Package 'ResDisMapper'

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Type Package

Title Calculates and maps environmental resistance to dispersal over a landscape

Version 1.1

Description Provides functions to (1) Read in genetic data and geographic coordinates for individuals over a landscape, model Isolation by Distance (IBD) and calculate IBD residuals; (2) Plot IBD residuals for pairs of individuals in a population, as represented by line segments over the defined landscape; (3) Calculate environmental resistance to dispersal over the landscape using the IBD residuals and a novel method; and (4) Create a map of the resistance values over the landscape. The novel method of calculating resistance is detailed in Tang et al. (2020).

Depends R (>= 3.3.3)

Imports adegenet, ggplot2, poppr, raster, rgl, Rmisc, sp

License GPL (>= 3)

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ResDisMapper-package   *Calculates and maps environmental resistance to dispersal over a landscape*

Description

The Resistance to Dispersal Mapper (ResDisMapper) package provides functions to calculate and map environmental resistance to dispersal over a landscape, for a population of individuals. Firstly, there is a function called `rdm_IBD`, which reads in the geographic coordinates and genetic data for the individuals and computes the geographic and genetic distance between each pair of individuals. This function compares the geographic and genetic distance for each pair of individuals to expected values in the case of Isolation by distance (IBD), and calculates the corresponding residuals. Secondly, there is a function `rdm_residual`, which takes the residuals and visualizes them using a 3-D plot, and outputs the residuals together with line segments representing pairs of individuals over the landscape. Thirdly, there is a function `rdm_resistance`, which uses the residuals and line segments to calculate the environmental resistance to dispersal over the landscape. Lastly, the function `rdm_mapper` visualizes the resistance values using a raster map, with contour lines indicating areas of high and low resistance.

Author(s)

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References

Tang, Q., Fung, T., Rheindt, F.E. (2020). ResDisMapper: An R package for fine-scale mapping of resistance to dispersal. Molecular Ecology Resources 20 (3), 819-831 https://doi.org/10.1111/1755-0998.13127

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rdm_IBD   *Calculates Isolation by Distance (IBD) residuals for each pair of individuals in a population*

Description

`rdm_IBD`: Reads genotype data for individuals in a population together with the geographic coordinates of the individuals, models overall IBD trend for the population, and then calculates IBD residuals for each pair of individuals.

Usage

```
rdm_IBD(Gen_raw, Geo_raw, Dist_method = 1, IBD_method = 1)
```

Arguments

`Gen_raw`	A string specifying the path to a file of genotype data in GENEPOP format, with alleles specified using three digits. The GENEPOP file must have the extension *.gen*.
`Geo_raw`	A string specifying the path to a text file showing the name (1st column) and geographical x and y coordinates (2nd and 3rd columns) of each individual (each row). The first row needs to specify the column headings, and all entries need to be tab-delimited.
`Dist_method`	An integer from 1 to 6 specifying the method used to calculate genetic distance among individuals. Integers 1 to 6 correspond to the methods incorporated into the following six functions from the `poppr` R package, respectively: `diss.dist`, `nei.dist`, `rogers.dist`, `reynolds.dist`, `edwards.dist`, and `provesti.dist`. The default value is 1.
`IBD_method`	An integer specifying the method used to calculate the IBD residual for each pair of individuals. A value of 1 means that the residuals are calculated by fitting a straight line to all pairs of genetic and geographic distances, and measuring the vertical distance from each pair to the fitted line. The fitted straight line represents the combinations of genetic and geographic distances that are expected from IBD. A value of 2 means that a non-linear curve of the form $y = a + b*(1-\exp(-\exp(c)*x))$ is fitted instead of a straight line, where *a*, *b* and *c* are the fitted parameters. The default value is 1. The function `rdm_IBD` automatically plots the data points together with the fitted line or curve.

Value

An object of class `dist`, containing a matrix showing the IBD residuals for pairs of individuals.

Examples

```
rdm_IBD("files/genotypes.gen", "files/coordinates.txt")
```

`rdm_mapper`	*Visualizes the resistance to dispersal over a landscape, for individuals in a population*

Description

`rdm_mapper`: Reads in the resistance to dispersal for individuals of a population, over a grid of cells defining the landscape containing the individuals, and then creates a raster map of resistance.

Usage

```
rdm_mapper(
  F.df,
  Geo_raw,
  p_signf = 0.05,
  p_size = 2,
  p_col = "yellow",
  disp_all_cells = 0,
  disp_contours = 1
)
```

Arguments

`F.df`	A data frame containing eight columns with resistance information for each grid cell in a landscape. Each row corresponds to one cell, and the eight different columns refer to the resistance, the number of intersecting line segments (lines connecting pairs of individuals in the landscape), the x and y coordinates specifying the location of the mid-point of the cell, the lower and upper limits of the confidence interval for the resistance, the sign of the product of the upper and lower limits of the confidence interval, and the percentile of the null distribution of resistances corresponding to the observed resistance. A .csv file with this information is produced by the function `rdm_resistance`.
`Geo_raw`	A string specifying the path to a text file showing the name (1st column) and geographical x and y coordinates (2nd and 3rd columns) of each individual (each row). The first row needs to specify the column headings, and all entries need to be tab-delimited.
`p_signf`	Specifies the percentiles of the null distribution of resistances used to define areas of high and low resistance that are statistically significant. In a grid cell, a resistance value that is above the 100*(1-`p_signf`)% percentile is considered to be a high resistance that is statistically significant, whereas a resistance value that is below the 100*(`p_signf`)% percentile is considered to be a low resistance that is statistically significant. Default value of 0.05.
`p_size`	Specifies the size of the sampling points in the plotted raster map of resistances. Default value of 2.
`p_col`	Specifies the color of the sampling points in the plotted raster map of resistances. Default color is yellow.
`disp_all_cells`	Specifies whether to display all cells (1) or just cells with resistances that are statistically different from zero (0). For a further description of the meaning of resistances that are statistically different from zero, please refer to the description of the function `rdm_resistance`. Default value of 0.
`disp_contours`	Specifies whether to display red and green contour lines that delineate areas with statistically significant high and low resistance values respectively (1), or not (0). For a further description of the meaning of a statistically significant high or low resistance value, please refer to the description of the function `rdm_resistance`. Default value of 1.

Value

Function plots a map of resistance, but does not return an output object.

Examples

```
F.df <- read.csv("files/resistance_map.csv")
rdm_mapper(F.df, "files/coordinates.txt")
```

`rdm_residual`	*Creates and plots IBD residuals for pairs of individuals in a population, represented as line segments over a defined landscape*

Description

`rdm_residual`: Reads the IBD residuals for each pair of individuals in a population (as calculated by function `rdm_IBD`) together with their geographic coordinates, and then creates a 3-D graph showing the residuals for each pair of individuals, represented as a line segment over the landscape considered. The 3-D graph can be rotated to obtain a better view.

Usage

```
rdm_residual(IBD.res, Geo_raw, min.dist = 1, max.dist = Inf,
  n_resolution = 50, proj = sp::CRS("+init=epsg:4326"))
```

Arguments

`IBD.res`	An object of class `dist`, containing a matrix with the IBD residuals for pairs of individuals in a population.
`Geo_raw`	A string specifying the path to a text file showing the name (1st column) and geographical x and y coordinates (2nd and 3rd columns) of each individual (each row). The first row needs to specify the column headings, and all entries need to be tab-delimited.
`min.dist`	IBD residuals are only calculated for pairs of individuals that are separated by a distance greater than `min.dist`. The default value is 1.
`max.dist`	IBD residuals are only calculated for pairs of individuals that are separated by a distance less than `max.dist`. The default value is Inf.
`n_resolution`	Specifies the number of cells that the landscape is divided into, for the purposes of creating the 3-D plot. The landscape is divided into `n_resolution` cells along both coordinate axes. Individuals that appear in the same cell are represented by a single point on the plot. The default value is 50.
`proj`	The coordinate system that is used for plotting. The default is EPSG 4326.

Value

An object of class `SpatialLinesDataFrame`, containing coordinates of the line segments joining each pair of individuals and the corresponding IBD residuals.

Examples

```
IBD_res <- rdm_IBD("files/genotypes.gen", "files/coordinates.txt")
rdm_residual(IBD_res, "files/coordinates.txt")
```

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rdm_resistance	*Produces environmental resistance to dispersal over a landscape, for individuals in a population*

Description

`rdm_resistance`: Reads in IBD residuals for pairs of individuals in a population, represented as line segments connecting the pairs of individuals over a defined landscape, and then applies a novel method (Tang et al., in review) to the residuals to calculate environmental resistance to dispersal over the landscape. Essentially, the method splits the landscape into a grid of cells and for each cell, calculates the resistance as the average of the IBD residuals of all line segments that intersect the cell.

Usage

```
rdm_resistance(IBD.res, Res_SLDF, nrows = 30, ncols = 30,
  conf_intervals = 0.95, random_rep = 1000,
  outputfile = "resistance_map.csv")
```

Arguments

IBD.res	An object of class `dist`, containing a matrix with the IBD residuals for pairs of individuals in a population.
Res_SLDF	An object of class `SpatialLinesDataFrame`, containing the IBD residuals for each pair of individuals in a population and the coordinates of line segments connecting the pairs of individuals over the defined landscape. This object is produced by the function `rdm_residual`.
nrows	Number of grid cells in each row of the raster map of resistance. The default value is 30.
ncols	Number of grid cells in each column of the raster map of resistance. The default value is 30.
conf_intervals	The coverage of the confidence interval generated for each resistance value in a grid cell, expressed as a proportion. This interval measures the uncertainty in the (observed) resistance in each cell. If a cell has no intersecting line segments or only one, then a confidence interval cannot be calculated and the cell is no longer considered for further calculation. If the confidence interval does not overlap 0, then the resistance is statistically different from 0. The default value is 0.95 (corresponding to 95% intervals).
random_rep	Number of random resamples of the IBD residuals used to construct the null distribution of resistances in each grid cell. For a grid cell with *n* intersecting line segments and *n* corresponding IBD residuals, a random resample consists of randomly sampling *n* IBD residuals from the set of all IBD residuals over the entire landscape, without replacement. If the observed resistance is above a threshold percentile of the null distribution, then the cell is considered to have a high resistance that is statistically significant. If instead the observed resistance is below another threshold percentile of the null distribution, then the cell is considered to have a low resistance that is statistically significant. The default value is 1,000.
outputfile	Name of the .csv file that is produced, containing resistance information in the output data frame. The default is 'resistance_map.csv'.

Value

A data frame with resistance information for each grid cell in the landscape with more than one intersecting line segment. Each row corresponds to one cell, and the eight different columns refer to the resistance, the number of intersecting line segments, the x and y coordinates specifying the location of the mid-point of the cell, the lower and upper limits of the confidence interval for the resistance, the sign of the product of the lower and upper limits of the confidence interval, and the percentile of the null distribution of resistances corresponding to the observed resistance. When calculating this data, the function `rdm_resistance` prints out messages showing the current stage of calculation. There are four stages: Calculating (1) the resistances, (2) the numbers of intersecting line segments, (3) the lower limits of the confidence intervals for the resistances, and (4) the upper limits of the confidence intervals for the resistances.

References

Tang, Q., Fung, T., Rheindt, F.E. (In review). ResDisMapper: An R package for fine-scale mapping of resistance to dispersal.

Examples

```
IBD_res <- rdm_IBD("files/genotypes.gen", "files/coordinates.txt")
Res_SLDF <- rdm_residuals(IBD_res, "files/coordinates.txt")
rdm_resistance(IBD_res, Res_SLDF)
```

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