# Package ‘popgraph’

February 20, 2015

**Type** Package

**Title** This is an R package that constructs and manipulates population graphs.

**Version** 1.4

**Date** 2014-01-06

**Author** Rodney J. Dyer

**Maintainer** Rodney J. Dyer <rjdyer@vcu.edu>

**Description** This is a generic package that produces "Population Graphs" a graph-theoretic topology based upon conditional genetic covariance. This functionality used to be within the gstudio package, but has been taken out to focus on spatial integration of graph topologies with existing packages like sp, raster, and ggplot2.

**License** GPL (>= 2)

**LazyLoad** yes

**Depends** R (>= 2.15), ggplot2, igraph

**Imports** MASS, sp, Matrix, sampling

**Suggests** testthat, maps, fields, grid

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2014-06-03 01:34:35

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popgraph-package

Package for the creation of population graph objects

Description

popgraph is a package that is designed to create and manipulate population graph objects (Dyer & Nason 2004, MolEcol). This specific package was made in conjunction with the book "Applied Landscape Genetics" by R.J. Dyer.

Details

Package: popgraph
Type: Package
Version: 1.0
Date: 2013-03-06
License: GPL (>= 2)
LazyLoad: yes

There are some very good examples of the components of this package are used in the vignettes for this package.
Overload `-` operator for pairs of `popgraph` objects

Description
An overload of the `-` operator for `popgraph` objects that removes the edges in the first one that are in the second one.

Usage
```
## S3 method for class 'popgraph'
e1 - e2
```

Arguments
- `e1`: A `popgraph` object representing the offspring.
- `e2`: A `popgraph` object representing the parent.

Value
A new `popgraph` object that represents the genotypes left over after removing the parental part (if possible).

Examples
```
library(igraph)
e1 <- as.popgraph( graph.atlas(716) )
e2 <- as.popgraph( graph.atlas(886) )
e3 <- e1 - e2
par(mfrow=c(1,3))
l <- layout.fruchterman.reingold( e1 )
plot(e1, layout=l)
plot(e2, layout=l)
plot(e3, layout=l)
par(mfrow=c(1,1))
```
alt  Sonoran desert altitude.

Description
This is a raster file for altitude in the Sonoran desert region coincident with the Lophocereus and Upiga data sets.

arapat_mv  Araptus attenuatus data

Description
This is the Araptus attenuatus data in mv format

arapat_pop  Arapat population data

Description
The population strata for the arapat_mv data

as.popgraph  Converts an object of type matrix or igraph into popgraph

Description
This is a simple conversion routine for matrix or igraph objects into popgraph objects

Usage
as.popgraph(graph)

Arguments

graph  An object of type matrix or igraph

Value
An object of type popgraph

Author(s)
Rodney J. Dyer <rjdyer@vcu.edu>
Metadata for Baja Populations.

Description

This is metadata associated with the sampling locations for the Lophocereus and Upiga data sets.

centroid_distance

This function takes a data set and a group set and returns centroid distances

Description

This is a convenience function for a reduce and distance operation based upon multivariate predictor variables.

Usage

centroid_distance(x, grouping)

Arguments

x
The NxP matrix of raw data.
grouping
The Nx1 vector of grouping factors.

Value

An NxN pairwise distance matrix.

Author(s)

Rodney J. Dyer <rjdyer@vcu.edu>
### centroid_variance

*This function takes a data set and a group set and returns centroid variances*

**Description**

This is a convenience function for a reduce and distance operation based upon multivariate predictor variables.

**Usage**

```r
centroid_variance(x, grouping)
```

**Arguments**

- `x` The NxP matrix of raw data.
- `grouping` The Nx1 vector of grouping factors.

**Value**

The sum of the within stratum variance for each group

**Author(s)**

Rodney J. Dyer <rjdyer@vcu.edu>

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### congruence_topology

*Returns congruence topology*

**Description**

Takes two graphs and returns topology that is the intersection of the edge sets.

**Usage**

```r
congruence_topology(graph1, graph2, warn.nonoverlap = TRUE)
```

**Arguments**

- `graph1` An object of type `popgraph`
- `graph2` An object of type `popgraph`
- `warn.nonoverlap` A flag indicating that a warning should be thrown if the node sets are not equal (default = TRUE)
Value

An object of type popgraph where the node and edge sets are the intersection of the two.

Author(s)

Rodney J. Dyer <rjdyer@vcu.edu>

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decorate_graph Merge data into popgraph node-wise

Description

This function takes a data frame and a popgraph object and attempts to add the node data (from the data frame) to the graph as vertex attributes.

Usage

decorate_graph(graph, data, stratum = "Population")

Arguments

graph An object of type igraph to populate
data An object of type data.frame that has a Node column that is the same as the V(graph)$name values.
stratum The column name of node labels to match up with graph.stratum (default 'Population') to be matched with V(graph)$name attribute

Value

A populated igraph object with as much of the metadata in the data.frame as possible stitched into the igraph object

Author(s)

Rodney J. Dyer <rjdyer@vcu.edu>
geom_edgelabels  

Plotting of a population graph edge labels using ggplot mnemonic

**Description**

This function allows you to layer the edgeset labels from a popgraph object.

**Usage**

```r
geom_edgelabels(mapping = NULL, graph = NULL, directed = FALSE,
offset = c(0, 0), ...)
```

**Arguments**

- `mapping`: The aesthetic mapping as an `aes()` object. This aesthetic must at least have values for x, y, and label.
- `graph`: The popgraph/igraph object to be plot.
- `directed`: A flag indicating that you should only plot the edge with the largest weight if more than one edge connects nodes.
- `offset`: The amount added to each X,Y coordinate to move the label off the line (default=c(0,0)).
- `...`: Options passed to `geom_text` like color, etc.

**Value**

A formatted geom_text object for addition to a ggplot()

**Author(s)**

Rodney J. Dyer <rjdyer@vcu.edu>

**Examples**

```r
a <- matrix( c(0,1,0,1,1,0,0,1,0,0,1,1,1,1,1,0), nrow=4)
rownames(a) <- colnames(a) <- LETTERS[1:4]
graph <- as.popgraph(a)
igraph::V(graph)$x <- runif(4)
igraph::V(graph)$y <- runif(4)
igraph::E(graph)$Label <- LETTERS[1:4]

require(ggplot2)
p <- ggplot() + geom_edgeset(aes(x=x,y=y), graph )
p + geom_edgelabels(aes(x=x,y=y,label=Label), graph)
p + geom_edgelabels(aes(x=x,y=y,label=Label), graph, color="red")
p + geom_edgelabels(aes(x=x,y=y,label=Label), graph, color="red", offset=c(.005,-.004))
```
geom_edgeset

Plotting of a population graph edge set using ggplot neumonic

Description

This function allows you to layer the edgeset of a popgraph object

Usage

geom_edgeset(mapping = NULL, graph = NULL, directed = FALSE, ...)

Arguments

mapping
The aesthetic mapping as an aes() object. This aesthetic must at least have values for x and y

graph
The popgraph/igraph object to be plot

directed
A flag indicating that you should only plot the edge with the largest weight if more than one edge connects nodes.

Value

A formatted geom_segment object for addition to a ggplot()

Author(s)

Rodney J. Dyer <rjdyer@vcu.edu>

Examples

```r
a <- matrix( c(0,1,0,1,1,0,0,1,0,0,0,1,1,1,0,nrow=4)
rownames(a) <- colnames(a) <- LETTERS[1:4]
graph <- as.popgraph(a)
igraph::V(graph)$x <- runif(4)
igraph::V(graph)$y <- runif(4)
require(ggplot2)
ggplot() + geom_edgeset( aes(x=x,y=y), graph )
ggplot() + geom_edgeset( aes(x=x,y=y), graph, color="darkblue" )
require(grid)
ggplot() + geom_edgeset( aes(x=x,y=y), graph, directed=TRUE, arrow=arrow(length=unit(0.5,"cm")) )
```
**geom_nodeset**

*Plotting of a population graph edge set using ggplot mnemonic*

**Description**

This function allows you to layer the edgeset of a popgraph object.

**Usage**

```r
gemm_nodeset(mapping = NULL, graph = NULL, ...)
```

**Arguments**

- `mapping` The aesthetic mapping as an `aes()` object. This aesthetic must at least have values for x and y but you can also specify color, fill, alpha, label, and size. Color, alpha, and fill may be a single value for all nodes or vertex attributes for each node.
- `graph` The popgraph/igraph object to be plot
- `...` Largely ignored.

**Value**

A formatted geom_segment object for addition to a ggplot()

**Author(s)**

Rodney J. Dyer <rjdyer@vcu.edu>

**Examples**

```r
library(igraph)
a <- matrix( c(0,1,0,1,0,0,1,0,0,0,1,1,1,1,0), nrow=4)
rownames(a) <- colnames(a) <- LETTERS[1:4]
graph <- as.popgraph(a)
igraph::V(graph)$x <- runif(4)
igraph::V(graph)$y <- runif(4)
require(ggplot2)
ggplot() + geom_nodeset( aes(x=x,y=y), graph )
igraph::V(graph)$group <- c("A","A","B","B")
ggplot() + geom_nodeset( aes(x=x,y=y,color=group), graph, size=4 )
```

**lopho**

*Lophocereus population graph*

**Description**

This is the population graph for the Lophocereus data that is discussed in Dyer & Nason (2004).
**overlay_popgraph**

*Convenience function to plot edges from popgraph*

**Description**

This is a quick convenience function for plotting nodes and edges on a normal R plot by iterating through edges and connecting nodes.

**Usage**

`overlay_popgraph(graph)`

**Arguments**

- **graph**: An object of type `popgraph`

**Author(s)**

Rodney J. Dyer <rjdyer@vcu.edu>

---

**permute_popgraph**

*Bootstraps individuals to see stability of graph topology.*

**Description**

This function uses a permutation test to look at edge stability. What we do is resample individuals and re-estimate the topology several times. This provides an estimate of edge stability.

**Usage**

`permute_popgraph(data, groups, nboot = 50, ...)`

**Arguments**

- **data**: The raw multivariate data as submitted to `popgraph`
- **groups**: The grouping of the data into nodes as submitted to `popgraph`
- **nboot**: The number of times to bootstrap the individuals per group (default=50)
- **...**: Other arguments to be passed to `popgraph`

**Value**

A weighted graph where edge weights represent the proportion of times the edge was found in the permuted data sets.
**popgraph**

*Default constructor for a PopulationGraph object*

**Description**

This function is the default constructor for PopulationGraph objects. Mechanistically, a PopulationGraph is a class that has some meta data and an igraph object within it.

**Usage**

```
popgraph(x, groups, alpha = 0.05, tol = 1e-04)
```

**Arguments**

- `x` An object of type matrix that holds the data to be analyzed.
- `groups` A factor indicating population membership of each row in `x`
- `alpha` The significance level to test edge retention (default = 0.05).
- `tol` A measure of tolerance for the retention of multivariate data columns (default sd dev = 1e-4)

**Value**

An object of type popgraph.

**Author(s)**

Rodney J. Dyer <rjdyer@vcu.edu>

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**read.popgraph**

*Reads in a population graph text file*

**Description**

This function imports a popgraph from the older text format.

**Usage**

```
read.popgraph(file, sep = "\t")
```

**Arguments**

- `file` The path to the file that is to be saved.
- `sep` The column separator in the file. By default it is a tab but sometimes a space or other object may be used.
test_congruence

Value

A fully created popgraph file (e.g., an igraph object with an extra class property)

Author(s)

Rodney J. Dyer <rjdyer@vcu.edu>

describe_tests
test_congruence

Returns distance congruence between the two graphs

Description

This function makes the shortest path matrices for both graphs and determines the correlation between pairwise distance.

Usage

test_congruence(graph1, graph2, method = c("distance", "combinatorial"))[1])

Arguments

g1hraph1
An object of type igraph or popgraph

g2hraph2
An object of type igraph or popgraph

method
An option on how congruence is to be estimated possible values are 'distance' (a measure of similarity in separation of nodes independent of connectivity, the default) 'structural' a measure of similarity in actual edges, and 'combinatorial' a combinatorial measure of similarity.

Value

A non-parametric rank sum test

Author(s)

Rodney J. Dyer <rjdyer@vcu.edu>
theme_empty

A blank theme for plotting networks

Description

This function defines a blank theme for plotting graph objects in ggplot.

Usage

theme_empty(base_size = 12, base_family = "Helvetica")

Arguments

base_size       The base size of the font
base_family     The font family to use

Value

A ggplot theme blank and transparent for plotting in another program.

Author(s)

Rodney J. Dyer <rjdyer@vcu.edu>

Examples

data(lopho)
require(ggplot2)
require(igraph)
layout <- layout.fruchterman.reingold(lopho)
V(lopho)$x <- layout[,1]
V(lopho)$y <- layout[,2]
p <- ggplot() + geom_edgeset(aes(x,y), lopho)
p <- p + geom_nodeset(aes(x,y), lopho)
p
p + theme_empty()
p <- ggplot() + geom_edgeset(aes(x,y,color=weight), lopho)
p
to_data.frame

Converts popgraph to data.frame based upon node attributes

Description

This is a quick conversion of vertex attributes to a data.frame, essentially the reverse operation as decorate_graph function.

Usage

to_data.frame(x, ...)

Arguments

x The popgraph to grab stuff from.
... Ignored (generally).

Value

An object of type data.frame with all the node attributes.

Author(s)

Rodney J. Dyer <rjdyer@vcu.edu>

to_html

Converts population graph to html file for interactive viewing

Description

This function takes a population graph that has been ‘decorated’ with sufficient spatial data to make a html file that uses the D3 visualization javascript materials to view it interactively.

Usage

to_html(graph, file)

Arguments

graph A popgraph object.
file The path to the html file to be saved. If not given then the html text is returned by the function.

Value

The text of the html file to be saved or viewed in the appropriate browser.
to_json

*Description*

This is a nice function that takes a graph structure and converts it to a json format for use on the web.

*Usage*

```
to_json(graph, file)
```

*Arguments*

- **graph**: An object of type igraph
- **file**: A file to write the output to (default missing)

*Value*

A textual json representation of the graph

*Author(s)*

Rodney J. Dyer <rjdyer@vcu.edu>

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to_kml

*Description*

This function takes a population graph that has been ‘decorated’ with sufficient spatial data to make a KML file from it for viewing in GoogleEarth.

*Usage*

```
to_kml(graph, file)
```

*Arguments*

- **graph**: A popgraph object.
- **file**: The location to save the kml to (if not passed, it returns it)
to_matrix

Value

The text of the KML file to be saved or viewed in the appropriate editor.

Author(s)

Rodney J. Dyer <rjdyer@vcu.edu>

to_matrix

Matrix conversion for Population Graph

Description

This function translates a Population to a matrix representing either the adjacency structure, the shortest path, or edge weights.

Usage

to_matrix(x, mode = c("adjacency", "shortest path", "edge weight") [1], ...)

Arguments

x An object of type popgraph
mode The kind of matrix to make. At present, the following types are available:
• adjacency A binary matrix representing the pairs of connected nodes (default)
• shortest path The shortest path between all nodes.
• edge weight Similar to the adjacency matrix but using edge weights instead of binary values
... Optional arguments passed on to the distance functions.

Value

A matrix (KxK) in size (where K is the number of nodes)

Author(s)

Rodney J. Dyer <rjdyer@vcu.edu>
to_pgraph

Converts graph to a pgraph file format

Description

This is a simple function that takes the graph and converts it into a *.pgraph file for visualization in other software.

Usage

```r
to_pgraph(graph, file)
```

Arguments

- `graph` An object of type popgraph
- `file` The name and location of where the *.pgraph file is to be saved. If omitted, this function will return a single text file.

Value

Nothing if passed a file or the raw text of the *.pgraph file if you do not provide a file object.

Author(s)

Rodney J. Dyer <rjdyer@vcu.edu>

to_SpatialLines

Converts edge set to SpatialLines object

Description

This is a convenience function that takes the edge set and returns a SpatialLines object.

Usage

```r
to_SpatialLines(graph, latitude = "Latitude", longitude = "Longitude", ...)
```

Arguments

- `graph` An object of type popgraph. This graph must already be decroated with latitude and longitude attributes.
- `latitude` The name of the Latitude attribute (default="Latitude")
- `longitude` The name of the Longitude attribute (default="Longitude")
- `...` Ignored
to\textunderscore SpatialPoints

Value

A SpatialLines object

Author(s)

Rodney J. Dyer <rjdyer@vcu.edu>

\textbf{Description}

Returns spatial points object

Usage

to\_SpatialPoints(x, \texttt{stratum} = "Name", \texttt{longitude} = "Longitude", \texttt{latitude} = "Latitude", ...)

Arguments

\begin{itemize}
\item \texttt{x} \hspace{1cm} The object containing coordinates.
\item \texttt{stratum} \hspace{1cm} The name of the variable in \texttt{x} that represents the stratum to be used as points.
\item \texttt{longitude} \hspace{1cm} The key for the attribute representing \texttt{Longitude} (default="Longitude")
\item \texttt{latitude} \hspace{1cm} The key for the attribute representing \texttt{Latitude} (default="Latitude")
\item ... \hspace{1cm} Optional arguments passed to overridden objects
\end{itemize}

Value

An object of type SpatialPoints

Author(s)

Rodney J. Dyer <rjdyer@vcu.edu>

upiga

\textbf{Description}

This is the population graph for the Upiga data that is currently unpublished.
write_popgraph  Convience function for file exports

Description
This function is a chokepoint for exporting popgraph objects to other formats.

Usage
write_popgraph(graph, file, format = "pgraph", ...)

Arguments

graph An object of type popgraph.
file The path to save the graph into.
format The type of output file to use. Options are:

- json Save as JSON format
- kml Save to KML format to view in GoogleEarth
- graphml Save as Graph Markup Language
- html Save to an interactive html format viewable in your browser
- pajek Save as input to Pajek
- pgraph Save as input for GeneticStudio (default)
- adjacency Saves as an adjacency matrix in csv format
- paths Saves as shortest paths matrix in csv format
- weights Saves as weighted adjacency matrix in csv format

... Ignored

Value
Nothing

Author(s)
Rodney J. Dyer <rjdyer@vcu.edu>
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