# Package 'paleotools'

December 10, 2021

**Title** Perform Standard Analyses for Palaeoenvironmental Studies

**Version** 0.0.0.9000

**Description** What the package does (one paragraph).

**License** MIT + file LICENSE

**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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`biomise` *A wrapper for all the crest functions.*

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### Description

Runs all the different steps of a CREST reconstruction in one function.

### Usage

```
biomise(s, pol2pft, pft2biome)
```

### Arguments

| | |
|---|---|
| s | . |
| pol2pft | . |
| pft2biome | . |

### Value

A .

### Examples

```
1:5
```

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## EMD *A wrapper for all the crest functions.*

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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, 6:10)
m <- matrix(1:25, ncol=5)
for(i in 1:5) m[i,i] <- 0
EMD(1:5, 6:10, weight.m=m)
## Not run:
  EMD(1:5, 1:6)

## End(Not run)
```

## pft2biome *A wrapper for all the crest functions.*

### Description

Runs all the different steps of a CREST reconstruction in one function.

### Usage

```
pft2biome(s, pft2biome)
```

### Arguments

| | |
|---|---|
| s | . |
| pft2biome | . |

### Value

A .

### Examples

```
1:5
```

## pollen2pft *A wrapper for all the crest functions.*

### Description

Runs all the different steps of a CREST reconstruction in one function.

### Usage

```
pollen2pft(s, pol2pft)
```

### Arguments

| | |
|---|---|
| s | . |
| pol2pft | . |

### Value

As.

### Examples

```
1:5
```

`test.EMD` *Test if two set of samples are more similar than expected if random.*

## Description

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

## Usage

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

## Arguments

| | |
|---|---|
| `x, y` | The two matrices to compare |
| `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`). |
| `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 colour gradient. |
| `nrep` | The number of randomisation to perform (Default 1000). |

## 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

```
m1 <- matrix(abs(rnorm(25)), ncol=5)
m2 <- matrix(abs(rnorm(25)), ncol=5)
test.EMD(m1, m2)
res <- test.EMD(m1, m2, plot=FALSE, verbose=TRUE)
str(res)
## Not run:
  test.EMD(m1, m2, save=TRUE, filename='test-emd.png')

## End(Not run)
```

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