

Ecodist Package in R

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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
 - 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, allows for more than
- 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

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- 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



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- 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

MRM	Multiple Regression on distance Matrices
addord	Fit new points to an existing NMDS configuration.
bcdist	Bray-Curtis distance
bump	Nine-bump spatial pattern
bump.pgram	Nine-bump spatial pattern
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
iris.nmfs	Example for nmfs
iris.vf	Example for vector fitting on ordination
iris.vfrot	Example for vector fitting on rotated ordination
lower	Lower-triangular matrix
mantel	Mantel test
mgram	Mantel correlogram
mgroup	Mantel test for groups
min.nmfs	Find minimum stress configuration
nmfs	Non-metric multidimensional scaling
pco	Principal coordinates analysis
plot.mgram	Plot a Mantel correlogram
plot.nmfs	Plot information about NMDS ordination
plot.vf	Plots fitted vectors onto an ordination diagram
pgram	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 pgram
z.z1	Example for pgram

Demonstration

```
1 library(ecodist)
2 data(iris)
3 iris.bc <- distance(iris[, 1:4], "bray-curtis")
4
5 # The effect of specifying icov:
6
7 # calculate Mahalanobis distance for the full iris dataset
8 iris.md <- full(distance(iris[, 1:4], "mahal"))
9 iris.md[1, 2] # Mahalanobis distance between samples 1 and 2
10
11 # calculate Mahalanobis for just one species
12 setosa.md <- full(distance(iris[iris$Species == "setosa", 1:4], "mahal"))
13 setosa.md[1, 2] # Mahalanobis distance between samples 1 and 2
14
15 # use the covariance matrix for the full dataset to scale for one species
16 setosa.scaled.md <- full(distance(iris[iris$Species == "setosa", 1:4],
17                                "mahal", icov=var(iris[,1:4])))
18 setosa.scaled.md[1, 2] # Mahalanobis distance between samples 1 and 2
19 |
```

```
• library(ecodist)
• iris.bc <- distance(iris[, 1:4], "bray-curtis")
• # calculate Mahalanobis distance for the full iris dataset
• iris.md <- full(distance(iris[, 1:4], "mahal"))
• iris.md[1, 2] # Mahalanobis distance between samples 1 and 2
[1] 1.834554
• # calculate Mahalanobis for just one species
• setosa.md <- full(distance(iris[iris$Species == "setosa", 1:4], "mahal"))
• setosa.md[1, 2] # Mahalanobis distance between samples 1 and 2
[1] 2.169407
• # use the covariance matrix for the full dataset to scale for one species
• setosa.scaled.md <- full(distance(iris[iris$Species == "setosa", 1:4],
•                                "mahal", icov=var(iris[,1:4])))
• setosa.scaled.md[1, 2] # Mahalanobis distance between samples 1 and 2
[1] 1.834554
```

R ▾ Global Environment ▾

Data

iris	150 obs. of 5 variables
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 ...

Values

iris.bc	'dist' num [1:11175] 0.0355 0.0408 0.051 0.0098 0.0556 ...
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