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Description Obtain network structures from animal GPS telemetry observations and statistically analyse them to assess their adequacy for social network analysis. Methods include pre-network data permutations, bootstrapping techniques to obtain confidence intervals for global network metrics, and correlation and regression analysis of the local network metrics.

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Description

Obtain network structures from animal GPS telemetry observations and statistically analyse them to assess their adequacy for social network analysis. Methods include pre-network data permutations, bootstrapping techniques to obtain confidence intervals for global network metrics, and correlation and regression analysis of the local network metrics.

Author(s)

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`bootstrapped_difference_pvalues`

To obtain two non-overlapping bootstrapped versions and obtain p-values for the significance of difference between them

Description

To obtain two non-overlapping bootstrapped versions and obtain p-values for the significance of difference between them

Usage

```
bootstrapped_difference_pvalues(  
  network,  
  n_versions = 1000,  
  seed = 12345,  
  n.iter = 10,  
  network_metrics = c("mean_degree", "mean_strength", "density", "diameter",  
    "transitivity")  
)
```

Arguments

<code>network</code>	An igraph object
<code>n_versions</code>	Number of bootstrapped versions to be used
<code>seed</code>	seed number
<code>n.iter</code>	Number of iterations at each level
<code>network_metrics</code>	Network metrics to be evaluated. This should be supplied as a character vector and the values should be chosen from "mean_degree", "mean_strength", "density", "diameter", "transitivity". (default = c("mean_degree", "mean_strength", "density", "diameter", "transitivity")).

Value

A matrix of p-values whose rows correspond to the sub-sample size and columns correspond to the chosen network metric.

Examples

```
data(elk_network_2010)  
bootstrapped_difference_pvalues(elk_network_2010, n_versions = 100)
```

correlation_analyze *To perform correlation analysis for local network metrics*

Description

To perform correlation analysis for local network metrics

Usage

```
correlation_analyze(  
  network,  
  n_simulations = 10,  
  subsampling_proportion = c(0.1, 0.3, 0.5, 0.7, 0.9),  
  network_metrics = c("degree", "strength", "betweenness", "clustering_coefficient",  
    "eigenvector_centrality")  
)
```

Arguments

network An igraph graph object consisting of observed network

n_simulations Number of sub-samples to be obtained at each level

subsampling_proportion
 A vector depicting proportions of sub-sampled nodes

network_metrics
 A vector depicting names of local global network metrics

Value

A list of network metrics of class `list_correlation_matrices`. Each element of list is a matrix whose columns correspond to `subsampling_proportion` and rows correspond to `n_simulations`. The entries of the matrix provide value of correlation between the nodes in full network and the sub-sampled network for the corresponding metric.

Examples

```
data(elk_network_2010)  
correlation_analyze(elk_network_2010)
```

`distance_radian_coordinates`*Calculate distance between two pairs of radian coordinates*

Description

Calculate distance between two pairs of radian coordinates

Usage

```
distance_radian_coordinates(latf, lonf, latt, lont)
```

Arguments

<code>latf</code>	latitude from
<code>lonf</code>	longitude from
<code>latt</code>	latitude to
<code>lont</code>	longitude to

Value

distance value in meters

`elk_2010_permutations` *A list of 100 igraph objects obtained by permuting the raw elk_data_2010 and obtaining network from those*

Description

A list of 100 igraph objects obtained by permuting the raw elk_data_2010 and obtaining network from those

Usage

```
elk_2010_permutations
```

Format

A list of 100 igraph objects

Examples

```
data(elk_2010_permutations)
```

elk_all_interactions_2010

Dataset of all possible interactions from elk_data_2010

Description

Dataset of all possible interactions from elk_data_2010

Usage

```
elk_all_interactions_2010
```

Format

A dataframe with 7615 rows and 5 variables

Animal_A First animal ID

Animal_B Second animal ID

Timestamp_A Observation timestamp of first animal

Timestamp_B Observation timestamp of second animal

distance Distance in metres between the two animals

Examples

```
data(elk_all_interactions_2010)
```

elk_data_2010

Data to showcase functions in our package

Description

Contains GPS telemetry observations of the species elk in year 2010

Usage

```
elk_data_2010
```

Format

A dataframe with 123568 rows and 4 variables:

animal_id Unique ID of individuals in the observed sample

datetime Date and timestamp of the observation

latitude_rad Latitude of individual observation in radians

longitude_rad Longitude of individual observation in radians

Examples

```
data(elk_data_2010)
```

`elk_interactions_2010` *Dataset of interactions from elk_data_2010 using first mode as the spatial threshold*

Description

Dataset of interactions from elk_data_2010 using first mode as the spatial threshold

Usage

```
elk_interactions_2010
```

Format

A dataframe with 2393 rows and 5 variables

Animal_A First animal ID

Animal_B Second animal ID

Timestamp_A Observation timestamp of first animal

Timestamp_B Observation timestamp of second animal

distance Distance in metres between the two animals

Examples

```
data(elk_interactions_2010)
```

`elk_network_2010` *An igraph object depicting the network obtained from elk_interactions_2010*

Description

An igraph object depicting the network obtained from elk_interactions_2010

Usage

```
elk_network_2010
```

Format

An igraph object with 57 nodes and 114 edges

Examples

```
igraph::E(elk_network_2010)
```

get_coordinates_in_radian

To obtain latitude and longitude values in radian

Description

To obtain latitude and longitude values in radian

Usage

```
get_coordinates_in_radian(species_raw)
```

Arguments

species_raw A DataFrame consisting of GPS observations. The DataFrame must have a "latitude" column and a "longitude" column

Value

The same DataFrame that has been passed as the argument with two additional columns namely "latitude_rad" and "longitude_rad"

get_interactions

To obtain interactions from raw GPS observations

Description

To obtain interactions from raw GPS observations

Usage

```
get_interactions(species_raw, temporal_thresh = 7, spatial_thresh, n_cores = 1)
```

Arguments

species_raw A DataFrame consisting of GPS observations. It should have at least four columns namely "animal_id", "datetime", "latitude_rad", and "longitude_rad". "latitude_rad", and "longitude_rad" are latitude and longitude values in radians respectively. See function "get_coordinates_in_radian" to get these values.

temporal_thresh

Temporal threshold in minutes with default 7 minutes

spatial_thresh

The maximum distance in meters within which two animals are considered interacting

n_cores

Number of cores for parallel processing with default 1

Value

A dataframe consisting of five columns. The first two columns contain animal ids, third and fourth column contain timestamp of their observations and the final column contains the distance between the two individuals.

Examples

```
data(elk_data_2010)
get_interactions(elk_data_2010, temporal_thresh = 7, spatial_thresh = 15)
```

get_network_summary *Calculates and prints network summary statistics*

Description

Calculates and prints network summary statistics

Usage

```
get_network_summary(network)
```

Arguments

network An undirected network with nodes representing animal IDs and edges representing associations between them.

Value

No return value, called for side effects. The function prints values of network metrics to the console.

Examples

```
data(elk_network_2010)
get_network_summary(elk_network_2010)
```

`get_spatial_threshold` *To obtain spatial threshold for calculating interactions from raw GPS observations. The threshold is obtained as the distance interval that captures maximum number of inter-individual interactions.*

Description

To obtain spatial threshold for calculating interactions from raw GPS observations. The threshold is obtained as the distance interval that captures maximum number of inter-individual interactions.

Usage

```
get_spatial_threshold(species_interactions, interval_size)
```

Arguments

`species_interactions`
A dataframe consisting of individual interactions within maximum possible distance

`interval_size` Minimum interval size within which the number of interactions should be calculated

Value

Spatial threshold in meters

Examples

```
data(elk_all_interactions_2010)
get_spatial_threshold(elk_all_interactions_2010, interval_size = 2)
```

`interacting_pairs` *Function to obtain pairs of interacting animals*

Description

Function to obtain pairs of interacting animals

Usage

```
interacting_pairs(
  i,
  datetime,
  latitude,
  longitude,
  temporal_thresh,
  spatial_thresh
)
```

Arguments

i	Index of the animal
datetime	DateTime vector
latitude	latitude vector
longitude	longitude vector
temporal_thresh	time threshold in minutes
spatial_thresh	spatial threshold in meters

Value

A matrix consisting of two row. The first row corresponds to the interacting indices and the second row to the respective distances.

network_from_interactions

Function to obtain a network structure from interactions dataframe

Description

Function to obtain a network structure from interactions dataframe

Usage

```
network_from_interactions(species_raw, interactions, n_cores = 1)
```

Arguments

species_raw	A dataframe consisting of raw GPS observations. It should have at least four columns namely "animal_id", "datetime", "latitude_rad", and "longitude_rad". "latitude_rad", and "longitude_rad" are latitude and longitude values in radians respectively. See function "get_coordinates_in_radian" to get these values.
interactions	A dataframe of interactions obtained from raw GPS observations using the function "get_interactions"
n_cores	Number of cores for parallel processing, default is 1

Value

An object of class igraph

Examples

```
data(elk_data_2010, elk_interactions_2010)
network_from_interactions(elk_data_2010, elk_interactions_2010)
```

network_subsamples *To generate subsamples and obtain network metrics of the subsamples*

Description

To generate subsamples and obtain network metrics of the subsamples

Usage

```
network_subsamples(  
  network,  
  n_simulations = 100,  
  subsampling_proportion = c(0.1, 0.3, 0.5, 0.7, 0.9),  
  network_metrics = c("density", "mean_strength", "diameter", "transitivity")  
)
```

Arguments

network An igraph graph object consisting of observed network

n_simulations Number of sub-samples to be obtained at each level

subsampling_proportion
 A vector depicting the levels (in proportion) at which subsamples to be taken

network_metrics
 A vector depicting names of global network metrics. Default = network_metrics = c("density", "mean_strength", "diameter", "transitivity")

Value

A list of network metrics of class "Subsampled_Network_Metrics". Each element of list is a matrix whose columns correspond to subsampling_proportion and rows correspond to n_simulations. The entries of the matrix provide values of the corresponding metric.

Examples

```
data(elk_network_2010)  
network_subsamples(elk_network_2010)
```

`obtain_bootstrapped_samples`*To obtain bootstrapped versions of a network*

Description

To obtain bootstrapped versions of a network

Usage

```
obtain_bootstrapped_samples(  
  network,  
  n_nodes = igraph::gorder(network),  
  n_versions = 1000,  
  seed = 12345  
)
```

Arguments

<code>network</code>	An igraph object
<code>n_nodes</code>	Number of nodes to be selected in bootstrapped versions (default : All nodes)
<code>n_versions</code>	Number of bootstrapped versions required
<code>seed</code>	seed number

Value

A list of class `bootstrapped_pvalue_matrix` consisting of two elements. The first element contains the original network and the second element contains bootstrapped versions.

Examples

```
data(elk_network_2010)  
obtain_bootstrapped_samples(elk_network_2010, n_versions = 100)
```

`obtain_permuted_network_versions`*Function to obtain permuted networks from raw datastream*

Description

Function to obtain permuted networks from raw datastream

Usage

```
obtain_permuted_network_versions(  
  species_raw,  
  temporal_thresh,  
  spatial_thresh,  
  n_permutations,  
  n_cores = 1  
)
```

Arguments

species_raw	A dataframe consisting of raw GPS observations
temporal_thresh	Temporal threshold in minutes
spatial_thresh	Spatial threshold
n_permutations	Number of permuted versions to obtain
n_cores	Number of cores for parallel processing with default 1

Value

A list of size n_permutations where each element is a network of class igraph obtained by permuting raw datastream

Examples

```
data(elk_data_2010)  
permuted_versions <- obtain_permuted_network_versions(elk_data_2010,  
  temporal_thresh = 7, spatial_thresh = 15, n_permutations = 10, n_cores = 2)
```

```
plot.bootstrapped_pvalue_matrix
```

To plot the results obtained from bootstrapped_difference_pvalues function

Description

To plot the results obtained from bootstrapped_difference_pvalues function

Usage

```
## S3 method for class 'bootstrapped_pvalue_matrix'  
plot(x, ...)
```

Arguments

x A matrix of p-values obtained from bootstrapped_difference_pvalues function
... Further arguments are ignored.

Value

No return value, called for side effects. The plot shows p-values between 0 and 1 corresponding to each sample size.

Examples

```
data(elk_network_2010)
mean_pvalue_matrix <- bootstrapped_difference_pvalues(elk_network_2010, n_versions = 100)
plot(mean_pvalue_matrix)
```

plot.list_correlation_matrices

To plot correlation analysis results

Description

To plot correlation analysis results

Usage

```
## S3 method for class 'list_correlation_matrices'
plot(x, ...)
```

Arguments

x A list of matrices obtained from correlation_analyze function
... Further arguments are ignored

Value

No return value, called for side effects. The plots show mean and standard deviation of correlation coefficients obtained over multiple iterations.

Examples

```
data(elk_network_2010)
elk_correlation_analysis <- correlation_analyze(elk_network_2010)
plot(elk_correlation_analysis)
```

```
plot.list_permuted_networks
```

Function to plot the network metrics distribution of permuted networks

Description

Function to plot the network metrics distribution of permuted networks

Usage

```
## S3 method for class 'list_permuted_networks'  
plot(  
  x,  
  species_original_network,  
  network_metrics = c("density", "mean_strength", "diameter", "transitivity"),  
  ...  
)
```

Arguments

`x` A list of igraph objects obtained obtained using the function `obtain_permuted_network_versions`

`species_original_network` An igraph object which is the original network

`network_metrics` A vector depicting names of global network metrics. This should be supplied as a character vector and the values should be chosen from "mean_strength", "density", "diameter", "transitivity". (default = c("mean_strength", "density", "diameter", "transitivity")).

... Further arguments are ignored.

Value

No return value, called for side effects.

Examples

```
data(elk_data_2010, elk_network_2010)  
permuted_versions <- obtain_permuted_network_versions(elk_data_2010,  
  temporal_thresh = 7, spatial_thresh = 15, n_permutations = 10, n_cores = 2)  
plot(permuted_versions, elk_network_2010)
```

`plot.list_regression_matrices`
To plot regression analysis results

Description

To plot regression analysis results

Usage

```
## S3 method for class 'list_regression_matrices'  
plot(x, ...)
```

Arguments

`x` A list of matrices obtained from `regression_slope_analyze` function
`...` Further arguments are ignored

Value

No return value, called for side effects. The plots show regression slope values corresponding to proportion of individuals in the sample.

Examples

```
data(elk_network_2010)  
elk_regression_analysis <- regression_slope_analyze(elk_network_2010)  
plot(elk_regression_analysis)
```

`plot.Subsampled_Network_Metrics`
To plot sub-sampling results

Description

To plot sub-sampling results

Usage

```
## S3 method for class 'Subsampled_Network_Metrics'  
plot(x, network, ...)
```

Arguments

x	A list of matrices obtained from network_subsamples function of class "Subsampled_Network_Metrics"
network	An igraph graph object consisting of observed network
...	Further arguments are ignored

Value

No return value, called for side effects. The boxplots depict range of values, network metrics take when multiple subsamples are chosen from the observed sample.

Examples

```
data(elk_network_2010)
elk_subsamples <- network_subsamples(elk_network_2010)
plot(elk_subsamples, elk_network_2010)
```

```
plot.Subsampled_Per-muted_Network_Metrics
```

To plot sub-sampling results of the original network and permuted networks

Description

To plot sub-sampling results of the original network and permuted networks

Usage

```
## S3 method for class 'Subsampled_Per-muted_Network_Metrics'
plot(x, network, ...)
```

Arguments

x	A list of matrices obtained from subsamples_permuted_networks function of class "Subsampled_Per-muted_Network_Metrics"
network	An igraph graph object consisting of observed network
...	Further arguments are ignored

Value

No return value, called for side effects. The boxplots show side-by-side comparison of network metrics distribution from subsamples of observed network and subsamples from permuted networks.

Examples

```
data(elk_2010_permutations, elk_network_2010)
elk_subsamples_permuted_networks <- subsamples_permuted_networks(elk_2010_permutations)
plot(elk_subsamples_permuted_networks, elk_network_2010)
```

`plot.Width_CI_matrix` *To plot the results obtained from width_CI function*

Description

To plot the results obtained from `width_CI` function

Usage

```
## S3 method for class 'Width_CI_matrix'
plot(x, ...)
```

Arguments

`x` A matrix of width of Confidence Intervals obtained from `width_CI` function

`...` Further arguments are ignored.

Value

No return value, called for side effects. Plots show width of confidence intervals corresponding to number of individuals in the sub-sample.

Examples

```
data(elk_network_2010)
width_CI_elk <- width_CI(elk_network_2010, n_versions = 100)
plot(width_CI_elk)
```

plot_network	<i>Visualize Animal Network</i>
--------------	---------------------------------

Description

Visualize Animal Network

Usage

```
plot_network(species_network, seed = 1)
```

Arguments

species_network	An igraph graph object consisting of observed network.
seed	Seed to be set for layout.

Value

No return value, called for side effects. The plots depict a visualisation of network structure.

Examples

```
data(elk_network_2010)
plot_network(elk_network_2010)
```

rcpp_hello_world	<i>Simple function using Rcpp</i>
------------------	-----------------------------------

Description

Simple function using Rcpp

Usage

```
rcpp_hello_world()
```

Examples

```
## Not run:
rcpp_hello_world()

## End(Not run)
```

`regression_slope_analyze`*To perform regression analysis for local network metrics*

Description

To perform regression analysis for local network metrics

Usage

```
regression_slope_analyze(  
  network,  
  n_simulations = 10,  
  subsampling_proportion = c(0.1, 0.3, 0.5, 0.7, 0.9),  
  network_metrics = c("degree", "strength", "betweenness", "clustering_coefficient",  
    "eigenvector_centrality")  
)
```

Arguments

<code>network</code>	An igraph graph object consisting of observed network
<code>n_simulations</code>	Number of sub-samples to be obtained at each level
<code>subsampling_proportion</code>	A vector depicting proportions of sub-sampled nodes
<code>network_metrics</code>	A vector depicting names of local global network metrics

Value

A list of network metrics of class `list_regression_matrices`. Each element of list is a matrix whose columns correspond to `subsampling_proportion` and rows correspond to `n_simulations`. The entries of the matrix provide value of the slope of regression when the nodal values in sub-sampled network are regressed upon the values of the same nodes in the full network for the corresponding metric.

Examples

```
data(elk_network_2010)  
regression_slope_analyze(elk_network_2010)
```

subsamples_permuted_networks

To generate subsamples of the permuted networks and obtain network metrics of those subsamples

Description

To generate subsamples of the permuted networks and obtain network metrics of those subsamples

Usage

```
subsamples_permuted_networks(  
  networks_list,  
  subsampling_proportion = c(0.1, 0.3, 0.5, 0.7, 0.9),  
  network_metrics = c("density", "mean_strength", "diameter", "transitivity")  
)
```

Arguments

`networks_list` A list of igraph objects obtained by permuting the observed network

`subsampling_proportion`

A vector depicting the levels (in proportion) at which subsamples to be taken

`network_metrics`

A vector depicting names of global network metrics. Default = `network_metrics = c("density", "mean_strength", "diameter", "transitivity")`

Value

A list of network metrics of class "Subsampled_Permuted_Network_Metrics". Each element of list is a matrix whose columns correspond to `subsampling_proportion` and rows correspond to the number of networks in `networks_list`. The entries of the matrix provide values of the corresponding metric.

Examples

```
data(elk_2010_permutations)  
subsamples_permuted_networks(elk_2010_permutations)
```

width_CI	<i>To obtain width of confidence intervals using bootstrapped versions at each level of sub-sampling</i>
----------	--

Description

To obtain width of confidence intervals using bootstrapped versions at each level of sub-sampling

Usage

```
width_CI(
  network,
  n_versions = 100,
  seed = 12345,
  n.iter = 10,
  network_metrics = c("mean_degree", "mean_strength", "density", "diameter",
    "transitivity"),
  scaled_metrics = NULL
)
```

Arguments

network	An igraph object
n_versions	Number of bootstrapped versions to be used. (default = 100)
seed	seed number
n.iter	Number of iterations at each level. (default = 10)
network_metrics	Network metrics to be evaluated. This should be supplied as a character vector and the values should be chosen from "mean_degree", "mean_strength", "density", "diameter", "transitivity". (default = c("mean_degree", "mean_strength", "density", "diameter", "transitivity"))
scaled_metrics	Optional. A vector subset of network_metrics with the names of metrics that should be scaled. Values can be chosen from c("mean_degree", "mean_strength", "diameter").

Value

A matrix of class `Width_CI_matrix` containing width of Confidence Intervals where each row corresponds to the sub-sample size and columns correspond to the chosen network metric.

Examples

```
data(elk_network_2010)
width_CI(elk_network_2010, n_versions = 100)
```

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