

Package: ecotraj (via r-universe)

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Type Package

Title Ecological Trajectory Analysis

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Description Assists ecologists in the analysis of temporal changes of ecosystems, defined as trajectories on a chosen multivariate space, by providing a set of trajectory metrics and visual representations [De Caceres et al. (2019) <doi:10.1002/ecm.1350>; and Sturbois et al. (2021) <doi:10.1016/j.ecolmodel.2020.109400>]. Includes functions to estimate metrics for individual trajectories (length, directionality, angles, ...) as well as metrics to relate pairs of trajectories (dissimilarity and convergence). Functions are also provided to estimate the ecological quality of ecosystem with respect to reference conditions [Sturbois et al. (2023) <doi:10.1002/ecs2.4726>].

Depends R (>= 3.4.0), Rcpp (>= 0.12.12)

Imports Kendall, MASS

LinkingTo Rcpp

License GPL (>= 2)

URL <https://emf-creaf.github.io/ecotraj/>

LazyLoad yes

Encoding UTF-8

NeedsCompilation yes

RoxygenNote 7.3.2

Suggests ape, vegclust, knitr, rmarkdown, RColorBrewer, smacof, vegan, ggplot2, hrbthemes, reshape2, scales, tidyr, viridis, testthat (>= 3.0.0)

LazyData true

BugReports <https://github.com/emf-creaf/ecotraj/issues>

Config/testthat/edition 3

Roxygen list(markdown = TRUE)

Repository <https://emf-creaf.r-universe.dev>

RemoteUrl <https://github.com/emf-creaf/ecotraj>

RemoteRef HEAD

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avoca	<i>Avoca permanent plot dataset</i>
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Description

Example dataset with data from 8 permanent forest plots located on slopes of a valley in the New Zealand Alps. The study area is mountainous and centered on the Craigieburn Range (Southern Alps), South Island, New Zealand. Forests plots are almost monospecific, being the mountain beech (*Fuscospora cliffortioides*) the main dominant tree species. Previously forests consisted of largely mature stands, but some of them were affected by different disturbances during the sampling period (1972-2009) which includes 9 surveys.

Format

Three data items are included:

avoca_strat An object of class `stratifiedvegdata` (see function `stratifyvegdata` from package `'vegclust'`) with structural and compositional data.

avoca_sites A vector identifying sampled sites of each element in `avoca_strat`.

avoca_surveys A vector identifying surveys of each element in `avoca_strat`.

Source

New Zealand National Vegetation Survey (NVS) Databank (<https://nvs.landcareresearch.co.nz/>).

References

- Allen, R. B., P. J. Bellingham, and S. K. Wiser. 1999. Immediate damage by an earthquake to a temperate montane forest. *Ecology* 80:708–714.
- Harcombe, P. A., R. B. Allen, J. A. Wardle, and K. H. Platt. 1998. Spatial and temporal patterns in stand structure, biomass, growth and mortality in a monospecific *Nothofagus solandri* var. *cliffortioides* (Hook. f.) Poole forest in New Zealand. *Journal of Sustainable Forestry* 6:313–343.
- Hurst, J. M., R. B. Allen, D. A. Coomes, and R. P. Duncan. 2011. Size-specific tree mortality varies with neighbourhood crowding and disturbance in a montane *Nothofagus* forest. *PLoS ONE* 6.

furseals

furseals dataset

Description

This is a subset of a data sets from Kernaléguen et al. (2015).

Format

furseals is an object of class data.frame composed of 1414 observations and 8 variables.

ID_SITA Fur seal ID used by Sturbois et al. (under review), from 1 to 47

ID Fur seal ID used by Kernaléguen et al. (2015) in the initial data set.

Species Fur seal species: the Antarctic fur seal *Arctocephalus gazella* or the subantarctic fur seal *A. tropicalis*.

Sex Fur seal gender, either 'Male' or 'Female'.

Time Number of the whisker sections from 1 to 30.

Place Breeding place: Crozet, Amsterdam or Kerguelen

d13C delta 13C value

d15N delta 15N value

Details

Briefly, fur seals the Antarctic fur seal *Arctocephalus gazella* and subantarctic fur seal *A. tropicalis* whisker SI values yield unique long-term information on individual behaviour which integrates the spatial, trophic and temporal dimensions of the ecological niche. The foraging strategies of this two species of sympatric fur seals were examined in the winter 2001/2002 at Crozet, Amsterdam and Kerguelen Islands (Southern Ocean) using the stable isotope values of serially sampled whiskers. The subset of the initial data set is composed of consecutive whisker sections (3 mm-long) starting from the proximal (facial) end, with the most recently synthesized tissue remaining under the skin. Only individuals ($n = 47$) with whiskers totalizing at least 30 sections were selected in the initial data, and only those 30 sections were selected.

Author(s)

Kernaléguen, L., Arnould, J.P.Y., Guinet, C., Cherel, Y.

References

Kernaléguen, L., Arnould, J.P.Y., Guinet, C., Cherel, Y., 2015. Determinants of individual foraging specialization in large marine vertebrates, the Antarctic and subantarctic fur seals. *Journal of Animal Ecology* 1081–1091.

glenan

Glenan dataset

Description

Maerl bed data set to illustrate Ecological Quality Assessment (EQA)

Format

Glenan is an object of class `data.frame` composed of 32 observations and 252 variables.

Abundance.x Abundance (number of individuals) of each taxon *x*

Surveys Indicates different Maerl bed surveys.

Treatment Combinations of fishing dredges and pressure levels. 'CTRL' stands for control. Fishing dredges are:

- (1) a clam dredge (CD), 70 to 90 kg, 1.5 m wide, 40 teeth of 11 cm each;
- (2) a queen scallop dredge (QSD), 120 kg, 1.8 m wide, with a blade;
- (3) a king scallop dredge (KSD), 190 kg, 1.8 m wide, 18 teeth of 10 cm each every 9 cm.

Details

Experimental data set built by Tauran et al. (2020) to study the impact of fishing dredges and varying fishing pressures on maerl beds, in the bay of Brest (Brittany, France).

References

Tauran, A., Dubreuil, J., Guyonnet, B., Grall, J., 2020. Impact of fishing gears and fishing intensities on maerl beds: An experimental approach. *Journal of Experimental Marine Biology and Ecology* 533, 151472. <https://doi.org/10.1016/j.jembe.2020.151472>

See Also

[envelope](#)

glomel

Glomel vegetation dataset

Description

Vegetation data set to illustrate Ecological Quality Assessment (EQA)

Format

Glomel is an object of class `data.frame` composed of 23 observations and 46 variables.

ID Station ID.

Ref Logical flag to indicate stations used to define the reference envelope.

Complementary Comments regarding the quality of the ecosystem.

... Percent cover values (derived from Braun-Blanquet ordinal scale) for 43 species of vascular plants.

Details

The nature reserve of Landes et Marais de Glomel (Brittany, France) is composed of temperate Atlantic wet heaths whose reference state is commonly considered dominated by plant communities associated to acid, nutrient poor soils that are at least seasonally water logged and dominated by *Erica tetralix* and *E. ciliaris*. The data set consists of 23 rows and 46 columns. The first five stations (rows) were used to define the reference envelope, and the next 18 stations (rows) were those for which the conservation status was to be assessed.

Author(s)

Aline Bifolchi, Réserve Naturelle des landes et marais de Glomel

See Also

[envelope](#)

heatmapdata

heatmapdata dataset

Description

Espinasse et al. (2020) tested the application of isoscapes modelled from satellite data to the description of secondary production in the Northeast Pacific. The output model fits in a $0.25^\circ \times 0.25^\circ$ spatial grid covering the region spanning from 46° to 62° N and from 195° to 235° E and supporting delta ^{13}C and delta ^{15}N isoscapes from 1998 to 2017.

Format

heatmapdata is an object of class dataframe composed of 9206 observations of 9 variables.

Latitude Latitude coordinate of the station, in degrees

Longitude Longitude coordinate of the station, in degrees

d13C delta 13C modelled value

d15N delta 15N modelled value

station Station ID

Years Period corresponding to the calculation of trajectory metrics

Angles Angle alpha (i.e direction) in the stable isotope space

Lengths Net change values (i.e direction) in the stable isotope space

Angles2 Angle alpha values (i.e direction) in the stable isotope space transformed for a potential use with function geom_spoke

Details

This data sets is composed of trajectory metrics calculated by Sturbois et al. (2021) for all stations within all inter-annual consecutive periods between 1998 and 2017 calculated from the whole data set of Espinasse et al. (2020) for a 1° x 1° spatial grid.

Author(s)

Espinasse, B., Hunt, B.P.V., Batten, S.D., Pakhomov, E.A.

References

Espinasse, B., Hunt, B.P.V., Batten, S.D., Pakhomov, E.A., 2020. Defining isoscapes in the North-east Pacific as an index of ocean productivity. *Global Ecol Biogeogr* 29, 246–261.

See Also

isoscape

isoscape

isoscape dataset

Description

This data sets is a subset from Espinasse et al. (2020).

Format

isoscape is an object of class dataframe composed of 978 observations of 6 variables.

Latitude Latitude coordinate of the station, in degrees

Longitude Longitude coordinate of the station, in degrees

d13C delta 13C modelled value

d15N delta 15N modelled value

station station ID

Year Year corresponding to modelled stable isotope values

Details

Briefly, Espinasse et al. (2020) tested the application of isoscapes modelled from satellite data to the description of secondary production in the Northeast Pacific. The output model fits in a $0.25^\circ \times 0.25^\circ$ spatial grid covering the region spanning from 46 to 62°N and from 195 to 235°E and supporting delta 13C and delta 15N isoscapes from 1998 to 2017. The subset is composed of modelled delta 13C and delta 15N values of a $1^\circ \times 1^\circ$ spatial grid from the original modelled dataset for 2013 and 2015.

Author(s)

Espinasse, B., Hunt, B.P.V., Batten, S.D., Pakhomov, E.A.

References

Espinasse, B., Hunt, B.P.V., Batten, S.D., Pakhomov, E.A., 2020. Defining isoscapes in the North-east Pacific as an index of ocean productivity. *Global Ecol Biogeogr* 29, 246–261.

See Also

heatmapdata

pike

pike dataset

Description

This data sets comes from Cucherousset et al. (2013).

Format

pike is an object of class dataframe composed of 58 observations of 10 variables.

trophic_status_initial Initial trophic status at release

ID ID used for each individual by Cucherousset et al. (2013)

Time Time of the stable isotope measurement: 1 (Release) or 2 (Departure)

Time_L Time of the stable isotope measurement as string, either 'Release' or 'Departure'

Date Date of release (common for all individuals) or recapture (variable dependind of the date of departure)

Size_mm Size (length) of juvenile pike, in mm

d13C delta 13C values

d15N delta 15N values

Residence_time Number of days between the release and the recapture

Trophic_status_final Trophic status at the end of the study

Details

Briefly, Cucherousset et al. (2013) released 192 individually tagged, hatchery-raised, juvenile pike (*Esox lucius* L.) with variable initial trophic position (fin delta 13C/delta 15N values). Based on delta values, individuals were classified into zooplanktivorous (delta 15N < 10 ‰) and piscivorous (delta 15N > 10 ‰) as cannibalism is commonly observed in this species. Individuals were released in a temporarily flooded grassland where pike eggs usually hatch of the Brière marsh (France) to identify the determinants of juvenile natal departure. The release site was connected through a unique point to an adjacent pond used as a nursery habitat. Fish were continuously recaptured when migrating from flooded grassland to adjacent pond. Recaptured individuals (n = 29) were anaesthetized, checked for tags, measured for fork length, fin-clipped to quantify changes in delta 13C and delta 15N values, and released.

Author(s)

Cucherousset, J., Paillisson, J.-M., Roussel, J.-M.

References

Cucherousset, J., Paillisson, J.-M., Roussel, J.-M., 2013. Natal departure timing from spatially varying environments is dependent of individual ontogenetic status. *Naturwissenschaften* 100, 761–768.

Description

Functions to assess the variability of ecological reference envelopes and to assess the ecological quality of target stations/observations with respect to reference envelopes (Sturbois et al., under review).

Usage

```
trajectoryEnvelopeVariability(  
  d,  
  sites,  
  surveys = NULL,  
  envelope = NULL,  
  nboot.ci = NULL,  
  alpha.ci = 0.05,  
  ...  
)  
  
stateEnvelopeVariability(d, envelope = NULL, nboot.ci = NULL, alpha.ci = 0.05)  
  
compareToTrajectoryEnvelope(  
  d,  
  sites,  
  envelope,  
  surveys = NULL,  
  m = 1.5,  
  comparison_target = "trajectories",  
  distances_to_envelope = FALSE,  
  distance_percentiles = FALSE,  
  ...  
)  
  
compareToStateEnvelope(  
  d,  
  envelope,  
  m = 1.5,  
  nboot.ci = NULL,  
  alpha.ci = 0.05,  
  distances_to_envelope = FALSE,  
  distance_percentiles = FALSE,  
  ...  
)
```

Arguments

d	A symmetric <code>matrix</code> or an object of class <code>dist</code> containing the distance values between pairs of ecosystem states (see details).
sites	A vector indicating the site corresponding to each ecosystem state.
surveys	A vector indicating the survey corresponding to each ecosystem state (only necessary when surveys are not in order).
envelope	A vector indicating the set of sites that conform the reference envelope (other sites will be compared to the envelope)
nboot.ci	Number of bootstrap samples for confidence intervals. If nboot.ci = NULL then confidence intervals are not estimated.
alpha.ci	Error in confidence intervals.
...	Additional parameters for function <code>trajectoryDistances</code>
m	Fuzziness exponent for quality value assessment
comparison_target	String indicating the component to be compared to the reference envelope. Either 'trajectories' (to compare complete trajectories) or 'states' (to compare individual trajectory states).
distances_to_envelope	Flag to indicate that distances to envelope should be included in the result
distance_percentiles	Flag to include the percentage of distances to the envelope (among sites corresponding to the reference) that are smaller than that of the site.

Details

Functions `stateEnvelopeVariability` and `trajectoryEnvelopeVariability` are used to assess the variability of reference envelopes. Functions `compareToStateEnvelope` and `compareToTrajectoryEnvelope` are used to evaluate the ecological quality of stations/observations with respect to a predefined reference envelope.

Value

- Functions `stateEnvelopeVariability` and `trajectoryEnvelopeVariability` are used to assess the
- Functions `compareToStateEnvelope` and `compareToTrajectoryEnvelope` return data frame with columns identifying the envelope and the Q statistic for the ecological quality with respect to the envelope. If `nboot.ci != NULL` extra columns are added to indicate the boundaries of a confidence interval for Q, built using bootstrap samples of the reference envelope.

Author(s)

Miquel De Cáceres, CREAF

Anthony Sturbois, Vivarmor nature, Réserve Naturelle nationale de la Baie de Saint-Brieuc

References

Sturbois, A., De Cáceres, M., Bifulchi, A., Bioret, F., Boyé, A., Gauthier, O., Grall, J., Grémare, A., Labruno, C., Robert, A., Schaal, G., Desroy, N. (2023). Ecological Quality Assessment: a general multivariate framework to report the quality of ecosystems and their dynamics with respect to reference conditions. *Ecosphere*.

See Also

[trajectorymetrics](#), [glomel](#)

Examples

```
data(glomel)

# Extract compositional data matrix
glomel_comp <- as.matrix(glomel[!(names(glomel) %in% c("ID", "Ref", "Complementary"))])
rownames(glomel_comp) <- glomel$ID

# Calculate Bray-Curtis distance matrix
glomel_bc <- vegan::vegdist(glomel_comp, method = "bray")

# Define reference envelope (5 stations) by observation ID
glomel_env <- glomel$ID[glomel$Ref]

# Assess quality with respect to reference envelope
compareToStateEnvelope(glomel_bc, glomel_env)
```

trajectorymetrics

Metrics for Ecological Trajectory Analysis

Description

Ecological Trajectory Analysis (ETA) is a framework to analyze dynamics of ecosystems described as trajectories in a chosen space of multivariate resemblance (De Cáceres et al. 2019). ETA takes trajectories as objects to be analyzed and compared geometrically.

Usage

```
segmentDistances(
  d,
  sites,
  surveys = NULL,
  distance.type = "directed-segment",
  add = TRUE,
  verbose = FALSE
)
```

```
trajectoryDistances(  
  d,  
  sites,  
  surveys = NULL,  
  distance.type = "DSPD",  
  symmetrization = "mean",  
  add = TRUE,  
  verbose = FALSE  
)  
  
trajectoryLengths(  
  d,  
  sites,  
  surveys = NULL,  
  relativeToInitial = FALSE,  
  all = FALSE,  
  verbose = FALSE  
)  
  
trajectoryLengths2D(  
  xy,  
  sites,  
  surveys,  
  relativeToInitial = FALSE,  
  all = FALSE,  
  verbose = FALSE  
)  
  
trajectoryAngles(  
  d,  
  sites,  
  surveys = NULL,  
  all = FALSE,  
  relativeToInitial = FALSE,  
  stats = TRUE,  
  add = TRUE,  
  verbose = FALSE  
)  
  
trajectoryAngles2D(  
  xy,  
  sites,  
  surveys,  
  relativeToInitial = FALSE,  
  betweenSegments = TRUE  
)  
  
trajectoryProjection(d, target, trajectory, tol = 1e-06, add = TRUE)
```

```
trajectoryConvergence(
  d,
  sites,
  surveys = NULL,
  symmetric = FALSE,
  add = TRUE,
  verbose = FALSE
)
```

```
trajectoryDirectionality(d, sites, surveys = NULL, add = TRUE, verbose = FALSE)
```

Arguments

d	A symmetric matrix or an object of class dist containing the distance values between pairs of ecosystem states (see details).
sites	A vector indicating the site corresponding to each ecosystem state.
surveys	A vector indicating the survey corresponding to each ecosystem state (only necessary when surveys are not in order).
distance.type	The type of distance index to be calculated (Besse et al. 2016; De Cáceres et al. submitted). For <code>segmentDistances</code> the available indices are: <ul style="list-style-type: none"> • Hausdorff: Hausdorff distance between two segments. • directed-segment: Directed segment distance (default). • PPA: Perpendicular-parallel-angle distance. whereas for <code>trajectoryDistances</code> the available indices are: <ul style="list-style-type: none"> • Hausdorff: Hausdorff distance between two trajectories. • SPD: Segment path distance. • DSPD: Directed segment path distance (default).
add	Flag to indicate that constant values should be added (local transformation) to correct triplets of distance values that do not fulfill the triangle inequality.
verbose	Provides console output informing about process (useful for large dataset).
symmetrization	Function used to obtain a symmetric distance, so that $DSPD(T1,T2) = DSPD(T2,T1)$ (e.g., mean or min). If <code>symmetrization = NULL</code> then the symmetrization is not conducted and the output dissimilarity matrix is not symmetric.
relativeToInitial	Flag to indicate that lengths or angles should be calculated with respect to initial survey.
all	A flag to indicate that angles are desired for all triangles (i.e. all pairs of segments) in the trajectory. If <code>FALSE</code> , angles are calculated for consecutive segments only.
xy	Matrix with 2D coordinates in a Cartesian space (typically an ordination of ecosystem states).
stats	A flag to indicate that circular statistics are desired (mean, standard deviation and mean resultant length, i.e. rho)

betweenSegments	Flag to indicate that angles should be calculated between trajectory segments or with respect to X axis.
target	An integer vector of the ecosystem states to be projected.
trajectory	An integer vector of the trajectory onto which target states are to be projected.
tol	Numerical tolerance value to determine that projection of a point lies within the trajectory.
symmetric	A logical flag to indicate a symmetric convergence comparison of trajectories.

Details

Given a distance matrix between ecosystem states, the set of functions that provide ETA metrics are:

- Functions `segmentDistances` and `trajectoryDistances` calculate the distance between pairs of directed segments and ecosystem trajectories, respectively.
- Function `trajectoryLengths` calculates lengths of directed segments and total path lengths of trajectories.
- Function `trajectoryLengths2D` calculates lengths of directed segments and total path lengths of trajectories from 2D coordinates given as input.
- Function `trajectoryAngles` calculates the angle between consecutive pairs of directed segments or between segments of ordered triplets of points.
- Function `trajectoryAngles2D` calculates the angle between consecutive pairs of directed segments or between segments of ordered triplets of points.
- Function `trajectoryProjection` projects a set of target points onto a specified trajectory and returns the distance to the trajectory (i.e. rejection) and the relative position of the projection point within the trajectory.
- Function `trajectoryConvergence` performs the Mann-Kendall trend test on the distances between trajectories (symmetric test) or the distance between points of one trajectory to the other.
- Function `trajectoryDirectionality` returns (for each trajectory) a statistic that measures directionality of the whole trajectory.

Details of calculations are given in De Cáceres et al (2019). The input distance matrix `d` should ideally be metric. That is, all subsets of distance triplets should fulfill the triangle inequality (see utility function `is.metric`). All ETA functions that require metricity include a parameter `'add'`, which by default is `TRUE`, meaning that whenever the triangle inequality is broken the minimum constant required to fulfill it is added to the three distances. If such local (and hence, inconsistent across triplets) corrections are not desired, users should find another way to modify `d` to achieve metricity, such as PCoA, metric MDS or non-metric MDS (see vignette 'Introduction to Ecological Trajectory Analysis'). If parameter `'add'` is set to `FALSE` and problems of triangle inequality exist, ETA functions may provide missing values in some cases where they should not.

The resemblance between trajectories is done by adapting concepts and procedures used for the analysis of trajectories in space (i.e. movement data) (Besse et al. 2016).

Function `trajectoryAngles` calculates angles between consecutive segments in degrees. For each pair of segments, the angle between the two is defined on the plane that contains the two segments,

and measures the change in direction (in degrees) from one segment to the other. Angles are always positive, with zero values indicating segments that are in a straight line, and values equal to 180 degrees for segments that are in opposite directions. If `all = TRUE` angles are calculated between the segments corresponding to all ordered triplets. Alternatively, if `relativeToInitial = TRUE` angles are calculated for each segment with respect to the initial survey.

Function `trajectoryAngles2D` calculates angles between consecutive segments in degrees from 2D coordinates given as input. For each pair of segments, the angle between the two is defined on the plane that contains the two segments, and measures the change in direction (in degrees) from one segment to the other. Angles are always positive (0 to 360), with zero values indicating segments that are in a straight line, and values equal to 180 degrees for segments that are in opposite directions. If `all = TRUE` angles are calculated between the segments corresponding to all ordered triplets. Alternatively, if `relativeToInitial = TRUE` angles are calculated for each segment with respect to the initial survey. If `betweenSegments = TRUE` angles are calculated between segments of trajectory, otherwise, If `betweenSegments = FALSE`, angles are calculated considering Y axis as the North (0°).

Value

Function `trajectoryDistances` returns an object of class `dist` containing the distances between trajectories (if `symmetrization = NULL` then the object returned is of class `matrix`).

Function `trajectorySegments` returns a list with the following elements:

- `Dseg`: Distance matrix between segments.
- `Dini`: Distance matrix between initial points of segments.
- `Dfin`: Distance matrix between final points of segments.
- `Dinifin`: Distance matrix between initial points of one segment and the final point of the other.
- `Dfinini`: Distance matrix between final points of one segment and the initial point of the other.

Function `trajectoryLengths` returns a data frame with the length of each segment on each trajectory and the total length of all trajectories. If `relativeToInitial = TRUE` lengths are calculated between the initial survey and all the other surveys. If `all = TRUE` lengths are calculated for all segments.

Function `trajectoryLengths2D` returns a data frame with the length of each segment on each trajectory and the total length of all trajectories. If `relativeToInitial = TRUE` lengths are calculated between the initial survey and all the other surveys. If `all = TRUE` lengths are calculated for all segments.

Function `trajectoryAngles` returns a data frame with angle values on each trajectory. If `stats=TRUE`, then the mean, standard deviation and mean resultant length of those angles are also returned.

Function `trajectoryAngles2D` returns a data frame with angle values on each trajectory. If `betweenSegments=TRUE`, then angles are calculated between trajectory segments, alternatively, If `betweenSegments=FALSE`, angles are calculated considering Y axis as the North (0°).

Function `trajectoryProjection` returns a data frame with the following columns:

- `distanceToTrajectory`: Distances to the trajectory, i.e. rejection (NA for target points whose projection is outside the trajectory).

- **segment**: Segment that includes the projected point (NA for target points whose projection is outside the trajectory).
- **relativePosition**: Relative position of the projected point within the trajectory, i.e. values from 0 to 1 with 0 representing the start of the trajectory and 1 representing the end (NA for target points whose projection is outside the trajectory).

Function `trajectoryConvergence` returns a list with two elements:

- **tau**: A matrix with the statistic (Mann-Kendall's tau) of the convergence/divergence test between trajectories. If `symmetric=TRUE` then the matrix is square. Otherwise the statistic of the test of the row trajectory approaching the column trajectory.
- **p.value**: A matrix with the p-value of the convergence/divergence test between trajectories. If `symmetric=TRUE` then the matrix is square. Otherwise the p-value indicates the test of the row trajectory approaching the column trajectory.

Function `trajectoryDirectionality` returns a vector with directionality values (one per trajectory).

Author(s)

Miquel De Cáceres, CREAM

Anthony Sturbois, Vivarmor nature, Réserve Naturelle nationale de la Baie de Saint-Brieuc

References

Besse, P., Guillouet, B., Loubes, J.-M. & François, R. (2016). Review and perspective for distance based trajectory clustering. *IEEE Trans. Intell. Transp. Syst.*, 17, 3306–3317.

De Cáceres M, Coll L, Legendre P, Allen RB, Wiser SK, Fortin MJ, Condit R & Hubbell S. (2019). Trajectory analysis in community ecology. *Ecological Monographs* 89, e01350.

See Also

[trajectoryplots](#), [trajectoryutils](#)

Examples

```
#Description of sites and surveys
sites = c(1,1,1,2,2,2)
surveys=c(1,2,3,1,2,3)

#Raw data table
xy<-matrix(0, nrow=6, ncol=2)
xy[2,2]<-1
xy[3,2]<-2
xy[4:6,1] <- 0.5
xy[4:6,2] <- xy[1:3,2]
xy[6,1]<-1

#Draw trajectories
trajectoryPlot(xy, sites, surveys,
```



```

traj.colors = c("black","red"), lwd = 2)

#Distance matrix
d = dist(xy)
d

trajectoryLengths(d, sites, surveys)
trajectoryLengths2D(xy, sites, surveys)
trajectoryAngles(d, sites, surveys)
trajectoryAngles2D(xy, sites, surveys, betweenSegments = TRUE)
trajectoryAngles2D(xy, sites, surveys, betweenSegments = FALSE)
segmentDistances(d, sites, surveys)$Dseg
trajectoryDistances(d, sites, surveys, distance.type = "Hausdorff")
trajectoryDistances(d, sites, surveys, distance.type = "DSPD")

#Should give the same results if surveys are not in order
#(here we switch surveys for site 2)
temp = xy[5,]
xy[5,] = xy[6,]
xy[6,] = temp
surveys[5] = 3
surveys[6] = 2

trajectoryPlot(xy, sites, surveys,
              traj.colors = c("black","red"), lwd = 2)
trajectoryLengths(dist(xy), sites, surveys)
trajectoryLengths2D(xy, sites, surveys)
segmentDistances(dist(xy), sites, surveys)$Dseg
trajectoryAngles(dist(xy), sites, surveys)
trajectoryAngles2D(xy, sites, surveys, betweenSegments = TRUE)
trajectoryAngles2D(xy, sites, surveys, betweenSegments = FALSE)
trajectoryDistances(dist(xy), sites, surveys, distance.type = "Hausdorff")
trajectoryDistances(dist(xy), sites, surveys, distance.type = "DSPD")

```

trajectoryplots

Trajectory plots

Description

Set of plotting functions for Ecological Trajectory Analysis:

Usage

```

trajectoryPCoA(
  d,
  sites,
  surveys = NULL,
  selection = NULL,

```

```

    traj.colors = NULL,
    axes = c(1, 2),
    survey.labels = FALSE,
    ...
)

trajectoryPlot(
  x,
  sites,
  surveys = NULL,
  selection = NULL,
  traj.colors = NULL,
  axes = c(1, 2),
  survey.labels = FALSE,
  ...
)

```

Arguments

d	A symmetric matrix or an object of class dist containing the distance values between pairs of ecosystem states (see details).
sites	A vector indicating the site corresponding to each ecosystem state.
surveys	A vector indicating the survey corresponding to each ecosystem state (only necessary when surveys are not in order).
selection	A character vector of sites, a numeric vector of site indices or logical vector of the same length as <code>sites</code> , indicating a subset of site trajectories to be selected.
traj.colors	A vector of colors (one per site). If <code>selection != NULL</code> the length of the color vector should be equal to the number of sites selected.
axes	The pair of principal coordinates to be plotted.
survey.labels	A boolean flag to indicate whether surveys should be plotted as text next to arrow endpoints
...	Additional parameters for function arrows .
x	A <code>data.frame</code> or matrix where rows are ecosystem states and columns are coordinates in an arbitrary space

Details

- Function `trajectoryPCoA` performs principal coordinates analysis (**cmdscale**) and draws trajectories in the ordination scatterplot.
- Function `trajectoryPlot` Draws trajectories in a scatterplot corresponding to the input coordinates.

Details of calculations are given in De Cáceres et al (2019). The input distance matrix `d` should ideally be metric. That is, all subsets of distance triplets should fulfill the triangle inequality (see function `is.metric`). All CTA functions that require metricity include a parameter `'add'`, which by default is `TRUE`, meaning that whenever the triangle inequality is broken the minimum constant required to fulfill it is added to the three distances. If such local (and hence, inconsistent across

triplets) corrections are not desired, users should find another way modify `d` to achieve metricity, such as PCoA, metric MDS or non-metric MDS (see CTA vignette). If parameter `'add'` is set to `FALSE` and problems of triangle inequality exist, CTA functions may provide missing values in some cases where they should not.

The resemblance between trajectories is done by adapting concepts and procedures used for the analysis of trajectories in space (i.e. movement data) (Besse et al. 2016).

Value

Function `trajectoryPCoA` returns the result of calling `cmdscale`.

Author(s)

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References

Besse, P., Guillouet, B., Loubes, J.-M. & François, R. (2016). Review and perspective for distance based trajectory clustering. *IEEE Trans. Intell. Transp. Syst.*, 17, 3306–3317.

De Cáceres M, Coll L, Legendre P, Allen RB, Wiser SK, Fortin MJ, Condit R & Hubbell S. (2019). Trajectory analysis in community ecology. *Ecological Monographs* 89, e01350.

Anderson (2017). Permutational Multivariate Analysis of Variance (PERMANOVA). *Wiley Stat- sRef: Statistics Reference Online*. 1-15. Article ID: stat07841.

See Also

[trajectorymetrics](#), [trajectoryutils](#), [cmdscale](#)

Examples

```
#Description of sites and surveys
sites = c(1,1,1,2,2,2)
surveys=c(1,2,3,1,2,3)

#Raw data table
xy<-matrix(0, nrow=6, ncol=2)
xy[2,2]<-1
xy[3,2]<-2
xy[4:6,1] <- 0.5
xy[4:6,2] <- xy[1:3,2]
xy[6,1]<-1

#Draw trajectories
trajectoryPlot(xy, sites, surveys,
              traj.colors = c("black","red"), lwd = 2)

#Should give the same results if surveys are not in order
#(here we switch surveys for site 2)
```

```
temp = xy[5,]  
xy[5,] = xy[6,]  
xy[6,] = temp  
surveys[5] = 3  
surveys[6] = 2  
  
trajectoryPlot(xy, sites, surveys,  
              traj.colors = c("black", "red"), lwd = 2)
```

trajectorySmoothing *Trajectory smoothing*

Description

Trajectory smoothing using a Gaussian kernel

Usage

```
trajectorySmoothing(  
  d,  
  sites,  
  surveys = NULL,  
  survey_times = NULL,  
  kernel_scale = 1,  
  fixed_endpoints = TRUE  
)
```

Arguments

d	A symmetric matrix or an object of class dist containing the distance values between pairs of ecosystem states.
sites	A vector indicating the site corresponding to each ecosystem state.
surveys	A vector indicating the survey corresponding to each ecosystem state (only necessary when surveys are not in order).
survey_times	A vector indicating the survey time for all surveys (if NULL, time between consecutive surveys is considered to be one)
kernel_scale	Scale of the Gaussian kernel, related to survey times
fixed_endpoints	A logical flag to force keeping the location of trajectory endpoints unmodified

Value

An object of class **dist**

Description

The set following set of utility functions are provided:

- Function `trajectorySelection` allows selecting the submatrix of distances corresponding to a given subset of trajectories.
- Function `centerTrajectories` shifts all trajectories to the center of the compositional space and returns a modified distance matrix.
- Function `is.metric` checks whether the input dissimilarity matrix is metric (i.e. all triplets fulfill the triangle inequality).

Usage

```
trajectorySelection(d, sites, selection)
```

```
centerTrajectories(d, sites, verbose = FALSE)
```

```
is.metric(d, tol = 1e-04)
```

Arguments

<code>d</code>	A symmetric <code>matrix</code> or an object of class <code>dist</code> containing the distance values between pairs of ecosystem states (see details).
<code>sites</code>	A vector indicating the site corresponding to each ecosystem state.
<code>selection</code>	A character vector of sites, a numeric vector of site indices or logical vector of the same length as <code>sites</code> , indicating a subset of site trajectories to be selected.
<code>verbose</code>	Provides console output informing about process (useful for large dataset).
<code>tol</code>	Tolerance value for metricity

Details

Details of calculations are given in De Cáceres et al (2019). Function `centerTrajectories` performs centering of trajectories using matrix algebra as explained in Anderson (2017).

Value

Function `centerTrajectories` and `trajectorySelection` return an object of class `dist`.

Author(s)

Miquel De Cáceres, CREAF

References

De Cáceres M, Coll L, Legendre P, Allen RB, Wiser SK, Fortin MJ, Condit R & Hubbell S. (2019). Trajectory analysis in community ecology. *Ecological Monographs* 89, e01350.

Anderson (2017). Permutational Multivariate Analysis of Variance (PERMANOVA). *Wiley StatsRef: Statistics Reference Online*. 1-15. Article ID: stat07841.

See Also

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