Package ‘AnimalHabitatNetwork’

Type Package

Title Networks Characterising the Physical Configurations of Animal Habitats

Version 0.1.0

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Description Functions for generating and visualising networks for characterising the physical attributes and spatial organisations of habitat components (i.e. habitat physical configurations). The network generating algorithm first determines the X and Y coordinates of N nodes within a rectangle with a side length of L and an area of A. Then it computes the pair-wise Euclidean distance Dij between node i and j, and then a complete network with 1/Dij as link weights is constructed. Then, the algorithm removes links from the complete network with the probability as shown in the function `ahn_prob()`. Such link removals can make the network disconnected whereas a connected network is wanted. In such cases, the algorithm rewrites one network component to its spatially nearest neighbouring component and repeat doing this until the network is connected again. Finally, it outputs an undirected network (weighted or unweighted, connected or disconnected). This package came with a manuscript on modelling the physical configurations of animal habitats using networks (in preparation).

License GPL-3

Imports stats, igraph (>= 1.2.4.1), ggplot2 (>= 3.2.0)

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ahn_gen

Generate networks characterising habitat physical configurations

### Description

Generate undirected networks (weighted or unweighted, connected or disconnected) characterising the physical attributes and spatial organizations (or distributions) of habitat components (i.e. habitat configurations).

### Usage

```
ahn_gen(N, L, mu, lamda, Connected = TRUE, Weighted = TRUE, eta = 1, 
        A = 25, X = NULL, Y = NULL, U = NULL, V = NULL)
```

### Arguments

- **N**: The number of nodes
- **L**: A side length of the rectangle landscape within which nodes are anchored
- **mu**: The critical \( D_{ij} \) (i.e. Euclidean distance between node i and j) at which the link removing probability curve \( P(D_{ij}, mu, lamda) \) transits from concave to convex (see \ahn_prob\)
- **lamda**: The steepness of the link removing probability curve \( P(D_{ij}, mu, lamda) \), see \ahn_prob\.
- **Connected**: TRUE for connected while FALSE ignores whether the networks are connected or not
- **Weighted**: TRUE for weighted while FALSE for unweighted networks
- **eta**: Mediates the weight, i.e. \((D_{ij})^{-\eta}\), of the link rewiring node i from one network component and node j from another network component (i and j are with an Euclidean distance of \( D_{ij} \)) when the network becomes disconnected after removing links from the initial complete network with the probability \( P(D_{ij}, mu, lamda) = [1 + \exp(-lamda(D_{ij} - mu))]^{-1} \) when both Connected = TRUE and Weighted = TRUE
- **A**: The area of the rectangle landscape within which the network is defined
- **X**: A vector of \( X \) coordinates for the \( N \) nodes (sampled from \([0, L]\) uniformly at random if NULL)
- **Y**: A vector of \( Y \) coordinates for the \( N \) nodes (sampled from \([0, A/L]\) uniformly at random if NULL)
- **U**: A vector with \( N \) elements specifying node attributes (qualitative or quantitative), by default NULL
- **V**: A vector with \( N \) elements specifying node attributes (qualitative or quantitative), by default NULL
ah\_plot

**Value**

Return an animal habitat network (an igraph object)

**Examples**

# generate a connected and weighted network
ah\_gen(N = 10, L = 5, mu = 1, lamda = 5)

```r
N <- 10
x <- runif(N, 0, 5)
ql <- sample(LETTERS, N, replace = TRUE)
qn <- sample(1:20, N, replace = TRUE)

# specify the X coordinates, node attributes U and V for a connected and unweighted network
ah\_gen(N, L = 5, mu = 1, lamda = 5, Weighted = FALSE, X = x, U = ql, V = qn)

# specify the Y coordinates, node attributes U and V for a weighted network, no matter if the
# network will be connected or not
ah\_gen(N, L = 5, mu = 1, lamda = 5, Weighted = TRUE, Connected = FALSE, Y = x, U = ql, V = qn)
```

**ahn\_plot**

Plot networks

**Description**

Visualise networks generated by the function `ahn\_gen`.

**Usage**

```
ahn\_plot(ahn, NodeLabels = unname(V(ahn)), NodeColors = unname(V(ahn)),
    NodeSizes = rep(3, length(V(ahn))))
```

**Arguments**

- **ahn**
  Networks returned by `ahn\_gen`
- **NodeLabels**
  The labels of nodes in `ahn` (node IDs by default)
- **NodeColors**
  The colors of nodes in `ahn` (each node has a unique color by default)
- **NodeSizes**
  The sizes of nodes in `ahn` (nodes are with the identical size of 3 by default)

**Value**

Return a plot of the network
Examples

# generate a weighted and connected network and plot it by default
N <- 10
x <- runif(N, 0, 5)
ahn <- ahn_gen(N, L = 5, mu = 1, lamda = 5, X = x)
ahn_plot(ahn)

# plot the network with specified colors, labels and sizes for nodes
ahn_plot(
  ahn,
  NodeColors = sample(4, N, replace = TRUE),
  NodeLabels = letters[1:N],
  NodeSizes = seq(1, 5, length.out = N))

ahn_prob

Plot probability curves

Description

Plot the probability curve $P(D_{ij}, \mu, \lambda)$ for removing links from the initial complete network

Usage

ahn_prob(Dij = seq(0.05, 10, length.out = 30), mu = c(0.1, 2, 5, 10),
  lamda = c(1e-04, 0.15, 0.35, 0.75, 1.25, 5, 30))

Arguments

- **Dij**: A vector of Euclidean distances between node $i$ and $j$
- **mu**: The concave-to-convex transition point of the probability curves $P(D_{ij}, \mu, \lambda) = [1 + \exp(-\lambda(D_{ij} - \mu))]^{-1}$, where $D_{ij}$ is the Euclidean distance between node $i$ and $j$
- **lamda**: The steepness of the probability curves

Value

Return a plot with probability curves
Examples

# plot the probabilities for removing network links between node i and j with
# Euclidean distances D_{ij}

dis <- seq(.05, 10, length.out = 20)
m <- c(.1, 2, 5, 10)
l <- c(.0001, .15, .35, .75, 1.25, 5, 30)
ahn_prob(dis, m, l)
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