

# Package ‘fossil’

October 13, 2022

**Type** Package

**Title** Palaeoecological and Palaeogeographical Analysis Tools

**Version** 0.4.0

**Date** 2020-03-20

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**Depends** sp, maps, shapefiles

**Description** A set of analytical tools useful in analysing ecological and geographical data sets, both ancient and modern. The package includes functions for estimating species richness (Chao 1 and 2, ACE, ICE, Jackknife), shared species/beta diversity, species area curves and geographic distances and areas.

**License** GPL (>= 2)

**URL** <http://matthewvavrek.com/programs-and-code/fossil/>

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2020-03-23 11:30:05 UTC

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 fossil-package

*fossil: Palaeoecological and Palaeogeographical Analysis Tools*


---

## Description

A set of analytical tools useful in analysing ecological and geographical data sets, both ancient and modern. The package includes functions for estimating species richness (Chao 1 and 2, ACE, ICE, Jackknife), shared species/beta diversity, species area curves and geographic distances.

## Details

The fossil package is designed to be used by palaeoecologists and palaeobiogeographers, providing to them a set of useful tools including species similarity indices, species estimators, minimum spanning tree/forest functions, and an assortment of other useful tools.

## Author(s)

Matthew Vavrek <matthew@matthewvavrek.com>

**Description**

Computes the extrapolated species richness of a population using the Abundance- and Incidence-based Coverage Estimators

**Usage**

```
ACE(x, taxa.row = TRUE)
ICE(x, taxa.row = TRUE)
```

**Arguments**

x	a vector, matrix or data frame of positive integers or zero of any size
taxa.row	whether each row of the matrix is a different taxon; if so, value is T

**Details**

These functions compute the ACE and ICE richness estimators, respectively. Both functions will accept a vector, matrix or data frame of any size made up of positive integers and zeros. Matrices are by default treated such that each row is a different taxon and each column is a sample or locality, however if they are arranged with the taxa as columns, change the argument `taxa.row` to FALSE. Take note that ACE is intended only for use with abundance data, and not presence absence data. While ICE will accept abundance matrices, it will internally convert the matrix to presence absence data. Note that if ACE returns NaN or Inf as a value, that Chao1 will be used in its place as per the recommendation made by Colwell in EstimateS.

**Value**

A value representing a minimum number of species present in the assemblage if the entire population were to be censused.

**Author(s)**

Matthew Vavrek, with recommendations from the EstimateS reference manual by R.K. Colwell

**References**

- Chao, A., M.-C. Ma, & M. C. K. Yang. 1993. Stopping rules and estimation for recapture debugging with unequal failure rates. *Biometrika* 80, 193-201.
- Chao, A., W.-H. Hwang, Y.-C. Chen, and C.-Y. Kuo. 2000. Estimating the number of shared species in two communities. *Statistica Sinica* 10:227-246.
- Chazdon, R. L., R. K. Colwell, J. S. Denslow, & M. R. Guariguata. 1998. Statistical methods for estimating species richness of woody regeneration in primary and secondary rain forests of NE Costa Rica. Pp. 285-309 in F. Dallmeier and J. A. Comiskey, eds. *Forest biodiversity research, monitoring and modeling: Conceptual background and Old World case studies*. Parthenon Publishing, Paris.

**See Also**

For related species estimators, see [chao1](#), [bootstrap](#) and [jack1](#), and [spp.est](#) to calculate multiple indices at once.

**Examples**

```
## sample vector
a<-c(0,5,1,1,2,0,0,1,0,0,8,45)
ACE(a)

## matrix format
a<-matrix(c(0,5,1,1,2,0,0,1,0,0,8,45),4,3)
ACE(a)
ICE(a)

## presence absence matrix
a<-matrix(c(0,1,1,1,1,0,0,1,0,0,1,1),4,3)
ACE(a)
ICE(a)
```

---

aic.nest

*Nestedness of samples using AIC*

---

**Description**

Test if two empirical samples are drawn from the same or different communities

**Usage**

```
aic.nest(comm1, comm2, base=exp(1))
```

**Arguments**

comm1, comm2     lists of abundance data from two empirical samples  
base             base of the log used in the calculation of Shannon's diversity

**Details**

This function tests if two empirical samples are drawn from the same community, based on the AIC scores.

**Value**

returns two AIC scores, the first assuming the two empirical samples are drawn from the same distribution, the other assuming the two empirical samples are from different distributions

**Author(s)**

Matthew Vavrek

**See Also**[simpson](#)**Examples**

```
#for example, two different communities
a<-c(12,4,12,1,4,0,6,5,0,0,0)
b<-c(0,11,4,3,6,7,7,2,23,5,8)

#if the aic score is lower, it is the better model
aic.nest(a,b)

#from the same community
a<-c(5,6,5,6,5,6,5,6,5,2,1,1)
b<-c(2,3,2,3,2,3,2,3,2,3,2,1,0,0)
aic.nest(a,b)
```

---

**bootstrap***Bootstrap Species Richness Estimator*

---

**Description**

Computes the bootstrap species richness estimator for abundance or presence-absence data

**Usage**

```
bootstrap(x, taxa.row = TRUE, abund = TRUE, samples = NA)
```

**Arguments**

x	a vector, matrix or data frame of positive integers or zero of any size
taxa.row	whether each row of the matrix is a different taxon
abund	whether the input is abundance (or presence/absence) based
samples	if input is a vector file, the number of samples must be included

**Details**

The bootstrap estimator

**Value**

Returns a single value for the Bootstrap Species Estimator

**Author(s)**

Matthew Vavrek

**References**

Smith, E.P. & van Belle, G. 1984. Nonparametric estimation of species richness. *Biometrics* 40, 119-129.

**See Also**

[jack1](#), [ACE](#), [chao1](#)

**Examples**

```
## sample vector
a<-c(0,5,1,1,2,0,0,1,0,0,8,45)
bootstrap(a,samples=45)

## matrix format
a<-matrix(c(0,5,1,1,2,0,0,1,0,0,8,45),4,3)
bootstrap(a)
bootstrap(a,,FALSE)

## presence absence matrix
a<-matrix(c(0,1,1,1,1,0,0,1,0,0,1,1),4,3)
bootstrap(a,,FALSE)
```

---

chao.sd

*Chao's estimation of standard error*

---

**Description**

Computes the standard error for chao1 or chao2

**Usage**

```
chao.sd(x)
```

**Arguments**

x                    a vector of abundances or frequencies of occurrences

**Details**

primarily designed to be used internally by `spp.est` to calculate the errors for the chao estimators

**Value**

returns a value for standard deviation for chao1 or chao2

**Author(s)**

Matthew Vavrek

**References**

Colwell, R.K. 2010. EstimateS: Statistical estimation of species richness and shared species from samples. Version 8.2. User's Guide and application published at: <http://purl.oclc.org/estimates>.

**See Also**

[chao1](#), [spp.est](#)

**Examples**

```
## sample vector
a<-c(0,5,1,1,2,0,0,1,0,0,8,45)
chao.sd(a)
```

---

chao.sorenson

*Chao's Jaccard and Sorenson Estimators of Shared Species*

---

**Description**

Chao's Jaccard and Sorenson shared species estimators for use with incomplete datasets

**Usage**

```
chao.sorenson(x, y)
chao.jaccard(x, y)
```

**Arguments**

x	species from group A
y	species from group B

**Details**

You must provide two separate vectors, with species arranged in the same order, from area A and B. If species are present in one site but not the other, these must be recorded for both sites; the site where they are not found should be coded as a zero. Species not present at either site are ignored.

**Value**

Returns the Chao-Jaccard or Chao-Sorenson similarity index for the two sites in question.

**Author(s)**

Matthew Vavrek

**References**

Chao, A., R. L. Chazdon, et al. 2005. A new statistical approach for assessing similarity of species composition with incidence and abundance data. *Ecology Letters* 8: 148-159.

**See Also**

[bray.curtis](#)

**Examples**

```
##Species counts from two different locations
a <- c(1,0,4,3,5,0,0,7)
b <- c(2,1,3,0,0,1,0,6)
chao.sorenson(a,b)
chao.jaccard(a,b)
```

---

chao1

*Chao's Species Estimators*

---

**Description**

Computes the Chao species estimator for abundance or presence-absence data

**Usage**

```
chao1(x, taxa.row = TRUE)
chao2(x, taxa.row = TRUE)
```

**Arguments**

x                    a vector, matrix or data frame with species by samples  
taxa.row            a logical argument if the species are the rows or columns

**Details**

chao1 will return an estimate of species richness based on a vector or matrix of abundance data, while chao2 will return an estimate of species richness based on incidence data. Note that chao1 estimator is for abundance data only. The chao2 estimator can be given abundance data and it will automatically convert it to incidence data, but due to the nature of the estimator, the data must contain more than one sample (ie the data must be arranged in a minimum 2 by 2 matrix).



**Value**

returns a value for the Chao Species Estimator for a the given data.

**Note**

While the function will still return a value, if all the species abundances are equal to 1 in the input to `chao1`, a warning will be raised, and the value returned will be equal to the number of species observed.

**Author(s)**

Matthew Vavrek

**References**

Chao, A. 1984. Non-parametric estimation of the number of classes in a population. *Scandinavian Journal of Statistics* 11: 265-270.

Chao, A. 1987. Estimating the Population Size for Capture-Recapture Data with Unequal Catchability. *Biometrics* 43: 783-791.

**See Also**

[jack1](#), [bootstrap](#)

**Examples**

```
## sample vector
a<-c(0,5,1,1,2,0,0,1,0,0,8,45)
chao1(a)

## matrix format
a<-matrix(c(0,5,1,1,2,0,0,1,0,0,8,45),4,3)
chao1(a)
chao2(a)

## presence absence matrix
a<-matrix(c(0,1,1,1,1,0,0,1,0,0,1,1),4,3)
chao1(a)
chao2(a)
```

**Description**

Computes Cohesiveness Index for a Cluster Analysis

**Usage**

```
coi(mst, groups)
```

**Arguments**

mst	A minimum spanning tree matrix (binary)
groups	A vector with the group/cluster assignments for each sample

**Value**

Returns a something

**Note**

While the function will still return a value, if all the species abundances are equal to 1 in the input to `chao1`, a warning will be raised, and the value returned will be equal to the number of species observed.

**Author(s)**

Matthew Vavrek

**See Also**

[rclust](#)

**Examples**

```
## sample vector
a<-c(0,5,1,1,2,0,0,1,0,0,8,45)
chao1(a)

## matrix format
a<-matrix(c(0,5,1,1,2,0,0,1,0,0,8,45),4,3)
chao1(a)
chao2(a)

## presence absence matrix
a<-matrix(c(0,1,1,1,1,0,0,1,0,0,1,1),4,3)
chao1(a)
chao2(a)
```

---

`create.lats`*Creating a table of Latitudes and Longitudes*

---

**Description**

Create a matrix of locations with a column of latitudes and longitudes

**Usage**

```
create.lats(x, loc="locality", long="longitude", lat="latitude")
```

**Arguments**

<code>x</code>	a table arranged in columnar format, with one column indicating the locations, another the latitude and another the longitude
<code>loc</code>	the name or number of the column giving the names of the locations to be used
<code>long</code>	the name or number of the column giving the longitude of the locations
<code>lat</code>	the name or number of the column giving the latitude of the locations

**Details**

This function will create a location table with longitude (X) and latitude (Y) or their equivalents for every location. This function ceates a matrix in the format needed for most of the geographic functions found in the fossil package.

**Value**

A matrix with a column of longitude and latitude, respectively with rownames corresponding to each location

**Author(s)**

Matthew Vavrek

**See Also**

[create.matrix](#)

**Examples**

```
#to reproduce the fdata.lats dataset
data(fdata.list)
create.lats(fdata.list, loc="locality", long="longitude", lat="latitude")
```

---

 create.matrix

*Creating species locality matrices*


---

### Description

Create a matrix with taxa as rows and occurrences or samples as columns

### Usage

```
create.matrix(
  x,
  tax.name="genus",
  locality="locality",
  time.col=NULL,
  time=NULL,
  abund=FALSE,
  abund.col="abundance"
)
```

### Arguments

x	a table arranged in columnar format, with at least one column indicating name of taxa and another giving location or sample
tax.name	the name or number of the column giving the taxonomic names to be used (the rows of the matrix to be created)
locality	the name or number of the column giving the locations of the samples (the columns of the matrix to be created)
time.col	what is the column name or number containing the time periods; if left null, filtering for time will be ignored
time	what time periods to keep for the matrix; if left null, filtering for time will be ignored
abund	whether to record abundances of taxa; if left FALSE, a binary (presence/absence) matrix is created
abund.col	column name or number containing abundance values

### Details

This is a helper function to convert large lists of data into matrices of species (rows) and locations (columns). The parameters can be adjusted to create either a binary (presence/absence) or abundance matrix. The setup of the table is largely flexible; simply input the column names or numbers containing the pertinent information. To filter data according to time, both the time column and the time period must be specified. For abundance, the default title for the abundance column is simply "abundance"; the function will not work if you have chosen to include abundances (abund = TRUE) but the name of the abundance column is incorrect.

**Value**

A matrix of taxa (rows) by localities (columns).

**Note**

At present, the function will ignore rows where the taxon name is NA, NULL, ' ' (empty character value) or ' ' (single space), as these labels typically represent an unknown taxa, which would be inappropriate to include in most analyses.

**Author(s)**

Matthew Vavrek

**See Also**

[create.lats](#)

**Examples**

```
#converting the fdata.list dataset into a matrix of species (rows)
#by samples (columns) with abundance data
data(fdata.list)
create.matrix(fdata.list, tax.name = "species", abund=TRUE)

#same data set, but now for an occurrence matrix
create.matrix(fdata.list, tax.name = "species", locality = "locality")
```

---

deg.dist

*Haversine Distance Formula*

---

**Description**

Haversine formula to calculate distances between points on the earth

**Usage**

```
deg.dist(
  long1,
  lat1,
  long2,
  lat2
)
```

**Arguments**

long1	longitude of location 1
lat1	latitude of location 1
long2	longitude of location 2
lat2	latitude of location 2

**Details**

This function will calculate the shortest distance (portion of a Great Circle) in kilometers between two points on the Earth given their latitude and longitude.

**Value**

Arc distance between two points on the Earth's surface in kilometers.

**Note**

The distance calculated may be up to 0.2% inaccurate, as this function treats the Earth as a sphere with a circumference of 40041.47 km (mean circumference), rather than an ellipsoid like it actually is.

**Author(s)**

Matthew Vavrek

**References**

The formulas for the Haversine distance function were taken from the Dr. Math website at <http://mathforum.org/library/drmath/view/55417.html>

**See Also**

To calculate pairwise distances between a list of points see [earth.dist](#), or to calculate an area enclosed by three points on the Earth's surface, see [earth.tri](#)

**Examples**

```
##distance between 23 degrees N 54 degrees E and 32 degrees S 67 degrees E  
deg.dist(23,54,-32,67)
```

---

`dino.mst`*Calculate a Minimum Spanning Tree or Network*

---

**Description**

Methods for calculating a minimum spanning tree or network between a number of points given a distance matrix.

**Usage**

```
dino.mst(x, random.start = TRUE, random.search = TRUE)
dino.msn(x)
```

**Arguments**

<code>x</code>	a distance matrix for any number of points
<code>random.start</code>	If the minimum spanning tree is to start at a random point and not the first given site (default is TRUE)
<code>random.search</code>	If there is more than one shortest possible branch, should one be chosen randomly

**Details**

Ensure that a distance matrix is used, and not a similarity matrix, otherwise the result given will be highly incorrect.

**Value**

Returns a binary matrix where connections between points are denoted by a 1.

**Author(s)**

Yvonnick Noel, Julien Claude and Emmanuel Paradis with modifications from Matthew Vavrek

**See Also**

[dino.dist](#)

**Examples**

```
#minimum spanning tree for the fdata set
data(fdata.mat)
fdata.dist<-dino.dist(fdata.mat)
dino.mst<-dino.mst(fdata.dist)
```

---

`earth.bear`*Bearings Between Geographic Locations*

---

**Description**

Calculate the bearing in degrees clockwise from True North between any two points on the globe.

**Usage**

```
earth.bear(long1, lat1, long2, lat2)
```

**Arguments**

<code>long1</code>	Longitude of site 1
<code>lat1</code>	Latitude of site 1
<code>long2</code>	Longitude of site 2
<code>lat2</code>	Latitude of site 2

**Details**

Calculate the bearing in degrees clockwise from True North between any two points on the globe. Primarily designed to be used with other included geographic tools.

**Value**

Returns a value in degrees from True North between two geographic points.

**Author(s)**

Matthew Vavrek

**References**

Haversine formula from Math Forums: Ask Dr. Math at <http://mathforum.org/dr.math/>

**See Also**

[earth.poly](#)

**Examples**

```
earth.bear(-100, 30, 20, -40)
```



**Description**

Create a distance matrix (lower triangle) between a list of points

**Usage**

```
earth.dist(lats, dist = TRUE)
```

**Arguments**

lats	a table with a longitude and latitude column respectively as the first two columns
dist	A logical argument whether to create a distance matrix (lower triangle) or full matrix

**Details**

This function will calculate the pairwise distances between all points given and return either a distance or full matrix as specified. All coordinates must be in decimal degrees.

**Value**

Returns a matrix of distances in kilometers between a list of longitudes and latitudes.

**Note**

Large datasets may take some time to process, as the number of distances to calculate is factorial in nature.

**Author(s)**

Matthew Vavrek, with suggestions from Anton Korobeynikovs

**See Also**

[deg.dist](#)

**Examples**

```
data(fdata.lats)
earth.dist(fdata.lats)
```

---

`earth.poly`*Calculating a Minimum Convex Polygon*

---

### Description

Calculate a minimum convex polygon for a collection of points without knowing what points form the vertices.

### Usage

```
earth.poly(lats)
```

### Arguments

`lats` a table with a longitude and latitude column respectively as the first two columns, or a `SpatialPoints` object with longitude/latitude

### Details

This function will calculate the area of a minimum convex polygon/convex hull for a spherical surface (ie points on a globe).

### Value

The function will return a list consisting of the area in  $\text{km}^2$  (`\$area`) and a vector with the row numbers of the vertices (`\$vertices`)

### Author(s)

Matthew Vavrek

### See Also

[earth.tri](#)

### Examples

```
#1/8th the surface area of the earth
a <- matrix(c(0, 0, 0, 90, 90, 0, 25, 25), 4, 2, byrow = TRUE)
earth.poly(a)
```

---

`earth.tri`*Calculating the Surface Area Enclosed by Three Geographic Points*

---

**Description**

Calculate the true area on a sphere enclosed by three points on the earth's surface

**Usage**

```
earth.tri(long1, lat1, long2, lat2, long3, lat3)
```

**Arguments**

<code>long1</code>	Longitude of site 1
<code>lat1</code>	Latitude of site 1
<code>long2</code>	Longitude of site 2
<code>lat2</code>	Latitude of site 2
<code>long3</code>	Longitude of site 3
<code>lat3</code>	Latitude of site 3

**Details**

A function to find the area enclosed by three points on the surface of the earth, given their latitudes and longitudes. This function is primarily designed to be a component of [earth.poly](#), which is likely a more useful function for most applications.

**Value**

Returns a value in kilometers squared of the area enclosed by the three points.

**Note**

The distance calculated may be up to 0.2% inaccurate, as this function treats the Earth as a sphere with a circumference of 40041.47 km (mean circumference), rather than an ellipsoid like it actually is.

**Author(s)**

Matthew Vavrek

**References**

Wolfram Mathworld, <http://mathworld.wolfram.com/SphericalTriangle.html>

**See Also**

[earth.poly](#)

## Examples

```
#1/8th the surface area of the earth  
earth.tri(0, 0, 0, 90, 90, 0)
```

---

ecol.dist

*Creating a Distance Matrix*

---

## Description

Create a distance matrix between any number of locations

## Usage

```
ecol.dist(x, method = sorensen, type = "dis")  
dino.dist(x, method = sorensen, type = "dis")
```

## Arguments

x	matrix of taxa (or equivalent data) in rows by columns of localities (or equivalent)
method	the distance/similarity index to compute
type	if the matrix is to be a distance ('dis') or similarity ('sim') matrix

## Details

This will create a distance (or similarity) matrix using any of the provided indices: [sorensen](#), [simpson](#), [bray.curtis](#), [jaccard](#), [morisita.horn](#), [chao.jaccard](#) and [chao.sorensen](#). Creating a distance matrix will give a value of 1 for the most distantly related sites, while similarity index will give a value of 1 for the most similar sites.

`dino.dist` is an old name for the function, and is in the process of being deprecated.

## Value

A distance matrix (lower triangle) giving the pairwise distance indices between all points.

## Note

To use a user generated distance index, type the name of the function to be used for method, and the function will use that function instead. Note that the function internally provides two equal length vectors at a time to the distance calculation function.

## Author(s)

Matthew Vavrek

**See Also**

[sorenson](#), [simpson](#), [bray.curtis](#), [jaccard](#), [morisita.horn](#), [chao.jaccard](#) and [chao.sorenson](#)

**Examples**

```
##example using fdata.mat
data(fdata.mat)
ecol.dist(fdata.mat)
ecol.dist(fdata.mat,simpson,"sim")
```

---

euler.rot

*Calculate the Euler Rotation of a Point*

---

**Description**

Calculate the rotation of a point on the Earth for a given Euler pole. The rotation assumes a spherical earth.

**Usage**

```
euler.rot(lat1, long1, rotdeg, lat2, long2)
```

**Arguments**

lat1	Euler-pole latitude
long1	Euler-pole longitude
rotdeg	Rotation about Euler-pole
lat2	Latitude of point to be converted
long2	longitude of point to be converted

**Details**

Locations of the Euler pole and the point to be rotated must be given in decimal degrees.

**Value**

Rotated latitude and longitude of the provided point in decimal degrees.

**Author(s)**

Matthew Vavrek

**References**

~put references to the literature/web site here ~

---

`fdata`*A Sample Species Abundance Dataset*

---

**Description**

A simple hypothetical data set used in many of the examples.

**Value**

There are 3 datasets, however 2 of them (`fdata.mat` and `fdata.lats`) derive from the first (`fdata.list`). `fdata.list` is a table with 5 columns describing the sample site, species name, abundance, and location in latitude/longitude. `fdata.mat` is a 12 by 12 species abundance matrix (12 unique species and 12 unique samples/localities) that can be recreated from the original table of occurrences using the `create.matrix()` function; likewise, the `fdata.lats()` contains the locations of each of the samples, and can be created using the `create.lats()`

**Author(s)**

Matthew Vavrek

**Examples**

```
data(fdata.list)
```

---

`int.chao`*Internal function for chao estimators*

---

**Description**

Computes the Chao species estimator for both `chao1` and `chao2` estimators

**Usage**

```
int.chao(x)
```

**Arguments**

`x` a vector of positive integers or zero of any length

**Details**

This function is typically only called internally by the functions `chao1` and `chao2`. The function has a built in bias correction, such that it will not return values of infinity or non-numbers.

**Value**

Estimated number of species using the Chao estimator.

**Author(s)**

Matthew Vavrek

**References**

Chao, A. 1984. Nonparametric estimation of the number of classes in a population. Scandinavian Journal of Statistics 11: 265-270.

**See Also**

For the more useful implementations of the Chao estimator, see [chao1](#) for the abundance based estimator or [chao2](#) for the incidence based estimator

**Examples**

```
## create example data set
a<-c(4,5,1,1,2,0,0,1,3,0,8,45,23)
int.chao(a)

## a data set which would give NaN using classic (ie not bias corrected) version
a<-c(4,5,0,0,2,0,0,0,3,0,8,45,23)
int.chao(a)
```

---

jack1

*First- and second-order jackknife estimators*

---

**Description**

Computes the extrapolated species richness of a population using first- or second-order jackknife estimators

**Usage**

```
jack1(x, taxa.row = TRUE, abund = TRUE)
jack2(x, taxa.row = TRUE, abund = TRUE)
```

**Arguments**

x	a vector, matrix or data frame of positive integers or zero of any size
taxa.row	whether each row of the matrix is a different taxon; if so, value is set to TRUE
abund	If true, data is assumed to be abundance, if false, presence absence is assumed

**Details**

These functions compute the first and second-order jackknife species richness estimators, respectively. Both functions will accept a vector, matrix or data frame of any size made up of positive integers and zeros. Matrices are by default treated such that each row is a different taxon and each column is a sample or locality, however if they are arranged with the taxa as columns, change the argument `taxa.row` to `FALSE`. If the data is abundance based, `abund` should be set to `TRUE`. If `abund` is set to `FALSE`, the data will be converted to presence/absence if not already in that format. For single vectors/columns, `taxa.row` and `abund` are ignored.

**Value**

The value returned is the Jackknife estimated species diversity of the dataset in question.

**Author(s)**

Matthew Vavrek

**References**

- Burnham, K.P. & W.S. Overton. 1978. Estimation of the size of a closed population when capture probabilities vary among animals. *Biometrika* 65, 623-633.
- Burnham, K.P. & W.S. Overton. 1979. Robust estimation of population size when capture probabilities vary among animals. *Ecology* 60, 927-936.
- Heltsh, J. & Forrester, N.E. 1983 . Estimating species richness using the jackknife procedure. *Biometrics* 39, 1-11.

**See Also**

[ACE](#)

**Examples**

```
## sample vector
a<-c(0,5,1,1,2,0,0,1,0,0,8,45)
jack1(a)

## matrix format
a<-matrix(c(0,5,1,1,2,0,0,1,0,0,8,45),4,3)
jack1(a)
jack2(a)
jack2(a,abund = FALSE)

## presence absence matrix of the above abundance matrix
a<-matrix(c(0,1,1,1,1,0,0,1,0,0,1,1),4,3)
jack1(a)
jack2(a)
jack2(a, abund = FALSE)
```



---

`lats2Shape`*Converting a Table of Latitudes and Longitudes to a Shapefile*

---

**Description**

A helper function to convert a table of latitudes and longitudes (and associated attributes, if applicable) into a shapefile

**Usage**

```
lats2Shape(lats)
```

**Arguments**

`lats` a table with a latitude and longitude column respectively with associated attributes

**Details**

The table to be converted must contain as it's first two columns the latitude (or Y) and longitude (or X) values to be converted. Any other number of columns in any format can also be attached, and will be included in the attribute table.

**Value**

A shapefile object which can be written to file using `write.shapefile`

**Author(s)**

Matthew Vavrek

**See Also**

[msn2Shape](#)

**Examples**

```
## Not run:
#use fdata.lats as dataset
data(fdata.lats)
shape.lats<-lats2Shape(fdata.lats)
write.shapefile(shape.lats, file='/path/to/write/lats')

## End(Not run)
```

---

`loc.map`*Mapping Points on a Global Map*

---

**Description**

A function to plot any number of points given their latitude and longitude respectively on a map of the world.

**Usage**

```
loc.map(x, ...)
```

**Arguments**

<code>x</code>	a table with a longitude and latitude column respectively with optional associated attributes
<code>...</code>	arguments to be passed to the plot call

**Details**

This is a helper function, which automatically zooms in and centers the map view on the input points. The `...` allow the user to adjust the usual parameters for a scatterplot outlined by [par](#).

**Value**

Plots a map of the world focused on the locations provided.

**Author(s)**

Matthew Vavrek

**See Also**

[msn.map](#)

**Examples**

```
#plotting the fdata sample set
data(fdata.lats)
loc.map(fdata.lats)
```

---

`localoptima`*Function to Find Local Optimization for clustering*

---

**Description**

A function meant to be used internally by the `relational.clustering` function

**Usage**

```
localoptima(dist, group)
```

**Arguments**

<code>dist</code>	Distance matrix to be used
<code>group</code>	group designations

**Details**

The function takes a distance matrix and a vector with the group identifications for each sample locality (or equivalent). It is mainly meant to be used internally by the `relational.clustering` function to optimize the initial clustering and find the local (which hopefully is also the global) optimal organization, such that each member of a group is more similar to the other members in it's group (on average) than to any other groups.

**Value**

Arc distance between two points on the Earth's surface in kilometers.

**Note**

The distance calculated may be up to 0.2% inaccurate, as this function treats the Earth as a sphere with a circumference of 40003 km, rather than an ellipsoid like it actually is.

**Author(s)**

Matthew Vavrek

**See Also**

To calculate pairwise distances between a list of points see [earth.dist](#), or to calculate an area enclosed by three points on the Earth's surface, see [earth.tri](#)

**Examples**

```
##distance between 23 degrees N 54 degrees E and 32 degrees S 67 degrees E  
deg.dist(23,54,-32,67)
```

---

`msn.map`*Mapping a Minimum Spanning Tree*

---

**Description**

Creating a quick and focused map using a world map for geographically referenced visualization within R of a minimum spanning tree or network.

**Usage**

```
msn.map(msn, lat, ...)
```

**Arguments**

<code>msn</code>	minimum spanning tree or network to be used
<code>lat</code>	the lats
<code>...</code>	arguments to be passed to <code>plot</code>

**Details**

This is a helper function for quick visualization of georeferenced minimum spanning trees, and is not meant for creating figure quality images due to lack of fine control over many functions

**Value**

Returns a map of the globe, focused in on any set of georeferenced localities.

**Author(s)**

Matthew Vavrek

**See Also**

[dino.msn](#)

**Examples**

```
##add examples
```

---

`msn2Shape`*Convert a Minimum spanning Network or Tree to Shapefile*

---

**Description**

A helper function to convert a minimum spanning tree or network into shapefile format.

**Usage**

```
msn2Shape(msn, lats, dist = NULL)
```

**Arguments**

<code>msn</code>	a minimum spanning tree or network (binary matrix)
<code>lats</code>	a matrix or data frame with the latitude and longitude of the sites as the first two columns respectively
<code>dist</code>	Optional argument to include distance values in final output; if wanted, a distance matrix (lower triangle) with the localities in the same order as in the MSN are required

**Details**

This function will take a minimum spanning tree or network object, along with the georeferenced locations of the sites, and convert it into a shapefile for use with GIS. The `msn` argument requires a minimum spanning tree or network object, and the `lat` argument requires some form of location for each of the points, typically a matrix with latitude and longitude columns respectively.

**Value**

A shapefile which can be output using the `write.shapefile` function for use with a GIS program.

**Author(s)**

Matthew Vavrek

**See Also**

[lats2Shape](#) for a function to convert a lat/long table to a shapefile

**Examples**

```
## Not run:  
#import both fdata.lats and fdata.mat  
data(fdata.lats)  
data(fdata.mat)  
fdata.dist<-dino.dist(fdata.mat)  
fdata.mst<-dino.mst(fdata.dist)  
shape.mst<-msn2Shape(fdata.mst, fdata.lats)
```

```
write.shapefile(shape.mst, file='/path/to/write/mst')  
  
## End(Not run)
```

---

mstlines

*Display a Minimum Spanning Tree or Network*

---

### Description

a method of displaying a Minimum Spanning Tree/Network over a given set of points

### Usage

```
mstlines(mst, x, y = NULL, pts.names = NULL, ...)
```

### Arguments

mst	a minimum spanning tree or network object
x	either a table with the first two columns that of the x and y coordinates respectively, or simply that of the x coordinate
y	an optional argument if the y coordinates were not given in argument x
pts.names	If there is more than one shortest possible branch, should one be chosen randomly
...	arguments to be passed to lines()

### Details

A function to plot the lines of a minimum spanning tree/forest on a plot; works as a frontend for lines.

### Author(s)

Matthew Vavrek

### See Also

[dino.dist](#)

### Examples

```
#plot with overlain MST for fdata dataset  
data(fdata.lats)  
data(fdata.mat)  
fdata.dist<-dino.dist(fdata.mat)  
fdata.mst<-dino.mst(fdata.dist)  
plot(coordinates(fdata.lats))  
mstlines(fdata.mst, coordinates(fdata.lats))
```

---

`new.lat.long`*Find a New Latitude and Longitude*

---

**Description**

Find a new location using an original location (latitude and longitude) along with a bearing and distance

**Usage**

```
new.lat.long(long, lat, bearing, distance)
```

**Arguments**

<code>long</code>	original longitude
<code>lat</code>	original latitude
<code>bearing</code>	bearing from original point to new location, degrees from North
<code>distance</code>	distance to location

**Value**

a vector of length 2 with the new latitude and longitude respectively

**Author(s)**

Matthew Vavrek

**See Also**

[deg.dist](#), [earth.bear](#)

**Examples**

```
#Travel from 0,0 to a new location at a bearing of 45 degrees  
#from North (clockwise) and 1000 km away  
new.lat.long(long = 0, lat = 0, bearing = 45, distance = 1000)
```

---

`nmds.mst`*Creating NMDS plots with overlain Minimum Spanning Trees*

---

**Description**

This is a helper function which will plot an NMDS with an overlain MST

**Usage**

```
nmds.mst(nmds, mst, ...)
```

**Arguments**

<code>nmds</code>	an NMDS created using the <code>ecodist</code> program
<code>mst</code>	a minimum spanning tree or network (binary matrix)
<code>...</code>	arguments to be passed to the <code>plot</code> function

**Details**

At the moment, the function requires an NMDS created using the `ecodist` program, however the minimum spanning tree can be any one which creates a binary matrix showing connections (ie [dino.mst](#)).

**Value**

Plots a non-metric multidimensional scaling plot with an overlain minimum spanning tree showing connections between the points.

**Author(s)**

Matthew Vavrek

**See Also**

[dino.msn](#), [dino.mst](#)

**Examples**

```
## Not run:
#use fdata.mat as dataset, and use the \code{ecodist} package for the \code{nmds()} function
data(fdata.mat)
z <- ecol.dist(fdata.mat)
a <- dino.msn(z)
b <- nmds(z)
nmds.mst(b, a)

## End(Not run)
```



---

rand.index	<i>Rand Index and Adjusted Rand Index</i>
------------	---

---

**Description**

Measures to compare the similarity of two clustering outcomes

**Usage**

```
rand.index(group1, group2)
adj.rand.index(group1, group2)
```

**Arguments**

group1	first cluster identity matrix
group2	second cluster identity matrix

**Details**

This function calculates the Rand Index for two different clustering outcomes. The Rand Index gives a value between 0 and 1, where 1 means the two clustering outcomes match identically.

The Adjusted Rand Index rescales the index, taking into account that random chance will cause some objects to occupy the same clusters, so the Rand Index will never actually be zero.

**Value**

a single value between 0 and 1

**Author(s)**

Matthew Vavrek

**References**

Rand, W.M. 1971. Objective criteria for the evaluation of clustering methods. *Journal of the American Statistical Association* 66: 846–850.

Hubert, L. and Arabie, P. 1985. Comparing partitions. *Journal of Classification*. 2: 193–218.

**See Also**

To cluster the data, use the function [rclust](#)

**Examples**

```
#create a hypothetical clustering outcome with 2 distinct clusters
g1 <- sample(1:2, size=10, replace=TRUE)
g2 <- sample(1:3, size=10, replace=TRUE)
rand.index(g1, g2)
```

---

`rclust`*Relational Clustering*

---

**Description**

A method to cluster a number of samples using a relational (dissimila

**Usage**

```
rclust(dist, clusters = 2, runs = 10, counter = FALSE)
```

**Arguments**

<code>dist</code>	pairwise distance matrix
<code>clusters</code>	final number of clusters
<code>runs</code>	number of randomizations to run
<code>counter</code>	use counter to display current run number

**Details**

This function will return a cluster identity vector. The number of clusters requested must be 2 or greater, but 1/2 or less than the total number of samples, as the function requires at least 2 samples per cluster.

**Value**

The vector returned will be the same length as the number of samples provided in the original `dist` matrix. The samples will have been clustered into the same number of clusters as defined in `clusters`

**Author(s)**

Matthew Vavrek

**See Also**

[rclust.dist](#), [rclust.null](#), [rclust.weights](#) and [coi](#)

**Examples**

```
#a null solution for the fdata example data set
data(fdata.mat)
fd.dist <- dino.dist(fdata.mat)
rclust(fd.dist, clusters = 2, runs = 10)
```

---

rclust.dist	<i>Relational Clustering</i>
-------------	------------------------------

---

**Description**

Provides a distance matrix intra- and inter-group average distances based on a clustering solution and a dissimilarity matrix.

**Usage**

```
rclust.dist(groups, dist)
```

**Arguments**

groups	cluster identity vector
dist	original pairwise distance matrix

**Details**

This function calculates a distance matrix for each cluster, giving the average within group pairwise distance and the average between group pairwise distance.

**Value**

A matrix  $c$  by  $c$  in size, where  $c$  is the number of clusters

**Author(s)**

Matthew Vavrek

**See Also**

To cluster the data, use the function [rclust](#); see as well [rclust.weights](#), [rclust.null](#)

**Examples**

```
#a null solution for the fdata example data set
data(fdata.mat)
fd.dist <- dino.dist(fdata.mat)
fd.clust <- rclust(fd.dist, 2)
rclust.dist(fd.clust, fd.dist)
```

---

rclust.null	<i>Relational Clustering</i>
-------------	------------------------------

---

**Description**

A Monte Carlo method for calculating a null/random clustering solution based on the type and arrangement of a known clustering solution.

**Usage**

```
rclust.null(groups, dist)
```

**Arguments**

groups	cluster identity vector
dist	original pairwise distance matrix

**Details**

This function calculates a random/null clustering solution based on a given solution. It resamples the data and reassigns samples to groups, keeping the same group sizes.

**Value**

A matrix equal in rows to the number of clusters originally given, with two columns for mean within group distance and standard deviation respectively.

**Author(s)**

Matthew Vavrek

**See Also**

To cluster the data, use the function [rclust](#); see as well [rclust.weights](#), [rclust.dist](#)

**Examples**

```
#a null solution for the fdata example data set
data(fdata.mat)
fd.dist <- dino.dist(fdata.mat)
fd.clust <- rclust(fd.dist, 2)
rclust.null(fd.clust, fd.dist)
```

---

rclust.weights	<i>Relational Clustering</i>
----------------	------------------------------

---

### Description

A method to cluster a number of samples using a relational (dissimila

### Usage

```
rclust.weights(groups, dist)
```

### Arguments

groups	cluster identity vector
dist	original pairwise distance matrix

### Details

This function creates an  $n$  by  $c$  sized matrix, where  $n$  is the number of samples and  $c$  is the number of groups, of the average distances for each sample from itself to all the members of another group ( $c_i$ ).

### Value

A matrix of of size  $n$  (samples) by  $c$  (groups).

### Author(s)

Matthew Vavrek

### See Also

To cluster the data, use the function [rclust](#); see as well [rclust.dist](#), [rclust.null](#)

### Examples

```
data(fdata.mat)
fd.dist <- dino.dist(fdata.mat)
fd.clust <- rclust(fd.dist, 2)
rclust.weights(fd.clust, fd.dist)
```

---

relational.clustering *Relational Clustering*

---

**Description**

A method to cluster a number of samples using a relational (dissimilarity)

**Usage**

```
relational.clustering(dist, clusters = 2)
```

**Arguments**

dist	pairwise distance matrix
clusters	number of clusters required

**Details**

This function will calculate the shortest distance (portion of a Great Circle) in kilometers between two points on the Earth given their latitude and longitude.

**Value**

Arc distance between two points on the Earth's surface in kilometers.

**Note**

The distance calculated may be up to 0.2% inaccurate, as this function treats the Earth as a sphere with a circumference of 40003 km, rather than an ellipsoid like it actually is.

**Author(s)**

Matthew Vavrek

**References**

The formulas for the Haversine distance function were taken from the Dr. Math website at <http://mathforum.org/library/drmath/view/55417.html>

**See Also**

To calculate pairwise distances between a list of points see [earth.dist](#), or to calculate an area enclosed by three points on the Earth's surface, see [earth.tri](#)

**Examples**

```
##distance between 23 degrees N 54 degrees E and 32 degrees S 67 degrees E  
deg.dist(23,54,-32,67)
```

---

sac *Calculate Species Area Curves*

---

**Description**

Calculating a species area curve for a set of georeferenced localities

**Usage**

```
sac(lats, spp)
```

**Arguments**

lats	a table with a longitude and latitude column respectively as the first two columns, or a SpatialPoints object with longitude/latitude
spp	A matrix/data frame of species (rows) by samples/localities (columns)

**Details**

This will take a set of geographic coordinates along with a table of species by localities and return a list consisting of a matrix (`$areavsspp`) with a column of total area and of total species present, and a vector (`ranks`) with the order the samples were added in. The area is calculated by starting with the most central point, and adding those points closest to it, calculating a minimum spanning polygon as each new site is added, until all points are used.

**Value**

Returns a list of a matrix with columns of total area and total species recorded respectively and a vector of sample orders.

**Author(s)**

Matthew Vavrek

**See Also**

[earth.dist](#), [earth.poly](#)

**Examples**

```
#fdata species/area relationship
data(fdata.lats)
data(fdata.mat)
a<-sac(fdata.lats, fdata.mat)
plot(log(a$areavsspp))
```

---

sim.occ                      *Simulated Species Occurrence data*

---

### Description

A function to simulate a species occurrence data set

### Usage

```
sim.occ(total.species = 100, endemics = 0.1, regions = 3, locs = 30, avg.abund = 1)
```

### Arguments

total.species	The total number of species in the region (i.e. the number of rows in the result matrix)
endemics	The proportion of endemic species for the entire region
regions	The number of areas of endemism
locs	The number of samples/localities per region of endemism
avg.abund	The 'average' abundance of a species for any given sample

### Details

The function creates a matrix of  $c$  rows of species (given by `total.species`) with  $n$  number of sample columns (where  $n$  equals `regions*locs`). The given abundance of any species at a given sample is determined by a log normal distribution, with each species being randomly assigned a value from `rnorm()`. The number of endemics for any given region is equal to `total.species*endemics/regions`. An endemic is considered to only occur within a given region, and all other non-endemic species are considered to be 'cosmopolitan' and can occur in any region. The `avg.abund` value affects how many species are recovered at a given site, and for any given run there are typically species that are not present in the sample but are present in the region.

### Value

Returns a matrix of simulated species abundances per locality.

### Author(s)

Matthew Vavrek

### See Also

[ecol.dist](#)

### Examples

```
## create a dataset with 2 regions and 5 samples per region
sim.occ(regions=2, locs=5)
```



---

similarity

*Similarity/Dissimilarity Indices*

---

### **Description**

Functions to calculate the ecological distance between two groups

### **Usage**

```
braun.blanquet(x, y)
bray.curtis(x, y)
euclidean(x,y)
kulczynski(x,y)
jaccard(x, y)
manhattan(x, y)
morisita.horn(x, y)
ochiai(x, y)
simpson(x, y)
sorenson(x, y)
```

### **Arguments**

x	species from group A
y	species from group B

### **Details**

You must provide two separate vectors, with species arranged in the same order, from area A and B. If species are present in one site but not the other, these must be recorded for both sites; the site where they are not found should be coded as a zero. For details on each index, please consult the references.

### **Value**

Returns the similarity index for the two sites in question.

### **Author(s)**

Matthew Vavrek

### **References**

Shi, G. R. 1993. Multivariate data analysis in palaeoecology and palaeobiogeography – a review. *Palaeogeography, Palaeoclimatology, Palaeoecology* 105: 199–234.

Magurran, A. E. 2004. *Measuring Biological Diversity*. Oxford, Blackwell.

**See Also**[dino.dist](#)**Examples**

```
##Species counts from two different locations
a <- c(1,0,4,3,5,0,0,7)
b <- c(2,1,3,0,0,1,0,6)
bray.curtis(a,b)
jaccard(a,b)
simpson(a,b)
sorensen(a,b)
morisita.horn(a,b)
```

---

`spp.est`*Estimating Species Diversity*

---

**Description**

Estimate the diversity of a sample(s) using a number of species diversity estimators.

**Usage**

```
spp.est(x, rand = 10, abund = TRUE, counter = FALSE, max.est = 'all')
```

**Arguments**

<code>x</code>	A vector, matrix or data frame with species as rows and locations/samples as columns
<code>rand</code>	The number of times to run the internal randomizations; default is set to 10
<code>abund</code>	If the data is abundance or presence/absence; default is set to TRUE for abundance
<code>counter</code>	Whether or not to provide a running total of progress of randomizations
<code>max.est</code>	The value to go up to for the analysis; default is set to the same as the total number of samples

**Details**

This function will accept a vector, matrix or data frame of species by samples and return a large matrix with various species estimation values.

**Value**

Returns a table with the following column names if abund=TRUE:

N.obs	Total sample size
S.obs	Number of observed species
S.obs(+95%)	95% upper confidence interval
S.obs(-95%)	95% lower confidence interval
Chao1	Chao Species Estimation
Chao1(upper)	95% upper confidence interval
Chao1(lower)	95% lower confidence interval
ACE	Abundance-based Coverage Estimator
ACE(upper)	95% upper confidence interval
ACE(lower)	95% lower confidence interval
Jack1	First Order Jackknife Estimator
Jack1(upper)	95% upper confidence interval
Jack1(lower)	95% lower confidence interval

Returns a table with the following column names if abund=FALSE:

N.obs	Total sample size
S.obs	Number of observed species
S.obs(+95%)	95% upper confidence interval
S.obs(-95%)	95% lower confidence interval
Chao2	Chao Species Estimation
Chao2(upper)	95% upper confidence interval
Chao2(lower)	95% lower confidence interval
ICE	Incidence-based Coverage Estimator
ICE(upper)	95% upper confidence interval
ICE(lower)	95% lower confidence interval
Jack1	First Order Jackknife Estimator
Jack1(upper)	95% upper confidence interval
Jack1(lower)	95% lower confidence interval

**Note**

This function can be very long to run due to its iterative nature. The randomizations are initially set to 10 so the process will run relatively quickly, but a low value for randomizations will not give nicely smoothed curves.

Also, in some cases due to the nature of some of the functions, they provide no answer, such as is common with the Chao standard deviation. In this case, the Chao upper and lower bounds are simply 95% confidence intervals based on the actual Chao estimator.

**Author(s)**

Matthew Vavrek

**References**

The original idea for a program similar to this came from the extremely useful EstimateS program by Robert K. Colwell

Colwell, R.K. 2010. EstimateS: Statistical estimation of species richness and shared species from samples. Version 8.2. User's Guide and application published at: <http://purl.oclc.org/estimates>.

**See Also**

[chao1](#), [jack1](#), [bootstrap](#)

**Examples**

```
#abundance example with sample data set
data(fdata.mat)
spp.est(fdata.mat, abund = TRUE, counter = FALSE)

#occurrence example with sample data set
data(fdata.mat)
spp.est(fdata.mat, abund = FALSE, counter = FALSE)
```

---

tri.ineq

*Testing for the Triangle Inequality*

---

**Description**

Determines if a distance matrix obeys the triangle inequality

**Usage**

```
tri.ineq(dist)
```

**Arguments**

dist            A distance matrix

**Details**

Tests if a distance matrix respects the triangle inequality. Often with non-monotonic distance measures and complex data a situation can arise where the triangle inequality (where no single side of a triangle is greater in length than the sum of the other two sides) is not respected.

**Value**

Returns a TRUE if the inequality is respected, and a FALSE if there is any situation where the triangle inequality is not respected.

**Author(s)**

Matthew Vavrek

**See Also**

[ecol.dist](#)

**Examples**

```
## sample distance matrix with an impossible triangle
a<-matrix(0.2, 4,4)
a[4,2]<-0.8
a<-as.dist(a)
tri.ineq(a)
```

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