Ecodist Package in R

Leah Bargnesi

Introduction to Ecodist

- First published in 2007, most recently updated May 2022
- Intended for community and landscape ecologists
- Deals with multidimensional or spatially-structured data
- Package includes standard methods and a novel extension to the mantel correlogram
 - Correlogram→ spatial correlation plotted on the y-axis and geographic distance classes on the x-axis
 - o Mantel correlogram→ (Mantel, 1967) multivariate distance matrix
 - E.g. multiple species
- The novel extension removes linearity assumption of the Mantel methods
 - Relationship between variables at different scales
- Simple Mantel test→ determines whether environmentally similar sites have similar species composition and if different sites have different species composition
 - Determines whether shorter distant sites are more similar than farther apart sites
- Partial Mantel test→ the partial correlation of A and B given any number of other variables
- Includes geographic distance, while requiring minimal assumptions about nature of the data→ more flexibility
- If relationships are linear, use standard Mantel methods, if not, use the multivariate correlogram method (novel extension)
 - Space-free analysis → Piecewise removal of spatial variation

About the Authors

Sarah C. Goslee [aut, cre]



- Ecologist at USDA
- Field and landscape scales
- Plant diversity in managed grasslands, plant diversity to improve agricultural management, use of satellite imagery to measure grazing land productivity and how forage and biofuel species respond to climate change



Dean L. Urban [aut]

- Professor at Duke University
- Landscape ecology
- Integration of field work, spatial analysis, and simulation modeling
- Fine scale empirical environmental issues→larger time and space scales for management and policy

Functions in package

- Includes worked examples, since analysis can be time consuming, that can be loaded using data()
- bump is a data set included in the package that shows a 2D artificial landscape of the kind of spatial pattern that might be seen across two mountain peaks
- distance() calculates distance or dissimilarity metrics, similar to dist() but allows for new metrics to easily be added
- xmantel() allows for simple and partial cross mantel tests

bump	Nine-bump spatial pattern		
bcdist	Bray-Curtis distance		
	configuration.		
addord	Fit new points to an existing NMDS		
MRM	Multiple Regression on distance Matrices		
мрм	Multiple Degression on distance Matrices		

bump	Nine-bump	spatial	pattern	
bump.pmgram	Nine-bump	spatial	pattern	
cor2m	Two-matrix	correl	etion tab	a

cor2m Two-matrix correlation table corgen Generate correlated data crosstab Data formatting

distance Calculate dissimilarity/distance metrics
ecodist-package Dissimilarity-Based Functions for Ecological
Analysis

fixdmat Distance matrix conversion
full Full symmetric matrix
graze Site information and grazed vegetation data.
iris.fit Example of adding to an ordination

Lower-triangular matrix

Plots fitted vectors onto an ordination diagram

iris.nmds Example for nmds
iris.vf Example for vector fitting on ordination
iris.vfrot Example for vector fitting on rotated
ordination

mantel Mantel test
mgram Mantel correlogram
mgroup Mantel test for groups

lower

plot.vf

min.nmds Find minimum stress configuration
nmds Non-metric multidimensional scaling
pco Principal coordinates analysis
plot.mgram Plot a Mantel correlogram
plot.nmds Plot information about NMDS ordination

pmgram Partial Mantel correlogram
residuals.mgram Residuals of a Mantel correlogram
vf Vector fitting
xdistance Cross-distance between two datasets.

xmantel Cross-Mantel test
xmgram Cross-Mantel correlogram
z.no Example for pmgram

z.zl Example for pmgram

Demonstration

```
🗀 🚽 🔚 🗀 Source on Save 🔍 🎢 🗸 📋
                                                                                   Run P Source - =
  1 library(ecodist)
     data(iris)
                                                                       R . Global Environment .
    iris.bc <- distance(iris[, 1:4], "bray-curtis")</pre>
                                                                       Data
                                                                       O iris
                                                                                             150 obs. of 5 variables
     # The effect of specifying icov:
                                                                        iris.md
                                                                                             num [1:150, 1:150] 0 1.835 0.938 1.976 0.348 ...
                                                                        setosa, md
                                                                                             num [1:50, 1:50] 0 2.169 1.55 3.014 0.593 ...
                                                                        setosa.scaled.md
                                                                                             num [1:50, 1:50] 0 1.835 0.938 1.976 0.348 ...
     # calculate Mahalanobis distance for the full iris dataset
                                                                       values
    iris.md <- full(distance(iris[, 1:4], "mahal"))</pre>
                                                                        iris.bc
                                                                                             'dist' num [1:11175] 0.0355 0.0408 0.051 0.0098 0.0556 ...
     iris.md[1, 2] # Mahalanobis distance between samples 1 and 2
 10
     # calculate Mahalanobis for just one species
     setosa.md <- full(distance(iris[iris$Species == "setosa", 1:4], "mahal"))</pre>
     setosa.md[1, 2] # Mahalanobis distance between samples 1 and 2
14
     # use the covariance matrix for the full dataset to scale for one species
     setosa.scaled.md <- full(distance(iris[iris$Species == "setosa", 1:4],</pre>
                                         "mahal", icov=var(iris[,1:4])))
17
18
     setosa.scaled.md[1, 2] # Mahalanobis distance between samples 1 and 2
                                                  library(ecodist)
19
                                                  iris.bc <- distance(iris[, 1:4], "bray-curtis")</pre>

    # calculate Mahalanobis distance for the full iris dataset

                                                  iris.md <- full(distance(iris[, 1:4], "mahal"))</pre>
                                                  · iris.md[1, 2] # Mahalanobis distance between samples 1 and 2
                                                  11 1.834554

    # calculate Mahalanobis for just one species

                                                  - setosa.md <- full(distance(iris[iris$Species == "setosa", 1:4], "mahal"))</pre>

    setosa.md[1, 2] # Mahalanobis distance between samples 1 and 2

                                                  11 2.169407
```

Works Cited

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