Package ‘mapi’

January 19, 2022

Title  Mapping Averaged Pairwise Information

Version  1.0.5

Description  Mapping Averaged Pairwise Information (MAPI) is an exploratory method providing graphical representations summarizing the spatial variation of pairwise metrics (eg. distance, similarity coefficient, ...) computed between georeferenced samples.

License  GPL (>= 3)

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LazyData  true

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Author  Sylvain Piry [aut, cre] (<https://orcid.org/0000-0002-7717-7555>),
        Thomas Campolunghi [aut],
        Florent Cestier [aut],
        Karine Berthier [aut] (<https://orcid.org/0000-0002-2260-7968>)

Maintainer  Sylvain Piry <sylvain.piry@inrae.fr>

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MAPI, general presentation

Description

MAPI is an exploratory method providing graphical representations of the spatial variation of pairwise metrics (e.g. distance, similarity coefficient, ...) computed between georeferenced samples.

Principle: As schematically illustrated Figure 1, MAPI relies on spatial joins between a hexagonal grid and a network of georeferenced samples connected by ellipses, i.e. polygons with 32 segments approaching an elliptical shape.

The shape of the ellipses can be controlled through the eccentricity value and the sample locations can be "blurred" by applying an error circle of a given radius on the geographic coordinates. Each elliptical polygon is associated to 1) the value of the pairwise metric computed between the samples it connects and 2) a weight corresponding to the inverse of its area (i.e. larger ellipses have lower weights).

Each cell of the grid receives the weighted mean of the pairwise metric values associated to the ellipses intersecting the cell.
Input data: The analysis requires two tables (data.frame or data.table):

1. Information on samples: table with three mandatory columns and column names: 'ind' (sample name), 'x' and 'y' (projected coordinates). An optional column 'errRad' (radius of error circle on sample coordinates) can be provided.

MAPI requires cartesian coordinates (ie. projected, such as UTM or Lambert) NOT (yet?) angular coordinates (eg. latitude/longitude). The package sf provides the st_transform function for coordinates transformation and projection. GIS software such as QGis can also help with datum transformation.

Example of 'samples' data:

<table>
<thead>
<tr>
<th>ind</th>
<th>x</th>
<th>y</th>
<th>errRad</th>
</tr>
</thead>
<tbody>
<tr>
<td>2_42</td>
<td>12000</td>
<td>5000</td>
<td>10</td>
</tr>
<tr>
<td>2_47</td>
<td>17000</td>
<td>5000</td>
<td>10</td>
</tr>
<tr>
<td>1_82</td>
<td>2000</td>
<td>9000</td>
<td>10</td>
</tr>
<tr>
<td>2_100</td>
<td>20000</td>
<td>10000</td>
<td>10</td>
</tr>
<tr>
<td>2_87</td>
<td>17000</td>
<td>9000</td>
<td>10</td>
</tr>
<tr>
<td>1_11</td>
<td>1000</td>
<td>2000</td>
<td>10</td>
</tr>
</tbody>
</table>

1. Values of the pairwise metric computed between samples provided, either, as a complete matrix with the same number of columns and rows (column and row names must match the sample names provided in the 'samples' data) or as a table with three mandatory columns and column names: 'ind1', 'ind2' (sample names) and 'value' (pairwise metric values).

Example of 'metric' data:

<table>
<thead>
<tr>
<th>ind1</th>
<th>ind2</th>
<th>value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1_1</td>
<td>1_2</td>
<td>0.05556</td>
</tr>
<tr>
<td>1_1</td>
<td>1_3</td>
<td>0.02083</td>
</tr>
<tr>
<td>1_1</td>
<td>1_4</td>
<td>0.12500</td>
</tr>
<tr>
<td>1_1</td>
<td>1_5</td>
<td>0.12500</td>
</tr>
<tr>
<td>1_1</td>
<td>1_6</td>
<td>0.02083</td>
</tr>
<tr>
<td>1_1</td>
<td>1_7</td>
<td>0.090278</td>
</tr>
</tbody>
</table>

Try it: Using the test dataset ('samples' and 'metric') included in the package, let's run an (almost) automatic MAPI analysis.

Test data result from population genetic simulations in which two panmictic populations are separated by a barrier to dispersal. As we use dummy coordinates, there is no appropriate crs, so we just use 'crs=3857' (a pseudo-mercator projection). Of course, in this case, sample position on earth is meaningless. For a real dataset, 'crs' must be the EPSG code of the projection of your cartesian coordinates.

# Load the package
library(mapi)
# Load 'samples' data
data("samples")

# Load 'metric' data. For our simulated data set the pairwise metric
# computed between samples is the individual genetic distance \( \alpha \) of Rousset (2000).
data("metric")

# Run MAPI the lazy way (automatic) with 1000 permutations
# for detection of significant (dis)continuous areas.
# As crs must be set, we go with crs=3857 even if we use dummy coordinates.
# Of course, this have no geographical meaning.
# As we have a regular sampling, we use beta=0.5
my.results <- MAPI_RunAuto(samples, metric, crs=3857, beta=0.5, nbPermut=1000)

# Get significant areas with a FDR control at alpha=0.05 (5%, by default)
my.tails <- MAPI_Tails(my.results, alpha=0.05)

# Look at the result Figure 2.
MAPI_Plot2(my.results, tails=my.tails)

Spatial variation of the genetic distance is represented with a color scale from dark brown (lowest
values) to dark blue (higher value). The central blue area identified as a significant area of dis-
continuity corresponds to the position of the simulated barrier. Note that due to the permutation
procedure, delineation of the significant areas may vary slightly among runs.

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**Figure 2:** MAPI graphical Output produced using the MAPI_Plot2 function.

**To go deeper:** MAPI_RunAuto is a wrapper which calls three other functions: MAPI_CheckData,
MAPI_GridAuto and MAPI_RunOnGrid.

MAPI_GridAuto is itself another wrapper around MAPI_EstimateHalfwidth and MAPI_GridHexagonal.

Typically, a "manual" MAPI analysis will involve the following ordered steps:

1. MAPI_CheckData
2. MAPI_EstimateHalfwidth
3. MAPI_GridHexagonal
4. MAPI_RunOnGrid
5. MAPI_Tails
6. MAPI_Plot2

Within this general framework, you may, for example:

- set your own value for 'halfwidth' (ignore step 2)
- use your own grid, or reuse one from another run (ignore steps 2 & 3)
- tweak some MAPI parameters (such as dMin or dMax for filtering on geographic distances between samples)
- discard poorly supported cells prior detecting significant areas of (dis)continuity (parameter minQ) and/or change significance level (parameter alpha in MAPI_Tails)
- build your MAPI maps with a GIS software (ignore step 6). See 'Export results' section below

**Export results:** Output tables (weighted mean of the pairwise metric within cell and polygons delineating significant areas of (dis)continuity) are spatial objects built using the package **sf**. Refer to **sf** documentation to export MAPI results in various format. Below is an example of how MAPI results can be exported as ESRI Shapefiles:

```r
library(sf)
# Export results for our test dataset
st_write(my.results, dsn=".", layer="myFirstMapiResult",
         driver="ESRI Shapefile", append=FALSE, delete_layer=TRUE)
st_write(my.tails, dsn=".", layer="myFirstMapiResultTails",
         driver="ESRI Shapefile", append=FALSE, delete_layer=TRUE)
```

Alternatively, exporting layers in a geopackage is more convenient (only one file):

```r
library(sf)
# Export results for our test dataset
st_write(my.results, dsn="myFirstMapi.gpkg", layer="Result",
         driver="GPKG", append=FALSE, delete_layer=TRUE)
st_write(my.tails, dsn="myFirstMapi.gpkg", layer="Tails",
         driver="GPKG", append=FALSE, delete_layer=TRUE)
```

You may now open these files 'myFirstMapiResult.shp' and 'myFirstMapiResultTails.shp' or 'myFirstMapi.gpkg' in a GIS software such as QGis and customize the layout.

**NOTE:** recent versions of sf/gdal packages does not allow to export the 'permuts' column. As it was never used, MAPI >=1.0.4 releases does not returns anymore this column. If you still use older MAPI versions, you can remove this column before exporting using the following command:

```r
my.results$permuts <- NULL
```

**NOTE:** If the area of significant zones is very large, the measure may not fit in Shapefiles fields. It is then possible to convert the area measure in km² by dividing the value by 1,000,000:

```r
my.tails$area <- as.numeric(my.tails$area) / 1e6
```

Overlaying MAPI results with landscape layouts can help in analyzing the relationship between environmental features and spatial genetic patterns (eg. Piry & al., 2016; Piry & al., 2018).
References

**Description of the MAPI method:**

**Applications of MAPI in Landscape Genetics:**

- Stragier C., Piry S., et al. 2020. Interplay between historical and current features of the cityscape in shaping the genetic structure of the house mouse (*Mus musculus domesticus*) in Dakar (Senegal, West Africa) *bioRxiv*; Version 4 of this preprint has been peer-reviewed and is recommended by Peer Community In Ecology (DOI:10.24072/pci.ecology.100044) doi: 10.1101/557066

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**MAPI_CheckData**

**Function MAPI_CheckData**

**Description**

Check the validity of the ’samples’ and ’metric’ data loaded.

Missing data are removed from ’metric’, samples with missing coordinates are removed and samples that are not present in both dataset (’samples’ and ’metric’) are discarded.

**Usage**

```r
MAPI_CheckData(  
samples,  
metric,  
isMatrix = all((class(metric) == "matrix"), (nrow(metric) == ncol(metric)))
)
```

**Arguments**

- `samples` a data.frame with names and geographical coordinates of samples. Column names must be: ‘ind’, ‘x’, ‘y’. Optional column ‘errRad’ with an error radius for sample locations (eg. GPS uncertainty). Coordinates must be projected (not latitude/longitude).
MAPI_EstimateHalfwidth

Description

This function computes the side length (= halfwidth) of the hexagonal cells. Halfwidth value can be further used to build a MAPI grid.

Usage

MAPI_EstimateHalfwidth(samples, crs, beta = 0.25)

Arguments

samples a data.frame with names and geographical coordinates of samples. Column names must be: 'ind', 'x', 'y'. Optional column 'errRad' with an error radius for sample locations (eg. GPS uncertainty). Coordinates must be projected (not latitude/longitude).
MAPI_GridAuto

```r
MAPI_GridAuto(samples, crs, beta = 0.25, buf = 0)
```

**Description**

Wrapper that computes cell halfwidth for a given beta value, and then builds a grid of hexagonal cells (call to `MAPI_GridHexagonal`).

**Usage**

`MAPI_GridAuto(samples, crs, beta = 0.25, buf = 0)`

**Arguments**

- `samples` a data.frame with names and geographical coordinates of samples. Column names must be: 'ind', 'x', 'y'. Optional column 'errRad' with an error radius for sample locations (e.g., GPS uncertainty). Coordinates must be projected (not latitude/longitude).
- `crs` coordinate reference system: integer with the EPSG code, or character with proj4string. The coordinates system must be a projection, not latitude/longitude.
- `beta` A value depending on spatial regularity of sampling: 0.5 for regular sampling, 0.25 for random sampling (Hengl, 2006).

**Details**

\[ h_w = \beta \frac{\sqrt{A/N}}{2.5980} \], where A is the study area (convex hull of sampling points) and N the number of samples. Parameter beta allows to respect the Nyquist-Shannon sampling theorem depending on sampling regularity.

**Value**

Halfwidth cell value (side length of hexagonal cells).

**References**

**MAPI_GridHexagonal**

**beta**
A value depending on sampling regularity: 0.5 for regular sampling, 0.25 for random sampling (Hengl, 2006).

**buf**
Optional. This parameter allows to expand or shrink the grid by a number of units in the same reference system as the sample geographical coordinates (0 by default).

**Details**

The halfwidth cell value used to build the grid is computed as \( h_w = \beta \sqrt{\frac{A/N}{2.5980}} \), where \( A \) is the study area (convex hull of sampling points) and \( N \) the number of samples. Parameter beta allows to respect the Nyquist-Shannon sampling theorem depending on sampling regularity (call to `MAPI_EstimateHalfwidth`).

**Value**

A spatial object of class 'sf' including the x and y coordinates of cell centers, cell geometry (polygons) and cell id (gid).

**Examples**

```r
data("samples")
grid <- MAPI_GridAuto(samples, crs=3857, beta=0.5)
```

**Description**

Build a grid of hexagonal cells according to samples coordinates and a given halfwidth cell value provided by users (can be computed using `MAPI_EstimateHalfwidth`).

**Usage**

`MAPI_GridHexagonal(samples, crs, hw, buf = 0)`

**Arguments**

- **samples**: a data.frame with names and geographical coordinates of samples. Column names must be: 'ind', 'x', 'y'. Optional column 'errRad' with an error radius for sample locations (eg. GPS uncertainty). Coordinates must be projected (not latitude/longitude).
- **crs**: coordinate reference system: integer with the EPSG code, or character with proj4string. When using dummy coordinates (eg. simulation output) you may use EPSG:3857 for example. This allows computation but, of course, has no geographical meaning.
- **hw**: Halfwidth: side length of hexagonal cells.
buf
optional. This parameter allows to expand or shrink the grid by a number of units in the same reference system as the sample geographical coordinates (0 by default).

Value

a spatial object of class 'sf' including the x and y coordinates of cell centers, cell geometry (polygons) and cell id (gid).

Examples

data(“samples”)
# Builds a grid of hexagonal cells according to samples coordinates (columns x and y)
# using the EPSG:3857 projection and an halfwidth cell value of hw=250m.
grid <- MAPI_GridHexagonal(samples, crs=3857, hw=250)

MAPI_Plot

Function MAPI_Plot

Description

Plot a MAPI analysis result

Usage

MAPI_Plot(
resu,
tails = NULL,
samples = NULL,
pal = c("#994000", "#CC5800", "#FF8F33", "#FFAD66", "#FFCA99", "#FFE6CC", "#FBFBFB",
"#CCFDFF", "#99F8FF", "#66F0FF", "#33E4FF", "#00AACC", "#007A99"),
shades = 20,
main = NA,
upper = TRUE,
lower = TRUE,
upper.border = "black",
lower.border = "gray"
)

Arguments

resu A spatial object of class 'sf' resulting from a MAPI analysis done using MAPI_RunAuto or MAPI_RunOnGrid.
tails An optional spatial object of class 'sf' resulting from the post-process with MAPI_Tails of a MAPI analysis result. Default = NULL (no tails shown).
samples A data.frame with names and geographical coordinates of samples. Column names must be: 'ind', 'x', 'y'. Optional column 'errRad' with an error radius for sample locations (e.g. GPS uncertainty). Coordinates must be projected (not latitude/longitude).

pal A color ramp, e.g. from RColorBrewer (default: orange > light gray > blue)

shades Number of breaks for the color ramp (default 20)

main Plot title (none by default)

upper If TRUE and tails is not NULL, upper-tail significant areas are plotted. TRUE by default.

lower If TRUE and tails is not NULL, lower-tail significant areas are plotted. TRUE by default.

upper.border Border color of the upper-tail significant area. "black" by default.

lower.border Border color of the lower-tail significant area. "gray" by default.

Value

Returns the "trellis" object.

Examples

## Not run:
data("metric")data("samples")resu <- MAPI_RunAuto(samples, metric, crs=3857, nbPermuts = 1000)tails <- MAPI_Tails(resu)pl <- MAPI_Plot(resu, tails=tails, samples=samples)# Open png driverpng("mapiPlotOutput.png", width=1000, type="cairo-png")print(pl) # Do plot in filedev.off() # Close driver

## End(Not run)
pal = c("#994000", ",#CC5800", ",#FF8F33", ",#FFAD66", ",#FFE6CC", ”#FBFBFB”,

“#CCFDFF”, “#99F8FF”, “#66F0FF”, “#33E4FF”, “#00AACC”, “#007A99"),
shades = 20,
main = "",
upper = TRUE,
lower = TRUE,
upper.border = "black",
lower.border = "gray"
)

Arguments

resu A spatial object of class 'sf' resulting from a MAPI analysis done using MAPI_RunAuto or MAPI_RunOnGrid.
tails An optional spatial object of class 'sf' resulting from the post-process with MAPI_Tails of a MAPI analysis result. Default = NULL (no tails shown).
samples A data.frame with names and geographical coordinates of samples. Column names must be: 'ind', 'x', 'y'. Optional column 'errRad' with an error radius for sample locations (eg. GPS uncertainty). Coordinates must be projected (not latitude/longitude).
pal A color ramp, eg. from RColorBrewer (default: orange > light gray > blue)
shades Number of breaks for the color ramp (default 20)
main Plot title (none by default)
upper If TRUE and tails is not NULL, upper-tail significant areas are plotted. TRUE by default.
lower If TRUE and tails is not NULL, lower-tail significant areas are plotted. TRUE by default.
upper.border Border color of the upper-tail significant area. "black" by default.
lower.border Border color of the lower-tail significant area. "gray" by default.

Value

Returns the ggplot object.

Examples

## Not run:
library(ggplot2)
data("metric")
data("samples")
resu <- MAPI_RunAuto(samples, metric, crs=3857, nbPermut = 1000)
tails <- MAPI_Tails(resu)
pl <- MAPI_Plot2(resu, tails=tails, samples=samples)
# Save to image
ggsave("mapiPlotOutput.png", plot=pl)
## End(Not run)
Function MAPI_RunAuto

Description

This function is a wrapper allowing to run a complete MAPI analysis.

Usage

```r
MAPI_RunAuto(
  samples,
  metric,
  crs,
  isMatrix = all(class(metric) == "matrix", nrow(metric) == ncol(metric)),
  beta = 0.25,
  ecc = 0.975,
  buf = 0,
  errRad = 10,
  nbPermut = 0,
  dMin = 0,
  dMax = Inf,
  nbCores = ifelse(requireNamespace("parallel", quietly = TRUE),
                   parallel::detectCores() - 1, 1),
  N = 8
)
```

Arguments

- **samples**
  a data.frame with names and geographical coordinates of samples. Column names must be: 'ind', 'x', 'y'. Optional column 'errRad' with an error radius for sample locations (eg. GPS uncertainty). Coordinates must be projected (not latitude/longitude).

- **metric**
  a data.frame or a square matrix with the pairwise metric computed for all pairs of samples. If data.frame, column names must be: 'ind1', 'ind2', 'value'. If matrix, sample names must be the row- and column names.

- **crs**
  coordinate reference system: integer with the EPSG code, or character with proj4string. When using dummy coordinates (eg. simulation output) you may use EPSG:3857 for example. This allows computation but, of course, has no geographical meaning.

- **isMatrix**
  Boolean. Depends on the 'metric' data:
  TRUE if 'metric' is a square matrix with column names = row names and standing for sample names.
  FALSE if 'metric' is a three columns data.frame ('ind1', 'ind2', 'value').
  The default value is determined using a "matrix" class detection for 'metric' as well as identity between row and column number.
beta  A value depending on spatial regularity of sampling: 0.5 for regular sampling, 0.25 for random sampling (Hengl, 2006).

ecc  ellipse eccentricity value (0.975 by default).

buf  optional. This parameter allows to expand or shrink the grid by a number of units in the same reference system as the sample geographical coordinates (0 by default).

errRad  global error radius for sample locations (same radius for all samples, 10 by default). Units are in the same reference system as the sample geographical coordinates. To use different error radius values for sample locations, add a column ‘errRad’ in the ‘sample’ data (see mapi).

nbPermits  number of permutations of sample locations (0 by default).

dMin  minimum distance between individuals. 0 by default.

dMax  maximal distance between individuals. +Inf by default.

nbCores  number of CPU cores you want to use during parallel computation. The default value is estimated as the number of available cores minus 1, suitable for a personal computer. On a cluster you might have to set it to a reasonable value (eg. 8) in order to keep resources for other tasks.

N  number of points used per quarter of ellipse, 8 by default. Don’t change it unless you really know what you are doing.

Details

Following functions are called by MAPI_RunAuto in following order:

- MAPI_CheckData cleans the dataset;
- MAPI_GridAuto generates a grid of hexagons by calling MAPI_EstimateHalfwidth then MAPI_GridHexagonal;
- MAPI_RunOnGrid performs the MAPI analysis.

NOTE: The call to MAPI_Tails is not included. It should be done afterwards on the object returned by MAPI_RunAuto.

Value

a spatial object of class `sf` providing for each cell:

- gid: Cell ID
- x and y coordinates of cell center
- nb_ell: number of ellipses used to compute the weighted mean
- avg_value: weighted mean of the pairwise metric
• sum_wgts: sum of weights of ellipses used to compute the weighted mean

• w_stdev: weighted standard deviation of the pairwise metric

• swQ: percentile of the sum of weights

• geometry
  When permutations are performed:

• proba: proportion of the permuted weighted means below the observed weighted mean

• ltP: lower-tail p-value adjusted using the FDR procedure of Benjamini and Yekutieli

• utP: upper-tail p-value adjusted using the FDR procedure of Benjamini and Yekutieli

References


Examples

```r
## Not run:
data("metric")
data("samples")
# Run a MAPI analysis without permutation
my.results <- MAPI_RunAuto(samples, metric, crs=3857, beta=0.5, nbPermut=0)

# eg. Export results to shapefile "myFirstMapiResult" in current directory
# to further visualize and customize the MAPI plot in SIG software.
library(sf)
st_write(my.results, dsn=".", layer="myFirstMapiResult", driver="ESRI Shapefile")

## End(Not run)
```

Function MAPI_RunOnGrid

Description

Launch a MAPI analysis for a given grid computed with `MAPI_GridAuto` or `MAPI_GridHexagonal` or provided by users.
Usage

MAPI_RunOnGrid(
  samples,
  metric,
  grid,
  isMatrix = FALSE,
  ecc = 0.975,
  errRad = 10,
  nbPermuts = 0,
  dMin = 0,
  dMax = Inf,
  nbCores = ifelse(base::requireNamespace("parallel", quietly = TRUE),
                   parallel::detectCores() - 1, 1),
  N = 8
)

Arguments

samples a data.frame with names and geographical coordinates of samples. Column names must be: 'ind', 'x', 'y'. Optional column 'errRad' with an error radius for sample locations (eg. GPS uncertainty). Coordinates must be projected (not latitude/longitude).

metric a data.frame or a square matrix with the pairwise metric computed for all pairs of samples. If data.frame, column names must be: 'ind1', 'ind2', 'value'. If matrix, sample names must be the row- and column names.

grid a spatial object of class 'sf' with the geometry of each cell. When using your own grid, please check that the object structure is the same as returned by MAPI_GridAuto or MAPI_GridHexagonal.

isMatrix Boolean. Depends on the 'metric' data:
TRUE if 'metric' is a square matrix with column names = row names and standing for sample names.
FALSE if 'metric' is a three columns data.frame ('ind1', 'ind2', 'value').
The default value is determined using a "matrix" class detection for metric as well as identity between row and column number.

ecc ellipse eccentricity value (0.975 by default).

errRad global error radius for sample locations (same radius for all samples, 10 by default). Units are in the same reference system as the sample geographical coordinates. To use different error radius values for sample locations, add a column 'errRad' in the 'sample' data (see mapi).

nbPermuts number of permutations of sample locations (0 by default).

dMin minimum distance between individuals. 0 by default.

dMax maximal distance between individuals. +Inf by default.

nbCores number of CPU cores you want to use during parallel computation. The default value is estimated as the number of available cores minus 1, suitable for a personal computer. On a cluster you might have to set it to a reasonable value (eg. 8) in order to keep resources for other tasks.
number of points used per quarter of ellipse, 8 by default. Don’t change it unless you really know what you are doing.

Details
To test whether the pairwise metric values associated with the ellipses are independent of the sample locations, those are permuted 'nbPermuts' times. At each permutation, new cell values are computed and stored to build a cumulative null distribution for each cell of the grid. Each cell value from the observed data set is then ranked against its null distribution. For each cell, the proportion of permuted values that are smaller or greater than the observed value provides a lower-tailed (ltP) and upper-tailed (utP) test p-value.

A false discovery rate (FDR) procedure (Benjamini and Yekutieli, 2001) is applied to account for multiple testing (number of cells) under positive dependency conditions (spatial autocorrelation). An adjusted p-value is computed for each cell using the function `p.adjust` from the 'stats' package with the method 'BY'.

Value
a spatial object of class 'sf' providing for each cell:

- gid: Cell ID
- x and y coordinates of cell center
- nb_ell: number of ellipses used to compute the weighted mean
- avg_value: weighted mean of the pairwise metric
- sum_wgts: sum of weights of ellipses used to compute the weighted mean
- w_stdev: weighted standard deviation of the pairwise metric
- swQ: percentile of the sum of weights
- geometry
  When permutations are performed:
  - proba: proportion of the permuted weighted means below the observed weighted mean
  - ltP: lower-tail p-value adjusted using the FDR procedure of Benjamini and Yekutieli
  - utP: upper-tail p-value adjusted using the FDR procedure of Benjamini and Yekutieli
References


Examples

```r
## Not run:
data(metric)
data(samples)
my.grid <- MAPI_GridHexagonal(samples, crs=3857, 500) # 500m halfwidth
# Note: 10 permutations is only for test purpose, increase to >=1000 in real life!
my.results <- MAPI_RunOnGrid(samples, metric, grid=my.grid, nbPermuts=10, nbCores=1)
# eg. Export results to shapefile "myFirstMapiResult" in current directory
library(sf)
st_write(my.results, dsn=".", layer="myFirstMapiResult", driver="ESRI Shapefile")
## End(Not run)
```

### MAPI_Tails

#### Function MAPI_Tails

**Description**

Determine significant continuous and discontinuous areas from the result of a MAPI analysis when run with permutations.

**Usage**

```r
MAPI_Tails(resu, minQ = 0, alpha = 0.05)
```

**Arguments**

- `resu`: A spatial object of class `sf` resulting from a MAPI analysis done using either `MAPI_RunAuto` or `MAPI_RunOnGrid`.
- `minQ`: Threshold under which cells with the smallest sum-of-weights percentile (range 1 .. 100) are discarded (default value = 0). This parameter allows to discard cells for which the average value of the pairwise metric is computed using either a small number and/or only long-distance ellipses.
- `alpha`: Significance level (default=0.05)
Details

When permutations are performed, in `MAPI_RunOnGrid` for each cell, the proportion of permuted values that are smaller or greater than the observed value provides a lower-tailed (ltP) and upper-tailed (utP) test p-value. A false discovery rate (FDR) procedure (Benjamini and Yekutieli, 2001) is applied to account for multiple testing (number of cells) under positive dependency conditions (spatial autocorrelation). An adjusted p-value is computed for each cell using the function `p.adjust` from the 'stats' package with the method 'BY'. The significance level at which FDR is controlled is set through the parameter alpha. For example, when alpha is set to 0.05, this means that 5% of the cells belonging to the lower (or upper) tail that are spatially connected are aggregated together to form the significant areas with the lowest (or greater) average values of the pairwise metric analyzed.

Value

a spatial object of class ‘sf’ with the area and geometry of the polygons delineating the significant areas. A column provides the tail for each polygon (upper or lower).

References


Examples

```r
## Not run:
data("metric")
data("samples")
# Run MAPI computation
resu <- MAPI_RunAuto(samples, metric, crs=3857, nbPermuts=1000)
# Discards the 10% cells with the smallest sum-of-weights
# and aggregates adjacent cells belonging to the same tail
# at a 5% significance level
tails <- MAPI_Tails(resu, minQ=10, alpha=0.05)
## End(Not run)
```

Description

The individuals were simulated as described in the `samples` section. The value is a genetic distance (À estimator in Rousset, 2000) computed between the 200 simulated samples using SPAGeDi v1.4 (Hardy & Vekemans, 2002).

Usage

data("metric")
Value

A data.table object with 19900 rows (one per sample pair, non symmetrical) and 3 columns ("ind1", "ind2", "value") containing respectively the first sample name, the second sample name and the value of their relation.

References


Examples

data("metric")

Description

Test dataset provided with the MAPI package. We used generation-by-generation coalescent algorithms (Hudson et al., 1990) to simulate 10 microsatellite genotypes at migration-mutation-drift equilibrium for 200 diploid individuals, distributed on the nodes of a 20x10 lattice.

Mutations for each locus followed a symmetric generalized stepwise model with a variance equal to 0.36 (Estoup et al., 2001) and a maximum range of allelic states of 40. The mutation rate was fixed so that heterozygosity ranged from 0.6 to 0.8 as frequently observed at microsatellite markers (Chapuis et al., 2012).

Two panmictic populations are separated by a barrier. We used Simcoal2 (Laval and Excoffier, 2004) to generate two panmictic populations of equal effective size $N_e = 100$ and exchanging $N_e m = 0.1$ migrants at each generation. The barrier to gene flow bisected the lattice from north to south in its center.

The differentiation values computed between these samples is described in the metric section.

Usage

data("samples")

Value

A data.table object with 200 simulated individuals (one per row) and 4 columns ("ind", "x", "y", "errRad") including the sample names, coordinates x and y and an error circle radius on coordinates.
References


Examples

data("samples")
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