

Package ‘paleotools’

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Title Perform Standard Analyses for Palaeoenvironmental Studies

Version 0.0.0.9000

Description What the package does (one paragraph).

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Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

Suggests testthat

Imports emdist,
Hmisc,
crestr

R topics documented:

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EMD	<i>Calculates the EMD for two vectors x and y.</i>
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Description

Calculates the EMD for two vectors x and y.

Usage

```
EMD(  
  x,  
  y,  
  weight.m = matrix(rep(1, length(x)^2), ncol = length(x), byrow = TRUE) - diag(1,  
    length(x), length(x))  
)
```

Arguments

`x, y` The two vectors to compare
`weight.m` Matrix of weights. Values should be 'numeric'.

Value

The EMD between `x` and `y`.

Examples

```
EMD(1:5/sum(1:5), 6:10/sum(6:10))
EMD(1:5, 6:10) # The vectors are normalised by the function
m <- matrix(1:25, ncol=5)
for(i in 1:5) m[i,i] <- 0
EMD(1:5, 6:10, weight.m=m)
```

signif_struct

Test if two set of samples share a similar spatial structure.

Description

Calculates the EMD for two matrices `x` and `y` and test if the spatial structure of the two is better than random.

Usage

```
signif_struct(
  x,
  y,
  nrep = 200,
  alpha = 0.05,
  weight.m = matrix(1, ncol = ncol(x), nrow = ncol(x)) - diag(1, ncol = ncol(x), nrow =
    ncol(x)),
  plot = TRUE,
  verbose = TRUE,
  emd.step = 0.002,
  save = FALSE,
  filename = paste0("test", ifelse(as.png, ".png", ".pdf")),
  as.png = TRUE,
  png.res = 300,
  width = 9,
  height = 9,
  col = c("#66a182", "#d95f02")
)
```

Arguments

`x, y` Two matrices of the same dimensions to compare.
`nrep` The number of randomisation to perform (Default 1000).
`alpha` The significance threshold of the test (Default 0.05).

weight.m	Matrix of weights. Values should be 'numeric'.
plot	A boolean to indicate if the results of the test should be plotted. Default is FALSE.
verbose	A boolean to indicate if the results of the test should be printed on the screen (default TRUE).
emd.step	Graphical parameter that defines the width of the histogram bins.
save	A boolean to indicate if the diagram should be saved as a pdf file. Default is FALSE.
filename	An absolute or relative path that indicates where the diagram should be saved. Also used to specify the name of the file. Default: the file is saved in the working directory under the name 'Reconstruction_climate.pdf'.
as.png	A boolean to indicate if the output should be saved as a png. Default is TRUE. If FALSE, the figure is saved as a pdf.
png.res	The resolution of the png file (default 300 pixels per inch).
width, height	The dimensions of the output file in cm (default 9x9cm).
col	A vector of two colours to use for significant and non-significant tests, respectively.

Value

A list containing 3 items: 1. The mean EMD derived the comparison of x and y. 2. The ensemble of EMDs calculated from the nrep randomised data. 3. The pvalue of the test.

Examples

```
##> We generate two tables of random, positive data
m1 <- matrix(abs(rnorm(500)), ncol=5) ; m1 <- m1 / apply(m1, 1, sum)
m2 <- matrix(abs(rnorm(500)), ncol=5) ; m2 <- m2 / apply(m2, 1, sum)
signif_struct(m1, m2, plot=FALSE)
res <- signif_struct(m1, m2, plot=TRUE, verbose=TRUE)
res <- signif_struct(m1, 1+m1, plot=TRUE, verbose=TRUE, nrep=100)
str(res)
## Not run:
  signif_struct(m1, m2, save=TRUE, filename='test-emd.png')

## End(Not run)
```

signif_threshold	<i>Test if two set of samples share a similar spatial structure.</i>
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Description

Calculates the EMD for two matrices x and y and test if the spatial structure of the two is better than random.

Usage

```
signif_threshold(
  x,
  nrep = 1000,
  alpha = 0.05,
  weight.m = matrix(1, ncol = ncol(x), nrow = ncol(x)) - diag(1, ncol = ncol(x), nrow =
    ncol(x)),
  plot = TRUE,
  verbose = TRUE,
  emd.step = 0.002,
  save = FALSE,
  filename = paste0("test", ifelse(as.png, ".png", ".pdf")),
  as.png = TRUE,
  png.res = 300,
  width = 9,
  height = 9,
  col = "cornflowerblue"
)
```

Arguments

x	A matrix of samples (rows) to compare.
nrep	The number of randomisation to perform (Default 1000).
alpha	The significance threshold of the test (Default 0.05).
weight.m	Matrix of weights. Values should be 'numeric'.
plot	A boolean to indicate if the results of the test should be plotted. Default is FALSE.
verbose	A boolean to indicate if the results of the test should be printed on the screen (default TRUE).
emd.step	Graphical parameter that defines the width of the histogram bins.
save	A boolean to indicate if the diagram should be saved as a pdf file. Default is FALSE.
filename	An absolute or relative path that indicates where the diagram should be saved. Also used to specify the name of the file. Default: the file is saved in the working directory under the name 'Reconstruction_climate.pdf'.
as.png	A boolean to indicate if the output should be saved as a png. Default is TRUE. If FALSE, the figure is saved as a pdf.
png.res	The resolution of the png file (default 300 pixels per inch).
width, height	The dimensions of the output file in cm (default 9x9cm).
col	A vector of two colours to use for significant and non-significant tests, respectively.

Value

A list containing 3 items: 1. The mean EMD derived the comparison of x and y. 2. The ensemble of EMDs calculated from the nrep randomised data. 3. The pvalue of the test.

Examples

```
##> We generate two tables of random, positive data
m1 <- matrix(abs(rnorm(500)), ncol=5) ; m1 <- m1 / apply(m1, 1, sum)
signif_threshold(m1, plot=FALSE)
res <- signif_threshold(m1, plot=TRUE, verbose=TRUE)
str(res)
## Not run:
  signif_threshold(m1, save=TRUE, filename='test-emd.png')

## End(Not run)
```

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