Package 'GGoutlieR'

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Type Package

Title Identify Individuals with Unusual Geo-Genetic Patterns

Version 1.0.2

Description

Identify and visualize individuals with unusual association patterns of genetics and geography using the approach of Chang and Schmid (2023) <doi:10.1101/2023.04.06.535838>. It detects potential outliers that violate the isolation-by-distance assumption using the K-nearest neighbor approach. You can obtain a table of outliers with statistics and visualize unusual geo-genetic patterns on a geographical map. This is useful for landscape genomics studies to discover individuals with unusual geography and genetics associations from a large biological sample.

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Depends R (>= 3.5.0)

Imports stats4, FastKNN, foreach, doParallel, parallel, scales,
RColorBrewer, ggforce, rlang, stats, tidyr, utils,
rnaturalearth, sf, ggplot2, cowplot

Suggests rnaturalearthdata

Encoding UTF-8

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R topics documented:

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anc_coeff_to_GeneticSimilarityMatrix
calculate genetic similarity from ancestry coefficients.

Description

calculate genetic similarity from ancestry coefficients.

Usage

```
anc_coeff_to_GeneticSimilarityMatrix(anc_coef)
```

Arguments

anc_coef   a matrix of ancestry coefficients with samples by rows. Each column corresponds to an ancestral population.

Details

Since ancestry coefficients can be interpreted as a propotion of genome derived from a specific ancestral population, this function calculate genetic similarity as the probability of a random genome segment of two individuals derived from the same ancestral population.

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get_GGNet_adjacency_matrix
obtain an adjacency matrix to make a network graph

Description

'get_GGNet_adjacency_matrix' calculates p-values based on the KNNs and heuristic Gamma distribution obtained in the outlier identification processes. The matrices of p-values are then multiplied with the given genetic similarity matrix to form adjacency matrices.

Usage

```
get_GGNet_adjacency_matrix(
  ggoutlier_res,
  geo_coord,
  gen_coord,
  mutual = FALSE,
  adjust_p_value = TRUE
)
```

Arguments

ggoutlier_res	an output from 'ggoutlier'
geo_coord	a two-column matrix or data.frame. the first column is longitude and the second one is latitude.
gen_coord	a matrix of "coordinates in a genetic space". Users can provide ancestry coefficients or eigenvectors for calculation. If, for example, ancestry coefficients are given, each column corresponds to an ancestral population. Samples are ordered in rows as in 'geo_coord'. Users have to provide 'pgdM' if 'gen_coord' is not given.
mutual	logic. If a multi-stage test is used in the outlier identification, some samples could not be a mutual neighbor with its K nearest neighbors. In this case, setting 'mutual=TRUE' can force those samples to become mutual neighbors in the output adjacency matrix.
adjust_p_value	logic. If 'adjust_p_value=TRUE', p values are adjusted for each nearest neighbor of a given sample.

Value

a list consisting of four matrices that can be used in building network graphs. The default is 'TRUE' 'GeoSP_pvalue' is a matrix describing the strength of edges as p values from the empirical Gamma distribution identified by 'detect_outlier_in_GeoSpace' 'GenSP_pvalue' is a matrix describing the strength of edges as p values from the empirical Gamma distribution identified by 'detect_outlier_in_GeneticSpace'

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ggoutlier *Identify outliers with unusual geo-genetic patterns*

Description

This function is used to identify outliers with unusual geo-genetic patterns using the KNN approach. For the details of the outlier detection approach, please see Chang and Schmid 2023 (doi:https://doi.org/10.1101/2023.04.06.535838)

Usage

```
ggoutlier(
  geo_coord,
  gen_coord,
  pgdM = NULL,
  method = c("geneticKNN", "geoKNN", "composite"),
  K = NULL,
  k_geneticKNN = NULL,
  k_geoKNN = NULL,
  klim = c(3, 50),
  make_fig = FALSE,
  plot_dir = ".",
  w_geo = 1,
  w_genetic = 2,
  p_thres = 0.05,
  s = 100,
  min_nn_dist = 100,
  cpu = 1,
  geneticKNN_output = NULL,
  geoKNN_output = NULL,
  verbose = TRUE,
  multi_stages = TRUE,
  maxIter = NULL,
  keep_all_stg_res = FALSE,
  warning_minR2 = 0.9
)
```

Arguments

geo_coord	matrix or data.frame with two columns. The first column is longitude and the second one is latitude.
gen_coord	matrix. A matrix of "coordinates in a genetic space". Users can provide ancestry coefficients or eigenvectors for calculation. If, for example, ancestry coefficients are given, each column corresponds to an ancestral population. Samples are ordered in rows as in 'geo_coord'.
pgdM	matrix. A pairwise genetic distance matrix. Users can provide a customized genetic distance matrix with this argument. Samples are ordered in rows and columns as in the rows of 'geo_coord'. The default of 'pgdM' is 'NULL'. If 'pgdM' is not provided, a genetic distance matrix will be calculated from 'gen_coord'.
method	string. The method to run 'GGoutlieR'. It can be '"composite"', '"geneticKNN"', or '"geoKNN"'.
K	integer. Number of the nearest neighbors. If 'K' is not 'NULL', the value will pass to 'k_geneticKNN' and 'k_geoKNN'.
k_geneticKNN	integer. Number of the nearest neighbors in a genetic space. The default is 'NULL'. The 'ggoutlier' will search the optimal K if 'k_geneticKNN = NULL'.

k_geoKNN	integer. Number of the nearest neighbors in a geographical space. the default is 'NULL'. The 'ggoutlier' will search the optimal K if 'k_geoKNN = NULL'.
klim	vector. A range of K to search for the optimal number of nearest neighbors. The default is 'klim = c(3, 50)'
make_fig	logic. If 'make_fig = TRUE', plots for diagnosing GGoutlieR analysis will be generated and saved to 'plot_dir'. The default is 'FALSE'
plot_dir	string. The path to save plots
w_geo	numeric. A value controlling the power of distance weight in geographical KNN prediction.
w_genetic	numeric. A value controlling the power of distance weight in genetic KNN prediction.
p_thres	numeric. A significance level
s	integer. A scalar of geographical distance. The default 's=100' scales the distance to a unit of 0.1 kilometer.
min_nn_dist	numeric. A minimal geographical distance for searching KNNs. Neighbors of a focal sample within this distance will be excluded from the KNN searching procedure.
cpu	integer. Number of CPUs to use for searching the optimal K.
geneticKNN_output	
	output of 'ggoutlier_geneticKNN'. Users can use this argument if running 'ggoutlier_geneticKNN' in advance.
geoKNN_output	output of 'ggoutlier_geoKNN'. Users can use this argument if running 'ggoutlier_geoKNN' in advance.
verbose	logic. If 'verbose = FALSE', 'ggoutlier' will suppress printout messages.
multi_stages	logic. A multi-stage test will be performed if is 'TRUE' (the default is 'TRUE').
maxIter	numeric. Maximal iteration number of multi-stage KNN test.
keep_all_stg_res	
	logic. Results from all iterations of the multi-stage test will be retained if it is 'TRUE'. (the default is 'FALSE')
warning_minR2	numeric. The prediction accuracy of KNN is evaluated as R^2 to assess the violation of isolation-by-distance expectation. If any R^2 is larger than 'warning_minR2', a warning message will be reported at the end of your analysis.

Value

an object of 'list'. If you set 'method = "composite"', 'ggoutlier' will return a nested 'list' with two subsidiary 'list' which are '"geneticKNN_result"' and '"geoKNN_result"'. Each subsidiary list includes five items: 'statistics' is a 'data.frame' consisting of the D_geography ("Dgeo") or D_genetics ("Dg") values, p values and a column of logic values showing if a sample is an outlier or not. 'threshold' is a 'data.frame' recording the significance threshold. 'gamma_parameter' is a vector recording the parameter of the heuristic Gamma distribution. 'knn_index' and 'knn_name' are a 'data.frame' recording the K nearest neighbors of each sample. The subsidiary list 'geneticKNN_result' has an additional item called '"scalar"', which records the value of geographical distance scalar used in the computation. If you set 'method = "geneticKNN"', or 'method = "geoKNN"', 'ggoutlier' will return a 'list' respectively corresponding to '"geneticKNN_result"' or '"geoKNN_result"'.

Examples

```
library(GGoutlieR)
data("ipk_anc_coef") # get ancestry coefficients
data("ipk_geo_coord") # get geographical coordinates


#DON'T RUN: this analysis will take a few minutes
## Not run:
ggoutlier_example <-
                 ggoutlier(geo_coord = ipk_geo_coord,
                           gen_coord = ipk_anc_coef,
                           klim = c(3,6),
                           p_thres = 0.01,
                           cpu = 2,
                           method = "composite",
                           verbose = FALSE,
                           min_nn_dist = 1000,
                           multi_stages = FALSE)

head(summary_ggoutlier(ggoutlier_example)) # get a summary table

## End(Not run)
```

---

ggoutlier_compositeKNN

GGoutlieR with the composite approach

Description

perform outlier identification with genetic space KNN and geographical space KNN. For the details of the outlier detection approach, please see the supplementary material of Chang and Schmid 2023 (doi:https://doi.org/10.1101/2023.04.06.535838)

Usage

```
ggoutlier_compositeKNN(
  geo_coord,
  gen_coord,
  pgdM = NULL,
  k_geneticKNN = NULL,
  k_geoKNN = NULL,
  klim = c(3, 50),
  make_fig = FALSE,
  plot_dir = ".",
  w_geo = 1,
  w_genetic = 2,
  p_thres = 0.05,
  n = 10^6,
```

```
    s = 100,
    min_nn_dist = 1000,
    multi_stages = TRUE,
    maxIter = NULL,
    keep_all_stg_res = FALSE,
    warning_minR2 = 0.9,
    cpu = 1,
    geneticKNN_output = NULL,
    geoKNN_output = NULL,
    verbose = TRUE
)
```

Arguments

geo_coord	matrix or data.frame with two columns. The first column is longitude and the second one is latitude.
gen_coord	matrix. A matrix of "coordinates in a genetic space". Users can provide ancestry coefficients or eigenvectors for calculation. If, for example, ancestry coefficients are given, each column corresponds to an ancestral population. Samples are ordered in rows as in 'geo_coord'.
pgdM	matrix. A pairwise genetic distance matrix. Users can provide a customized genetic distance matrix with this argument. Samples are ordered in rows and columns as in the rows of 'geo_coord'. The default of 'pgdM' is 'NULL'. If 'pgdM' is not provided, a genetic distance matrix will be calculated from 'gen_coord'. NOTE: the genetic distance matrix is used in the search of KNN and as weights of KNN regression.
k_geneticKNN	integer. Number of the nearest neighbors in a genetic space. The default is 'NULL'. The 'ggoutlier' will search the optimal K if 'k_geneticKNN = NULL'.
k_geoKNN	integer. Number of the nearest neighbors in a geographical space. the default is 'NULL'. The 'ggoutlier' will search the optimal K if 'k_geoKNN = NULL'.
klim	vector. A range of K to search for the optimal number of nearest neighbors. The default is 'klim = c(3, 50)'
make_fig	logic. If 'make_fig = TRUE', plots for diagnosing GGoutlieR analysis will be generated and saved to 'plot_dir'. The default is 'FALSE'
plot_dir	string. The path to save plots
w_geo	numeric. A value controlling the power of distance weight in geographical KNN prediction.
w_genetic	numeric. A value controlling the power of distance weight in genetic KNN prediction.
p_thres	numeric. A significance level
n	numeric. A number of random samples to draw from the null distribution for making a graph.
s	integer. A scalar of geographical distance. The default 's=100' scales the distance to a unit of 0.1 kilometer.

min_nn_dist	numeric. A minimal geographical distance for searching KNNs. Neighbors of a focal sample within this distance will be excluded from the KNN searching procedure.
multi_stages	logic. A multi-stage test will be performed if is 'TRUE' (the default is 'TRUE').
maxIter	numeric. Maximal iteration number of multi-stage KNN test.
keep_all_stg_res	
	logic. Results from all iterations of the multi-stage test will be retained if it is'TRUE'. (the default is 'FALSE')
warning_minR2	numeric. The prediction accuracy of KNN is evaluated as R^2 to assess the violation of isolation-by-distance expectation. If any R^2 is larger than 'warning_minR2', a warning message will be reported at the end of your analysis.
cpu	integer. Number of CPUs to use for searching the optimal K.
geneticKNN_output	
	output of 'ggoutlier_geneticKNN'. Users can use this argument if running 'ggoutlier_geneticKNN' in advance.
geoKNN_output	output of 'ggoutlier_geoKNN'. Users can use this argument if running 'ggoutlier_geoKNN' in advance.
verbose	logic. If 'verbose = FALSE', 'ggoutlier' will suppress printout messages.

Value

an object of nested 'list' with two subsidiary 'list' which are '"geneticKNN_result"' and '"geoKNN_result"'. Each subsidiary list includes five items: 'statistics' is a 'data.frame' consisting of the D_geography ("Dgeo") or D_genetics ("Dg") values, p values and a column of logic values showing if a sample is an outlier or not. 'threshold' is a 'data.frame' recording the significance threshold. 'gamma_parameter' is a vector recording the parameter of the heuristic Gamma distribution. 'knn_index' and 'knn_name' are a 'data.frame' recording the K nearest neighbors of each sample. The subsidiary list 'geneticKNN_result' has an additional item called '"scalar"', which records the value of geographical distance scalar used in the computation.

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ggoutlier_example	*Example of 'ggoutlier' output*

Description

Example of 'ggoutlier' output

Format

list

---

ggoutlier_geneticKNN   *GGoutlieR with the genetic KNN approach*

Description

identify samples geographically remote from K genetically nearest neighbors (genetic KNN). For the details of the outlier detection approach, please see the supplementary material of Chang and Schmid 2023 (doi:https://doi.org/10.1101/2023.04.06.535838)

Usage

```
ggoutlier_geneticKNN(
  geo_coord,
  gen_coord = NULL,
  pgdM = NULL,
  k = NULL,
  klim = c(3, 50),
  make_fig = FALSE,
  plot_dir = ".",
  w_power = 2,
  p_thres = 0.05,
  n = 10^6,
  s = 100,
  multi_stages = TRUE,
  maxIter = NULL,
  keep_all_stg_res = FALSE,
  warning_minR2 = 0.9,
  cpu = 1,
  verbose = TRUE
)
```

Arguments

geo_coord   matrix or data.frame with two columns. The first column is longitude and the second one is latitude.

gen_coord   matrix. A matrix of "coordinates in a genetic space". Users can provide ancestry coefficients or eigenvectors for calculation. If, for example, ancestry coefficients are given, each column corresponds to an ancestral population. Samples are ordered in rows as in 'geo_coord'.

pgdM   matrix. A pairwise genetic distance matrix. Users can provide a customized genetic distance matrix with this argument. Samples are ordered in rows and columns as in the rows of 'geo_coord'. The default of 'pgdM' is 'NULL'. If 'pgdM' is not provided, a genetic distance matrix will be calculated from 'gen_coord'.

k   integer. Number of the nearest neighbors.

klim	vector. A range of K to search for the optimal number of nearest neighbors. The default is 'klim = c(3, 50)'
make_fig	logic. If 'make_fig = TRUE', plots for diagnosing GGoutlieR analysis will be generated and saved to 'plot_dir'. The default is 'FALSE'
plot_dir	string. The path to save plots
w_power	numanceric. A value controlling the power of distance weight in genetic KNN prediction.
p_thres	numeric. A significe level
n	numeric. A number of random samples to draw from the null distribution for making a graph.
s	integer. A scalar of geographical distance. The default 's=100' scales the distance to a unit of 0.1 kilometer.
multi_stages	logic. A multi-stage test will be performed if is 'TRUE' (the default is 'TRUE').
maxIter	numeric. Maximal iteration number of multi-stage KNN test.
keep_all_stg_res	
	logic. Results from all iterations of the multi-stage test will be retained if it is'TRUE'. (the default is 'FALSE')
warning_minR2	numeric. The prediction accuracy of KNN is evaluated as R^2 to assess the violation of isolation-by-distance expectation. If any R^2 is larger than 'warning_minR2', a warning message will be reported at the end of your analysis.
cpu	integer. Number of CPUs to use for searching the optimal K.
verbose	logic. If 'verbose = FALSE', 'ggoutlier' will suppress printout messages.

Value

an object of 'list' including six items. 'statistics' is a 'data.frame' consisting of the 'D geography' "Dgeo" values, p values and a column of logic values showing if a sample is an outlier or not. 'threshold' is a 'data.frame' recording the significance threshold. 'gamma_parameter' is a vector recording the parameter of the heuristic Gamma distribution. 'knn_index' and 'knn_name' are a 'data.frame' recording the K nearest neighbors of each sample. 'scalar' is the value of geographical distance scalar used in the computation.

---

ggoutlier_geoKNN	*GGoutlieR with the geographical KNN approach*

Description

identify samples genetically different from K nearest geographical neighbors (geographical KNN). For the details of the outlier detection approach, please see the supplementary material of Chang and Schmid 2023 (doi:https://doi.org/10.1101/2023.04.06.535838)

Usage

```
ggoutlier_geoKNN(
  geo_coord,
  gen_coord,
  min_nn_dist = 100,
  k = NULL,
  klim = c(3, 50),
  s = 100,
  make_fig = FALSE,
  plot_dir = ".",
  w_power = 1,
  p_thres = 0.05,
  n = 10^6,
  multi_stages = TRUE,
  maxIter = NULL,
  keep_all_stg_res = FALSE,
  warning_minR2 = 0.9,
  cpu = 1,
  verbose = TRUE
)
```

Arguments

geo_coord   matrix or data.frame with two columns. The first column is longitude and the
                 second one is latitude.

gen_coord   matrix. A matrix of "coordinates in a genetic space". Users can provide ancestry
                 coefficients or eigenvectors for calculation. If, for example, ancestry coefficients
                 are given, each column corresponds to an ancestral population. Samples are
                 ordered in rows as in 'geo_coord'.

min_nn_dist   numeric. A minimal geographical distance for searching KNNs. Neighbors of
                 a focal sample within this distance will be excluded from the KNN searching
                 procedure.

k   integer. Number of the nearest neighbors.

klim   vector. A range of K to search for the optimal number of nearest neighbors. The
                 default is 'klim = c(3, 50)'

s   integer. A scalar of geographical distance. The default 's=100' scales the dis-
                 tance to a unit of 0.1 kilometer.

make_fig   logic. If 'make_fig = TRUE', plots for diagnosing GGoutlieR analysis will be
                 generated and saved to 'plot_dir'. The default is 'FALSE'

plot_dir   string. The path to save plots

w_power   numeric. A value controlling the power of distance weight in geographical KNN
                 prediction.

p_thres   numeric. A significance level

n   numeric. A number of random samples to draw from the null distribution for
                 making a graph.

multi_stages	logic. A multi-stage test will be performed if is 'TRUE' (the default is 'TRUE').
maxIter	numeric. Maximal iteration number of multi-stage KNN test.
keep_all_stg_res	
	logic. Results from all iterations of the multi-stage test will be retained if it is'TRUE'. (the default is 'FALSE')
warning_minR2	numeric. The prediction accuracy of KNN is evaluated as R^2 to assess the violation of isolation-by-distance expectation. If any R^2 is larger than 'warning_minR2', a warning message will be reported at the end of your analysis.
cpu	integer. Number of CPUs to use for searching the optimal K.
verbose	logic. If 'verbose = FALSE', 'ggoutlier' will suppress printout messages.

Value

an object of 'list' including five items. 'statistics' is a 'data.frame' consisting of the 'D genetics' ("Dg") values, p values and a column of logic values showing if a sample is an outlier or not. 'threshold' is a 'data.frame' recording the significance threshold. 'gamma_parameter' is a vector recording the parameter of the heuristic Gamma distribution. 'knn_index' and 'knn_name' are a 'data.frame' recording the K nearest neighbors of each sample.

---

ipk_anc_coef   *Ancestry coefficients of IPK barley landraces*

Description

Ancestry coefficients of IPK barley landraces

Format

matrix

---

ipk_geo_coord   *Geographical origins of IPK barley landraces*

Description

Geographical origins of IPK barley landraces

Format

data.frame

---

plot_ggoutlier   *Visualize GGoutlieR results on a geographical map*

Description

Visualize geo-genetic patterns of outliers with their K nearest neighbors

Usage

```
plot_ggoutlier(
  ggoutlier_res,
  geo_coord,
  anc_coef = NULL,
  gen_coord = NULL,
  pie_color = NULL,
  map_color = "black",
  p_thres = NULL,
  color_res = 10,
  dot_cex = NULL,
  map_type = c("geographic_knn", "genetic_knn", "both"),
  select_xlim = c(-180, 180),
  select_ylim = c(-90, 90),
  plot_xlim = NULL,
  plot_ylim = NULL,
  only_edges_in_xylim = TRUE,
  pie_r_scale = 1,
  map_resolution = "medium",
  show_knn_pie = FALSE,
  which_sample = NULL,
  add_benchmark_graph = TRUE,
  adjust_p_value_projection = FALSE,
  linewidth_range = c(0.5, 3),
  plot_labels = "auto"
)
```

Arguments

ggoutlier_res	output of 'ggoutlier'
geo_coord	matrix or data.frame with two columns. The first column is longitude and the second one is latitude.
anc_coef	matrix. A matrix of ancestry coefficients with samples ordered by rows. Ancestry coefficients are used to make pie charts on a geographical map. This argument is optional.
gen_coord	matrix. A matrix of "coordinates in a genetic space". It should be identical to the 'gen_coord' used for running 'ggoutlier'

pie_color	string. Colors of pie charts. colors are automatically assigned if 'pie_color = NULL' (which is the default). This argument is optional.
map_color	string. Colors of map contours. The default is 'map_color = "black"'
p_thres	numeric. A value of significant level. Only outliers (p values less than 'p_thres') are mapped on a geographical map if 'p_thres' is provided (the default is 'NULL'). This argument is optional.
color_res	integer. The resolution of color scale.
dot_cex	numeric. The size of dots denoting the positions of samples on a geographical map.
map_type	string. The type of plot to draw. It can be '"geographic_knn"', '"genetic_knn"' and '"both"'.
select_xlim	vector. Values controlling longitude boundaries of a window to select outliers to present on a geographical map. The default is 'select_xlim = c(-180,180)'.
select_ylim	vector. Values controlling latitude boundaries of a window to select outliers to present on a geographical map. The default is 'select_ylim = c(-90,90)'.
plot_xlim	vector. Values controlling longitude boundaries of a map.
plot_ylim	vector. Values controlling latitude boundaries of a map.
only_edges_in_xylim	
	logic. only the edges with starting points within the given 'select_xlim' and 'select_ylim' will display on a geographical map. If 'FALSE', the edges out of the given boundaries will be removed from your plot. The default is 'TRUE'.
pie_r_scale	numeric. A scale controlling the radius of pie charts
map_resolution	a character string. The resolution of the geographical map. See details of the 'scale' argument in the manual of 'rnaturalearth::ne_countries()'. The default is 'map_resolution = "medium"'
show_knn_pie	logic. If 'TRUE', the ancestry coefficients of K nearest neighbors of significant samples will display on the map. The default is 'FALSE'.
which_sample	a string vector of sample ID(s). If users want to only show specific sample(s)
add_benchmark_graph	
	logic. If 'TRUE', a benchmark graph with only pie charts of ancestry coefficients for comparison with the outlier graph.
adjust_p_value_projection	
	logic. If 'TRUE', the function will perform KNN prediction by forcing K=1 and compute new p-values for visualization.
linewidth_range	
	numeric. A vector of two values. It is used to control the minimal and maximal width of KNN network on the geographical map.
plot_labels	character. A string of labels for plots. The default is 'plot_labels = "auto"'. This parameter is for 'cowplot::plot_grid'.

Details

Red links on the map denote individual pairs that are genetically similar but geographically remote. The color depth and thickness of red links are proportional to -log10(p) based on the empirical Gamma distribution obtained from 'detect_outlier_in_GeneticSpace'. Blue links on the map denote individual pairs that are genetically different but geographically close. The color depth and thickness of blue links are proportional to -log10(p) based on the empirical Gamma distribution obtained from 'detect_outlier_in_GeoSpace'

Value

ggplot object. The plot is geographical map(s) with colored lines showing sample pairs with unusual geo-genetic associations.

Examples

```
library(GGoutlieR)
data("ipk_anc_coef") # get ancestry coefficients
data("ipk_geo_coord") # get geographical coordinates
data(ggoutlier_example) # get an example output of ggoutlier
## Not run:
plot_ggoutlier(ggoutlier_res = ggoutlier_example,
               gen_coord = ipk_anc_coef,
               geo_coord = ipk_geo_coord,
               p_thres = 0.025,
               map_type = "both",
               select_xlim = c(-20,140),
               select_ylim = c(10,62),
               plot_xlim = c(-20,140),
               plot_ylim = c(10,62),
               pie_r_scale = 1.8,
               map_resolution = "medium")

## End(Not run)
```

---

summary_ggoutlier   *Summarize GGoutlieR results*

Description

Get a summary table from the 'ggoutlier' output

Usage

```
summary_ggoutlier(ggoutlier_res)
```

Arguments

ggoutlier_res   output from the function 'ggoutlier'

Value

a table contains IDs of outliers and p-values.

Examples

```
library(GGoutlieR)
data(ggoutlier_example) # get an example output of ggoutlier
head(summary_ggoutlier(ggoutlier_example))
```

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