sums of zero.*
`lattice.plot`	*Function to produce multi-figure plot of species abundance vs covariates.*
`LinCCor`	*Function to calculate maximum value of* stat *for a linear gradient.*
`plot.NCAP`	*Function to plot gradient, and residuals. Residuals are not produced when* `stat="RDA"`.
`plot.pco`	*Function to produce scatter plots of pco's and plot of pco's vs covariates.*
`PermNLCor`	*Function to calculate permutation test statistics.*
`PermNLCor`	*Function to calculate permutation test statistics.*