

# Package ‘palaeoSig’

October 14, 2022

**Type** Package

**Title** Significance Tests for Palaeoenvironmental Reconstructions

**Version** 2.0-3

**URL** <https://github.com/richardjtelford/palaeoSig>

**BugReports** <https://github.com/richardjtelford/palaeoSig/issues>

**Depends** R (>= 2.10)

**Suggests** fields, knitr, rmarkdown, gstat, sp, tidyverse

**Imports** TeachingDemos, rioja, mgcv, MASS, tibble, dplyr, magrittr, ggplot2, forcats, assertr, vegan, rlang, ggrepel, tidyr, purrr

**Description** Several tests of quantitative palaeoenvironmental reconstructions from microfossil assemblages, including the null model tests of the statistically significant of reconstructions developed by Telford and Birks (2011) <[doi:10.1016/j.quascirev.2011.03.002](https://doi.org/10.1016/j.quascirev.2011.03.002)>, and tests of the effect of spatial autocorrelation on transfer function model performance using methods from Telford and Birks (2009) <[doi:10.1016/j.quascirev.2008.12.020](https://doi.org/10.1016/j.quascirev.2008.12.020)> and Trachsel and Telford (2016) <[doi:10.5194/cp-12-1215-2016](https://doi.org/10.5194/cp-12-1215-2016)>. Age-depth models with generalized mixed-effect regression from Heegaard et al (2005) <[doi:10.1191/0959683605hl836r](https://doi.org/10.1191/0959683605hl836r)> are also included.

**License** GPL-3

**LazyLoad** yes

**RoxygenNote** 6.0.1

**VignetteBuilder** knitr

**Encoding** UTF-8

**NeedsCompilation** no

**Author** Richard Telford [aut, cre, cph],  
Mathias Trachsel [ctb]

**Maintainer** Richard Telford <[Richard.Telford@bio.uib.no](mailto:Richard.Telford@bio.uib.no)>

**Repository** CRAN

**Date/Publication** 2019-06-28 08:00:03 UTC

## R topics documented:

palaeoSig-package	2
abundances	3
agelme	4
anamorph	6
arctic.pollen	7
Atlantic	7
centipede_plot	8
cor.mat.fun	9
coverage_plot	10
Hill.N2.core	11
jointsig	12
make.env	13
make.set	14
multi.mat	16
obs.cor	17
plot.fittedAgelme	20
predict.agelme	20
randomTF	22
rne	24
species	26
STOR	28

<b>Index</b>	<b>30</b>
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palaeoSig-package	<i>Significance Tests of Quantitative Palaeoenvironmental Reconstructions</i>
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## Description

Significance tests for quantitative palaeoenvironmental reconstructions derived from transfer functions. Functions from the **autocorTF** package are now included in **palaeoSig**.

## Details

This package includes:

significance tests for quantitative palaeoenvironmental reconstructions (`randomTF`, `obs.cor`)

graphical methods to show autocorrelation in transfer functions (`rne`)

null model test of transfer functions performance in a spatially autocorrelated environment - see vignette.

Several functions have from **autocorTF** version 1.0 and **palaeoSig** version 1.0 have been rewritten or replaced with more flexible or user friendly functions. See `news(package="palaeoSig")` for details.

See also my blog at <https://quantpalaeo.wordpress.com/>

Package: palaeoSig  
 Type: Package  
 Version: 1.1-2  
 Date: 2013-04-17  
 License: GPL - 3  
 LazyLoad: yes

### Author(s)

Richard Telford <[richard.telford@bio.uib.no](mailto:richard.telford@bio.uib.no)>

### References

Telford, R. J. and Birks, H. J. B. (2009) Evaluation of transfer functions in spatially structured environments. *Quaternary Science Reviews* **28**: 1309–1316. DOI: 10.1016/j.quascirev.2008.12.020

Telford, R. J. and Birks, H. J. B. (2011) A novel method for assessing the statistical significance of quantitative reconstructions inferred from biotic assemblages. *Quaternary Science Reviews* **30**: 1272–1278. DOI: 10.1016/j.quascirev.2011.03.002

### See Also

[rioja, rda](#)

---

abundances

*Generates abundances*

---

### Description

Generates species abundances based on species response functions and environmental variables.

### Usage

```
abundances(env, spp, nc)
```

### Arguments

env	Environmental variables. Usually generated by <a href="#">make.env</a> . Users may as well supply own environmental variables.
spp	Species parameters. Usually generated by <a href="#">species</a> .
nc	Number of counts to be simulated. If omitted no simulation of the counting process is carried out.

### Value

spp	Data frame containing species abundances.
env	Data frame containing environmental variables.

**Author(s)**

Mathias Trachsel and Richard J Telford

**References**

Minchin, P.R. (1987) Multidimensional Community Patterns: Towards a Comprehensive Model. *Vegetatio*, 71, 145-156.

**See Also**

[make.env](#), [species](#)

**Examples**

```
spec <- species(nspp = 30, ndim = 10, Amax = runif, fun = runif, xpar = c(-50, 150),
  srange = 200, alpha = 4, gamma = 4)
env.var <- make.env(100, elen = rep(100, 10), emean = rep(50, 10), edistr = 'uniform',
  ndim = 10)
spec.abun <- abundances(env.var, spec, 200)
```

---

 agelme

---

*Estimation of the relationship between Calibrated age and depth*


---

**Description**

Estimates the relationship of Calibrated age and depth for paleorecords. The function uses a smooth spline of the `mgcv` library by Simon Wood. It produces predicted confidence interval for the relationship approximating a mixed effect model, as there are two levels of uncertainty, i.e. within dated object and between dated objects.

**Usage**

```
agelme(depup, depdo, bpup, bpdo, use, weights=c(1, rep(0, length(depup)-1)),
  vspan=1, k=length(depup)-1, m=2, diagnostic=FALSE)
```

**Arguments**

depup	The upper depths of the dated slides
depdo	The lower depths of the dated slides
bpup	The younger calibrated ages of the dated slides
bpdo	The older calibrated ages of the dated slides
use	Logical vector of dates to include in the model. Default is to use all.
weights	Weights to be used for the estimation, default is fixed top-layer followed by inverse variance of within dated object
vspan	The span to be used for the diagnostic plots, default span = 1

k	Number of base function to start the shrinkage in the gam estimation procedure
m	The order of penalty for the term, i.e. the degree of continuity at the knots (default, m = 2 gives cubic smooth spline)
diagnostic	Logical, should diagnostic plots be made.

### Details

Note that the fixation of the top layer is done by a weight = 1, whereas the other weights follows inverse variance within object.

The diagnostic plots is used to check the quality of the estimation and to see if there is a need for an assumption of between object variance proportional to mean. The latter however is rarely encountered for paleodata.

### Value

tdf	Degrees of freedom used by the cubic smooth spline, a vector with first value for constant variance and second vector for variance equal to mu.
weights	A vector of the weights used by the cubic smooth spline
RES	A vector of the Residual sum of squares
Models	A list with the models from the cubic smooth spline, constant and mu variance, respectively
Data	A data.frame including the data used for the estimation

### Author(s)

Einar Heegaard <einar.heegaard@bio.uib.no>

### References

Heegaard, E., Birks, HJB. & Telford, RJ. 2005. Relationships between calibrated ages and depth in stratigraphical sequences: an estimation procedure by mixed-effect regression. *The Holocene* 15: 612-618

### Examples

```
data(STOR)

fit.mod <- with(STOR, agelme(depthup, depthdo, cageup, cagedo))

#Predicting using the constant variance model,
#for each cm between 70 and 400 cm.
fit.pre <- predict(fit.mod, 1, 70:400)
plot(fit.pre)
```

---

anamorph

*Anamorph*

---

### Description

Creates functions that transform arbitrary distributions into a Gaussian distributions, and vice versa.

### Usage

```
anamorph(x, k, plot = FALSE)
```

### Arguments

x	data
k	number of Hermite polynomials
plot	plot

### Details

Increasing k can give a better fit.

### Value

Returns two function in a list

xtog	Function to transform arbitrary variable x into a Gaussian distribution
gtox	The back transformation

### Author(s)

Richard Telford <Richard.Telford@bio.uib.no>

### References

Wackernagel, H. (2003) *Multivariate Geostatistics*. 3rd edition, Springer-Verlag, Berlin.

### Examples

```
set.seed(42)
x <- c(rnorm(50, 0, 1), rnorm(50, 6, 1))
hist(x)
ana.fun <- anamorph(x, 30, plot = TRUE)
xg <- ana.fun$xtog(x)
qqnorm(xg)
qqline(xg)
all.equal(x, ana.fun$gtox(xg))
```

---

`arctic.pollen`*Arctic Pollen and associated environmental data*

---

**Description**

Arctic pollen percent data and associated environmental data

**Usage**

```
arctic.env
```

**Format**

**arctic.pollen** A data frame with 828 observations on the percentage of 39 pollen taxa

**arctic.env** Environmental data for the pollen sites

**Source**

Data extracted from North American Pollen Database and New *et al.* (2002) by Fréchette *et al.* (2008). Following Fréchette (Pers. Comm.), three duplicate sites have been deleted.

**References**

Fréchette, B., de Vernal, A., Guiot, J., Wolfe, A. P., Miller, G. H., Fredskild, B., Kerwin, M. W. and Richard, P. J. H. (2008) Methodological basis for quantitative reconstruction of air temperature and sunshine from pollen assemblages in Arctic Canada and Greenland. *Quaternary Science Reviews* **27**, 1197–1216 doi:[10.1016/j.quascirev.2008.02.016](https://doi.org/10.1016/j.quascirev.2008.02.016)

**Examples**

```
data(arctic.pollen)
data(arctic.env)
```

---

`Atlantic`*Atlantic core-top foram assemblages*

---

**Description**

A dataset containing over 1000 foram assemblages from the Atlantic from Kucera et al (2005) and the 50m SST for the warmest season. Rare taxa and co-located assemblages are removed.

**Usage**

```
Atlantic
```

**Format**

A data frame with 1093 rows and 33 variables. summ50 is 50m water temperature of the warmest season

**Source**

<https://doi.pangaea.de/10.1594/PANGAEA.227322> <https://www.nodc.noaa.gov/cgi-bin/OC5/woa13/woa13.pl?parameter=t>

**Examples**

```
data(Atlantic)
```

---

centipede_plot	<i>centipede_plot</i>
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---

**Description**

Plot of species WA optima and tolerance

**Usage**

```
centipede_plot(x, spp, minN2 = 1, mult = 1)
```

**Arguments**

x	A tolerance weighted weighted-average model from <a href="#">WA</a>
spp	data.frame of species data used to train the WA model
minN2	numeric giving minimum N2 for inclusion in plot
mult	numeric multiplier for the tolerances

**Details**

Extracts and sorts [WA](#) optima and tolerances and generates a ggplot. Tends only to work well when there are a reasonable number of taxa, otherwise it is difficult to read the names on the axis. Rare taxa can be excluded with the minN2 argument. The tol.cut argument in [WA](#) may need to be set to prevent very small tolerances in rare taxa. This function is very similar to the [caterpillar](#) plot, but produces a ggplot

**Value**

A [ggplot](#) object.

**Examples**

```
library(rioja)
data(SWAP)
mod <- WA(SWAP$spec, SWAP$pH, to1DW=TRUE)
coef(mod)
centipede_plot(mod, spp = SWAP$spec, minN2 = 20)
```

---

`cor.mat.fun`*Generates correlation matrix*

---

**Description**

Generates a correlation matrix for the environmental variables generated in [make.env](#) and for correlated species optima in [species](#). Only used when correlated environmental variables or optima are generated.

**Usage**

```
cor.mat.fun(ndim, cors)
```

**Arguments**

<code>ndim</code>	Number of environmental variables that are subsequently generated with <a href="#">make.env</a> .
<code>cors</code>	List of correlations between environmental variables. Each element of the list consists of three numbers, the first two numbers indicate the variables that are correlated, the third number is the correlation coefficient. If correlations between two variables are omitted the correlation remains 0.

**Value**

Correlation matrix

**Author(s)**

Mathias Trachsel

**See Also**

[make.env](#), [species](#)

**Examples**

```
correlations <- list(c(1, 2, 0.5), c(1, 4, 0.1), c(2, 5, 0.6))
cor.mat <- cor.mat.fun(5, correlations)
```

---

coverage_plot	<i>coverage_plot</i>
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---

### Description

A simple diagnostic plot showing the coverage of fossil taxa in modern calibration set

### Usage

```
coverage_plot(spp, fos, n2_rare = 5, label = NULL)
```

### Arguments

spp	data.frame of modern species abundances
fos	data.frame of fossil species abundances
n2_rare	numeric value of Hill's N2 below which species are highlighted as rare
label	numeric label taxa where maximum fossil abundance - maximum modern abundance > label. Defaults to NULL which does not add labels

### Details

Finds the maximum abundance of fossil taxa and plots this against the maximum abundance the taxa in the modern calibration set. Taxa with a Hill's N2 less than rare in the calibration set are highlighted in blue. Taxa absent from the calibration set are highlighted in red. If there are many taxa above the 1:1 line, or important fossil taxa have a low N2 in the calibration set, reconstructions should be interpreted with caution.

### Value

A `ggplot` object.

### Examples

```
data("SWAP", package = "rioja")
data("RLGH", package = "rioja")
coverage_plot(spp = SWAP$spec, fos=RLGH$spec, n2_rare = 5, label = 0)
```

---

`Hill.N2.core`*Calculate the effective number of species in the fossil data*

---

**Description**

Gives a measure of the species diversity in the fossil data.

**Usage**

```
Hill.N2.core(spp)
```

**Arguments**

`spp`                      Species data

**Details**

Uses [Hill.N2](#) from the rioja package

**Value**

Minimum, first quartile and median effective number of species

**Note**

If the effective number of species is small, WA based reconstructions are unlikely to be significant, and MAT based reconstructions should be tested instead.

**Author(s)**

Richard Telford

**References**

Hill, M. O. (1973) Diversity and evenness: a unifying notation and its consequences. *Ecology* **54**: 427–432.

**See Also**

[Hill.N2](#)

**Examples**

```
require(rioja)
data(RLGH)
```

```
Hill.N2.core(RLGH$spec)
```

jointsig

*Test if two variables jointly control changes in fossil data***Description**

Generates synthetic variables with different proportion of two environmental variables, and tests how much variance in the fossil data reconstructions of these synthetic variables explain.

**Usage**

```
jointsig(spp, fos, var1, var2, method = "randomTF", n = 99, r = 32, ...)
## S3 method for class 'js'
plot(x, names.v1, names.v2, ...)
```

**Arguments**

spp	Data frame of modern training set species data, transformed as required for example with sqrt
fos	Data frame of fossil species data, with same species codes and transformations as spp
var1	Training set environmental variable 1.
var2	Training set environmental variable 2.
n	number of random training sets used to generate the null model
method	Which significance test to use. Current options are randomTF and obs.cor. The latter may give strange results - use with caution.
r	How many synthetic variables to make. More is better but slower.
x	Output from jointsig
names.v1	Vector length 2 with names of the end members of the first environmental variable, e.g., c("cold", "warm") for temperature.
names.v2	Ditto for the second variable.
...	Other arguments to the significance test (some of these are required) or plot.

**Details**

With method="randomTF", the function calculates the proportion of variance in the fossil data explained by transfer function reconstructions of synthetic variables. The synthetic variables are composed of two environmental variables, weighted between -1 and +1, so to represent a circle. This is compared with a null distribution of the proportion of variance explained by reconstructions based on random environmental variables. Any transfer function in the rioja library can be used. With method="obs.cor", the aim is the same, but the function reports the correlation between the species weighted average optima on the synthetic variables and the species first axis scores. This option has some pathological behaviour and should probably be avoided.

**Value**

A list with components

PCA	The unconstrained ordination of the fossil data.
preds	A list of the containing the reconstructions for each environmental variable.
MAX	Proportion of the variance explained by the first axis of the unconstrained ordination. This is the maximum amount that a reconstruction of a single variable can explain.
EX	The proportion of the variance in the fossil data explained by each reconstruction.
sim.ex	The proportion of variance explained by each of the random environmental variables.
sig	The p-value of each reconstruction.

**Author(s)**

Richard Telford <richard.telford@bio.uib.no>

**References**

Unpublished method - use with caution. Can give spurious results with weighted averaging.

**See Also**

[randomTF,obs.cor](#)

**Examples**

```
require(rioja)
data(SWAP)
data(RLGH)

rlgh.js <- jointsig(spp = sqrt(SWAP$spec), fos = sqrt(RLGH$spec), var1 = SWAP$pH,
  var2 = sample(SWAP$pH), method = "randomTF", n = 99, r = 32, fun = WA, col = 1)
#nonsense second variable

plot(rlgh.js, c("acid", "alkaline"), c("down", "up"))
```

---

make.env

*Generates environmental variables*

---

**Description**

Generates environmental variables used for generating species abundances. Environmental variables may be correlated, and may follow different distributions.

**Usage**

```
make.env(n, elen, emean, edistr, ecor, ndim)
```

**Arguments**

n	Number of samples to be generated.
elen	Range of the environmental variables. Single number or vector of length ndim.
emean	Mean of the environmental variables. Single number or vector of length ndim.
edistr	Distribution of the environmental variables. Currently 'uniform' and 'Gaussian' are supported.
ecor	Correlation matrix of the environmental variables supplied by user. Object generated by <code>cor.mat.fun</code> . If omitted environmental variables are not correlated.
ndim	Number of environmental variables to generate.

**Value**

Matrix of environmental variables. n rows and ndim columns.

**Author(s)**

Mathias Trachsel and Richard J. Telford

**References**

Minchin, P.R. (1987) Multidimensional Community Patterns: Towards a Comprehensive Model. *Vegetatio*, 71, 145-156.

**See Also**

[cor.mat.fun](#)

**Examples**

```
env.vars <- make.env(100, elen = rep(100, 10), emean = rep(50, 10), edistr = 'uniform', ndim = 10)
```

---

make.set

*Function to simulate species data*

---

**Description**

Function to simulate species data following Minchin (1987). This functions generates species response functions, simulates environmental variables and simulates species assemblages based on species response functions and environmental variables. Users can as well supply own species parameters (e.g. when simulating calibration and fossil datasets) and own environmental variables.

**Usage**

```
make.set(ndim, n, elen, emean, edistr, ecor, cnt, spec, env,...)
```

**Arguments**

ndim	Number of environmental variables to generate.
n	Number of samples to be generated.
elen	Range of the environmental variables. Single number or vector of length ndim.
emean	Mean of the environmental variables. Single number or vector of length ndim.
edistr	Distribution of the environmental variables. Currently 'uniform' and 'Gaussian' are supported.
ecor	Correlation matrix of the environmental variables supplied by user. Object generated by <a href="#">cor.mat.fun</a> . If omitted environmental variables are uncorrelated.
cnt	Number of counts to be simulated.
spec	Users may supply their own species paramters.
env	Users may supply their own environmental variables.
...	Arguments passed to <a href="#">species</a>

**Value**

spp	Species abundance data.
env	Environmental variables used to simulate species abundance data.
spec	Species parameters.

**Author(s)**

Mathias Trachsel and Richard J. Telford

**References**

Minchin, P.R. (1987) Multidimensional Community Patterns: Towards a Comprehensive Model. *Vegetatio*, 71, 145-156.

**See Also**

[make.env](#), [species](#), [cor.mat.fun](#)

**Examples**

```
calib <- make.set(nspp = 90, ndim = 3, Amax = runif, fun = runif, xpar = c(-50, 150),
  srange = 400, alpha = 4, gamma = 4, n = 100, elen = rep(100, 3), emean = rep(50, 3),
  edistr = 'uniform', cnt = 1000)

# Provide species parameters generated above, so that the fossil data use the
# same species parameters.
fos <- make.set(ndim = 3, n = 100, elen = rep(100, 3), emean = rep(50, 3), edistr = 'uniform',
```

```

cnt = 1000, spec = calib$spec)

# Supplying own environmental variables and species parameters.
env.vars <- make.env(100,elen =rep(100,3),emean = rep(50,3), edistr = 'uniform', ndim = 3)
fos <- make.set(cnt = 1000, spec = calib$spec, env = env.vars)

```

---

multi.mat

*MAT for multiple variables*


---

### Description

MAT for many environmental variables simultaneously. More efficient than calculating them separately for each variable.

### Usage

```

multi.mat(training.spp, envs, core.spp, noanalogues = 10, method = "sq-chord",
run = "both")

```

### Arguments

training.spp	Community data
envs	Environmental variables - or simulations
core.spp	Optional fossil data to make predictions for
noanalogues	Number of analogues to use
method	distance metric to use
run	Return LOO predictions or predictions for fossil data

### Value

Matrix of predictions

### Author(s)

Richard Telford <Richard.Telford@bio.uib.no>

### References

Telford, R. J. and Birks, H. J. B. (2009) Evaluation of transfer functions in spatially structured environments. *Quaternary Science Reviews* **28**: 1309–1316. DOI: 10.1016/j.quascirev.2008.12.020

## Examples

```
data(arctic.env)
data(arctic.pollen)

mMAT <- multi.mat(arctic.pollen, arctic.env[,9:67], noanalogues = 5)
```

---

obs.cor	<i>Weighted correlation between weighted averaging optima and constrained ordination species scores.</i>
---------	--

---

## Description

obs.cor calculates the weighted correlation between the species weighted average optima and the axis one species scores of an ordination constrained by the WA reconstruction.

## Usage

```
obs.cor(spp, env, fos, ord = rda, n = 99, min.occure = 1, autosim,
  permute = FALSE)

## S3 method for class 'obscor'
plot(x, xlab, ylab, f = 5, which = 1,
  variable_names = "env", abund = "abund.calib", p_val = 0.05, ...)

## S3 method for class 'obscor'
identify(x, labels, ...)

## S3 method for class 'obscor'
autoplot(x, which = 1, variable_names = "env",
  abund = "abund.calib", p_val = 0.05, nbins = 20, top = 0.7, ...)
```

## Arguments

spp	Data frame of modern training set species data, transformed if required, for example with sqrt
env	Vector of a single environmental variable
fos	Data frame of fossil species data. Species codes and transformations should match those in spp.
ord	Constrained ordination method to use. <code>rda</code> is the default, <code>cca</code> should also work. <code>capscale</code> won't work without modifications to the code (or a wrapper).
n	number of random training sets. More is better.
min.occure	Minimum number of occurrences of species in the species and fossil data.

autosim	Optional data frame of random values. This is useful if the training set is spatially autocorrelated and the supplied data frame contains autocorrelated random variables. If autosim is missing, and permute is FALSE, the transfer functions are trained on random variables drawn from a uniform distribution.
permute	logical value. Generate random environmental variables by permuting existing variable. Only possible if there is only one environmental variable and autosim is missing.
x	An obscor object.
xlab	X-axis label if the default is unsatisfactory.
ylab	Y-axis label if the default is unsatisfactory.
f	Scale factor for the abundances, the maximum cex of points for the which=1 plot.
which	Which type of plot. which = 1 gives a plot of RDA scores against species optima. which = 2 gives a histogram showing the null distribution of correlations between RDA scores and species optima, together with the observed correlation.
variable_names	Name of environmental variable (only 1 currently) for the label on the observed correlation with which = 2
abun	Which species weighting required for plots. See details
p_val	P value to draw a line vertical line at (with which=2)
...	Other arguments to plot or identify
labels	Labels for the points in identify. By default, the species names from intersection of colnames(spp) and colnames(fos) are used.
nbins	integer giving number of bins for the histogram
top	Proportion of the figure below the environmental name labels.

### Details

Obs.cor calculates the (weighted) correlation between the species WA optima in the calibration set and their ordination axis one scores in the fossil data. Seven different weights for the species are implimented.

- "abun.fos" - weight by the mean abundance in the fossil data.
- "abun.calib" - weight by the mean abundance in the calibration data
- "abun.joint" - weight by the product of the mean abundance in the fossil and calibration data
- "n2.fos" - weight by the effective number of occurences (Hill's N2) of each species in the fossil data
- "n2.calib" - weight by the effective number of occurences (Hill's N2) of each species in the calibration data
- "n2.joint" - weight by the product of n2.calib and n2.fos
- "unweighted" - all species recieve same weight. This is unlikely to be the best option but is included for completeness.

It is unclear which of these weights is likely to be best, research is in progress. A square root transformation of the species data is often useful. n = 99 is too small in practice to give a smooth histogram of the null model. n = 999 is better.

**Value**

obs.cor returns an obscor object, which is a list

- ob Observed correlation. Data.frame with columns Optima, RDA1 and abun containing the species optima, ordination axis 1 scores, and abundance used to weight the species respectively and a vector containing the weighted and unweighted correlations between species optima and ordination scores.
- sim Matrix with the correlation between species weighted average optima and ordination scores in the first column and the weighted correlation in the second column. Each row represents a different random environmental variable.
- sigs p-value for the observed correlation between species weighted average optima and ordination scores for each of the weights.

**Methods (by generic)**

- plot: Plots for obscor object
- identify: Identify species on obs.cor plot
- autoplot: autoplots for obscor object

**Note**

The test of the weighted correlation between species optima and ordination axis scores is more powerful, especially with a small number of fossil observations, than the test of variance explained in [randomTF](#) but is only applicable to WA and will have a large type II error if there are few species.

**Author(s)**

Richard Telford <[richard.telford@uib.no](mailto:richard.telford@uib.no)>

**References**

Telford, R. J. and Birks, H. J. B. (2011) A novel method for assessing the statistical significance of quantitative reconstructions inferred from biotic assemblages. *Quaternary Science Reviews* **30**: 1272–1278. DOI: [10.1016/j.quascirev.2011.03.002](https://doi.org/10.1016/j.quascirev.2011.03.002)

**See Also**

[randomTF](#), [WA](#), [rda](#), [cca](#)

**Examples**

```
require(rioja)
data(SWAP)
data(RLGH)
rlgh.obs <- obs.cor(spp = sqrt(SWAP$spec), env = SWAP$pH, fos = sqrt(RLGH$spec))
rlgh.obs$sig
plot(rlgh.obs, which=1)
plot(rlgh.obs, which=2)
```

```
require(ggplot2)
autoplot(rlgh.obs, which=1)
autoplot(rlgh.obs, which=2, variable_names = "pH")
```

---

plot.fittedAgelme      *Plots fitted agelme model and dates*

---

### Description

Plots fitted agelme model and dates

### Usage

```
## S3 method for class 'fittedAgelme'
plot(x, main, xlab = "Depth",
     ylab = "Calibrated Age", ...)
```

### Arguments

x	Fitted agelme model.
main	Title of the plot.
xlab	xlabel of the plot.
ylab	ylabel of the plot.
...	Other arguments to plot.

### Examples

```
data(STOR)
fit.mod <- with(STOR, agelme(depthup, depthdo, cageup, cagedo))
#Predicting using the constant variance model,
#for each cm between 70 and 400 cm.
fit.pre <- predict(fit.mod, 1, 70:400)
plot(fit.pre)
```

---

predict.agelme      *Predicts the Calibrated age*

---

### Description

This function uses the output from 'agelme' to predict the Calibrated ages for specified depths.

### Usage

```
## S3 method for class 'agelme'
predict(object, v = 1, depth,...)
```

**Arguments**

object	An 'agelme' model
v	Using constant (1) or mu (2) variance
depth	A vector of the depths to be predicted
...	Other arguments, currently unused.

**Value**

A list with three items

- v Whether constant variance or mu variance used.
- fit A data.frame of the predictions including 95% confidence interval.
  - DepthThe depths for the predicted ages
  - EstagePredicted age
  - LowlimLower 95% confidence interval
  - UpplimUpper 95% confidence interval
  - TsdTotal standard deviation
- data A data.frame containing the age and depth information of the radiocarbon dates.

**Author(s)**

Einar Heegaard <einar.heegaard@bio.bui.no

**References**

Heegaard, E., Birks, HJB. & Telford, RJ. 2005. Relationships between calibrated ages and depth in stratigraphical sequences: an estimation procedure by mixed-effect regression. *The Holocene* 15: 612-618

**Examples**

```
data(STOR)

fit.mod <- with(STOR, agelme(depthup, depthdo, cageup, cagedo))

#Predicting using the constant variance model,
#for each cm between 70 and 400 cm.
fit.pre <- predict(fit.mod, 1, 70:400)
plot(fit.pre)
```

---

randomTF	<i>Proportion of variance in the fossil data explained by an environmental reconstruction</i>
----------	---

---

## Description

Calculate the proportion of variance in the fossil data explained by an environmental reconstruction with a constrained ordination. This value is compared with a null distribution calculated as the proportion of variance in the fossil data explained by reconstructions from transfer functions trained on random data.

## Usage

```
randomTF(spp, env, fos, n = 99, fun, col, condition, autosim, ord = rda,
         permute = FALSE, models, make_models = FALSE, ...)
```

```
## S3 method for class 'palaeoSig'
plot(x, variable_names, top = 0.7, adj = c(0, 0.5),
     p_val = 0.05, ...)
```

```
## S3 method for class 'palaeoSig'
autoplot(x, variable_names, nbins = 20, top = 0.7,
         p_val = 0.05)
```

## Arguments

spp	Data frame of modern training set species data, transformed as required for example with <code>sqrt</code>
env	Data frame of training set environmental variables or vector with single environmental variable
fos	Data frame of fossil species data, with same species codes and transformations as <code>spp</code>
n	number of random training sets. More is better.
fun	Transfer function method. Additional arguments to <code>fun</code> can be passed with <code>...</code>
col	Some transfer functions return more than one column of results, for example with different <a href="#">WAPLS</a> components. <code>col</code> selects which column to use. See the relevant transfer function method help file.
condition	Optional data frame of reconstructions to partial out when testing if multiple independent reconstructions are possible.
autosim	Optional data frame of random values. This is useful if the training set is spatially autocorrelated and the supplied data frame contains autocorrelated random variables. If <code>autosim</code> is missing, and <code>permute</code> is <code>FALSE</code> , the transfer functions are trained on random variables drawn from a uniform distribution.
ord	Constrained ordination method to use. <code>rda</code> is the default, <code>cca</code> should also work. <code>capscale</code> won't work without modifications to the code (or a wrapper).

permute	logical value. Generate random environmental variables by permuting existing variable. Only possible if there is only one environmental variable and autosim is missing.
models	list of models made by randomTF with argument make_models = TRUE
make_models	logical, should a list of transfer functions trained on random data be returned
...	Other arguments to the transfer function. For example to change the distance metric in <a href="#">MAT</a> . Also extra arguments to plot.
x	Output from randomTF
variable_names	Names of environmental variables. If missing, taken from env data.frame.
top	Proportion of the figure below the environmental name labels.
adj	Adjust the position that the environmental names are plotted at.
p_val	P value to draw a line vertical line at (with which=2)
nbins	integer giving number of bins for the histogram

## Details

The function calculates the proportion of variance in the fossil data explained by the transfer function reconstruction. This is compared with a null distribution of the proportion of variance explained by reconstructions based on random environmental variables. Reconstructions can be partialled out to test if multiple reconstructions are statistically significant. If the environment is spatially auto-correlated, a red-noise null should be used instead of the default white noise null. The red noise environmental variables can be generated with the **gstat** package.

Any transfer function in the **rioja** package can be used. Other methods (e.g. random forests) can be used by making a wrapper function.

If reconstructions from several sites are to be tested using the same training set it can be much faster to train the models on random environmental data once and then use them repeatedly. This can be done with `make_models = TRUE` and then running `randomTF` again giving the resultant models to the `models` argument. `make_models` does not work with `MAT`.

## Value

A list with components

- `PCA` The unconstrained ordination of the fossil data.
- `preds` A list of the containing the reconstructions for each environmental variable.
- `MAX` Proportion of the variance explained by the first axis of the unconstrained ordination. This is the maximum amount that a reconstruction of a single variable can explain.
- `EX` The proportion of the variance in the fossil data explained by each reconstruction.
- `sim.ex` The proportion of variance explained by each of the random environmental variables.
- `sig` The p-value of each reconstruction.

If `make_models = TRUE`, a list of transfer function models is returned.

`autoplot.palaeoSig` returns a `ggplot2` object

### Methods (by generic)

- plot: Plot palaeoSig object
- autoplot: autoplot function for palaeoSig object

### Note

If there are only a few fossil levels, [obs.cor](#) might have more power. If there are few taxa, tests on [MAT](#) reconstructions have more statistical power than those based on [WA](#).

### Author(s)

Richard Telford <[richard.telford@uib.no](mailto:richard.telford@uib.no)>

### References

Telford, R. J. and Birks, H. J. B. (2011) A novel method for assessing the statistical significance of quantitative reconstructions inferred from biotic assemblages. *Quaternary Science Reviews* **30**: 1272–1278. DOI: [10.1016/j.quascirev.2011.03.002](https://doi.org/10.1016/j.quascirev.2011.03.002)

### See Also

[obs.cor](#), [WA](#), [MAT](#), [WAPLS](#), [rda](#), [cca](#)

### Examples

```
require(rioja)
data(SWAP)
data(RLGH)
rlghr <- randomTF(spp = sqrt(SWAP$spec), env = data.frame(pH = SWAP$pH),
fos = sqrt(RLGH$spec), n = 99, fun = WA, col = 1)
rlghr$sig
plot(rlghr, "pH")

require("ggplot2")
autoplot(rlghr, "pH")
```

---

rne

*Random, neighbour, environment deletion analysis for transfer function model*

---

### Description

Calculates effect of deleting sites from training set at random, from a geographic neighbourhood, or from an environmental neighbourhood. A simple graphical technique for gauging the effect of spatial autocorrelation on the transfer function model.

**Usage**

```
rne(y, env, geodist, fun, neighbours, subsets = c(1, 0.75, 0.5, 0.25, 0.1), ...)
## S3 method for class 'RNE'
plot(x, which=1, ylim, ...)
```

**Arguments**

y	Community data, or distance object, or distance matrix
env	Environmental variable
geodist	Matrix of geographical distances between sites
fun	Transfer function
neighbours	Neighbourhood radii
subsets	Proportion of sites to retain in random deletion
...	Arguments passed to fun or plot
x	RNE object to be plotted
which	Which column of the results to plot eg if more than one WAPLS component is calculated
ylim	Y-limits of the plot

**Details**

Finds the leave-one-out transfer function performance if sites are deleted at random (repeated 10 times to reduce variance in results), from a neighbourhood zone, or by deleting environmentally close sites.

**Value**

Returns an RNE object, list with two components

random	Performance with random deletion.
neighbour	Performance with deletion by neighbourhood, or environment

**Author(s)**

Richard Telford <Richard.Telford@bio.uib.no>

**References**

Telford, R. J. and Birks, H. J. B. (2009) Evaluation of transfer functions in spatially structured environments. *Quaternary Science Reviews* **28**: 1309–1316. DOI: 10.1016/j.quascirev.2008.12.020

**Examples**

```
require(fields)
require(rioja)
data(arctic.env)
data(arctic.pollen)

#using just the first 100 sites so code runs in an reasonable time, but still slow
arctic.d <- rdist.earth(arctic.env[1:100,c("Longitude","Latitude")], miles = FALSE)

arctic.rne <- rne(y = arctic.pollen[1:100,], env = arctic.env$tjul[1:100],
  geodist = arctic.d, fun = MAT, neighbours = c(0,50,200),
  subsets = c(1,.5,.1), k = 5)
plot(arctic.rne)
```

---

species

*Generates species response parameters for n dimensions*


---

**Description**

Generates species response parameters to n environmental variables following Minchin (1987).

**Usage**

```
species(nspp=30, Amax, fun, xpar, srange, alpha = 4, gamma= 4, ndim, sdistr, ocor, odistr)
```

**Arguments**

nspp	Number of species to be generated.
Amax	Maximum abundance of a species. Amax currently allows three options: i) a function how to generate maximum abundances (e.g. runif, rgamma) ii) a vector of length nspp iii) a single number that is used as maximum abundance for all the species.
fun	Function to generate species optima (e.g. rnorm, runif). The two parameters in xpar are passed to function fun. If omitted species optima are generated at regular intervals between the two values in xpar.
xpar	Two numbers describing a distribution e.g mu and sigma for a normal distribution, lower and upper bound for a random uniform distribution.
srange	Length of the ecological gradient to which individual species respond. Either one number or a matrix with nspp rows and ndim columns. If srange should be different for different environmental variables a simpler solution is to change argument elen in <a href="#">make.env</a> accordingly. E.g. elen =c(100,50,50) when using three environmental gradients.

alpha	Shape parameter of the beta distribution. One number or a matrix with nspp rows and ndim columns.
gamma	Shape parameter of the beta distribution. One number or a matrix with nspp rows and ndim columns.
ndim	Number of environmental variables to which generated species should respond.
sdistr	Users may supply own distributions of species optima. Matrix with nspp rows and ndim columns (as well in the special case of ndim = 1).
ocor	Correlation matrix of the species optima. May be generated by code <a href="#">cor.mat.fun</a> .
odistr	Distribution of the correlated optima either 'uniform' or 'Gaussian'

### Details

Details on the exact generation of species response functions from parameters Amax, m, r, gamma and alpha are given in Minchin (1987). Species response curves are determined by five parameters: a parameter determining the maximum abundance (Amax) and one describing the location (m) of this mode. A parameter determining to which environmental range the species respond (srange in the input r in the output) and two parameters (alpha, gamma) describing the shape of the species response function. If alpha = gamma the response curve is symmetric (alpha = gamma = 4, yields Gaussian distributions). Additionally, species optima for several environmental variables may be correlated. Currently this is only possible for gaussian or uniform distributions of species optima. Users may as well supply previously generated optima (e.g. optima similar to a real dataset).

### Value

List with ndim elements. Each list contains the species response parameters to one environmental gradient.

### Author(s)

Mathias Trachsel and Richard J. Telford

### References

Minchin, P.R. (1987) Multidimensional Community Patterns: Towards a Comprehensive Model. *Vegetatio*, 71, 145-156.

### Examples

```
spec.par <- species(nspp = 30, Amax = runif, srange = 200, fun = runif, xpar = c(-50,150),
ndim = 5, alpha = 4, gamma = 4)
spec.par <- species(nspp = 30, ndim = 3, Amax = runif, xpar = c(-50,150),
srange = 200, alpha = 4, gamma = 4)

# example where srange, alpha and gamma are different for each species and environmental gradient.
spec.par <- species(nspp = 30, ndim = 3, Amax = runif, xpar = c(-50,150),
srange = matrix(ncol = 3, runif(90,100,200)), alpha = matrix(ncol = 3, runif(90,1,5)),
gamma = matrix(ncol = 3, runif(90,1,5)))

# example where species optima are correlated
```

```

correlations <- list(c(1, 2, 0.5),c(1, 3, 0.3),c(2, 3, 0.1))
spec.cor.mat <- cor.mat.fun(3, correlations)
spec.par <- species(nspp = 30, ndim = 3, Amax = runif, xpar = c(50, 50), srange = 200,
alpha = 4, gamma = 4, ocor = spec.cor.mat, odistr = 'Gaussian')

# example for species response curves (users should alter alpha and gamma)
spec.par <- species(nspp = 1, Amax = 200, srange = 200, fun = runif, xpar = c(50, 50),
  ndim = 1, alpha = 3, gamma = 1)
env <- -50:150
response <- palaeoSig:::make.abundances(env = -50:150, param = spec.par[[1]]$spp)
plot(env, response, type='l')

```

---

 STOR

*Storsandsvatnet*


---

## Description

Storsandsvatnet is a lake in western Norway. From the sediments a core was obtained, and 11 samples was submitted for radiocarbon dating. The data contain the depths of the slides dated and the younger and older calibrated ages for each slide.

## Usage

STOR

## Format

A data.frame with 11 observations on the following 4 variables.

**depthup** The upper border of the dated slide

**depthdo** The lower border of the dated slide

**ageup** The younger calibrated age of the dated slide

**agedo** The older calibrated age of the dated slide

## Details

The calibrated ages is obtained by calibration of the radiocarbon dates. The borders represent mean calibrated age +/- 1 SD of calibrated age.

## Source

The data are unpublished and provided by H. John B. Birks <john.birks@bio.uib.no> and Sylvia M. Peglar

## References

Heegaard, E., Birks, HJB. & Telford, RJ. 2005. Relationships between calibrated ages and depth in stratigraphical sequences: an estimation procedure by mixed-effect regression. *The Holocene* 15: 612-618

*STOR*

29

**Examples**

`data(STOR)`

# Index

- \* **attribute**
    - Hill.N2.core, 11
  - \* **datagen**
    - abundances, 3
    - cor.mat.fun, 9
    - make.env, 13
    - make.set, 14
    - species, 26
  - \* **datasets**
    - arctic.pollen, 7
    - Atlantic, 7
    - STOR, 28
  - \* **hplot**
    - jointsig, 12
    - obs.cor, 17
    - randomTF, 22
  - \* **htest**
    - jointsig, 12
    - obs.cor, 17
    - randomTF, 22
  - \* **manip**
    - anamorph, 6
  - \* **multivariate**
    - jointsig, 12
    - multi.mat, 16
    - obs.cor, 17
    - randomTF, 22
    - rne, 24
  - \* **package**
    - palaeoSig-package, 2
- abundances, 3  
agelme, 4  
anamorph, 6  
arctic.env (arctic.pollen), 7  
arctic.pollen, 7  
Atlantic, 7  
autoplot.obscor (obs.cor), 17  
autoplot.palaeoSig (randomTF), 22  
capscale, 17, 22  
caterpillar, 8  
cca, 17, 19, 22, 24  
centipede\_plot, 8  
cor.mat.fun, 9, 14, 15, 27  
coverage\_plot, 10  
ggplot, 8, 10  
Hill.N2, 11  
Hill.N2.core, 11  
identify.obscor (obs.cor), 17  
jointsig, 12  
make.env, 3, 4, 9, 13, 15, 26  
make.set, 14  
MAT, 23, 24  
multi.mat, 16  
obs.cor, 2, 13, 17, 24  
palaeoSig (palaeoSig-package), 2  
palaeoSig-package, 2  
plot.fittedAgelme, 20  
plot.js (jointsig), 12  
plot.obscor (obs.cor), 17  
plot.palaeoSig (randomTF), 22  
plot.RNE (rne), 24  
predict.agelme, 20  
randomTF, 2, 13, 19, 22  
rda, 3, 17, 19, 22, 24  
rioja, 3  
rne, 2, 24  
species, 3, 4, 9, 15, 26  
STOR, 28  
WA, 8, 19, 24  
WAPLS, 22, 24