Package 'BiodiversityR'

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Type Package

Title Package for Community Ecology and Suitability Analysis

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Description Graphical User Interface (via the R-Commander) and utility functions (often based on the vegan package) for statistical analysis of biodiversity and ecological communities, including species accumulation curves, diversity indices, Renyi profiles, GLMs for analysis of species abundance and presence-absence, distance matrices, Mantel tests, and cluster, constrained and unconstrained ordination analysis. A book on biodiversity and community ecology analysis is available for free download from the website. In 2012, methods for (ensemble) suitability modelling and mapping were expanded in the package.

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URL http://www.worldagroforestry.org/output/tree-diversity-analysis

Depends R (>= 3.2.2), tcltk, vegan (>= 2.5-1), vegan3d, rgl

Imports Rcmdr (>= 2.5-3)

Suggests permute, lattice, MASS, mgcv, cluster, car, RODBC, rpart, effects, multcomp, ellipse, maptree, sp, splancs, spatial, akima, nnet, dismo, raster (>= 2.8-19), rgdal, maxlike, gbm, randomForest, gam (>= 1.15), earth, mda, kernlab, e1071, glmnet, tools, methods, bootstrap, PresenceAbsence, geosphere, maptools, ENMeval, red, rgeos, igraph, Rlof, maxnet, party, readxl, colorspace

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`BiodiversityR-package` *GUI for biodiversity, suitability and community ecology analysis*

Description

This package provides a GUI (Graphical User Interface, via the R-Commander; `BiodiversityRGUI`) and some utility functions (often based on the vegan package) for statistical analysis of biodiversity and ecological communities, including species accumulation curves, diversity indices, Renyi profiles, GLMs for analysis of species abundance and presence-absence, distance matrices, Mantel tests, and cluster, constrained and unconstrained ordination analysis. A book on biodiversity and community ecology analysis is available for free download from the website.

Details

We warmly thank all that provided inputs that lead to improvement of the Tree Diversity Analysis manual that describes common methods for biodiversity and community ecology analysis and its accompanying software. We especially appreciate the comments received during training sessions with draft versions of this manual and the accompanying software in Kenya, Uganda and Mali. We are equally grateful to the thoughtful reviews by Dr Simoneta Negrete-Yankelevich (Instituto de Ecologia, Mexico) and Dr Robert Burn (Reading University, UK) of the draft version of this manual, and to Hillary Kipruto for help in editing of this manual. We also want to specifically thank Mikkel Grum, Jane Poole and Paulo van Breugel for helping in testing the packaged version of the software. We also want to give special thanks for all the support that was given by Jan Beniest, Tony Simons and Kris Vanhoutte in realizing the book and software.

We highly appreciate the support of the Programme for Cooperation with International Institutes (SII), Education and Development Division of the Netherlands Ministry of Foreign Affairs, and VVOB (The Flemish Association for Development Cooperation and Technical Assistance, Flanders, Belgium) for funding the development for this manual. We also thank VVOB for seconding Roeland Kindt to the World Agroforestry Centre (ICRAF). The tree diversity analysis manual was inspired by research, development and extension activities that were initiated by ICRAF on tree and landscape diversification. We want to acknowledge the various donor agencies that have funded these activities, especially VVOB, DFID, USAID and EU.

We are grateful for the developers of the R Software for providing a free and powerful statistical package that allowed development of BiodiversityR. We also want to give special thanks to Jari Oksanen for developing the vegan package and John Fox for developing the Rcmdr package, which are key packages that are used by BiodiversityR.

Author(s)

Maintainer: Roeland Kindt (World Agroforestry Centre)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

We suggest to use this citation for this software as well (together with citations of all other packages that were used)

`accumresult` *Alternative Species Accumulation Curve Results*

Description

Provides alternative methods of obtaining species accumulation results than provided by functions `specaccum` and `plot.specaccum` (**vegan**).

Usage

```
accumresult(x, y="", factor="", level, scale="", method="exact", permutations=100,
    conditioned=T, gamma="boot", ...)

accumplot(xr, addit=F, labels="", col=1, ci=2, pch=1, type="p", cex=1,
    xlim=c(1, xmax), ylim=c(1, rich),
    xlab="sites", ylab="species richness", cex.lab=1, cex.axis=1, ...)

accumcomp(x, y="", factor, scale="", method="exact", permutations=100,
    conditioned=T, gamma="boot", plotit=T, labelit=T, legend=T, rainbow=T,
    xlim=c(1, max), ylim=c(0, rich),type="p", xlab="sites",
    ylab="species richness", cex.lab=1, cex.axis=1, ...)
```

Arguments

`x`	Community data frame with sites as rows, species as columns and species abundance as cell values.
`y`	Environmental data frame.
`factor`	Variable of the environmental data frame that defines subsets to calculate species accumulation curves for.
`level`	Level of the variable to create the subset to calculate species accumulation curves.
`scale`	Continuous variable of the environmental data frame that defines the variable that scales the horizontal axis of the species accumulation curves.
`method`	Method of calculating the species accumulation curve (as in function `specaccum`). Method "collector" adds sites in the order they happen to be in the data, "random" adds sites in random order, "exact" finds the expected (mean) species richness, "coleman" finds the expected richness following Coleman et al. 1982, and "rarefaction" finds the mean when accumulating individuals instead of sites.

permutations	Number of permutations to calculate the species accumulation curve (as in function specaccum).
conditioned	Estimation of standard deviation is conditional on the empirical dataset for the exact SAC (as in function specaccum).
gamma	Method for estimating the total extrapolated number of species in the survey area (as in specaccum).
addit	Add species accumulation curve to an existing graph.
xr	Result from specaccum or accumresult.
col	Colour for drawing lines of the species accumulation curve (as in function plot.specaccum).
labels	Labels to plot at left and right of the species accumulation curves.
ci	Multiplier used to get confidence intervals from standard deviatione (as in function plot.specaccum).
pch	Symbol used for drawing the species accumulation curve (as in function points).
type	Type of plot (as in function plot).
cex	Character expansion factor (as in function plot).
xlim	Limits for the X = horizontal axis.
ylim	Limits for the Y = vertical axis.
xlab	Label for the X = horizontal axis (as in function title).
ylab	Label for the Y = vertical axis (as in function title).
cex.lab	The magnification to be used for X and Y labels relative to the current setting of cex. (as in function par).
cex.axis	The magnification to be used for axis annotation relative to the current setting of cex (as in function par).
plotit	Plot the results.
labelit	Label the species accumulation curves with the levels of the categorical variable.
legend	Add the legend (you need to click in the graph where the legend needs to be plotted).
rainbow	Use rainbow colouring for the different curves.
...	Other items passed to function specaccum or plot.specaccum.

Details

These functions provide some alternative methods of obtaining species accumulation results, although function specaccum is called by these functions to calculate the actual species accumulation curve.

Functions accumresult and accumcomp allow to calculate species accumulation curves for subsets of the community and environmental data sets. Function accumresult calculates the species accumulation curve for the specified level of a selected environmental variable. Method accumcomp calculates the species accumulation curve for all levels of a selected environmental variable separatedly. Both methods allow to scale the horizontal axis by multiples of the average of a selected continuous variable from the environmental dataset (hint: add the abundance of each site to the environmental data frame to scale accumulation results by mean abundance).

Functions accumcomp and accumplot provide alternative methods of plotting species accumulation curve results, although function plot.specaccum is called by these functions. When you choose to add a legend, make sure that you click in the graph on the spot where you want to put the legend.

Value

The functions provide alternative methods of obtaining species accumulation curve results, although results are similar as obtained by functions specaccum and plot.specaccum.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(dune.env)
data(dune)
dune.env$site.totals <- apply(dune,1,sum)
Accum.1 <- accumresult(dune, y=dune.env, scale='site.totals', method='exact', conditioned=TRUE)
Accum.1
accumplot(Accum.1)
accumcomp(dune, y=dune.env, factor='Management', method='exact', legend=FALSE, conditioned=TRUE)
## CLICK IN THE GRAPH TO INDICATE WHERE THE LEGEND NEEDS TO BE PLACED FOR
## OPTION WHERE LEGEND=TRUE (DEFAULT).
```

---

add.spec.scores *Add Species Scores to Unconstrained Ordination Results*

Description

Calculates scores (coordinates) to plot species for PCoA or NMS results that do not naturally provide species scores. The function can also rescale PCA results to use the choice of rescaling used in **vegan** for the rda function (after calculating PCA results via PCoA with the euclidean distance first).

Usage

```
add.spec.scores(ordi,comm,method="cor.scores",multi=1,Rscale=F,scaling="1")
```

Arguments

ordi	Ordination result as calculated by cmdscale, isoMDS, sammon, postMDS, metaMDS or NMSrandom.
comm	Community data frame with sites as rows, species as columns and species abundance as cell values.

method	Method for calculating species scores. Method "cor.scores" calculates the scores by the correlation between site scores and species vectors (via function cor), method "wa.scores" calculates the weighted average scores (via function wascores) and method "pcoa.scores" calculates the scores by weighing the correlation between site scores and species vectors by variance explained by the ordination axes.
multi	Multiplier for the species scores.
Rscale	Use the same scaling method used by **vegan** for rda.
scaling	Scaling method as used by rda.

Value

The function returns a new ordination result with new information on species scores. For PCoA results, the function calculates eigenvalues (not sums-of-squares as provided in results from function cmdscale), the percentage of explained variance per axis and the sum of all eigenvalues. PCA results (obtained by PCoA obtained by function cmdscale with the Euclidean distance) can be scaled as in function rda, or be left at the original scale.

Author(s)

Roeland Kindt

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(dune)
distmatrix <-vegdist(dune, method="euc")
# Principal coordinates analysis with 19 axes to estimate total variance
Ordination.model1 <- cmdscale (distmatrix, k=19, eig=TRUE, add=FALSE)
# Change scores for second axis
Ordination.model1$points[,2] <- -1.0 * Ordination.model1$points[,2]
Ordination.model1 <- add.spec.scores(Ordination.model1, dune,
    method='pcoa.scores', Rscale=TRUE, scaling=1, multi=1)
# Compare Ordination.model1 with PCA
Ordination.model2 <- rda(dune, scale=FALSE)
#
par(mfrow=c(1,2))
ordiplot(Ordination.model1, type="text")
abline(h = 0, lty = 3)
abline(v = 0, lty = 3)
plot(Ordination.model2, type="text", scaling=1)
```

`balanced.specaccum` *Balanced Species Accumulation Curves*

Description

Provides species accumulation results calculated from balanced (equal subsample sizes) subsampling from each stratum. Sites can be accumulated in a randomized way, or alternatively sites belonging to the same stratum can be kept together Results are in the same format as `specaccum` and can be plotted with `plot.specaccum` (**vegan**).

Usage

```
balanced.specaccum(comm, permutations=100, strata=strata, grouped=TRUE,
    reps=0, scale=NULL)
```

Arguments

`comm`	Community data frame with sites as rows, species as columns and species abundance as cell values.
`permutations`	Number of permutations to calculate the species accumulation curve.
`strata`	Categorical variable used to specify strata.
`grouped`	Should sites from the same stratum be kept together (TRUE) or not.
`reps`	Number of subsamples to be taken from each stratum (see details).
`scale`	Quantitative variable used to scale the sampling effort (see details).

Details

This function provides an alternative method of obtaining species accumulation results as provided by `specaccum` and `accumresult`.

Balanced sampling is achieved by randomly selecting the same number of sites from each stratum. The number of sites selected from each stratum is determined by `reps`. Sites are selected from strata with sample sizes larger or equal than `reps`. In case that `reps` is smaller than 1 (default: 0), then the number of sites selected from each stratum is equal to the smallest sample size of all strata. Sites from the same stratum can be kept together (grouped=TRUE) or the order of sites can be randomized (grouped=FALSE).

The results can be scaled by the average accumulation of a quantitative variable (default is number of sites), as in `accumresult` (hint: add the abundance of each site to the environmental data frame to scale accumulation results by mean abundance). When sites are not selected from all strata, then the average is calculated only for the strata that provided sites.

Value

The functions provide alternative methods of obtaining species accumulation curve results, although results are similar as obtained by functions `specaccum` and `accumresult`.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt, R., Kalinganire, A., Larwanou, M., Belem, M., Dakouo, J.M., Bayala, J. & Kaire, M. (2008) Species accumulation within landuse and tree diameter categories in Burkina Faso, Mali, Niger and Senegal. Biodiversity and Conservation. 17: 1883-1905.

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(dune.env)
data(dune)

# not balancing species accumulation
Accum.orig <- specaccum(dune)
Accum.orig

# randomly sample 3 quadrats from each stratum of Management
Accum.1 <- balanced.specaccum(dune, strata=dune.env$Management, reps=3)
Accum.1

# scale results by number of trees per quadrat
dune.env$site.totals <- apply(dune,1,sum)
Accum.2 <- balanced.specaccum(dune, strata=dune.env$Management, reps=3, scale=dune.env$site.totals)
Accum.2
```

BCI.env *Barro Colorado Island Quadrat Descriptions*

Description

Topography-derived variables and UTM coordinates and UTM coordinates of a 50 ha sample plot (consisting of 50 1-ha quadrats) from Barro Colorado Island of Panama. Dataset BCI provides the tree species composition (trees with diameter at breast height equal or larger than 10 cm) of the same plots.

Usage

```
data(BCI.env)
```

Format

A data frame with 50 observations on the following 6 variables.

`UTM.EW` UTM easting

`UTM.NS` UTM northing

`elevation` mean of the elevation values of the four cell corners

`convex` mean elevation of the target cell minus the mean elevation of the eight surrounding cells

`slope` mean angular deviation from horizontal of each of the four triangular planes formed by connecting three of its corners

`aspectEW` the sine of aspect

`aspectNS` the cosine of aspect

References

Pyke C.R., Condit R., Aguilar S. and Lao S. (2001). Floristic composition across a climatic gradient in a neotropical lowland forest. Journal of Vegetation Science 12: 553-566.

Condit R., Pitman N., Leigh E.G., Chave J., Terborgh J., Foster R.B., Nunez P., Aguilar S., Valencia R., Villa G., Muller-Landau H.C., Losos E. and Hubbell, S.P. (2002). Beta-diversity in tropical forest trees. Science 295: 666-669.

De Caceres M., P. Legendre, R. Valencia, M. Cao, L.-W. Chang, G. Chuyong, R. Condit, Z. Hao, C.-F. Hsieh, S. Hubbell, D. Kenfack, K. Ma, X. Mi, N. Supardi Noor, A. R. Kassim, H. Ren, S.-H. Su, I-F. Sun, D. Thomas, W. Ye and F. He. (2012). The variation of tree beta diversity across a global network of forest plots. Global Ecology and Biogeography 21: 1191-1202

Examples

```
data(BCI.env)
```

`BiodiversityR.changeLog`

changeLog file for BiodiversityR

Description

ChangeLog file

Usage

```
BiodiversityR.changeLog()
```

`BiodiversityRGUI` *GUI for Biodiversity, Community Ecology and Ensemble Suitability Analysis*

Description

This function provides a GUI (Graphical User Interface) for some of the functions of **vegan**, some other packages and some new functions to run biodiversity analysis, including species accumulation curves, diversity indices, Renyi profiles, rank-abundance curves, GLMs for analysis of species abundance and presence-absence, distance matrices, Mantel tests, cluster and ordination analysis (including constrained ordination methods such as RDA, CCA, db-RDA and CAP). In 2012 methods for ensemble suitability The function depends and builds on **Rcmdr**, performing all analyses on the community and environmental datasets that the user selects. A thorough description of the package and the biodiversity and ecological methods that it accomodates (including examples) is provided in the freely available Tree Diversity Analysis manual (Kindt and Coe, 2005) that is accessible via the help menu.

Usage

```
BiodiversityRGUI(changeLog = FALSE, backward.compatibility.messages = FALSE)
```

Arguments

`changeLog`	Show the changeLog file
`backward.compatibility.messages`	Some notes on backward compatiblity

Details

The function launches the R-Commander GUI with an extra menu for common statistical methods for biodiversity and community ecology analysis as described in the Tree Diversity Analysis manual of Roeland Kindt and Richard Coe (available via http://www.worldagroforestry.org/output/tree-diversity-analysis]) and expanded systematically with new functions that became available from the vegan community ecology package.

Since 2012, functions for ensemble suitability modelling were included in BiodiversityR. In 2016, a GUI was created for ensemble suitabilty modelling.

The R-Commander is launched by changing the location of the Rcmdr "etc" folder to the "etc" folder of BiodiversityR. As the files of the "etc" folder of BiodiversityR are copied from the Rcmdr, it is possible that newest versions of the R-Commander will not be launched properly. In such situations, it is possible that copying all files from the Rcmdr "etc" folder again and adding the BiodiversityR menu options to the Rcmdr-menus.txt is all that is needed to launch the R-Commander again. However, please alert Roeland Kindt about the issue.

BiodiversityR uses two data sets for biodiversity and community ecology analysis: the community dataset (or community matrix or species matrix) and the environmental dataset (or environmental matrix). The environmental dataset is the same dataset that is used as the "active dataset" of The R-Commander. (Note that you could sometimes use the same dataset as both the community and

environmental dataset. For example, you could use the community dataset as environmental dataset as well to add information about specific species to ordination diagrams. As another example, you could use the environmental dataset as community dataset if you first calculated species richness of each site, saved this information in the environmental dataset, and then use species richness as response variable in a regression analysis.) Some options of analysis of ecological distance allow the community matrix to be a distance matrix (the community data set will be interpreted as distance matrix via `as.dist` prior to further analysis).

For ensemble suitability modelling, different data sets should be created and declared such as the calibration stack, the presence data set and the absence data set. The ensemble suitability modelling menu gives some guidelines on getting started with ensemble suitability modelling.

Value

Besides launching the graphical user interface, the function gives some notes on backward compatibility.

Author(s)

Roeland Kindt (with some help from Jari Oksanen)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

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`CAPdiscrim` *Canonical Analysis of Principal Coordinates based on Discriminant Analysis*

Description

This function provides a method for CAP that follows the procedure as described by the authors of the ordination method (Anderson & Willis 2003). The CAP method implemented in **vegan** through `capscale` conforms more to distance-based Redundancy Analysis (Legendre & Anderson, 1999) than to the original description for CAP (Anderson & Willis, 2003).

Usage

```
CAPdiscrim(formula, data, dist="bray", axes=4, m=0, mmax=10, add=FALSE, permutations=0)
```

Arguments

`formula`	Formula with a community data frame (with sites as rows, species as columns and species abundance as cell values) or distance matrix on the left-hand side and a categorical variable on the right-hand side (only the first explanatory variable will be used).

data	Environmental data set.
dist	Method for calculating ecological distance with function vegdist: partial match to "manhattan", "euclidean", "canberra", "bray", "kulczynski", "jaccard", "gower", "morisita", "horn" or "mountford". This argument is ignored in case that the left-hand side of the formula already is a distance matrix.
axes	Number of PCoA axes (cmdscale) to provide in the result.
m	Number of PCoA axes to be investigated by discriminant analysis (lda). If m=0 then the number of axes that provides the best distinction between the groups is calculated (following the method of Anderson and Willis).
mmax	The maximum number of PCoA axes considered when searching (m=0) for the number of axes that provide the best classification success.
add	Add a constant to the non-diagonal dissimilarities such that the modified dissimilarities are Euclidean; see also cmdscale.
permutations	The number of permutations for significance testing.

Details

This function provides a method of Constrained Analysis of Principal Coordinates (CAP) that follows the description of the method by the developers of the method, Anderson and Willis. The method investigates the results of a Principal Coordinates Analysis (function cmdscale) with linear discriminant analysis (lda). Anderson and Willis advocate to use the number of principal coordinate axes that result in the best prediction of group identities of the sites.

Results may be different than those obtained in the PRIMER-e package because PRIMER-e does not consider prior probabilities, does not standardize PCOA axes by their eigenvalues and applies an additional spherical standardization to a common within-group variance/covariance matrix.

For permutations > 0, the analysis is repeated by randomising the observations of the environmental data set. The significance is estimated by dividing the number of times the randomisation generated a larger percentage of correct predictions.

Value

The function returns an object with information on CAP based on discriminant analysis. The object contains following elements:

PCoA	the positions of the sites as fitted by PCoA
m	the number of axes analysed by discriminant analysis
tot	the total variance (sum of all eigenvalues of PCoA)
varm	the variance of the m axes that were investigated
group	the original group of the sites
CV	the predicted group for the sites by discriminant analysis
percent	the percentage of correct predictions
percent.level	the percentage of correct predictions for different factor levels
x	the positions of the sites provided by the discriminant analysis
F	the squares of the singulare values of the discriminant analysis

manova	the results for MANOVA with the same grouping variable
signi	the significance of the percentage of correct predictions
manova	a summary of the observed randomised prediction percentages

The object can be plotted with ordiplot, and species scores can be added by add.spec.scores .

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Legendre, P. & Anderson, M.J. (1999). Distance-based redundancy analysis: testing multispecies responses in multifactorial ecological experiments. Ecological Monographs 69: 1-24.

Anderson, M.J. & Willis, T.J. (2003). Canonical analysis of principal coordinates: a useful method of constrained ordination for ecology. Ecology 84: 511-525.

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
library(MASS)
data(dune)
data(dune.env)
Ordination.model1 <- CAPdiscrim(dune~Management, data=dune.env,
    dist="bray", axes=2, m=0, add=FALSE)
Ordination.model1
plot1 <- ordiplot(Ordination.model1, type="none")
ordisymbol(plot1, dune.env, "Management", legend=TRUE)

# plot change in classification success against m
plot(seq(1:14), rep(-1000, 14), xlim=c(1, 14), ylim=c(0, 100), xlab="m",
    ylab="classification success (percent)", type="n")
for (mseq in 1:14) {
    CAPdiscrim.result <- CAPdiscrim(dune~Management, data=dune.env,
        dist="bray", axes=2, m=mseq)
    points(mseq, CAPdiscrim.result$percent)
}

#
```

caprescale *Rescaling of Capscale Results to Reflect Total Sums of Squares Of Distance Matrix*

Description

This is a simple function that rescales the ordination coordinates obtained from the distance-based redundancy analysis method implemented in **vegan** through capscale. The rescaling of the ordination coordinates results in the distances between fitted site scores in ordination results (scaling=1 obtained via ordiplot to be equal to the distances between sites on the axes corresponding to positive eigenvalues obtained from principal coordinates analysis (cmdscale).

Usage

```
caprescale(x,verbose=FALSE)
```

Arguments

x	Ordination result obtained with capscale.
verbose	Give some information on the pairwise distances among sites (TRUE) or not.

Details

The first step of distance-based redundancy analysis involves principal coordinates analysis whereby the distances among sites from a distance matrix are approximated by distances among sites in a multidimensional configuration (ordination). In case that the principal coordinates analysis does not result in negative eigenvalues, then the distances from the distance matrix are the same as the distances among the sites in the ordination. In case that the principal coordinates analysis results in negative eigenvalues, then the distances among the sites on all ordination axes are related to the sum of positive eigenvalues, a sum which is larger than the sum of squared distances of the distance matrix.

The distance-based redundancy analysis method implemented in **vegan** through capscale uses a specific rescaling method for ordination results. Function caprescale modifies the results of capscale so that an ordination with scaling=1 (a distance biplot) obtained viaordiplot preserves the distances reflected in the principal coordinates analysis implemented as the first step of the analysis. See Legendre and Legendre (1998) about the relationship between fitted site scores and eigenvalues.

Value

The function modifies and returns an object obtained via capscale.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Legendre, P. & Legendre, L. (1998). Numerical Ecology. Amsterdam: Elsevier. 853 pp.

Legendre, P. & Anderson, M.J. (1999). Distance-based redundancy analysis: testing multispecies responses in multifactorial ecological experiments. Ecological Monographs 69: 1-24.

Examples

```
library(vegan)
library(MASS)
data(dune)
data(dune.env)
Distmatrix.1 <- vegdist(dune,method='bray')
Ordination.model1 <- cmdscale(Distmatrix.1, k=19, eig=TRUE, add=FALSE)
# Sum of all eigenvalues
sum(Ordination.model1$eig)
# [1] 4.395807541512926
sum(Ordination.model1$eig[1:14])
# [1] 4.593946896588808
Distmatrix.2 <- as.matrix(vegdist(Ordination.model1$points[,1:14],method='euc'))
totalsumsquares1 <- sum(Distmatrix.2^2)/(2*20)
# Sum of distances among sites in principal coordinates analysis on axes
# corresponding to positive eigenvalues
totalsumsquares1
# [1] 4.593946896588808
Ordination.model2 <- capscale(dune ~ Management,dune.env,dist='bray', add=FALSE)
# Total sums of positive eigenvalues of the distance-based redundancy analysis
Ordination.model2$CA$tot.chi+Ordination.model2$CCA$tot.chi
# [1] 4.593946896588808
Ordination.model3 <- caprescale(Ordination.model2, verbose=TRUE)
sum1 <- summary(Ordination.model3,axes=17,scaling=1)$constraints
Distmatrix.3 <- as.matrix(vegdist(sum1 ,method='euc'))
totalsumsquares2 <- sum((Distmatrix.3)^2)/(2*20)/19
totalsumsquares2
# [1] 4.593946896588808
```

`crosstabanalysis` *Presence-absence Analysis by Cross Tabulation*

Description

This function makes a cross-tabulation of two variables after transforming the first variable to presence-absence and then returns results of `chisq.test`.

Usage

```
crosstabanalysis(x,variable,factor)
```

Arguments

x	Data set that contains the variables "variable" and "factor".
variable	Variable to be transformed in presence-absence in the resulting cross-tabulation.
factor	Variable to be used for the cross-tabulation together with the transformed variable.

Value

The function returns the results of chisq.test on a crosstabulation of two variables, after transforming the first variable to presence-absence first.

Author(s)

Roeland Kindt

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(dune.env)
crosstabanalysis(dune.env,"Manure","Management")
```

---

deviancepercentage *Calculate Percentage and Significance of Deviance Explained by a GLM*

Description

This function calculates the percentage of deviance explained by a GLM model and calculates the significance of the model.

Usage

```
deviancepercentage(x,data,test="F",digits=2)
```

Arguments

x	Result of GLM as calculated by glm or glm.nb.
data	Data set to be used for the null model (preferably the same data set used by the 'full' model).
test	Test statistic to be used for the comparison between the null model and the 'full' model as estimated by anova.glm or anova.negbin: partial match of one of "Chisq", "F" or "Cp".
digits	Number of digits in the calculation of the percentage.

Details

The function calculates the percentage of explained deviance and the significance of the 'full' model by contrasting it with the null model.

For the null model, the data is subjected to na.omit. You should check whether the same data are used for the null and 'full' models.

Value

The function calculates the percentage of explained deviance and the significance of the 'full' model by contrasting it with the null model by ANOVA. The results of the ANOVA are also provided.

Author(s)

Roeland Kindt

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(dune)
data(dune.env)
dune.env$Agrostol <- dune$Agrostol
Count.model1 <- glm(Agrostol ~ Management + A1, family=quasipoisson(link=log),
    data=dune.env, na.action=na.omit)
summary(Count.model1)
deviancepercentage(Count.model1, dune.env, digits=3)
```

dist.eval *Distance Matrix Evaluation*

Description

Function `dist.eval` provides one test of a distance matrix, and then continues with `distconnected` (**vegan**). Function `prepare.bioenv` converts selected variables to numeric variables and then excludes all categorical variables in preparation of applying `bioenv` (**vegan**).

Usage

```
dist.eval(x, dist)
prepare.bioenv(env, as.numeric = c())
```

Arguments

`x`	Community data frame with sites as rows, species as columns and species abundance as cell values.
`env`	Environmental data frame with sites as rows and variables as columns.
`dist`	Method for calculating ecological distance with function `vegdist`: partial match to "manhattan", "euclidean", "canberra", "clark", "bray", "kulczynski", "jaccard", "gower", "morisita", "horn" or "mountford".
`as.numeric`	Vector with names of variables in the environmental data set to be converted to numeric variables.

Details

Function `dist.eval` provides two tests of a distance matrix:

(i) The first test checks whether any pair of sites that share some species have a larger distance than any other pair of sites that do not share any species. In case that cases are found, then a warning message is given.

(ii) The second test is the one implemented by the `distconnected` function (**vegan**). The distconnected test is only calculated for distances that calculate a value of 1 if sites share no species (i.e. not manhattan or euclidean), using the threshold of 1 as an indication that the sites do not share any species. Interpretation of analysis of distance matrices that provided these warnings should be cautious.

Function `prepare.bioenv` provides some simple methods of dealing with categorical variables prior to applying `bioenv`.

Value

The function tests whether distance matrices have some desirable properties and provide warnings if this is not the case.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(dune)
dist.eval(dune,"euclidean")
dist.eval(dune,"bray")

## Not run:
data(dune.env)
dune.env2 <- dune.env[,c('A1', 'Moisture', 'Manure')]
dune.env2$Moisture <- as.numeric(dune.env2$Moisture)
dune.env2$Manure <- as.numeric(dune.env2$Manure)
sol <- bioenv(dune ~ A1 + Moisture + Manure, dune.env2)
sol
summary(sol)
dune.env3 <- prepare.bioenv(dune.env, as.numeric=c('Moisture', 'Manure'))
bioenv(dune, dune.env3)

## End(Not run)
```

---

dist.zeroes *Distance Matrix Transformation*

Description

Sample units without any species result in "NaN" values in the distance matrix for some of the methods of vegdist (**vegan**). The function replaces "NA" by "0" if both sample units do not contain any species and "NA" by "1" if only one sample unit does not have any species.

Usage

```
dist.zeroes(comm,dist)
```

Arguments

comm	Community data frame with sites as rows, species as columns and species abundance as cell values.
dist	Distance matrix as calculated with function vegdist.

Details

This functions changes a distance matrix by replacing "NaN" values by "0" if both sample units do not contain any species and by "1" if only one sample unit does not contain any species.

Please note that there is a valid reason (deliberate removal of zero abundance values from calculations) that the original distance matrix contains "NaN", so you may not wish to do this transformation and remove sample units with zero abundances from further analysis.

Value

The function provides a new distance matrix where "NaN" values have been replaced by "0" or "1".

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
matrix <- array(0,dim=c(5,3))
matrix[4,] <- c(1,2,3)
matrix[5,] <- c(1,0,0)
dist1 <- vegdist(matrix,method="kulc")
dist1
dist2 <- dist.zeroes(matrix,dist1)
dist2
```

---

distdisplayed *Compare Distance Displayed in Ordination Diagram with Distances of Distance Matrix*

Description

This function compares the distance among sites as displayed in an ordination diagram (generated by ordiplot) with the actual distances among sites as available from a distance matrix (as generated by vegdist).

Usage

```
distdisplayed(x, ordiplot, distx = "bray", plotit = T, addit = F,
    method = "spearman", permutations = 100, abline = F, gam = T, ...)
```

Arguments

x	Community data frame (with sites as rows, species as columns and species abundance as cell values) or distance matrix.
ordiplot	Ordination diagram generated by ordiplot or distance matrix.
distx	Ecological distance used to calculated the distance matrix (theoretically the same distance as displayed in the ordination diagram); passed to vegdist and partial match to "manhattan", "euclidean", "canberra", "bray", "kulczynski", "jaccard", "gower", "morisita", "horn", "mountford", "raup" , "binomial" or "chao". This argument is ignored in case that "x" is already a distance matrix.
plotit	Should a plot comparing the distance in ordination diagram (or the distance matrix) with the distance from the distance matrix be generated (or not).
addit	Should the GAM regression result be added to an existing plot (or not).
method	Method for calculating the correlation between the ordination distance and the complete distance; from function mantel passed to function cor: "pearson", "spearman" or "kendall".
permutations	Number of permutations to assess the significance of the Mantel test; passed to mantel.
abline	Should a reference line (y=x) be added to the graph (or not).
gam	Evaluate the correspondence between the original distance and the distance from the ordination diagram with GAMas estimated by gam.
...	Other arguments passed to mantel.

Details

This function compares the Euclidean distances (between sites) displayed in an ordination diagram with the distances of a distance matrix. Alternatively, the distances of one distance matrix are compared against the distances of another distance matrix.

These distances are compared by a Mantel test (mantel) and (optionally) a GAM regression (gam). Optionally, a graph is provided compairing the distances and adding GAM results. .

Value

The function returns the results of a Mantel test and (optionally) the results of a GAM analysis.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
library(mgcv)
data(dune)
distmatrix <- vegdist(dune,method="kulc")
ordination.model1 <- cmdscale(distmatrix,k=2)
ordiplot1 <- ordiplot(ordination.model1)
distdisplayed(dune,ordiplot=ordiplot1,distx="kulc",plotit=TRUE,
    method="spearman",permutations=100,gam=TRUE)
```

`disttransform` *Community Matrix Transformation*

Description

Transforms a community matrix. Some transformation methods are described by distances for the original community matrix that result in the same distance matrix as calculated with the euclidean distance from the transformed community matrix. In several cases (methods of "hellinger", "chord", "profiles" and "chi.square"), the method makes use of function `decostand`. In several other cases ("Braun.Blanquet", "Domin", "Hult", "Hill", "fix" and "coverscale.log"), the method makes use of function `coverscale`. For method "dispweight" a call is made to function `dispweight`.

Usage

```
disttransform(x, method="hellinger")
```

Arguments

`x`	Community data frame with sites as rows, species as columns and species abundance as cell values.
`method`	Distance measure for the original community matrix that the euclidean distance will calculate for the transformed community matrix: partial match to "hellinger", "chord", "profiles", "chi.square", "log", "square", "pa", "Braun.Blanquet", "Domin", "Hult", "Hill", "fix", "coverscale.log" and "dispweight".

Details

This functions transforms a community matrix.

Some transformation methods ("hellinger", "chord", "profiles" and "chi.square") have the behaviour that the euclidean distance from the transformed matrix will equal a distance of choice for the original matrix. For example, using method "hellinger" and calculating the euclidean distance will result in the same distance matrix as by calculating the Hellinger distance from the original community matrix.

Transformation methods ("Braun.Blanquet", "Domin", "Hult", "Hill", "fix" and "coverscale.log") call function `coverscale`.

Method "dispweight" uses function `dispweight` without specifying a grouping structure.

Value

The function returns a transformed community matrix.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Legendre, P. & Gallagher, E.D. (2001). Ecologically meaningful transformations for ordination of species data. Oecologia 129: 271-280.

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(dune)
Community.1 <- disttransform(dune, method='hellinger')
Distmatrix.1 <- vegdist(Community.1,method='euclidean')
Distmatrix.1
```

---

diversityresult *Alternative Diversity Results*

Description

Provides alternative methods of obtaining results on diversity statistics than provided directly by functions diversity, fisher.alpha, specpool and specnumber (all from **vegan**), although these same functions are called. Some other statistics are also calculated such as the reciprocal Berger-Parker diversity index and abundance (not a diversity statistic). The statistics can be calculated for the entire community, for each site separately, the mean of the sites can be calculated or a jackknife estimate can be calculated for the community.

Usage

```
diversityresult(x, y = NULL, factor = NULL, level = NULL,
    index=c("Shannon", "Simpson", "inverseSimpson", "Logalpha", "Berger",
        "richness", "abundance", "Jevenness", "Eevenness",
        "jack1", "jack2", "chao", "boot"),
    method=c("pooled", "each site", "mean", "sd", "max", "jackknife"),
    sortit = FALSE, digits = 8)

diversityvariables(x, y, digits=8)

diversitycomp(x, y = NULL,
```

```
factor1 = NULL ,factor2 = NULL,
index=c("Shannon", "Simpson", "inverseSimpson", "Logalpha", "Berger",
    "richness", "abundance", "Jevenness", "Eevenness",
    "jack1", "jack2", "chao", "boot"),
method=c("pooled", "mean", "sd", "max", "jackknife"),
sortit=FALSE, digits=8)
```

Arguments

x	Community data frame with sites as rows, species as columns and species abundance as cell values.
y	Environmental data frame.
factor	Variable of the environmental data frame that defines subsets to calculate diversity statistics for.
level	Level of the variable to create the subset to calculate diversity statistics.
index	Type of diversity statistic with "richness" to calculate species richness, "abundance" to calculate abundance, "Shannon" to calculate the Shannon diversity index, "Simpson" to calculate 1-Simpson concentration index, "inverseSimpson" to calculate the reciprocal Simpson diversity index, "Logalpha" to calculate the log series alpha diversity index, "Berger" to calculate the reciprocal Berger-Parker diversity index, "Jevenness" to calculate one Shannon evenness index, "Eevenness" to calculate another Shannon evenness index, "jack1" to calculate the first-order jackknife gamma diversity estimator, "jack2" to calculate the second-order jackknife gamma diversity estimator, "chao" to calculate the Chao gamma diversity estimator and "boot" to calculate the bootstrap gamma diversity estimator.
method	Method of calculating the diversity statistics: "pooled" calculates the diversity of the entire community (all sites pooled), "each site" calculates diversity for each site separetly, "mean" calculates the average diversity of the sites, "sd" calculates the standard deviation of the diversity of the sites, "max" calculates the maximum diversity of the sites, whereas "jackknife" calculates the jackknifed diversity for the entire data frame.
sortit	Sort the sites by increasing values of the diversity statistic.
digits	Number of digits in the results.
factor1	Variable of the environmental data frame that defines subsets to calculate diversity statistics for.
factor2	Optional second variable of the environmental data frame that defines subsets to calculate diversity statistics for in a crosstabulation with the other variable of the environmental data frame.

Details

These functions provide some alternative methods of obtaining results with diversity statistics, although functions diversity, fisher.alpha, specpool, estimateR and specnumber (all from **vegan**) are called to calculate the various statistics.

Function `diversityvariables` adds variables to the environmental dataset (richness, Shannon, Simpson, inverseSimpson, Logalpha, Berger, Jevenness, Eevenness).

The reciprocal Berger-Parker diversity index is the reciprocal of the proportional abundance of the most dominant species.

J-evenness is calculated as: H / ln(S) where H is the Shannon diversity index and S the species richness.

E-evenness is calculated as: exp(H) / S where H is the Shannon diversity index and S the species richness.

The method of calculating the diversity statistics include following options: "all" calculates the diversity of the entire community (all sites pooled together), "s" calculates the diversity of each site separatedly, "mean" calculates the average diversity of the sites, whereas "Jackknife" calculates the jackknifed diversity for the entire data frame. Methods "s" and "mean" are not available for function diversitycomp. Gamma diversity estimators assume that the method is "all".

Functions `diversityresult` and `diversitycomp` allow to calculate diversity statistics for subsets of the community and environmental data sets. Function `diversityresult` calculates the diversity statistics for the specified level of a selected environmental variable. Function `diversitycomp` calculates the diversity statistics for all levels of a selected environmental variable separatedly. When a second environmental variable is provided, function `diversitycomp` calculates diversity statistics as a crosstabulation of both variables.

Value

The functions provide alternative methods of obtaining diversity results. For function `diversitycomp`, the number of sites is provided as "n".

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(dune.env)
data(dune)

diversityresult(dune, y=NULL, index="Shannon", method="each site",
    sortit=TRUE, digits=5)
diversityresult(dune, y=dune.env, factor="Management", level="NM",
    index="Shannon", method="each site",
    sortit=TRUE, digits=5)
diversityresult(dune, y=NULL, index="Shannon", method="pooled", digits=5)
```

```
diversityresult(dune, y=dune.env, factor="Management", level="NM",
    index="Shannon", method="pooled", digits=5)
diversityresult(dune, y=NULL, index="Shannon", method="mean",
    digits=5)
diversityresult(dune, y=NULL, index="Shannon", method="sd",
    digits=5)
diversityresult(dune, y=NULL, index="Shannon", method="jackknife",
    digits=5)
diversityresult(dune, y=dune.env, factor="Management", level="NM",
    index="Shannon", method="jackknife", digits=5)

diversitycomp(dune, y=dune.env, factor1="Moisture", index="Shannon",
    method="pooled", sortit=TRUE)
diversitycomp(dune, y=dune.env, factor1="Moisture", index="Shannon",
    method="mean", sortit=TRUE)
diversitycomp(dune, y=dune.env, factor1="Management", index="Shannon",
    method="jackknife", sortit=TRUE)

diversitycomp(dune, y=dune.env, factor1="Management", factor2="Moisture",
    index="Shannon", method="pooled", digits=6)
diversitycomp(dune, y=dune.env, factor1="Management", factor2="Moisture",
    index="Shannon", method="mean", digits=6)
```

`ensemble.analogue` *Climate analogues from climatic distance raster layers.*

Description

Function `ensemble.analogue` creates the map with climatic distance and provides the locations of the climate analogues (defined as locations with smallest climatic distance to a reference climate). Function `ensemble.analogue.object` provides the reference values used by the prediction function used by `predict` .

Usage

```
ensemble.analogue(x = NULL, analogue.object = NULL, analogues = 1,
    RASTER.object.name = analogue.object$name, RASTER.stack.name = x@title,
    RASTER.format = "raster", RASTER.datatype = "INT2S", RASTER.NAflag = -32767,
    KML.out = T, KML.blur = 10, KML.maxpixels = 100000,
    limits = c(1, 5, 20, 50), limit.colours = c('red', 'orange', 'blue', 'grey'),
    CATCH.OFF = FALSE)

ensemble.analogue.object(ref.location, future.stack, current.stack, name = "reference1",
    method = "mahal", an = 10000, probs = c(0.025, 0.975), weights = NULL, z = 2)
```

Arguments

x	RasterStack object (stack) containing all environmental layers (climatic variables) for which climatic distance should be calculated.
analogue.object	Object listing reference values for the environmental layers and additional parameters (covariance matrix for method = "mahal" or normalization parameters for method = "quantile") that are used by the prediction function that is used internally by predict. This object is created with ensemble.analogue.object.
analogues	Number of analogue locations to be provided
RASTER.object.name	First part of the names of the raster file that will be generated, expected to identify the area and time period for which ranges were calculated
RASTER.stack.name	Last part of the names of the raster file that will be generated, expected to identify the predictor stack used
RASTER.format	Format of the raster files that will be generated. See writeFormats and writeRaster.
RASTER.datatype	Format of the raster files that will be generated. See dataType and writeRaster.
RASTER.NAflag	Value that is used to store missing data. See writeRaster.
KML.out	If TRUE, then kml files will be saved in a subfolder 'kml/zones'.
KML.maxpixels	Maximum number of pixels for the PNG image that will be displayed in Google Earth. See also KML.
KML.blur	Integer that results in increasing the size of the PNG image by KML.blur^2, which may help avoid blurring of isolated pixels. See also KML.
limits	Limits indicating the accumulated number of closest analogue sites. These limits will correspond to different colours in the KML map. In the default setting, the closest analogue will be coloured red and the second to fifth closest analogues will be coloured orange.
limit.colours	Colours for the different limits based on number of analogues.
CATCH.OFF	Disable calls to function tryCatch.
ref.location	Location of the reference location for which analogues are searched for and from which climatic distance will be calculated, typically available in 2-column (lon, lat) dataframe; see also extract.
future.stack	RasterStack object (stack) containing the environmental layers (climatic variables) to obtain the conditions of the reference location. For climate change research, this RasterStack object corresponds to the future climatic conditions of the reference location.
current.stack	RasterStack object (stack) containing all environmental layers (climatic variables) for which climatic distance should be calculated. For climate change research, this RasterStack object corresponds to the current climatic conditions and range where climate analogues are searched for.
name	Name of the object, expect to expected to identify the area and time period for which ranges were calculated and where no novel conditions will be detected

method	Method used to calculate climatic distance: method = "mahal" results in using the Mahalanobis distance (mahalanobis); method = "quantile" results in dividing the differences between reference climatic values and climatic values in the 'current' raster by a quantile range obtained from the 'current' raster; method = "sd" results in dividing the differences between reference climatic values and climatic values in the 'current' raster by standard deviations obtained from the 'current' raster; and method = "none" results in not dividing these differences.
an	Number of randomly selected locations points to calculate the covariance matrix (cov) to be used with mahalanobis, therefore only used for method = "mahal". See also randomPoints.
probs	Numeric vector of probabilities [0,1] as used by quantile). Only used for method = "quantile".
weights	Numeric vector of weights by which each variable (difference) should be multiplied by (can be used to give equal weight to 12 monthly rainfall values and 24 minimum and maximum monthly temperature values). Not used for method = "mahal".
z	Parameter used as exponent for differences calculated between reference climatic variables and variables in the 'current' raster and reciprocal exponent for the sum of all differences. Default value of 2 corresponds to the Euclidean distance. Not used for method = "mahal".

Details

Function ensemble.analogues maps the climatic distance from reference values determined by ensemble.analogues.object and provides the locations of the analogues closest analogues.

The method = "mahal" uses the Mahalanobis distance as environmental (climatic) distance: mahalanobis.

Other methods use a normalization method to handle scale differences between environmental (climatic) variables:

$ClimaticDistance = (\sum_i (weight_i * (|T_i - C_i|/norm_i)^z))^(1/z)$

where T_i are the target values for environmental (climatic) variable i, C_i are the values in the current environmental layers where analogues are searched for, $weight_i$ are the weights for environmental variable i, and $norm_i$ are the normalization parameters for environmental variable i

Value

Function ensemble.analogue.object returns a list with following objects:

name	name for the reference location
ref.location	coordinates of the reference location
stack.name	name for time period for which values are extracted from the future.stack
method	method used for calculating climatic distance
target.values	target environmental values to select analogues for through minimum climatic distance
cov.mahal	covariance matrix

norm.values	parameters by which each difference between target and 'current' value will be divided
weight.values	weights by which each difference between target and 'current' value will be multiplied
z	parameter to be used as exponent for differences between target and 'current' values

Author(s)

Roeland Kindt (World Agroforestry Centre) and Eike Luedeling (World Agroforestry Centre)

References

Bos, Swen PM, et al. "Climate analogs for agricultural impact projection and adaptation-a reliability test." Frontiers in Environmental Science 3 (2015): 65. Luedeling, Eike, and Henry Neufeldt. "Carbon sequestration potential of parkland agroforestry in the Sahel." Climatic Change 115.3-4 (2012): 443-461.

See Also

ensemble.novel

Examples

```
## Not run:
# get predictor variables
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
predictors <- subset(predictors, subset=c("bio1", "bio5", "bio6", "bio7", "bio8",
    "bio12", "bio16", "bio17"))
predictors
predictors@title <- "base"

# instead of searching for current analogue of future climate conditions,
# search for analogue in southern hemisphere
future.stack <- stack(crop(predictors, y=extent(-125, -32, 0, 40)))
future.stack@title <- "north"
current.stack <- stack(crop(predictors, y=extent(-125, -32, -56, 0)))
current.stack@title <- "south"

# reference location in Florida
# in this case future.stack and current.stack are both current
ref.loc <- data.frame(t(c(-80.19, 25.76)))
names(ref.loc) <- c("lon", "lat")

# climate analogue analysis based on the Mahalanobis distance
Florida.object.mahal <- ensemble.analogue.object(ref.location=ref.loc,
    future.stack=future.stack, current.stack=current.stack,
```

```
    name="FloridaMahal", method="mahal", an=10000)
Florida.object.mahal

Florida.analogue.mahal <- ensemble.analogue(x=current.stack,
    analogue.object=Florida.object.mahal, analogues=50)
Florida.analogue.mahal

# climate analogue analysis based on the Euclidean distance and dividing each variable by the sd
Florida.object.sd <- ensemble.analogue.object(ref.location=ref.loc,
    future.stack=future.stack, current.stack=current.stack,
    name="FloridaSD", method="sd", z=2)
Florida.object.sd

Florida.analogue.sd <- ensemble.analogue(x=current.stack,
    analogue.object=Florida.object.sd, analogues=50)
Florida.analogue.sd

# plot analogues on climatic distance maps
par(mfrow=c(1,2))
analogue.file <- paste(getwd(), "//ensembles//analogue//FloridaMahal_south_analogue.grd", sep="")
plot(raster(analogue.file), main="Mahalanobis climatic distance")
points(Florida.analogue.sd[3:50, "lat"] ~ Florida.analogue.sd[3:50, "lon"],
    pch=1, col="red", cex=1)
points(Florida.analogue.mahal[3:50, "lat"] ~ Florida.analogue.mahal[3:50, "lon"],
    pch=3, col="black", cex=1)
points(Florida.analogue.mahal[2, "lat"] ~ Florida.analogue.mahal[2, "lon"],
    pch=22, col="blue", cex=2)
legend(x="topright", legend=c("closest", "Mahalanobis", "SD"), pch=c(22, 3 , 1),
    col=c("blue" , "black", "red"))

analogue.file <- paste(getwd(), "//ensembles//analogue//FloridaSD_south_analogue.grd", sep="")
plot(raster(analogue.file), main="Climatic distance normalized by standard deviation")
points(Florida.analogue.mahal[3:50, "lat"] ~ Florida.analogue.mahal[3:50, "lon"],
    pch=3, col="black", cex=1)
points(Florida.analogue.sd[3:50, "lat"] ~ Florida.analogue.sd[3:50, "lon"],
    pch=1, col="red", cex=1)
points(Florida.analogue.sd[2, "lat"] ~ Florida.analogue.sd[2, "lon"],
    pch=22, col="blue", cex=2)
legend(x="topright", legend=c("closest", "Mahalanobis", "SD"), pch=c(22, 3 , 1),
    col=c("blue" , "black", "red"))
par(mfrow=c(1,1))

## End(Not run)
```

`ensemble.batch` *Suitability mapping based on ensembles of modelling algorithms: batch processing*

Description

The main function allows for batch processing of different species and different environmental RasterStacks. The function makes internal calls to ensemble.calibrate.weights, ensemble.calibrate.models and ensemble.raster.

Usage

```
ensemble.batch(x = NULL, xn = c(x),
    species.presence = NULL, species.absence = NULL,
    presence.min = 20, thin.km = 0.1,
    an = 1000, excludep = FALSE, target.groups = FALSE,
    get.block = FALSE, block.default = runif(1) > 0.5, get.subblocks = FALSE,
    SSB.reduce = FALSE, CIRCLES.d = 250000,
    k.splits = 4, k.test = 0,
    n.ensembles = 1,
    VIF.max = 10, VIF.keep = NULL,
    SINK = FALSE, CATCH.OFF = FALSE,
   RASTER.format = "raster", RASTER.datatype = "INT2S", RASTER.NAflag = -32767,
    KML.out = FALSE, KML.maxpixels = 100000, KML.blur = 10,
    models.save = FALSE,
    threshold.method = "spec_sens", threshold.sensitivity = 0.9,
    threshold.PresenceAbsence = FALSE,
    ENSEMBLE.best = 0, ENSEMBLE.min = 0.7, ENSEMBLE.exponent = 1,
    ENSEMBLE.weight.min = 0.05,
    input.weights = NULL,
    MAXENT = 1, MAXNET = 1, MAXLIKE = 1, GBM = 1, GBMSTEP = 0, RF = 1, CF = 1,
    GLM = 1, GLMSTEP = 1, GAM = 1, GAMSTEP = 1, MGCV = 1, MGCVFIX = 0,
    EARTH = 1, RPART = 1, NNET = 1, FDA = 1, SVM = 1 , SVME = 1, GLMNET = 1,
    BIOCLIM.O = 0, BIOCLIM = 1, DOMAIN = 1, MAHAL = 1, MAHAL01 = 1,
    PROBIT = FALSE,
    Yweights = "BIOMOD",
    layer.drops = NULL, factors = NULL, dummy.vars = NULL,
    formulae.defaults = TRUE, maxit = 100,
    MAXENT.a = NULL, MAXENT.an = 10000,
    MAXENT.path = paste(getwd(), "/models/maxent", sep=""),
    MAXNET.classes = "default", MAXNET.clamp = FALSE, MAXNET.type = "cloglog",
    MAXLIKE.formula = NULL, MAXLIKE.method = "BFGS",
    GBM.formula = NULL, GBM.n.trees = 2001,
    GBMSTEP.tree.complexity = 5, GBMSTEP.learning.rate = 0.005,
    GBMSTEP.bag.fraction = 0.5, GBMSTEP.step.size = 100,
   RF.formula = NULL, RF.ntree = 751, RF.mtry = floor(sqrt(raster::nlayers(x))),
   CF.formula = NULL, CF.ntree = 751, CF.mtry = floor(sqrt(raster::nlayers(x))),
    GLM.formula = NULL, GLM.family = binomial(link = "logit"),
  GLMSTEP.steps = 1000, STEP.formula = NULL, GLMSTEP.scope = NULL, GLMSTEP.k = 2,
    GAM.formula = NULL, GAM.family = binomial(link = "logit"),
    GAMSTEP.steps = 1000, GAMSTEP.scope = NULL, GAMSTEP.pos = 1,
    MGCV.formula = NULL, MGCV.select = FALSE,
    MGCVFIX.formula = NULL,
```

```
    EARTH.formula = NULL,
    EARTH.glm = list(family = binomial(link = "logit"), maxit = maxit),
    RPART.formula = NULL, RPART.xval = 50,
    NNET.formula = NULL, NNET.size = 8, NNET.decay = 0.01,
    FDA.formula = NULL,
    SVM.formula = NULL, SVME.formula = NULL,
    GLMNET.nlambda = 100, GLMNET.class = FALSE,
    BIOCLIM.O.fraction = 0.9,
    MAHAL.shape = 1)

ensemble.mean(RASTER.species.name = "Species001", RASTER.stack.name = "base",
    positive.filters = c("grd", "_ENSEMBLE_"), negative.filters = c("xml"),
    RASTER.format = "raster", RASTER.datatype = "INT2S", RASTER.NAflag = -32767,
    KML.out = FALSE, KML.maxpixels = 100000, KML.blur = 10,
    abs.breaks = 6, pres.breaks = 6, sd.breaks = 9,
    p = NULL, a = NULL,
    pt = NULL, at = NULL,
    threshold = -1,
    threshold.method = "spec_sens", threshold.sensitivity = 0.9,
    threshold.PresenceAbsence = FALSE)

ensemble.plot(RASTER.species.name = "Species001", RASTER.stack.name = "base",
    plot.method=c("suitability", "presence", "count",
      "consensussuitability", "consensuspresence", "consensuscount", "consensussd"),
    dev.new.width = 7, dev.new.height = 7,
    main = paste(RASTER.species.name, " ", plot.method,
        " for ", RASTER.stack.name, sep=""),
    positive.filters = c("grd"), negative.filters = c("xml"),
    p=NULL, a=NULL,
    threshold = -1,
    threshold.method = "spec_sens", threshold.sensitivity = 0.9,
    threshold.PresenceAbsence = FALSE,
    abs.breaks = 6, abs.col = NULL,
    pres.breaks = 6, pres.col = NULL,
    sd.breaks = 9, sd.col = NULL,
    absencePresence.col = NULL,
    count.col = NULL,
    maptools.boundaries = TRUE, maptools.col = "dimgrey", ...)
```

Arguments

x	RasterStack object (stack) containing all layers to calibrate an ensemble.
xn	RasterStack object (stack) containing all layers that correspond to explanatory variables of an ensemble calibrated earlier with x. Several RasterStack objects can be provided in a format as c(stack1, stack2, stack3); these will be used sequentially. See also predict.
species.presence	presence points used for calibrating the suitability models, available in 3-column

(species, x, y) or (species, lon, lat) dataframe

`species.absence`
: background points used for calibrating the suitability models, either available in a 3-column (species, x, y) or (species, lon, lat), or available in a 2-column (x, y) or (lon, lat) dataframe. In case of a 2-column dataframe, the same background locations will be used for all species.

`presence.min`
: minimum number of presence locations for the organism (if smaller, no models are fitted).

`thin.km`
: Threshold for minimum distance (km) between presence point locations for focal species for model calibrations in each run. A new data set is randomly selected via `ensemble.spatialThin` in each of ensemble run.

`an`
: number of background points for calibration to be selected with `randomPoints` in case argument `a` or `species.absence` is missing

`excludep`
: parameter that indicates (if `TRUE`) that presence points will be excluded from the background points; see also `randomPoints`

`target.groups`
: Parameter that indicates (if `TRUE`) that the provided background points (argument `a`) represent presence points from a target group sensu Phillips et al. 2009 (these are species that are all collected or observed using the same methods or equipment). Setting the parameter to `TRUE` results in selecting the centres of cells of the target groups as background points, while avoiding to select the same cells twice. Via argument `excludep`, it is possible to filter out cells with presence observations (argument `p`).

`get.block`
: if `TRUE`, instead of creating k-fold cross-validation subsets randomly (`kfold`), create 4 subsets of presence and background locations with `get.block`.

`block.default`
: if `FALSE`, instead of making the first division of presence point locations along the y-coordinates (latitude) as in `get.block`, make the first division along the x-coordinates (longitude).

`get.subblocks`
: if `TRUE`, then 4 subsets of presence and background locations are generated in a checkerboard configuration by applying `get.block` to each of the 4 blocks generated by `get.block` in a first step.

`SSB.reduce`
: If `TRUE`, then new background points that will be used for evaluationg the suitability models will be selected (`randomPoints`) in circular neighbourhoods (created with `circles`) around presence locations (p and pt). The abbreviation of SSB refers to spatial sorting bias; see also `ssb`.

`CIRCLES.d`
: Radius in m of circular neighbourhoods (created with `circles`) around presence locations (p and pt).

`k`
: If larger than 1, the number of groups to split between calibration (k-1) and evaluation (1) data sets (for example, `k=5` results in 4/5 of presence and background points to be used for calibrating the models, and 1/5 of presence and background points to be used for evaluating the models). See also `kfold`.

`k.splits`
: If larger than 1, the number of splits for the `ensemble.calibrate.weights` step in batch processing. See also `kfold`.

`k.test`
: If larger than 1, the number of groups to split between calibration (k-1) and evaluation (1) data sets when calibrating the final models (for example, `k=5`

results in 4/5 of presence and background points to be used for calibrating the models, and 1/5 of presence and background points to be used for evaluating the models). See also kfold.

n.ensembles — If larger than 1, the number of different ensembles generated per species in batch processing.

VIF.max — Maximum Variance Inflation Factor of variables; see ensemble.VIF.

VIF.keep — character vector with names of the variables to be kept; see ensemble.VIF.

SINK — Append the results to a text file in subfolder 'outputs' (if TRUE). The name of file is based on species names. In case a file already exists, then results are appended. See also sink.

CATCH.OFF — Disable calls to function tryCatch.

RASTER.format — Format of the raster files that will be generated. See writeFormats and writeRaster.

RASTER.datatype — Format of the raster files that will be generated. See dataType and writeRaster.

RASTER.NAflag — Value that is used to store missing data. See writeRaster.

KML.out — if FALSE, then no kml layers (layers that can be shown in Google Earth) are produced. If TRUE, then kml files will be saved in a subfolder 'kml'.

KML.maxpixels — Maximum number of pixels for the PNG image that will be displayed in Google Earth. See also KML.

KML.blur — Integer that results in increasing the size of the PNG image by KML.blur^2, which may help avoid blurring of isolated pixels. See also KML.

models.save — Save the list with model details to a file (if TRUE). The filename will be species.name with extension .models; this file will be saved in subfolder of models. When loading this file, model results will be available as ensemble.models.

threshold.method — Method to calculate the threshold between predicted absence and presence; possibilities include spec_sens (highest sum of the true positive rate and the true negative rate), kappa (highest kappa value), no_omission (highest threshold that corresponds to no omission), prevalence (modeled prevalence is closest to observed prevalence) and equal_sens_spec (equal true positive rate and true negative rate). See threshold. Options specific to the BiodiversityR implementation are: threshold.mean (resulting in calculating the mean value of spec_sens, equal_sens_spec and prevalence) and threshold.min (resulting in calculating the minimum value of spec_sens, equal_sens_spec and prevalence).

threshold.sensitivity — Sensitivity value for threshold.method = 'sensitivity'. See threshold.

threshold.PresenceAbsence — If TRUE calculate thresholds with the PresenceAbsence package. See optimal.thresholds.

ENSEMBLE.best — The number of individual suitability models to be used in the consensus suitability map (based on a weighted average). In case this parameter is smaller than 1 or larger than the number of positive input weights of individual models, then all individual suitability models with positive input weights are included in the consensus suitability map. In case a vector is provided, ensemble.strategy is called internally to determine weights for the ensemble model.

ENSEMBLE.min — The minimum input weight (typically corresponding to AUC values) for a model to be included in the ensemble. In case a vector is provided, function ensemble.strategy is called internally to determine weights for the ensemble model.

ENSEMBLE.exponent — Exponent applied to AUC values to convert AUC values into weights (for example, an exponent of 2 converts input weights of 0.7, 0.8 and 0.9 into 0.7^2=0.49, 0.8^2=0.64 and 0.9^2=0.81). See details.

ENSEMBLE.weight.min — The minimum output weight for models included in the ensemble, applying to weights that sum to one. Note that ENSEMBLE.min typically refers to input AUC values.

input.weights — array with numeric values for the different modelling algorithms; if NULL then values provided by parameters such as MAXENT and GBM will be used. As an alternative, the output from ensemble.calibrate.weights can be used.

MAXENT — Input weight for a maximum entropy model (maxent). (Only weights > 0 will be used.)

MAXNET — number: if larger than 0, then a maximum entropy model (maxnet) will be fitted among ensemble

MAXLIKE — Input weight for a maxlike model (maxlike). (Only weights > 0 will be used.)

GBM — Input weight for a boosted regression trees model (gbm). (Only weights > 0 will be used.)

GBMSTEP — Input weight for a stepwise boosted regression trees model (gbm.step). (Only weights > 0 will be used.)

RF — Input weight for a random forest model (randomForest). (Only weights > 0 will be used.)

CF — number: if larger than 0, then a random forest model (cforest) will be fitted among ensemble

GLM — Input weight for a generalized linear model (glm). (Only weights > 0 will be used.)

GLMSTEP — Input weight for a stepwise generalized linear model (stepAIC). (Only weights > 0 will be used.)

GAM — Input weight for a generalized additive model (gam). (Only weights > 0 will be used.)

GAMSTEP — Input weight for a stepwise generalized additive model (step.gam). (Only weights > 0 will be used.)

MGCV — Input weight for a generalized additive model (gam). (Only weights > 0 will be used.)

MGCVFIX — number: if larger than 0, then a generalized additive model with fixed d.f. regression splines (gam) will be fitted among ensemble

EARTH — Input weight for a multivariate adaptive regression spline model (earth). (Only weights > 0 will be used.)

RPART — Input weight for a recursive partioning and regression tree model (rpart). (Only weights > 0 will be used.)

NNET — Input weight for an artificial neural network model (nnet). (Only weights > 0 will be used.)

FDA — Input weight for a flexible discriminant analysis model (fda). (Only weights > 0 will be used.)

SVM — Input weight for a support vector machine model (ksvm). (Only weights > 0 will be used.)

SVME — Input weight for a support vector machine model (svm). (Only weights > 0 will be used.)

GLMNET — Input weight for a GLM with lasso or elasticnet regularization (glmnet). (Only weights > 0 will be used.)

BIOCLIM.O — Input weight for the original BIOCLIM algorithm (ensemble.bioclim). (Only weights > 0 will be used.)

BIOCLIM — Input weight for the BIOCLIM algorithm (bioclim). (Only weights > 0 will be used.)

DOMAIN — Input weight for the DOMAIN algorithm (domain). (Only weights > 0 will be used.)

MAHAL — Input weight for the Mahalonobis algorithm (mahal). (Only weights > 0 will be used.)

MAHAL01 — Input weight for the Mahalanobis algorithm (mahal), using a transformation method afterwards whereby output is within the range between 0 and 1. (Only weights > 0 will be used.)

PROBIT — If TRUE, then subsequently to the fitting of the individual algorithm (e.g. maximum entropy or GAM) a generalized linear model (glm) with probit link family=binomial(link="probi will be fitted to transform the predictions, using the previous predictions as explanatory variable. This transformation results in all model predictions to be probability estimates.

Yweights — chooses how cases of presence and background (absence) are weighted; "BIOMOD" results in equal weighting of all presence and all background cases, "equal" results in equal weighting of all cases. The user can supply a vector of weights similar to the number of cases in the calibration data set.

layer.drops — vector that indicates which layers should be removed from RasterStack x. See also addLayer.

factors — vector that indicates which variables are factors; see also prepareData

dummy.vars — vector that indicates which variables are dummy variables (influences formulae suggestions)

formulae.defaults — Suggest formulae for most of the models (if TRUE). See also ensemble.formulae.

maxit — Maximum number of iterations for some of the models. See also glm.control, gam.control, gam.control and nnet.

MAXENT.a — background points used for calibrating the maximum entropy model (maxent), typically available in 2-column (lon, lat) dataframe; see also prepareData and extract.

MAXENT.an — number of background points for calibration to be selected with randomPoints in case argument MAXENT.a is missing. When used with the ensemble.batch function, the same background locations will be used for each of the species runs; this implies that for each species, presence locations are not excluded from the background data for this function.

MAXENT.path — path to the directory where output files of the maximum entropy model are stored; see also maxent

MAXNET.classes — continuous feature classes, either "default" or any subset of "lqpht" (linear, quadratic, product, hinge, threshold). Note that the "default" option chooses feature classes based on the number of presence locations as "l" (< 10 locations), "lq" (10 - 14 locations), "lqh" (15 - 79 locations) or "lqph" (> 79 locations). See also maxnet.

MAXNET.clamp — restrict predictors and features to the range seen during model training; see also predict.maxnet

MAXNET.type — type of response required; see also predict.maxnet

MAXLIKE.formula — formula for the maxlike algorithm; see also maxlike

MAXLIKE.method — method for the maxlike algorithm; see also optim

GBM.formula — formula for the boosted regression trees algorithm; see also gbm

GBM.n.trees — total number of trees to fit for the boosted regression trees model; see also gbm

GBMSTEP.tree.complexity — complexity of individual trees for stepwise boosted regression trees; see also gbm.step

GBMSTEP.learning.rate — weight applied to individual trees for stepwise boosted regression trees; see also gbm.step

GBMSTEP.bag.fraction — proportion of observations used in selecting variables for stepwise boosted regression trees; see also gbm.step

GBMSTEP.step.size — number of trees to add at each cycle for stepwise boosted regression trees (should be small enough to result in a smaller holdout deviance than the initial number of trees [50]); see also gbm.step

RF.formula — formula for the random forest algorithm; see also randomForest

RF.ntree — number of trees to grow for random forest algorithm; see also randomForest

RF.mtry — number of variables randomly sampled as candidates at each split for random forest algorithm; see also randomForest

CF.formula — formula for random forest algorithm; see also cforest

CF.ntree — number of trees to grow in a forest; see also cforest_control

CF.mtry — number of input variables randomly sampled as candidates at each node for random forest like algorithms; see also cforest_control

GLM.formula — formula for the generalized linear model; see also glm

GLM.family — description of the error distribution and link function for the generalized linear model; see also glm

GLMSTEP.steps	maximum number of steps to be considered for stepwise generalized linear model; see also stepAIC
STEP.formula	formula for the "starting model" to be considered for stepwise generalized linear model; see also stepAIC
GLMSTEP.scope	range of models examined in the stepwise search; see also stepAIC
GLMSTEP.k	multiple of the number of degrees of freedom used for the penalty (only k = 2 gives the genuine AIC); see also stepAIC
GAM.formula	formula for the generalized additive model; see also gam
GAM.family	description of the error distribution and link function for the generalized additive model; see also gam
GAMSTEP.steps	maximum number of steps to be considered in the stepwise generalized additive model; see also step.gam
GAMSTEP.scope	range of models examined in the step-wise search n the stepwise generalized additive model; see also step.gam
GAMSTEP.pos	parameter expected to be set to 1 to allow for fitting of the stepwise generalized additive model
MGCV.formula	formula for the generalized additive model; see also gam
MGCV.select	if TRUE, then the smoothing parameter estimation that is part of fitting can completely remove terms from the model; see also gam
MGCVFIX.formula	formula for the generalized additive model with fixed d.f. regression splines; see also gam (the default formulae sets "s(..., fx=TRUE, ...)"; see also s)
EARTH.formula	formula for the multivariate adaptive regression spline model; see also earth
EARTH.glm	list of arguments to pass on to glm; see also earth
RPART.formula	formula for the recursive partioning and regression tree model; see also rpart
RPART.xval	number of cross-validations for the recursive partioning and regression tree model; see also rpart.control
NNET.formula	formula for the artificial neural network model; see also nnet
NNET.size	number of units in the hidden layer for the artificial neural network model; see also nnet
NNET.decay	parameter of weight decay for the artificial neural network model; see also nnet
FDA.formula	formula for the flexible discriminant analysis model; see also fda
SVM.formula	formula for the support vector machine model; see also ksvm
SVME.formula	formula for the support vector machine model; see also svm
GLMNET.nlambda	The number of lambda values; see also glmnet
GLMNET.class	Use the predicted class to calculate the mean predictions of GLMNET; see also predict.glmnet
BIOCLIM.O.fraction	Fraction of range representing the optimal limits, default value of 0.9 as in the original BIOCLIM software (ensemble.bioclim).
MAHAL.shape	parameter that influences the transformation of output values of mahal.

RASTER.species.name
: First part of the names of the raster files, expected to identify the modelled species (or organism).

RASTER.stack.name
: Last part of the names of the raster files, expected to identify the predictor stack used.

positive.filters
: vector that indicates parts of filenames for files that will be included in the calculation of the mean probability values

negative.filters
: vector that indicates parts of filenames for files that will not be included in the calculation of the mean probability values

abs.breaks
: Number of breaks in the colouring scheme for absence (only applies to `suitability` mapping).

pres.breaks
: Number of breaks in the colouring scheme for presence (only applies to `suitability` mapping).

sd.breaks
: Number of breaks in the colouring scheme for standard deviation (only applies to `sd` mapping).

p
: presence points used for calibrating the suitability models, typically available in 2-column (x, y) or (lon, lat) dataframe; see also `prepareData` and `extract`

a
: background points used for calibrating the suitability models, typically available in 2-column (x, y) or (lon, lat) dataframe; see also `prepareData` and `extract`

pt
: presence points used for evaluating the suitability models, typically available in 2-column (lon, lat) dataframe; see also `prepareData`

at
: background points used for calibrating the suitability models, typicall available in 2-column (lon, lat) dataframe; see also `prepareData` and `extract`

threshold
: Threshold value that will be used to distinguish between presence and absence. If < 0, then a threshold value will be calculated from the provided presence `p` and absence `a` locations.

plot.method
: Choice of maps to be plotted: `suitability` plots suitability maps, `presence` plots presence-absence maps, `count` plots count maps (count of number of algorithms or number of ensembles predicting presence) and `sd` plots standard deviation maps.

dev.new.width
: Width for new graphics device (`dev.new`). If < 0, then no new graphics device is opened.

dev.new.height
: Heigth for new graphics device (`dev.new`). If < 0, then no new graphics device is opened.

main
: main title for the plots.

abs.col
: specify colours for absence (see examples on how not to plot areas where the species is predicted absent)

pres.col
: specify colours for presence

sd.col
: specify colours for standard deviation

absencePresence.col
: specify colours for absence - presence maps (see examples on how not to plot areas where the species is predicted absent)

count.col
: specify colours for number of algorithms or ensembles (see examples on how not to plot areas where the species is predicted absent)

maptools.boundaries
: If TRUE, then plot approximate country boundaries wrld_simpl

maptools.col
: Colour for approximate country boundaries plotted via wrld_simpl

...
: Other items passed to function plot.

Details

This function allows for batch processing of different species and different environmental RasterStacks. The function makes internal calls to ensemble.spatialThin, ensemble.VIF, ensemble.calibrate.weights, ensemble.calibrate.models and ensemble.raster.

Different ensemble runs allow for different random selection of k-fold subsets, background locations or spatial thinning of presence locations.

ensemble.calibrate.weights results in a cross-validation procedure whereby the data set is split in calibration and testing subsets and the best weights for the ensemble model are determined (including the possibility for weights = 0).

ensemble.calibrate.models is the step whereby models are calibrated using all the available presence data.

ensemble.raster is the final step whereby raster layers are produced for the ensemble model.

Function ensemble.mean results in raster layers that are based on the summary of several ensemble layers: the new ensemble has probability values that are the mean of the probabilities of the different raster layers, the presence-absence threshold is derived for this new ensemble layer, whereas the count reflects the number of ensemble layers where presence was predicted. Note the assumption that input probabilities are scaled between 0 and 1000 (as the output from ensemble.raster), whereas thresholds are based on actual probabilities (scaled between 0 and 1). After the mean probability has been calculated, the niche overlap (nicheOverlap) with the different input layers is calculated.

Function ensemble.plot plots suitability, presence-absence or count maps. In the case of suitability maps, the presence-absence threshold needs to be provide as suitabilities smaller than the threshold will be coloured red to orange, whereas suitabilities larger than the threshold will be coloured light blue to dark blue.

Value

The function finally results in ensemble raster layers for each species, including the fitted values for the ensemble model, the estimated presence-absence and the count of the number of submodels prediction presence and absence.

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References

Kindt R. 2018. Ensemble species distribution modelling with transformed suitability values. Environmental Modelling & Software 100: 136-145. https://doi.org/10.1016/j.envsoft.2017.11.009

Buisson L, Thuiller W, Casajus N, Lek S and Grenouillet G. 2010. Uncertainty in ensemble forecasting of species distribution. Global Change Biology 16: 1145-1157

Phillips SJ, Dudik M, Elith J et al. 2009. Sample selection bias and presence-only distribution models: implications for background and pseudo-absence data. Ecological Applications 19: 181-197.

See Also

ensemble.calibrate.weights, ensemble.calibrate.models, ensemble.raster

Examples

```
## Not run:
# based on examples in the dismo package

# get predictor variables
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
# subset based on Variance Inflation Factors
predictors <- subset(predictors, subset=c("bio5", "bio6",
    "bio16", "bio17", "biome"))
predictors
predictors@title <- "base"

# presence points
presence_file <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
pres <- read.table(presence_file, header=TRUE, sep=',')
pres[,1] <- rep("Bradypus", nrow(pres))

# choose background points
background <- randomPoints(predictors, n=1000, extf = 1.00)

# north and south for new predictions (as if new climates)
ext2 <- extent(-90, -32, 0, 23)
predictors2 <- crop(predictors, y=ext2)
predictors2 <- stack(predictors2)
predictors2@title <- "north"

ext3 <- extent(-90, -32, -33, 0)
predictors3 <- crop(predictors, y=ext3)
predictors3 <- stack(predictors3)
predictors3@title <- "south"

# fit 3 ensembles with batch processing, choosing the best ensemble model based on the
# average weights of 4-fold split of calibration and testing data
```

```
# final models use all available presence data and average weights determined by the
# ensemble.calibrate.weights function (called internally)
# batch processing can handle several species by using 3-column species.presence and
# species.absence data sets
# note that these calculations can take a while

ensemble.nofactors <- ensemble.batch(x=predictors,
    xn=c(predictors, predictors2, predictors3),
    species.presence=pres,
    species.absence=background,
    k.splits=4, k.test=0,
    n.ensembles=3,
    SINK=TRUE,
    layer.drops=c("biome"),
    ENSEMBLE.best=0, ENSEMBLE.exponent=c(1, 2, 3),
    ENSEMBLE.min=0.7,
    MAXENT=0, MAXNET=1, MAXLIKE=1, GBM=1, GBMSTEP=0, RF=1, CF=1,
    GLM=1, GLMSTEP=1, GAM=1, GAMSTEP=1, MGCV=1, MGCVFIX=1,
    EARTH=1, RPART=1, NNET=1, FDA=1, SVM=1, SVME=1, GLMNET=1,
    BIOCLIM.O=1, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=1,
    PROBIT=TRUE,
    Yweights="BIOMOD",
    formulae.defaults=TRUE)

# summaries for the 3 ensembles for the species
# summaries are based on files in folders ensemble/suitability,
# ensemble/presence and ensemble/count
# ensemble.mean is used internally in ensemble.batch

ensemble.mean(RASTER.species.name="Bradypus", RASTER.stack.name="base",
    p=pres, a=background)

# plot mean suitability without specifying colours
plot1 <- ensemble.plot(RASTER.species.name="Bradypus", RASTER.stack.name="base",
    plot.method="consensussuitability",
    p=pres, a=background, abs.breaks=4, pres.breaks=9)
plot1

# only colour the areas where species is predicted to be present
# option is invoked by having no absence breaks
# same colourscheme as \url{http://www.worldagroforestry.org/atlas-central-america}
LAatlascols <- grDevices::colorRampPalette(c("#FFFF80", "#38E009","#1A93AB", "#0C1078"))
plot2 <- ensemble.plot(RASTER.species.name="Bradypus", RASTER.stack.name="base",
    plot.method="consensussuitability",
    p=pres, a=background, abs.breaks=0, pres.breaks=9, pres.col=LAatlascols(8))
plot2

# only colour the areas where species is predicted to be present
# option is invoked by only setting one colour for absence-presence
plot3 <- ensemble.plot(RASTER.species.name="Bradypus", RASTER.stack.name="base",
    plot.method="consensuspresence",
    absencePresence.col=c("#90EE90"))
```

```
# only colour presence area by specifying colours > 0
plot4 <- ensemble.plot(RASTER.species.name="Bradypus", RASTER.stack.name="base",
    plot.method="consensuscount",
    count.col=LAatlascols(3))



## End(Not run)
```

---

ensemble.bioclim *Suitability mapping based on the BIOCLIM algorithm*

Description

Implementation of the BIOCLIM algorithm more similar to the original BIOCLIM algorithm and software than the implementation through bioclim. Function ensemble.bioclim creates the suitability map. Function ensemble.bioclim.object provides the reference values used by the prediction function used by predict .

Usage

```
ensemble.bioclim(x = NULL, bioclim.object = NULL,
   RASTER.object.name = bioclim.object$species.name, RASTER.stack.name = x@title,
    RASTER.format = "raster",
    KML.out = TRUE, KML.blur = 10, KML.maxpixels = 100000,
    CATCH.OFF = FALSE)

ensemble.bioclim.object(x = NULL, p = NULL, fraction = 0.9,
    quantiles = TRUE,
    species.name = "Species001",
    factors = NULL)
```

Arguments

x	RasterStack object (stack) containing all environmental layers for which suitability should be calculated, or alternatively a data.frame containing the bioclimatic variables.
bioclim.object	Object listing optimal and absolute minima and maxima for bioclimatic variables, used by the prediction function that is used internally by predict. This object is created with ensemble.bioclim.object.
RASTER.object.name	First part of the names of the raster file that will be generated, expected to identify the species or crop for which ranges were calculated
RASTER.stack.name	Last part of the names of the raster file that will be generated, expected to identify the predictor stack used

RASTER.format	Format of the raster files that will be generated. See writeFormats and writeRaster.
KML.out	If TRUE, then kml files will be saved in a subfolder 'kml/zones'.
KML.blur	Integer that results in increasing the size of the PNG image by KML.blur^2, which may help avoid blurring of isolated pixels. See also KML.
KML.maxpixels	Maximum number of pixels for the PNG image that will be displayed in Google Earth. See also KML.
CATCH.OFF	Disable calls to function tryCatch.
p	presence points used for calibrating the suitability models, typically available in 2-column (lon, lat) dataframe; see also prepareData and extract.
fraction	Fraction of range representing the optimal limits, default value of 0.9 as in the original BIOCLIM software.
quantiles	If TRUE then optimal limits are calculated as quantiles corresponding to 0.5-fraction/2 and 0.5+fraction/2 percentiles. If FALSE then optimal limits are calculated from the normal distribution with mean -cutoff*sd and mean + cutoff*sd with cutoff calculated as qnorm(0.5+fraction/2).
species.name	Name by which the model results will be saved.
factors	vector that indicates which variables are factors; these variables will be ignored by the BIOCLIM algorithm

Details

Function ensemble.bioclim maps suitability for a species based on optimal (percentiles, typically 5 and 95 percent) and absolute (minimum to maximum) limits for bioclimatic variables. If all values at a given location are within the optimal limits, suitability values are mapped as 1 (suitable). If not all values are within the optimal limits, but all values are within the absolute limits, suitability values are mapped as 0.5 (marginal). If not all values are within the absolute limits, suitability values are mapped as 0 (unsuitable).

Function ensemble.bioclim.object calculates the optimal and absolute limits. Optimal limits are calculated based on the parameter fraction, resulting in optimal limits that correspond to 0.5-fraction/2 and 0.5+fraction/2 (the default value of 0.9 therefore gives a lower limit of 0.05 and a upper limit of 0.95). Two methods are implemented to obtain optimal limits for the lower and upper limits. One method (quantiles = FALSE) uses mean, standard deviation and a cutoff parameter calculated with qnorm (see also http://openmodeller.sourceforge.net/algorithms/bioclim.html). The other method (quantiles = TRUE) calculates optimal limits via the quantile function. To handle possible asymmetrical distributions better, the second method is used as default.

When x is a RasterStack and point locations are provided, then optimal and absolute limits correspond to the bioclimatic values observed for the locations. When x is RasterStack and point locations are not provided, then optimal and absolute limits correspond to the bioclimatic values of the RasterStack.

Applying to algorithm without providing point locations will provide results that are similar to the ensemble.novel function, whereby areas plotted as not suitable will be the same areas that are novel.

Value

Function `ensemble.bioclim.object` returns a list with following objects:

`lower.limits`	vector with lower limits for each bioclimatic variable
`upper.limits`	vector with upper limits for each bioclimatic variable
`minima`	vector with minima for each bioclimatic variable
`maxima`	vector with maxima for each bioclimatic variable
`means`	vector with mean values for each bioclimatic variable
`medians`	vector with median values for each bioclimatic variable
`sds`	vector with standard deviation values for each bioclimatic variable
`cutoff`	cutoff value for the normal distribution
`fraction`	fraction of values within the optimal limits
`species.name`	name for the species

Author(s)

Roeland Kindt (World Agroforestry Centre) with inputs from Trevor Booth (CSIRO)

References

Nix HA. 1986. A biogeographic analysis of Australian elapid snakes. In: Atlas of Elapid Snakes of Australia. (Ed.) R. Longmore, pp. 4-15. Australian Flora and Fauna Series Number 7. Australian Government Publishing Service: Canberra.

Booth TH, Nix HA, Busby JR and Hutchinson MF. 2014. BIOCLIM: the first species distribution modelling package, its early applications and relevance to most current MAXENT studies. Diversity and Distributions 20: 1-9

See Also

`bioclim`, `ensemble.bioclim.graph` and `ensemble.novel`

Examples

```
## Not run:
# get predictor variables
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
# subset based on Variance Inflation Factors
predictors <- subset(predictors, subset=c("bio5", "bio6",
    "bio16", "bio17", "biome"))
predictors
predictors@title <- "base"

# presence points
```

```
presence_file <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
pres <- read.table(presence_file, header=TRUE, sep=',')[,-1]

background <- dismo::randomPoints(predictors, n=100)
colnames(background)=c('lon', 'lat')

pres.dataset <- data.frame(extract(predictors, y=pres))
names(pres.dataset) <- names(predictors)
pres.dataset$biome <- as.factor(pres.dataset$biome)

Bradypus.bioclim <- ensemble.bioclim.object(predictors, quantiles=T,
    p=pres, factors="biome", species.name="Bradypus")
Bradypus.bioclim
# obtain the same results with a data.frame
Bradypus.bioclim2 <- ensemble.bioclim.object(pres.dataset, quantiles=T,
    species.name="Bradypus")
Bradypus.bioclim2
# obtain results for entire rasterStack
Bradypus.bioclim3 <- ensemble.bioclim.object(predictors, p=NULL, quantiles=T,
    factors="biome", species.name="America")
Bradypus.bioclim3

ensemble.bioclim(x=predictors, bioclim.object=Bradypus.bioclim, KML.out=T)
ensemble.bioclim(x=predictors, bioclim.object=Bradypus.bioclim3, KML.out=T)

par.old <- graphics::par(no.readonly=T)
graphics::par(mfrow=c(1,2))

rasterfull1 <- paste("ensembles//Bradypus_base_BIOCLIM_orig", sep="")
raster::plot(raster(rasterfull1), breaks=c(-0.1, 0, 0.5, 1),
    col=c("grey", "blue", "green"), main="original method")
rasterfull2 <- paste("ensembles//America_base_BIOCLIM_orig", sep="")
raster::plot(raster(rasterfull2), breaks=c(-0.1, 0, 0.5, 1),
    col=c("grey", "blue", "green"), main="America")

graphics::par(par.old)

# compare with implementation bioclim in dismo
bioclim.dismo <- bioclim(predictors, p=pres)
rasterfull2 <- paste("ensembles//Bradypus_base_BIOCLIM_dismo", sep="")
raster::predict(object=predictors, model=bioclim.dismo, na.rm=TRUE,
    filename=rasterfull2, progress='text', overwrite=TRUE)

par.old <- graphics::par(no.readonly=T)
graphics::par(mfrow=c(1,2))

raster::plot(raster(rasterfull1), breaks=c(-0.1, 0, 0.5, 1),
    col=c("grey", "blue", "green"), main="original method")
raster::plot(raster(rasterfull2), main="dismo method")

graphics::par(par.old)

# use dummy variables to deal with factors
```

```
predictors <- stack(predictor.files)
biome.layer <- predictors[["biome"]]
biome.layer
ensemble.dummy.variables(xcat=biome.layer, most.frequent=0, freq.min=1,
    overwrite=TRUE)

predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
predictors.dummy <- subset(predictors, subset=c("biome_1", "biome_2",  "biome_3",
    "biome_4", "biome_5", "biome_7",  "biome_8",  "biome_9", "biome_10",
    "biome_12", "biome_13", "biome_14"))
predictors.dummy
predictors.dummy@title <- "base_dummy"

Bradypus.dummy <- ensemble.bioclim.object(predictors.dummy, quantiles=T,
    p=pres, species.name="Bradypus")
Bradypus.dummy
ensemble.bioclim(x=predictors.dummy, bioclim.object=Bradypus.dummy, KML.out=F)

par.old <- graphics::par(no.readonly=T)
graphics::par(mfrow=c(1,2))

rasterfull3 <- paste("ensembles//Bradypus_base_dummy_BIOCLIM_orig", sep="")
raster::plot(raster(rasterfull1), breaks=c(-0.1, 0, 0.5, 1), col=c("grey", "blue", "green"),
    main="numeric predictors")
raster::plot(raster(rasterfull3), breaks=c(-0.1, 0, 0.5, 1), col=c("grey", "blue", "green"),
    main="dummy predictors")

graphics::par(par.old)

## End(Not run)
```

`ensemble.bioclim.graph` *Graphs of bioclimatic ranges of species and climates*

Description

The main graph function makes graphs that show mean, median, minimum, maximum and lower and upper limits for species or climates. The `ensemble.bioclim.graph.data` function creates input data, using `ensemble.bioclim.object` internally.

Usage

```
ensemble.bioclim.graph(graph.data = NULL, focal.var = NULL,
    species.climates.subset = NULL, cols = NULL,
    var.multiply = 1.0, ref.lines = TRUE)
```

```
ensemble.bioclim.graph.data(
    x=NULL, p=NULL, fraction = 0.9,
    species.climate.name="Species001_base", factors = NULL)
```

Arguments

graph.data	Input data with same variables as created by ensemble.bioclim.graph
focal.var	Bioclimatic variable to be plotted in the graph
species.climates.subset	Character vector with subset of names of species and climates to be plotted in the graph (if not provided, then all species and climates will be plotted).
cols	colours for the different species and climates
var.multiply	multiplier for the values to be plotted; 0.1 should be used if the bioclimatic variable was multiplied by 10 in the raster layers as in WorldClim and AFRICLIM
ref.lines	If TRUE, then horizontal reference lines will be added for the minimum and maximum values of the species or climate plotted on the extreme left in the graph
x	RasterStack object (stack) containing all environmental layers for which statistics should be calculated; see also ensemble.bioclim.
p	presence points used for calibrating the suitability models, typically available in 2-column (lon, lat) dataframe; see also ensemble.bioclim.
fraction	Fraction of range representing the optimal limits, default value of 0.9 as in the original BIOCLIM software; see also ensemble.bioclim.
species.climate.name	Name for the species or climate that will be used as label in the graph.
factors	vector that indicates which variables are factors; these variables will be ignored by the BIOCLIM algorithm; see also ensemble.bioclim.

Details

The function creates a graph that shows mean, median, minimum, maximum and upper and lower limits for a range of species and climates. The graph can be useful in interpreting results of ensemble.bioclim or ensemble.novel.

In the graphs, means are indicated by an asterisk (pch=8 and medians as larger circles (pch=1)).

Value

function ensemble.bioclim.graph.data creates a data frame, function codeensemble.bioclim.graph allows for plotting.

Author(s)

Roeland Kindt (World Agroforestry Centre)

See Also

ensemble.bioclim

Examples

```
## Not run:

# get predictor variables
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
# subset based on Variance Inflation Factors
predictors <- subset(predictors, subset=c("bio5", "bio6",
    "bio16", "bio17", "biome"))
predictors
predictors@title <- "base"

# presence points
presence_file <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
pres <- read.table(presence_file, header=TRUE, sep=',')[,-1]

# climates for north and south (use same process for future climates)
ext2 <- extent(-90, -32, 0, 23)
predictors2 <- crop(predictors, y=ext2)
predictors2 <- stack(predictors2)
predictors2@title <- "north"

ext3 <- extent(-90, -32, -33, 0)
predictors3 <- crop(predictors, y=ext3)
predictors3 <- stack(predictors3)
predictors3@title <- "south"

graph.data1 <- ensemble.bioclim.graph.data(predictors, p=pres,
    factors="biome", species.climate.name="Bradypus")
graph.data2 <- ensemble.bioclim.graph.data(predictors, p=NULL,
    factors="biome", species.climate.name="baseline")
graph.data3 <- ensemble.bioclim.graph.data(predictors2, p=NULL,
    factors="biome", species.climate.name="north")
graph.data4 <- ensemble.bioclim.graph.data(predictors3, p=NULL,
    factors="biome", species.climate.name="south")
graph.data.all <- rbind(graph.data1, graph.data2, graph.data3, graph.data4)

par.old <- graphics::par(no.readonly=T)
graphics::par(mfrow=c(2, 2))

ensemble.bioclim.graph(graph.data.all, focal.var="bio5",
    var.multiply=0.1, cols=c("black", rep("blue", 3)))
ensemble.bioclim.graph(graph.data.all, focal.var="bio6",
    var.multiply=0.1, cols=c("black", rep("blue", 3)))
ensemble.bioclim.graph(graph.data.all, focal.var="bio16",
    var.multiply=1.0, cols=c("black", rep("blue", 3)))
ensemble.bioclim.graph(graph.data.all, focal.var="bio17",
    var.multiply=1.0, cols=c("black", rep("blue", 3)))

graphics::par(par.old)
```

```
## End(Not run)
```

---

ensemble.calibrate.models

Suitability mapping based on ensembles of modelling algorithms: calibration of models and weights

---

Description

The basic function ensemble.calibrate.models allows to evaluate different algorithms for (species) suitability modelling, including maximum entropy (MAXENT), boosted regression trees, random forests, generalized linear models (including stepwise selection of explanatory variables), generalized additive models (including stepwise selection of explanatory variables), multivariate adaptive regression splines, regression trees, artificial neural networks, flexible discriminant analysis, support vector machines, the BIOCLIM algorithm, the DOMAIN algorithm and the Mahalanobis algorithm. These sets of functions were developed in parallel with the biomod2 package, especially for inclusion of the maximum entropy algorithm, but also to allow for a more direct integration with the BiodiversityR package, more direct handling of model formulae and greater focus on mapping. Researchers and students of species distribution are strongly encouraged to familiarize themselves with all the options of the BIOMOD and dismo packages.

Usage

```
ensemble.calibrate.models(x = NULL, p = NULL,
    a = NULL, an = 1000, excludep = FALSE, target.groups = FALSE,
    k = 0, pt = NULL, at = NULL, SSB.reduce = FALSE, CIRCLES.d = 250000,
    TrainData = NULL, TestData = NULL,
    VIF = FALSE, COR = FALSE,
    SINK = FALSE, PLOTS = FALSE, CATCH.OFF = FALSE,
    threshold.method = "spec_sens", threshold.sensitivity = 0.9,
    threshold.PresenceAbsence = FALSE,
    evaluations.keep = FALSE,
    models.list = NULL, models.keep = FALSE,
    models.save = FALSE, species.name = "Species001",
    ENSEMBLE.tune = FALSE,
    ENSEMBLE.best = 0, ENSEMBLE.min = 0.7, ENSEMBLE.exponent = 1,
    ENSEMBLE.weight.min = 0.05,
    input.weights = NULL,
    MAXENT = 1, MAXNET = 1, MAXLIKE = 1, GBM = 1, GBMSTEP = 1, RF = 1, CF = 1,
    GLM = 1, GLMSTEP = 1, GAM = 1, GAMSTEP = 1, MGCV = 1, MGCVFIX = 0,
    EARTH = 1, RPART = 1, NNET = 1, FDA = 1, SVM = 1 , SVME = 1, GLMNET = 1,
    BIOCLIM.O = 0, BIOCLIM = 1, DOMAIN = 1, MAHAL = 1, MAHAL01 = 1,
    PROBIT = FALSE,
    Yweights = "BIOMOD",
    layer.drops = NULL, factors = NULL, dummy.vars = NULL,
```

```
    formulae.defaults = TRUE, maxit = 100,
    MAXENT.a = NULL, MAXENT.an = 10000,
    MAXENT.path = paste(getwd(), "/models/maxent_", species.name,  sep=""),
    MAXNET.classes = "default", MAXNET.clamp = FALSE, MAXNET.type = "cloglog",
    MAXLIKE.formula = NULL, MAXLIKE.method = "BFGS",
    GBM.formula = NULL, GBM.n.trees = 2001,
    GBMSTEP.gbm.x = 2:(ncol(TrainData.orig)), GBMSTEP.tree.complexity = 5,
    GBMSTEP.learning.rate = 0.005, GBMSTEP.bag.fraction = 0.5,
    GBMSTEP.step.size = 100,
  RF.formula = NULL, RF.ntree = 751, RF.mtry = floor(sqrt(ncol(TrainData.vars))),
  CF.formula = NULL, CF.ntree = 751, CF.mtry = floor(sqrt(ncol(TrainData.vars))),
    GLM.formula = NULL, GLM.family = binomial(link = "logit"),
    GLMSTEP.steps = 1000, STEP.formula = NULL, GLMSTEP.scope = NULL,
    GLMSTEP.k = 2,
    GAM.formula = NULL, GAM.family = binomial(link = "logit"),
    GAMSTEP.steps = 1000, GAMSTEP.scope = NULL, GAMSTEP.pos = 1,
    MGCV.formula = NULL, MGCV.select = FALSE,
    MGCVFIX.formula = NULL,
    EARTH.formula = NULL,
    EARTH.glm = list(family = binomial(link = "logit"), maxit = maxit),
    RPART.formula = NULL, RPART.xval = 50,
    NNET.formula = NULL, NNET.size = 8, NNET.decay = 0.01,
    FDA.formula = NULL,
    SVM.formula = NULL,
    SVME.formula = NULL,
    GLMNET.nlambda = 100, GLMNET.class = FALSE,
    BIOCLIM.O.fraction = 0.9,
    MAHAL.shape = 1)

ensemble.calibrate.weights(x = NULL, p = NULL, TrainTestData=NULL,
    a = NULL, an = 1000,
    get.block = FALSE, block.default = TRUE, get.subblocks = FALSE,
    SSB.reduce = FALSE, CIRCLES.d = 100000,
    excludep = FALSE, target.groups = FALSE,
    k = 4,
    VIF = FALSE, COR = FALSE,
    SINK = FALSE, PLOTS = FALSE, CATCH.OFF = FALSE,
    data.keep = FALSE,
    species.name = "Species001",
    threshold.method = "spec_sens", threshold.sensitivity = 0.9,
    threshold.PresenceAbsence = FALSE,
    ENSEMBLE.tune = FALSE,
    ENSEMBLE.best = 0, ENSEMBLE.min = 0.7, ENSEMBLE.exponent = 1,
    ENSEMBLE.weight.min = 0.05,
    input.weights = NULL,
    MAXENT = 1, MAXNET = 1, MAXLIKE = 1, GBM = 1, GBMSTEP = 1, RF = 1, CF = 1,
    GLM = 1, GLMSTEP = 1, GAM = 1, GAMSTEP = 1, MGCV = 1, MGCVFIX = 0,
    EARTH = 1, RPART = 1, NNET = 1, FDA = 1, SVM = 1 , SVME = 1, GLMNET = 1,
```

```
    BIOCLIM.O = 0, BIOCLIM = 1, DOMAIN = 1, MAHAL = 1, MAHAL01 = 1,
    PROBIT = FALSE,
    Yweights = "BIOMOD",
    layer.drops = NULL, factors = NULL, dummy.vars = NULL,
    formulae.defaults = TRUE, maxit = 100,
    MAXENT.a = NULL, MAXENT.an = 10000,
    MAXENT.path = paste(getwd(), "/models/maxent_", species.name,  sep=""),
    MAXNET.classes = "default", MAXNET.clamp = FALSE, MAXNET.type = "cloglog",
    MAXLIKE.formula = NULL, MAXLIKE.method = "BFGS",
    GBM.formula = NULL, GBM.n.trees = 2001,
    GBMSTEP.gbm.x = 2:(length(var.names)+1), GBMSTEP.tree.complexity = 5,
    GBMSTEP.learning.rate = 0.005,
    GBMSTEP.bag.fraction = 0.5, GBMSTEP.step.size = 100,
    RF.formula = NULL, RF.ntree = 751, RF.mtry = floor(sqrt(length(var.names))),
    CF.formula = NULL, CF.ntree = 751, CF.mtry = floor(sqrt(length(var.names))),
    GLM.formula = NULL, GLM.family = binomial(link = "logit"),
    GLMSTEP.steps = 1000, STEP.formula = NULL, GLMSTEP.scope = NULL, GLMSTEP.k = 2,
    GAM.formula = NULL, GAM.family = binomial(link = "logit"),
    GAMSTEP.steps = 1000, GAMSTEP.scope = NULL, GAMSTEP.pos = 1,
    MGCV.formula = NULL, MGCV.select = FALSE,
    MGCVFIX.formula = NULL,
    EARTH.formula = NULL,
    EARTH.glm = list(family = binomial(link = "logit"), maxit = maxit),
    RPART.formula = NULL, RPART.xval = 50,
    NNET.formula = NULL, NNET.size = 8, NNET.decay = 0.01,
    FDA.formula = NULL,
    SVM.formula = NULL,
    SVME.formula = NULL,
    GLMNET.nlambda = 100, GLMNET.class = FALSE,
    BIOCLIM.O.fraction = 0.9,
    MAHAL.shape = 1)

ensemble.calibrate.models.gbm(x = NULL, p = NULL, a = NULL, an = 1000, excludep = FALSE,
    k = 4,
    TrainData = NULL,
    VIF = FALSE, COR = FALSE,
    SINK = FALSE, PLOTS = FALSE,
    species.name = "Species001",
    Yweights = "BIOMOD",
    layer.drops = NULL, factors = NULL,
    GBMSTEP.gbm.x = 2:(ncol(TrainData.orig)),
    complexity = c(3:6), learning = c(0.005, 0.002, 0.001),
    GBMSTEP.bag.fraction = 0.5, GBMSTEP.step.size = 100)

ensemble.calibrate.models.nnet(x = NULL, p = NULL, a = NULL, an = 1000, excludep = FALSE,
    k = 4,
    TrainData = NULL,
    VIF = FALSE, COR = FALSE,
```

```
    SINK = FALSE, PLOTS = FALSE,
    species.name = "Species001",
    Yweights = "BIOMOD",
    layer.drops = NULL, factors = NULL,
    formulae.defaults = TRUE, maxit = 100,
    NNET.formula = NULL,
    sizes = c(2, 4, 6, 8), decays = c(0.1, 0.05, 0.01, 0.001) )

ensemble.drop1(x = NULL, p = NULL,
    a = NULL, an = 1000, excludep = FALSE, target.groups = FALSE,
    k = 0, pt = NULL, at = NULL, SSB.reduce = FALSE, CIRCLES.d = 100000,
    TrainData = NULL, TestData = NULL,
    VIF = FALSE, COR = FALSE,
    SINK = FALSE,
    species.name = "Species001",
    difference = FALSE, variables.alone = FALSE,
    ENSEMBLE.tune = FALSE,
    ENSEMBLE.best = 0, ENSEMBLE.min = 0.7, ENSEMBLE.exponent = 1,
    input.weights = NULL,
    MAXENT = 1, MAXNET = 1, MAXLIKE = 1, GBM = 1, GBMSTEP = 0, RF = 1, CF = 1,
    GLM = 1, GLMSTEP = 1, GAM = 1, GAMSTEP = 1, MGCV = 1, MGCVFIX = 0,
    EARTH = 1, RPART = 1, NNET = 1, FDA = 1, SVM = 1, SVME = 1, GLMNET = 1,
    BIOCLIM.O = 0, BIOCLIM = 1, DOMAIN = 1, MAHAL = 1, MAHAL01 = 1,
    PROBIT = FALSE,
    Yweights = "BIOMOD",
    layer.drops = NULL, factors = NULL, dummy.vars = NULL,
    maxit = 100,
    MAXENT.a = NULL, MAXENT.an = 10000,
    MAXENT.path = paste(getwd(), "/models/maxent_", species.name,  sep=""),
    MAXNET.classes = "default", MAXNET.clamp = FALSE, MAXNET.type = "cloglog",
    MAXLIKE.method = "BFGS",
    GBM.n.trees = 2001,
    GBMSTEP.tree.complexity = 5, GBMSTEP.learning.rate = 0.005,
    GBMSTEP.bag.fraction = 0.5, GBMSTEP.step.size = 100,
    RF.ntree = 751,
    CF.ntree = 751,
    GLM.family = binomial(link = "logit"),
    GLMSTEP.steps = 1000, GLMSTEP.scope = NULL, GLMSTEP.k = 2,
    GAM.family = binomial(link = "logit"),
    GAMSTEP.steps = 1000, GAMSTEP.scope = NULL, GAMSTEP.pos = 1,
    MGCV.select = FALSE,
    EARTH.glm = list(family = binomial(link = "logit"), maxit = maxit),
    RPART.xval = 50,
    NNET.size = 8, NNET.decay = 0.01,
    GLMNET.nlambda = 100, GLMNET.class = FALSE,
    BIOCLIM.O.fraction = 0.9,
    MAHAL.shape = 1)
```

```
ensemble.weights(weights = c(0.9, 0.8, 0.7, 0.5),
    best = 0, min.weight = 0,
    exponent = 1, digits = 6)

ensemble.strategy(TrainData = NULL, TestData = NULL,
    verbose = FALSE,
    ENSEMBLE.best = c(4:10), ENSEMBLE.min = c(0.7),
    ENSEMBLE.exponent = c(1, 2, 3) )

ensemble.formulae(x,
    layer.drops = NULL, factors = NULL, dummy.vars = NULL, weights = NULL)

ensemble.threshold(eval, threshold.method = "spec_sens", threshold.sensitivity = 0.9,
    threshold.PresenceAbsence = FALSE, Pres, Abs)

ensemble.VIF(x = NULL, a = NULL, an = 10000,
    VIF.max = 10, keep = NULL,
    layer.drops = NULL, factors = NULL, dummy.vars = NULL)

ensemble.VIF.dataframe(x=NULL,
    VIF.max=10, keep=NULL,
    car=TRUE, silent=F)

ensemble.pairs(x = NULL, a = NULL, an = 10000)
```

Arguments

x	RasterStack object (stack) containing all layers that correspond to explanatory variables
p	presence points used for calibrating the suitability models, typically available in 2-column (lon, lat) dataframe; see also prepareData and extract
a	background points used for calibrating the suitability models (except for maxent), typically available in 2-column (lon, lat) dataframe; see also prepareData and extract
an	number of background points for calibration to be selected with randomPoints in case argument a is missing
excludep	parameter that indicates (if TRUE) that presence points will be excluded from the background points; see also randomPoints
target.groups	Parameter that indicates (if TRUE) that the provided background points (argument a) represent presence points from a target group sensu Phillips et al. 2009 (these are species that are all collected or observed using the same methods or equipment). Setting the parameter to TRUE results in selecting the centres of cells of the target groups as background points, while avoiding to select the same cells twice. Via argument excludep, it is possible to filter out cells with presence observations (argument p).
k	If larger than 1, the number of groups to split between calibration (k-1) and evaluation (1) data sets (for example, k = 4 results in 3/4 of presence and background

points to be used for calibrating the models, and 1/4 of presence and background points to be used for evaluating the models). For `ensemble.calibrate.weights`, `ensemble.calibrate.models.gbm` and `ensemble.calibrate.models.nnet`, this procedure is repeated `k` times (k-fold cross-validation). See also `kfold`.

`pt` presence points used for evaluating the suitability models, available in 2-column (lon, lat) dataframe; see also `prepareData` and `extract`

`at` background points used for evaluating the suitability models, available in 2-column (lon, lat) dataframe; see also `prepareData` and `extract`

`SSB.reduce` If `TRUE`, then new background points that will be used for evaluationg the suitability models will be selected (`randomPoints`) in circular neighbourhoods (created with `circles`) around presence locations (p and pt). The abbreviation of SSB refers to spatial sorting bias; see also `ssb`.

`CIRCLES.d` Radius in m of circular neighbourhoods (created with `circles`) around presence locations (p and pt).

`TrainData` dataframe with first column 'pb' describing presence (1) and absence (0) and other columns containing explanatory variables; see also `prepareData`. In case that this dataframe is provided, then locations p and a are not used. For the maximum entropy model (`maxent`), a different dataframe is used for calibration; see parameter `MAXENT.TrainData`.

`TestData` dataframe with first column 'pb' describing presence (1) and absence (0) and other columns containing explanatory variables; see also `prepareData`. In case that this dataframe is provided, then locations pt and at are not used. For `ensemble.strategy`, this dataframe should be a dataframe that contains predictions for various models - such dataframe can be provided by the `ensemble.calibrate.models` or `ensemble.raster` functions.

`VIF` Estimate the variance inflation factors based on a linear model calibrated on the training data (if `TRUE`). Only background locations will be used and the response variable 'pb' will be replaced by a random variable. See also `vif`.

`COR` Provide information on the correlation between the numeric explanatory variables (if `TRUE`). See also `cor`.

`SINK` Append the results to a text file in subfolder 'outputs' (if `TRUE`). The name of file is based on argument `species.name`. In case the file already exists, then results are appended. See also `sink`.

`PLOTS` Disabled option of plotting evaluation results(BiodiversityR version 2.9-1) - see examples how to plot results afterwards and also `evaluate`.

`CATCH.OFF` Disable calls to function `tryCatch`.

`threshold.method`
Method to calculate the threshold between predicted absence and presence; possibilities include `spec_sens` (highest sum of the true positive rate and the true negative rate), `kappa` (highest kappa value), `no_omission` (highest threshold that corresponds to no omission), `prevalence` (modeled prevalence is closest to observed prevalence) and `equal_sens_spec` (equal true positive rate and true negative rate). See `threshold`. Options specific to the BiodiversityR implementation are: `threshold2005.mean`, `threshold2005.min`, `threshold2013.mean` and `threshold2013.min` (resulting in calculating the mean or minimum value

of recommended threshold values by studies published in 2005 and 2013; see details below).

`threshold.sensitivity`
: Sensitivity value for `threshold.method = 'sensitivity'`. See `threshold`.

`threshold.PresenceAbsence`
: If `TRUE` calculate thresholds with the PresenceAbsence package. See `optimal.thresholds`.

`evaluations.keep`
: Keep the results of evaluations (if `TRUE`). See also `evaluate`.

`models.list`
: list with 'old' model objects such as `MAXENT` or `RF`.

`models.keep`
: store the details for each suitability modelling algorithm (if `TRUE`). (This may be particularly useful when projecting to different possible future climates.)

`models.save`
: Save the list with model details to a file (if `TRUE`). The filename will be `species.name` with extension `.models`; this file will be saved in subfolder of `models`. When loading this file, model results will be available as `ensemble.models`.

`species.name`
: Name by which the model details will be saved to a file; see also argument `models.save`

`data.keep`
: Keep the data for each k-fold cross-validation run (if `TRUE`).

`ENSEMBLE.tune`
: Determine weights for the ensemble model based on AUC values (if `TRUE`). See details.

`ENSEMBLE.best`
: The number of individual suitability models to be used in the consensus suitability map (based on a weighted average). In case this parameter is smaller than 1 or larger than the number of positive input weights of individual models, then all individual suitability models with positive input weights are included in the consensus suitability map. In case a vector is provided, `ensemble.strategy` is called internally to determine weights for the ensemble model.

`ENSEMBLE.min`
: The minimum input weight (typically corresponding to AUC values) for a model to be included in the ensemble. In case a vector is provided, function `ensemble.strategy` is called internally to determine weights for the ensemble model.

`ENSEMBLE.exponent`
: Exponent applied to AUC values to convert AUC values into weights (for example, an exponent of 2 converts input weights of 0.7, 0.8 and 0.9 into 0.7^2=0.49, 0.8^2=0.64 and 0.9^2=0.81). See details.

`ENSEMBLE.weight.min`
: The minimum output weight for models included in the ensemble, applying to weights that sum to one. Note that `ENSEMBLE.min` typically refers to input AUC values.

`input.weights`
: array with numeric values for the different modelling algorithms; if `NULL` then values provided by parameters such as `MAXENT` and `GBM` will be used. As an alternative, the output from `ensemble.calibrate.weights` can be used.

`MAXENT`
: number: if larger than 0, then a maximum entropy model (`maxent`) will be fitted among ensemble

`MAXNET`
: number: if larger than 0, then a maximum entropy model (`maxnet`) will be fitted among ensemble

MAXLIKE	number: if larger than 0, then a maxlike model (maxlike) will be fitted among ensemble
GBM	number: if larger than 0, then a boosted regression trees model (gbm) will be fitted among ensemble
GBMSTEP	number: if larger than 0, then a stepwise boosted regression trees model (gbm.step) will be fitted among ensemble
RF	number: if larger than 0, then a random forest model (randomForest) will be fitted among ensemble
CF	number: if larger than 0, then a random forest model (cforest) will be fitted among ensemble
GLM	number: if larger than 0, then a generalized linear model (glm) will be fitted among ensemble
GLMSTEP	number: if larger than 0, then a stepwise generalized linear model (stepAIC) will be fitted among ensemble
GAM	number: if larger than 0, then a generalized additive model (gam) will be fitted among ensemble
GAMSTEP	number: if larger than 0, then a stepwise generalized additive model (step.gam) will be fitted among ensemble
MGCV	number: if larger than 0, then a generalized additive model (gam) will be fitted among ensemble
MGCVFIX	number: if larger than 0, then a generalized additive model with fixed d.f. regression splines (gam) will be fitted among ensemble
EARTH	number: if larger than 0, then a multivariate adaptive regression spline model (earth) will be fitted among ensemble
RPART	number: if larger than 0, then a recursive partioning and regression tree model (rpart) will be fitted among ensemble
NNET	number: if larger than 0, then an artificial neural network model (nnet) will be fitted among ensemble
FDA	number: if larger than 0, then a flexible discriminant analysis model (fda) will be fitted among ensemble
SVM	number: if larger than 0, then a support vector machine model (ksvm) will be fitted among ensemble
SVME	number: if larger than 0, then a support vector machine model (svm) will be fitted among ensemble
GLMNET	number: if larger than 0, then a GLM with lasso or elasticnet regularization (glmnet) will be fitted among ensemble
BIOCLIM.O	number: if larger than 0, then the original BIOCLIM algorithm (ensemble.bioclim) will be fitted among ensemble
BIOCLIM	number: if larger than 0, then the BIOCLIM algorithm (bioclim) will be fitted among ensemble
DOMAIN	number: if larger than 0, then the DOMAIN algorithm (domain) will be fitted among ensemble

MAHAL	number: if larger than 0, then the Mahalanobis algorithm (mahal) will be fitted among ensemble
MAHAL01	number: if larger than 0, then the Mahalanobis algorithm (mahal) will be fitted among ensemble, using a transformation method afterwards whereby output is within the range between 0 and 1 (see details)
PROBIT	If TRUE, then subsequently to the fitting of the individual algorithm (e.g. maximum entropy or GAM) a generalized linear model (glm) with probit link family=binomial(link="probi will be fitted to transform the predictions, using the previous predictions as explanatory variable. This transformation results in all model predictions to be probability estimates.
Yweights	chooses how cases of presence and background (absence) are weighted; "BIOMOD" results in equal weighting of all presence and all background cases, "equal" results in equal weighting of all cases. The user can supply a vector of weights similar to the number of cases in the calibration data set.
layer.drops	vector that indicates which layers should be removed from RasterStack x. This argument is especially useful for the ensemble.drop1 function. See also addLayer.
factors	vector that indicates which variables are factors; see also prepareData
dummy.vars	vector that indicates which variables are dummy variables (influences formulae suggestions)
formulae.defaults	Suggest formulae for most of the models (if TRUE). See also ensemble.formulae.
maxit	Maximum number of iterations for some of the models. See also glm.control, gam.control, gam.control and nnet.
MAXENT.a	background points used for calibrating the maximum entropy model (maxent), typically available in 2-column (lon, lat) dataframe; see also prepareData and extract.
MAXENT.an	number of background points for calibration to be selected with randomPoints in case argument MAXENT.a is missing
MAXENT.path	path to the directory where output files of the maximum entropy model are stored; see also maxent
MAXNET.classes	continuous feature classes, either "default" or any subset of "lqpht" (linear, quadratic, product, hinge, threshold). Note that the "default" option chooses feature classes based on the number of presence locations as "l" (< 10 locations), "lq" (10 - 14 locations), "lqh" (15 - 79 locations) or "lqph" (> 79 locations). See also maxnet.
MAXNET.clamp	restrict predictors and features to the range seen during model training; see also predict.maxnet
MAXNET.type	type of response required; see also predict.maxnet
MAXLIKE.formula	formula for the maxlike algorithm; see also maxlike
MAXLIKE.method	method for the maxlike algorithm; see also optim
GBM.formula	formula for the boosted regression trees algorithm; see also gbm
GBM.n.trees	total number of trees to fit for the boosted regression trees model; see also gbm

GBMSTEP.gbm.x indices of column numbers with explanatory variables for stepwise boosted regression trees; see also gbm.step

GBMSTEP.tree.complexity complexity of individual trees for stepwise boosted regression trees; see also gbm.step

GBMSTEP.learning.rate weight applied to individual trees for stepwise boosted regression trees; see also gbm.step

GBMSTEP.bag.fraction proportion of observations used in selecting variables for stepwise boosted regression trees; see also gbm.step

GBMSTEP.step.size number of trees to add at each cycle for stepwise boosted regression trees (should be small enough to result in a smaller holdout deviance than the initial number of trees [50]); see also gbm.step

RF.formula formula for random forest algorithm; see also randomForest

RF.ntree number of trees to grow for random forest algorithm; see also randomForest

RF.mtry number of variables randomly sampled as candidates at each split for random forest algorithm; see also randomForest

CF.formula formula for random forest algorithm; see also cforest

CF.ntree number of trees to grow in a forest; see also cforest_control

CF.mtry number of input variables randomly sampled as candidates at each node for random forest like algorithms; see also cforest_control

GLM.formula formula for the generalized linear model; see also glm

GLM.family description of the error distribution and link function for the generalized linear model; see also glm

GLMSTEP.steps maximum number of steps to be considered for stepwise generalized linear model; see also stepAIC

STEP.formula formula for the "starting model" to be considered for stepwise generalized linear model; see also stepAIC

GLMSTEP.scope range of models examined in the stepwise search; see also stepAIC

GLMSTEP.k multiple of the number of degrees of freedom used for the penalty (only k = 2 gives the genuine AIC); see also stepAIC

GAM.formula formula for the generalized additive model; see also gam

GAM.family description of the error distribution and link function for the generalized additive model; see also gam

GAMSTEP.steps maximum number of steps to be considered in the stepwise generalized additive model; see also step.gam

GAMSTEP.scope range of models examined in the step-wise search n the stepwise generalized additive model; see also step.gam

GAMSTEP.pos parameter expected to be set to 1 to allow for fitting of the stepwise generalized additive model

MGCV.formula	formula for the generalized additive model; see also gam
MGCV.select	if TRUE, then the smoothing parameter estimation that is part of fitting can completely remove terms from the model; see also gam
MGCVFIX.formula	formula for the generalized additive model with fixed d.f. regression splines; see also gam (the default formulae sets "s(..., fx = TRUE, ...)"; see also s)
EARTH.formula	formula for the multivariate adaptive regression spline model; see also earth
EARTH.glm	list of arguments to pass on to glm; see also earth
RPART.formula	formula for the recursive partioning and regression tree model; see also rpart
RPART.xval	number of cross-validations for the recursive partioning and regression tree model; see also rpart.control
NNET.formula	formula for the artificial neural network model; see also nnet
NNET.size	number of units in the hidden layer for the artificial neural network model; see also nnet
NNET.decay	parameter of weight decay for the artificial neural network model; see also nnet
FDA.formula	formula for the flexible discriminant analysis model; see also fda
SVM.formula	formula for the support vector machine model; see also ksvm
SVME.formula	formula for the support vector machine model; see also svm
GLMNET.nlambda	The number of lambda values; see also glmnet
GLMNET.class	Use the predicted class to calculate the mean predictions of GLMNET; see predict.glmnet
BIOCLIM.O.fraction	Fraction of range representing the optimal limits, default value of 0.9 as in the original BIOCLIM software (ensemble.bioclim).
MAHAL.shape	parameter that influences the transformation of output values of mahal. See details section.
TrainTestData	dataframe with first column 'pb' describing presence (1) and absence (0) and other columns containing explanatory variables; see also prepareData. In case that this dataframe is provided, then locations p and a are not used. This data set will also be used for the maximum entropy and maximum likelihood models.
get.block	if TRUE, instead of creating k-fold cross-validation subsets randomly (kfold), create 4 subsets of presence and background locations with get.block.
block.default	if FALSE, instead of making the first division of presence point locations along the y-coordinates (latitude) as in get.block, make the first division along the x-coordinates (longitude).
get.subblocks	if TRUE, then 4 subsets of presence and background locations are generated in a checkerboard configuration by applying get.block to each of the 4 blocks generated by get.block in a first step.
complexity	vector with values of complexity of individual trees (tree.complexity) for boosted regression trees; see also gbm.step
learning	vector with values of weights applied to individual trees (learning.rate) for boosted regression trees; see also gbm.step

sizes	vector with values of number of units in the hidden layer for the artificial neural network model; see also nnet
decays	vector with values of weight decay for the artificial neural network model; see also nnet
difference	if TRUE, then AUC values of the models with all variables are subtracted from the models where one explanatory variable was excluded. After subtraction, positive values indicate that the model without the explanatory variable has a higher AUC than the model with all variables.
variables.alone	if TRUE, then models are also fitted using each explanatory variable as single explanatory variable
weights	input weights for the ensemble.weights function
best	The number of final weights. In case this parameter is smaller than 1 or larger than the number of positive input weights of individual models, then this parameter is ignored.
min.weight	The minimum input weight to be included in the output.
exponent	Exponent applied to AUC values to convert AUC values into weights (for example, an exponent of 2 converts input weights of 0.7, 0.8 and 0.9 into 0.7^2=0.49, 0.8^2=0.64 and 0.9^2=0.81). See details.
digits	Number of number of decimal places in the output weights; see also round.
verbose	If TRUE, then provide intermediate results for ensemble.strategy)
eval	ModelEvaluation object obtained by evaluate
Pres	Suitabilities (probabilities) at presence locations
Abs	Suitabilities (probabilities) at background locations
VIF.max	Maximum Variance Inflation Factor of the selected subset of variables. In case that at least one of the variables has VIF larger than VIF.max, then the variable with the highest VIF will be removed in the next step.
keep	character vector with names of the variables to be kept.
car	Also provide results from vif.
silent	Limit textual output.

Details

The basic function ensemble.calibrate.models first calibrates individual suitability models based on presence locations p and background locations a, then evaluates these suitability models based on presence locations pt and background locations at. While calibrating and testing individual models, results obtained via the evaluate function can be saved (evaluations.keep).

As an alternative to providing presence locations p, models can be calibrated with data provided in TrainData. In case that both p and TrainData are provided, then models will be calibrated with TrainData.

Calibration of the maximum entropy (MAXENT) algorithm is not based on background locations a, but based on background locations MAXENT.a instead. However, to compare evaluations with evaluations of other algorithms, during evaluations of the MAXENT algorithm, presence locations p and background locations a are used (and not background locations MAXENT.a).

Output from the GLMNET algorithm is calculated as the mean of the output from predict.glmnet. With option GLMNET.class = TRUE, the mean output is the mean prediction of class 1. With option GLMNET.class = FALSE, the mean output is the mean of the responses.

As the Mahalanobis function (mahal) does not always provide values within the range of 0 - 1, the output values are rescaled with option MAHAL01 by first subtracting the value of 1 -MAHAL.shape from each prediction, followed by calculating the absolute value, followed by calculating the reciprocal value and finally multiplying this reciprocal value with MAHAL.shape. As this rescaling method does not estimate probabilities, inclusion in the calculation of a (weighted) average of ensemble probabilities may be problematic and the PROBIT transformation may help here (the same applies to other distance-based methods).

With parameter ENSEMBLE.best, the subset of best models (evaluated by the individual AUC values) can be selected and only those models will be used for calculating the ensemble model (in other words, weights for models not included in the ensemble will be set to zero). It is possible to further increase the contribution to the ensemble model for models with higher AUC values through parameter ENSEMBLE.exponent. With ENSEMBLE.exponent = 2, AUC values of 0.7, 0.8 and 0.9 are converted into weights of 0.7^2=0.49, 0.8^2=0.64 and 0.9^2=0.81). With ENSEMBLE.exponent = 4, AUC values of 0.7, 0.8 and 0.9 are converted into weights of 0.7^4=0.2401, 0.8^4=0.4096 and 0.9^2=0.6561).

ENSEMBLE.tune will result in an internal procedure whereby the best selection of parameter values for ENSEMBLE.min, ENSEMBLE.best or ENSEMBLE.exponent can be identified. Through a factorial procedure, the ensemble model with best AUC for a specific combination of parameter values is identified. The procedure also provides the weights that correspond to the best ensemble. In case that ENSEMBLE.tune is set to FALSE, then the ensemble is calculated based on the input weights.

Function ensemble.calibrate.weights splits the presence and background locations in a user-defined (k) number of subsets (i.e. k-fold cross-validation), then sequentially calibrates individual suitability models with (k-1) combined subsets and evaluates those with the remaining one subset, whereby each subset is used once for evaluation in the user-defined number (k) of runs. For example, k = 4 results in splitting the locations in 4 subsets, then using one of these subsets in turn for evaluations (see also kfold). Note that for the maximum entropy (MAXENT) algorithm, the same background data will be used in each cross-validation run (this is based on the assumption that a large number (~10000) of background locations are used).

Among the output from function ensemble.calibrate.weights are suggested weights for an ensemble model (output.weights and output.weights.AUC), and information on the respective AUC values of the ensemble model with the suggested weights for each of the (k) subsets. Suggested weights output.weights are calculated as the average of the weights of the different algorithms (submodels) of the k ensembles. Suggested weights output.weights.AUC are calculated as the average of the AUC of the different algorithms of the for the k runs.

Function ensemble.calibrate.models.gbm allows to test various combinations of parameters tree.complexity and learning.rate for the gbm.step model.

Function ensemble.calibrate.models.nnet allows to test various combinations of parameters size and decay for the nnet model.

Function ensemble.drop1 allows to test the effects of leaving out each of the explanatory variables, and comparing these results with the "full" model. Note that option of difference = TRUE may result in positive values, indicating that the model without the explanatory variable having larger AUC than the "full" model. A procedure is included to estimate the deviance of a model based on the fitted values, using -2 * (sum(x*log(x)) + sum((1-x)*log(1-x))) where x is a vector of the

fitted values for a respective model. (It was checked that this procedure results in similar deviance estimates for the null and 'full' models for glm, but note that it is not certain whether deviance can be calculated in a similar way for other submodels.)

Function `ensemble.formulae` provides suggestions for formulae that can be used for `ensemble.calibrate.models` and `ensemble.raster`. This function is always used internally by the `ensemble.drop1` function.

The `ensemble.weights` function is used internally by the `ensemble.calibrate.models` and `ensemble.raster` functions, using the input weights for the different suitability modelling algorithms. Ties between input weights result in the same output weights.

The `ensemble.strategy` function is used internally by the `ensemble.calibrate.models` function, using the train and test data sets with predictions of the different suitability modelling algorithms and different combinations of parameters `ENSEMBLE.best`, `ENSEMBLE.min` and `ENSEMBLE.exponent`. The final ensemble model is based on the parameters that generate the best AUC.

The `ensemble.threshold` function is used internally by the `ensemble.calibrate.models`, `ensemble.mean` and `ensemble.plot` functions. `threshold2005.mean` results in calculating the mean value of threshold methods that resulted in better results (calculated by `optimal.thresholds` with methods of `ObsPrev`, `MeanProb`, `MaxSens+Spec`, `Sens=Spec` and `MinROCdist`) in a study by Liu et al. (Ecography 28: 385-393. 2005). `threshold2005.min` results in calculating the mean value of threshold methods that resulted in better results (calculated by `optimal.thresholds` with methods of `ObsPrev`, `MeanProb` and `MaxSens+Spec`) in a study by Liu et al. (Ecography 28: 385-393. 2005). `threshold2013.mean` results in calculating the mean value of threshold methods that resulted in better results (calculated by `optimal.thresholds` with methods of `ObsPrev`, `MeanProb`, `MaxSens+Spec`, `Sens=Spec` and `MinROCdist`) in a study by Liu et al. (J. Biogeogr. 40: 778-789. 2013). `threshold2013.min` results in calculating the minimum value of threshold methods that resulted in better results (calculated by `optimal.thresholds` with methods of `ObsPrev`, `MeanProb`, `MaxSens+Spec`, `Sens=Spec` and `MinROCdist`) in a study by Liu et al. (J. Biogeogr. 40: 778-789. 2013).

Function `ensemble.VIF` implements a stepwise procedure whereby the explanatory variable with highest Variance Inflation Factor is removed from the list of variables. The procedure ends when no variable has VIF larger than parameter `VIF.max`.

Function `ensemble.pairs` provides a matrix of scatterplots similar to the example of `pairs` for version 3.4.3 of that package.

Value

Function `ensemble.calibrate.models` (potentially) returns a list with results from evaluations (via `evaluate`) of calibration and test runs of individual suitability models.

Function `ensemble.calibrate.weights` returns a matrix with, for each individual suitability model, the AUC of each run and the average AUC over the runs. Models are sorted by the average AUC. The average AUC for each model can be used as input weights for the `ensemble.raster` function.

Functions `ensemble.calibrate.models.gbm` and `ensemble.calibrate.models.nnet` return a matrix with, for each combination of model parameters, the AUC of each run and the average AUC. Models are sorted by the average AUC.

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Liu C, White M and Newell G. 2013. Selecting thresholds for the prediction of species occurrence with presence-only data. Journal of Biogeography 40: 778-789

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See Also

ensemble.raster, ensemble.batch

Examples

```
## Not run:
# based on examples in the dismo package

# get predictor variables
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
# subset based on Variance Inflation Factors
predictors <- subset(predictors, subset=c("bio5", "bio6",
    "bio16", "bio17", "biome"))
predictors
predictors@title <- "predictors"

# presence points
presence_file <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
pres <- read.table(presence_file, header=TRUE, sep=',')[,-1]

# the kfold function randomly assigns data to groups;
# groups are used as calibration (1/4) and training (3/4) data
groupp <- kfold(pres, 4)
pres_train <- pres[groupp !=  1, ]
pres_test <- pres[groupp ==  1, ]

# choose background points
background <- randomPoints(predictors, n=1000, extf=1.00)
colnames(background)=c('lon', 'lat')
groupa <- kfold(background, 4)
backg_train <- background[groupa != 1, ]
backg_test <- background[groupa == 1, ]
```

```
# formulae for random forest and generalized linear model
# compare with: ensemble.formulae(predictors, factors=c("biome"))

rfformula <- as.formula(pb ~ bio5+bio6+bio16+bio17)

glmformula <- as.formula(pb ~ bio5 + I(bio5^2) + I(bio5^3) +
    bio6 + I(bio6^2) + I(bio6^3) + bio16 + I(bio16^2) + I(bio16^3) +
    bio17 + I(bio17^2) + I(bio17^3) )

# fit four ensemble models (RF, GLM, BIOCLIM, DOMAIN)
# factors removed for BIOCLIM, DOMAIN, MAHAL
ensemble.nofactors <- ensemble.calibrate.models(x=predictors, p=pres_train, a=backg_train,
    pt=pres_test, at=backg_test,
    species.name="Bradypus",
    ENSEMBLE.tune=TRUE,
    ENSEMBLE.min = 0.65,
    MAXENT=0, MAXNET=0, MAXLIKE=0, GBM=0, GBMSTEP=0, RF=1, CF=0,
    GLM=1, GLMSTEP=0, GAM=0, GAMSTEP=0, MGCV=0, MGCVFIX=0,
    EARTH=0, RPART=0, NNET=0, FDA=0, SVM=0, SVME=0, GLMNET=0,
    BIOCLIM.O=0, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=0,
    Yweights="BIOMOD",
    factors="biome",
    evaluations.keep=TRUE, models.keep=TRUE,
    RF.formula=rfformula,
    GLM.formula=glmformula)

# with option models.keep, all model objects are saved in ensemble object
# the same slots can be used to replace model objects with new calibrations
ensemble.nofactors$models$RF
summary(ensemble.nofactors$models$GLM)
ensemble.nofactors$models$BIOCLIM
ensemble.nofactors$models$DOMAIN
ensemble.nofactors$models$formulae

# evaluations are kept in different slot
attributes(ensemble.nofactors$evaluations)
plot(ensemble.nofactors$evaluations$RF.T, "ROC")

# fit four ensemble models (RF, GLM, BIOCLIM, DOMAIN) using default formulae
# variable 'biome' is not included as explanatory variable
# results are provided in a file in the 'outputs' subfolder of the working
# directory
ensemble.nofactors <- ensemble.calibrate.models(x=predictors,
    p=pres_train, a=backg_train,
    pt=pres_test, at=backg_test,
    layer.drops="biome",
    species.name="Bradypus",
    ENSEMBLE.tune=TRUE,
    ENSEMBLE.min=0.65,
    SINK=TRUE,
    MAXENT=0, MAXNET=0, MAXLIKE=0, GBM=0, GBMSTEP=0, RF=1, CF=0,
    GLM=1, GLMSTEP=0, GAM=0,
```

```
    GAMSTEP=0, MGCV=0, MGCVFIX=0, EARTH=0, RPART=0, NNET=0, FDA=0,
    SVM=0, SVME=0, GLMNET=0,
    BIOCLIM.O=0, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=0,
    Yweights="BIOMOD",
    evaluations.keep=TRUE,
    formulae.defaults=TRUE)

# after fitting the individual algorithms (submodels),
# transform predictions with a probit link.
ensemble.nofactors <- ensemble.calibrate.models(x=predictors,
    p=pres_train, a=backg_train,
    pt=pres_test, at=backg_test,
    layer.drops="biome",
    species.name="Bradypus",
    SINK=TRUE,
    ENSEMBLE.tune=TRUE,
    ENSEMBLE.min=0.65,
    MAXENT=0, MAXNET=0, MAXLIKE=0, GBM=0, GBMSTEP=0, RF=1, CF=0,
    GLM=1, GLMSTEP=0, GAM=0, GAMSTEP=0, MGCV=0, MGCVFIX=0,
    EARTH=0, RPART=0, NNET=0, FDA=0, SVM=0, SVME=0, GLMNET=0,
    BIOCLIM.O=0, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=0,
    PROBIT=TRUE,
    Yweights="BIOMOD", factors="biome",
    evaluations.keep=TRUE,
    formulae.defaults=TRUE)

# Instead of providing presence and background locations, provide data.frames.
# Because 'biome' is a factor, RasterStack needs to be provided
# to check for levels in the Training and Testing data set.
TrainData1 <- prepareData(x=predictors, p=pres_train, b=backg_train,
    factors=c("biome"), xy=FALSE)
TestData1 <- prepareData(x=predictors, p=pres_test, b=backg_test,
    factors=c("biome"), xy=FALSE)
ensemble.factors1 <- ensemble.calibrate.models(x=predictors,
    TrainData=TrainData1, TestData=TestData1,
    p=pres_train, a=backg_train,
    pt=pres_test, at=backg_test,
    species.name="Bradypus",
    SINK=TRUE,
    ENSEMBLE.tune=TRUE,
    ENSEMBLE.min=0.65,
    MAXENT=0, MAXNET=1, MAXLIKE=1, GBM=1, GBMSTEP=0, RF=1, CF=1,
    GLM=1, GLMSTEP=1, GAM=1, GAMSTEP=1, MGCV=1, MGCVFIX=0,
    EARTH=1, RPART=1, NNET=1, FDA=1, SVM=1, SVME=1, GLMNET=1,
    BIOCLIM.O=1, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=1,
    Yweights="BIOMOD", factors="biome",
    evaluations.keep=TRUE)

# compare different methods of calculating ensembles
ensemble.factors2 <- ensemble.calibrate.models(x=predictors,
    TrainData=TrainData1, TestData=TestData1,
    p=pres_train, a=backg_train,
    pt=pres_test, at=backg_test,
```

```
    species.name="Bradypus",
    SINK=TRUE,
    ENSEMBLE.tune=TRUE,
    MAXENT=0, MAXNET=1, MAXLIKE=1, GBM=1, GBMSTEP=0, RF=1, CF=1,
    GLM=1, GLMSTEP=1, GAM=1, GAMSTEP=1, MGCV=1, MGCVFIX=1,
    EARTH=1, RPART=1, NNET=1, FDA=1, SVM=1, SVME=1, GLMNET=1,
    BIOCLIM.O=1, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=1,
    ENSEMBLE.best=c(4:10), ENSEMBLE.exponent=c(1, 2, 3),
    Yweights="BIOMOD", factors="biome",
    evaluations.keep=TRUE)

# test performance of different suitability models
# data are split in 4 subsets, each used once for evaluation
ensemble.nofactors2 <- ensemble.calibrate.weights(x=predictors,
    p=pres, a=background, k=4,
    species.name="Bradypus",
    SINK=TRUE, PROBIT=TRUE,
    MAXENT=0, MAXNET=1, MAXLIKE=1, GBM=1, GBMSTEP=0, RF=1, CF=1,
    GLM=1, GLMSTEP=1, GAM=1, GAMSTEP=1, MGCV=1, MGCVFIX=1,
    EARTH=1, RPART=1, NNET=1, FDA=1, SVM=1, SVME=1, GLMNET=1,
    BIOCLIM.O=1, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=1,
    ENSEMBLE.tune=TRUE,
    ENSEMBLE.best=0, ENSEMBLE.exponent=c(1, 2, 3),
    ENSEMBLE.min=0.7,
    Yweights="BIOMOD",
    formulae.defaults=TRUE)
ensemble.nofactors2$AUC.table

# test the result of leaving out one of the variables from the model
# note that positive differences indicate that the model without the variable
# has higher AUC than the full model
ensemble.variables <- ensemble.drop1(x=predictors,
    p=pres, a=background, k=4,
    species.name="Bradypus",
    SINK=TRUE,
    difference=TRUE,
    VIF=TRUE, PROBIT=TRUE,
    MAXENT=0, MAXNET=1, MAXLIKE=1, GBM=1, GBMSTEP=0, RF=1, CF=1,
    GLM=1, GLMSTEP=1, GAM=1, GAMSTEP=1, MGCV=1, MGCVFIX=1,
    EARTH=1, RPART=1, NNET=1, FDA=1, SVM=1, SVME=1, GLMNET=1,
    BIOCLIM.O=1, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=1,
    ENSEMBLE.tune=TRUE,
    ENSEMBLE.best=0, ENSEMBLE.exponent=c(1, 2, 3),
    ENSEMBLE.min=0.7,
    Yweights="BIOMOD", factors="biome")
ensemble.variables

# use function ensemble.VIF to select a subset of variables
# factor variables are not handled well by the function
# and therefore factors are removed
# however, one can check for factors with car::vif through
# the ensemble.calibrate.models function
# VIF.analysis$var.drops can be used as input for ensemble.calibrate.models or
```

```
# ensemble.calibrate.weights

predictors <- stack(predictor.files)
predictors <- subset(predictors, subset=c("bio1", "bio5", "bio6", "bio8",
    "bio12", "bio16", "bio17", "biome"))

ensemble.pairs(predictors)

VIF.analysis <- ensemble.VIF(predictors, factors="biome")
VIF.analysis
# alternative solution where bio1 and bio12 are kept
VIF.analysis <- ensemble.VIF(predictors, factors="biome",
    keep=c("bio1", "bio12"))
VIF.analysis

## End(Not run)
```

`ensemble.dummy.variables` *Suitability mapping based on ensembles of modelling algorithms: handling of categorical data*

Description

The basic function `ensemble.dummy.variables` creates new raster layers representing dummy variables (coded 0 or 1) for all or the most frequent levels of a caterogical variable. Sometimes the creation of dummy variables is needed for proper handling of categorical data for some of the suitability modelling algorithms.

Usage

```
ensemble.dummy.variables(xcat = NULL,
    freq.min = 50, most.frequent = 5,
    new.levels = NULL, overwrite = TRUE, ...)

ensemble.accepted.categories(xcat = NULL, categories = NULL,
    filename = NULL, overwrite = TRUE, ...)

ensemble.simplified.categories(xcat = NULL, p = NULL,
    filename = NULL, overwrite = TRUE, ...)
```

Arguments

`xcat`	RasterLayer object (`raster`) containing values for a categorical explanatory variable.
`freq.min`	Minimum frequency for a dummy raster layer to be created for the corresponding factor level. See also `freq`.

most.frequent	Number of dummy raster layers to be created (if larger than 0), corresponding to the same number of most frequent factor levels See also freq.
new.levels	character vector giving factor levels that are not encountered in xcat and for which dummy layers should be created (this could be useful in dealing with novel conditions)
overwrite	overwrite an existing file name with the same name (if TRUE). See also writeRaster.
...	additional arguments for writeRaster or (for ensemble.dummy.variables, writeRaster).
categories	numeric vector providing the accepted levels of a categorical raster layer; expected to correspond to the levels encountered during calibration
filename	name for the output file. See also writeRaster.
p	presence points that will be used for calibrating the suitability models, typically available in 2-column (x, y) or (lon, lat) dataframe; see also prepareData and extract

Details

The basic function ensemble.dummy.variables creates dummy variables from a RasterLayer object (see raster) that represents a categorical variable. With freq.min and most.frequent it is possible to limit the number of dummy variables that will be created. For example, most.frequent = 5 results in five dummy variables to be created.

Function ensemble.accepted.categories modifies the RasterLayer object (see raster) by replacing cell values for categories (levels) that are not accepted with missing values.

Function ensemble.simplified.categories modifies the RasterLayer object (see raster) by replacing cell values for categories (levels) where none of the presence points occur with the same level. This new level is coded by the maximum coding level for these 'outside categories'.

Value

The basic function ensemble.dummy.variables mainly results in the creation of raster layers that correspond to dummy variables.

Author(s)

Roeland Kindt (World Agroforestry Centre) and Evert Thomas (Bioversity International)

See Also

ensemble.calibrate.models, ensemble.raster

Examples

```
## Not run:

# get predictor variables
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
```

```
predictors <- stack(predictor.files)
biome.layer <- predictors[["biome"]]
biome.layer

# create dummy layers for the 5 most frequent factor levels

ensemble.dummy.variables(xcat=biome.layer, most.frequent=5,
    overwrite=TRUE)

# check whether dummy variables were created
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
predictors
names(predictors)

# once dummy variables were created, avoid using the original categorical data layer
predictors <- subset(predictors, subset=c("bio5", "bio6", "bio16", "bio17",
    "biome_1", "biome_2", "biome_7", "biome_8", "biome_13"))
predictors
predictors@title <- "base"

# presence points
presence_file <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
pres <- read.table(presence_file, header=TRUE, sep=',')[,-1]

# the kfold function randomly assigns data to groups;
# groups are used as calibration (1/5) and training (4/5) data
groupp <- kfold(pres, 5)
pres_train <- pres[groupp !=  1, ]
pres_test <- pres[groupp ==  1, ]

# choose background points
background <- randomPoints(predictors, n=1000, extf=1.00)
colnames(background)=c('lon', 'lat')
groupa <- kfold(background, 5)
backg_train <- background[groupa != 1, ]
backg_test <- background[groupa == 1, ]

# note that dummy variables with no variation are not used by DOMAIN
# note that dummy variables are not used by MAHAL and MAHAL01
# (neither are categorical variables)
ensemble.nofactors <- ensemble.calibrate.models(x=predictors, p=pres_train, a=backg_train,
    pt=pres_test, at=backg_test,
    species.name="Bradypus",
    VIF=T,
    MAXENT=1, MAXLIKE=1, GBM=1, GBMSTEP=0, RF=1, GLM=1, GLMSTEP=0, GAM=1,
    GAMSTEP=0, MGCV=1, MGCVFIX=0, EARTH=1, RPART=1, NNET=1, FDA=1,
    SVM=1, SVME=1, BIOCLIM.O=1, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=1,
    Yweights="BIOMOD",
    dummy.vars=c("biome_1", "biome_2", "biome_7", "biome_8", "biome_13"),
    PLOTS=FALSE, evaluations.keep=TRUE)
```

```
## End(Not run)
```

`ensemble.ecocrop` *Mapping of novel environmental conditions (areas where some of the environmental conditions are outside the range of environmental conditions of a reference area).*

Description

Function `ensemble.novel` creates the map with novel conditions. Function `ensemble.novel.object` provides the reference values used by the prediction function used by `predict` .

Usage

```
ensemble.ecocrop(x = NULL, ecocrop.object = NULL,
    RASTER.object.name = ecocrop.object$name, RASTER.stack.name = x@title,
    RASTER.format = "raster", RASTER.datatype = "INT2S", RASTER.NAflag = -32767,
    KML.out = TRUE, KML.blur = 10, KML.maxpixels = 100000,
    CATCH.OFF = FALSE)

ensemble.ecocrop.object(temp.thresholds, rain.thresholds, name = "crop01",
    temp.multiply = 10, annual.temps = TRUE, transform = 1)
```

Arguments

`x`	RasterStack object (`stack`) containing all environmental layers for which suitability should be calculated.
`ecocrop.object`	Object listing optimal and absolute minima and maxima for the rainfall and temperature values, used by the prediction function that is used internally by `predict`. This object is created with `ensemble.ecocrop.object`.
`RASTER.object.name`	First part of the names of the raster file that will be generated, expected to identify the species or crop for which ranges were calculated
`RASTER.stack.name`	Last part of the names of the raster file that will be generated, expected to identify the predictor stack used
`RASTER.format`	Format of the raster files that will be generated. See `writeFormats` and `writeRaster`.
`RASTER.datatype`	Format of the raster files that will be generated. See `dataType` and `writeRaster`.
`RASTER.NAflag`	Value that is used to store missing data. See `writeRaster`.
`KML.out`	If `TRUE`, then kml files will be saved in a subfolder 'kml/zones'.
`KML.maxpixels`	Maximum number of pixels for the PNG image that will be displayed in Google Earth. See also `KML`.

`KML.blur` Integer that results in increasing the size of the PNG image by `KML.blur^2`, which may help avoid blurring of isolated pixels. See also `KML`.

`CATCH.OFF` Disable calls to function `tryCatch`.

`temp.thresholds`
Optimal and absolute thresholds for temperatures. These will be sorted as: absolute minimum temperature, optimal minimum temperature, optimal maximum temperature and absolute maximum temperature.

`rain.thresholds`
Optimal and absolute thresholds for annual rainfall. These will be sorted as: absolute minimum rainfall, optimal minimum rainfall, optimal maximum rainfall and absolute maximum rainfall.

`name` Name of the object, expect to expected to identify the species or crop

`temp.multiply` Multiplier for temperature values. Default of 10 is to be used with raster layers where temperature was multiplied by 10 such as Worldclim or AFRICLIM.

`annual.temps` If `TRUE` then temperature limits are assumed to apply to mean annual temperature (bioclimatic variable bio1). If `FALSE` then minimum temperature limits are assumed to apply to the temperature of the coldest month (bioclimatic variable bio6) and maximum temperature limits are assumed to apply to the temperature of the hottest month (bioclimatic variable bio5). See also `biovars`.

`transform` Exponent used to transform probability values obtained from interpolating between optimal and absolute limits. Exponent of 2 results in squaring probabilities, for example input probabilities of 0.5 transformed to 0.5^2 = 0.25.

Details

Function `ensemble.ecocrop` maps suitability for a species or crop based on optimal and absolute temperature and rainfall limits. Where both temperature and rainfall are within the optimal limits, suitability of 1000 is calculated. Where both temperature and rainfall are outside the absolute limits, suitability of 0 is calculated. In situations where temperature or rainfall is in between the optimal and absolute limits, then suitability is interpolated between 0 and 1000, and the lowest suitability from temperature and rainfall is calculated. Setting very wide rainfall limits will simulate the effect of irrigation, i.e. where suitability only depends on temperature limits.

For a large range of crop and plant species, optimal and absolute limits are available from the FAO ecocrop database (http://www.fao.org/land-water/land/land-governance/land-resources-planning-toolbox/category/details/en/c/1027491/), hence the name of the function. A different implementation of suitability mapping based on ecocrop limits is available from `ecocrop`. Ecocrop thresholds for several species are available from: `getCrop`

Value

Function `ensemble.ecocrop.object` returns a list with following objects:

`name` name for the crop or species

`temp.thresholds`
optimal and absolute minimum and maximum temperature limits

`rain.thresholds`
optimal and absolute minimum and maximum annual rainfall limits

annual.temps	logical indicating whether temperature limits apply to annual temperatures
transform	exponent to transform suitability values

Author(s)

Roeland Kindt (World Agroforestry Centre)

See Also

biovars

Examples

```
## Not run:
#test with Brazil nut (limits from FAO ecocrop)
#temperature: (12) 20-36 (40)
#annnual rainfall: (1400) 2400-2800 (3500)

# get predictor variables
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
# subset based on Variance Inflation Factors
predictors <- subset(predictors, subset=c("bio5", "bio6", "bio12"))
predictors
predictors@title <- "base"

Brazil.ecocrop <- ensemble.ecocrop.object(temp.thresholds=c(20, 36, 12, 40),
    rain.thresholds=c(2400, 2800, 1400, 3500),
    annual.temps=FALSE, name="Bertholletia_excelsa")
Brazil.ecocrop
ensemble.ecocrop(predictors, ecocrop.object=Brazil.ecocrop)

dev.new()
par.old <- graphics::par(no.readonly=T)
graphics::par(mfrow=c(1,2))


rasterfull1 <- paste("ensembles//ecocrop//Bertholletia_excelsa_base.grd", sep="")
rasterfull1 <- raster(rasterfull1)
# raster file saved probabilities as integer values between 0 and 1000
rasterfull1 <- rasterfull1/1000
raster::plot(rasterfull1, main="Ecocrop suitability")

GBIFloc <- gbif(genus="Bertholletia", species="excelsa", geo=TRUE)
GBIFpres <- cbind(GBIFloc$lon, GBIFloc$lat)
GBIFpres <- GBIFpres[complete.cases(GBIFpres), ]
GBIFpres <- GBIFpres[duplicated(GBIFpres) == FALSE, ]
point.suitability <- extract(rasterfull1, y=GBIFpres)
point.suitability[is.na(point.suitability)] <- -1
```

```
GBIFpres.optimal <- GBIFpres[point.suitability == 1, ]
GBIFpres.suboptimal <- GBIFpres[point.suitability < 1 & point.suitability > 0, ]
GBIFpres.not <- GBIFpres[point.suitability == 0, ]

raster::plot(rasterfull1, main="GBIF locations",
    sub="blue: optimal, cyan: suboptimal, red: not suitable")
bg.legend <- c("blue", "cyan", "red")

points(GBIFpres.suboptimal, pch=21, cex=1.2, bg=bg.legend[2])
points(GBIFpres.optimal, pch=21, cex=1.2, bg=bg.legend[1])
points(GBIFpres.not, pch=21, cex=1.2, bg=bg.legend[3])

graphics::par(par.old)

## End(Not run)
```

`ensemble.evaluate` *Model evaluation including True Skill Statistic (TSS), AUCdiff and Symmetric Extremal Dependence Index (SEDI).*

Description

The main function of `ensemble.evaluate` calculates various model evaluation statistics. Function `ENSEMBLE.SEDI` calculates the Symmetric Extremal Dependence Index (SEDI) from the True Positive Rate (TPR = Sensitivity = Hit Rate) and the False Positive Rate (FPR = False Alarm Rate = 1 - Specificity).

Usage

```
ensemble.evaluate(eval, fixed.threshold = NULL, eval.train = NULL)

ensemble.SEDI(TPR, FPR, small = 1e-9)
```

Arguments

`eval`	ModelEvaluation object (`evaluate`), ideally obtained via model testing data that were not used for calibrating the model.
`fixed.threshold`	Absence-presence threshold to create the confusion matrix. See also (`threshold` and `ensemble.threshold`).
`eval.train`	ModelEvaluation object (`evaluate`), ideally obtained via model calibration data that were used for calibrating the model.
`TPR`	True Presence Rate, equal to correctly predicted presence observations divided by total number of presence observations. Also known as Sensitivity or Hit Rate.

FPR	False Presence Rate, equal to wrongly predicted absence observations divided by total number of absence observations. Also known as False Alarm Rate.
small	small amount that replaces zeroes in calculations.

Details

Details for the True Skill Statistic (TSS = TPR + TNR - 1 = TPR - FPR), Symmetric Extremal Dependence Index (SEDI), False Negative Rate (omission or miss rate) and AUCdiff (AUCtrain - AUCtest) are available from Ferro and Stephenson (2011), Wunderlich et al. (2019) and Castellanos et al. (2019).

Values for TSS and SEDI are given for the fixed absence-presence threshold, as well as their maximal values across the entire range of candidate threshold values calculate by `evaluate`.

In case that `fixed.threshold` is not provided, it is calculated from the calibration ModelEvaluation as the threshold that maximizes the sum of TPR (sensitivity) and TNR (specificity) (and thus also maximizes the TSS for the calibration).

Value

A numeric vector with following values.

AUC: Area Under The Curve for the testing ModelEvaluation TSS: maximum value of the True Skill Statistic over range of threshold values SEDI: maximum value of the Symmetric Extremal Dependence Index over range of threshold values TSS.fixed: True Skill Statistic at the fixed threshold value SEDI.fixed: SEDI at the fixed threshold value FNR.fixed: False Negative Rate (= omission rate) at the fixed threshold value MCR.fixed: Missclassification Rate at the fixed threshold value AUCdiff: Difference between AUC for calibration and the testing data

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Ferro CA, Stephenson DB. 2011. Extremal Dependence Indices: Improved Verification Measures for Deterministic Forecasts of Rare Binary Events. Wea. Forecasting 26: 699-713. https://doi.org/10.1175/WAF-D-10-05030.1

Wunderlich RF, Lin Y-P, Anthony J, Petway JR. 2019. Two alternative evaluation metrics to replace the true skill statistic in the assessment of species distribution models. Nature Conservation 35: 97-116. https://doi.org/10.3897/natureconservation.35.33918

Castellanos AA, Huntley JW, Voelker G, Lawing AM. 2019. Environmental filtering improves ecological niche models across multiple scales. https://doi.org/10.1111/2041-210X.13142

Kindt R. 2018. Ensemble species distribution modelling with transformed suitability values. Environmental Modelling & Software 100: 136-145. https://doi.org/10.1016/j.envsoft.2017.11.009

See Also

`ensemble.batch`

Examples

```
## check examples from Ferro and Stephenson (2011)
## see their Tables 2 - 5

TPR.Table2 <- 55/100
FPR.Table2 <- 45/900
ensemble.SEDI(TPR=TPR.Table2, FPR=FPR.Table2)

TPR.Table4 <- 195/300
FPR.Table4 <- 105/700
ensemble.SEDI(TPR=TPR.Table4, FPR=FPR.Table4)

## Not run:
## Not run:
# get predictor variables
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
# subset based on Variance Inflation Factors
predictors <- subset(predictors, subset=c("bio5", "bio6",
    "bio16", "bio17", "biome"))
predictors
predictors@title <- "predictors"

# presence points
presence_file <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
pres <- read.table(presence_file, header=TRUE, sep=',')[,-1]

# the kfold function randomly assigns data to groups;
# groups are used as calibration (1/4) and training (3/4) data
groupp <- kfold(pres, 4)
pres_train <- pres[groupp !=  1, ]
pres_test <- pres[groupp ==  1, ]

# choose background points
background <- randomPoints(predictors, n=1000, extf=1.00)
colnames(background)=c('lon', 'lat')
groupa <- kfold(background, 4)
backg_train <- background[groupa != 1, ]
backg_test <- background[groupa == 1, ]

# formulae for random forest and generalized linear model
# compare with: ensemble.formulae(predictors, factors=c("biome"))

rfformula <- as.formula(pb ~ bio5+bio6+bio16+bio17)

glmformula <- as.formula(pb ~ bio5 + I(bio5^2) + I(bio5^3) +
    bio6 + I(bio6^2) + I(bio6^3) + bio16 + I(bio16^2) + I(bio16^3) +
    bio17 + I(bio17^2) + I(bio17^3) )
```

```
# fit four ensemble models (RF, GLM, BIOCLIM, DOMAIN)
# factors removed for BIOCLIM, DOMAIN, MAHAL
ensemble.nofactors <- ensemble.calibrate.models(x=predictors, p=pres_train, a=backg_train,
    pt=pres_test, at=backg_test,
    species.name="Bradypus",
    ENSEMBLE.tune=TRUE,
    ENSEMBLE.min = 0.65,
    MAXENT=0, MAXNET=0, MAXLIKE=0, GBM=0, GBMSTEP=0, RF=1, CF=0,
    GLM=1, GLMSTEP=0, GAM=0, GAMSTEP=0, MGCV=0, MGCVFIX=0,
    EARTH=0, RPART=0, NNET=0, FDA=0, SVM=0, SVME=0, GLMNET=0,
    BIOCLIM.O=0, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=0,
    Yweights="BIOMOD",
    factors="biome",
    evaluations.keep=TRUE, models.keep=FALSE,
    RF.formula=rfformula,
    GLM.formula=glmformula)

# with option evaluations.keep, all model evaluations are saved in the ensemble object
attributes(ensemble.nofactors$evaluations)

# Get evaluation statistics for the ENSEMBLE model
eval.ENSEMBLE <- ensemble.nofactors$evaluations$ENSEMBLE.T
eval.calibrate.ENSEMBLE <- ensemble.nofactors$evaluations$ENSEMBLE.C
ensemble.evaluate(eval=eval.ENSEMBLE, eval.train=eval.calibrate.ENSEMBLE)

# TSS is maximum where specificity + sensitivity is maximum
threshold.specsens <- threshold(eval.ENSEMBLE, stat="spec_sens")
ensemble.evaluate(eval=eval.ENSEMBLE, fixed.threshold=threshold.specsens,
    eval.train=eval.calibrate.ENSEMBLE)

# usual practice to calculate threshold from calibration data
ensemble.evaluate(eval=eval.ENSEMBLE, eval.train=eval.calibrate.ENSEMBLE)


## End(Not run)
```

`ensemble.novel` *Mapping of novel environmental conditions (areas where some of the environmental conditions are outside the range of environmental conditions of a reference area).*

Description

Function `ensemble.novel` creates the map with novel conditions. Function `ensemble.novel.object` provides the reference values used by the prediction function used by `predict` .

Usage

```
ensemble.novel(x = NULL, novel.object = NULL,
    RASTER.object.name = novel.object$name, RASTER.stack.name = x@title,
    RASTER.format = "raster", RASTER.datatype = "INT1S", RASTER.NAflag = -127,
    KML.out = FALSE, KML.maxpixels = 100000, KML.blur = 10,
    CATCH.OFF = FALSE)

ensemble.novel.object(x = NULL, name = "reference1", mask.raster = NULL,
    quantiles = FALSE, probs = c(0.05, 0.95), factors = NULL)
```

Arguments

x	RasterStack object (stack) containing all environmental layers for which novel conditions should be calculated. With ensemble.novel.object, x can also be a data.frame.
novel.object	Object listing minima and maxima for the environmental layers, used by the prediction function that is used internally by predict. This object is created with ensemble.novel.object.
RASTER.object.name	First part of the names of the raster file that will be generated, expected to identify the area and time period for which ranges were calculated
RASTER.stack.name	Last part of the names of the raster file that will be generated, expected to identify the predictor stack used
RASTER.format	Format of the raster files that will be generated. See writeFormats and writeRaster.
RASTER.datatype	Format of the raster files that will be generated. See dataType and writeRaster.
RASTER.NAflag	Value that is used to store missing data. See writeRaster.
KML.out	If TRUE, then kml files will be saved in a subfolder 'kml/zones'.
KML.maxpixels	Maximum number of pixels for the PNG image that will be displayed in Google Earth. See also KML.
KML.blur	Integer that results in increasing the size of the PNG image by KML.blur^2, which may help avoid blurring of isolated pixels. See also KML.
CATCH.OFF	Disable calls to function tryCatch.
name	Name of the object, expect to expected to identify the area and time period for which ranges were calculated and where no novel conditions will be detected
mask.raster	RasterLayer object (raster) that can be used to select the area for which reference values are obtained (see mask)
quantiles	If TRUE, then replace minima and maxima with quantile values. See also quantile and quantile)
probs	Numeric vector of probabilities [0, 1] as used by quantile and quantile)
factors	vector that indicates which variables are factors; these variables will be ignored for novel conditions

Details

Function ensemble.novel maps zones (coded '1') that are novel (outside the minimum-maximum range) relative to the range provided by function ensemble.novel.object. Values that are not novel (inside the range of minimum-maximum values) are coded '0'. In theory, the maps show the same areas that have negative Multivariate Environmental Similarity Surface (MESS) values ((mess))

Value

Function ensemble.novel.object returns a list with following objects:

minima	minima of the reference environmental conditions
maxima	maxima of the reference environmental conditions
name	name for the reference area and time period

Author(s)

Roeland Kindt (World Agroforestry Centre)

See Also

ensemble.raster, ensemble.bioclim and ensemble.bioclim.graph

Examples

```
## Not run:
# get predictor variables
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
predictors <- subset(predictors, subset=c("bio1", "bio5", "bio6", "bio7", "bio8",
    "bio12", "bio16", "bio17"))
predictors
predictors@title <- "base"

# reference area to calculate environmental ranges
ext <- extent(-70, -50, -10, 10)
extent.values2 <- c(-70, -50, -10, 10)
predictors.current <- crop(predictors, y=ext)
predictors.current <- stack(predictors.current)

novel.test <- ensemble.novel.object(predictors.current, name="noveltest")
novel.test
novel.raster <- ensemble.novel(x=predictors, novel.object=novel.test, KML.out=T)
novel.raster

plot(novel.raster)
# no novel conditions within reference area
rect(extent.values2[1], extent.values2[3], extent.values2[2], extent.values2[4])
```

```
# use novel conditions as a simple species suitability mapping method
# presence points
presence_file <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
pres <- read.table(presence_file, header=TRUE, sep=',')[,-1]
pres.data <- data.frame(extract(predictors, y=pres))

# ranges and maps
Bradypus.ranges1 <- ensemble.novel.object(pres.data, name="Bradypus", quantiles=F)
Bradypus.ranges1
Bradypus.novel1 <- ensemble.novel(x=predictors, novel.object=Bradypus.ranges1, KML.out=T)
Bradypus.novel1

par.old <- graphics::par(no.readonly=T)
graphics::par(mfrow=c(1,2))

# suitable where there are no novel conditions
raster::plot(Bradypus.novel1, breaks=c(-0.1, 0, 1), col=c("green", "grey"),
    main="Suitability mapping using minimum to maximum range")
points(pres[, 2] ~ pres[, 1], pch=1, col="red", cex=0.8)

# use 90 percent intervals similar to BIOCLIM methodology
Bradypus.ranges2 <- ensemble.novel.object(pres.data, name="BradypusQuantiles", quantiles=T)
Bradypus.ranges2
Bradypus.novel2 <- ensemble.novel(x=predictors, novel.object=Bradypus.ranges2, KML.out=T)
Bradypus.novel2
raster::plot(Bradypus.novel2, breaks=c(-0.1, 0, 1), col=c("green", "grey"),
    main="Suitability mapping using quantile range")
points(pres[, 2] ~ pres[, 1], pch=1, col="red", cex=0.8)

graphics::par(par.old)

# deal with novel factor levels through dummy variables
predictors <- stack(predictor.files)
biome.layer <- predictors[["biome"]]
biome.layer
ensemble.dummy.variables(xcat=biome.layer, most.frequent=0, freq.min=1,
    overwrite=TRUE)

predictors.dummy <- stack(predictor.files)
predictors.dummy <- subset(predictors.dummy, subset=c("biome_1", "biome_2",  "biome_3",
    "biome_4", "biome_5", "biome_7",  "biome_8",  "biome_9",
    "biome_10", "biome_12", "biome_13", "biome_14"))
predictors.dummy
predictors.dummy@title <- "base_dummy"

predictors.dummy.current <- crop(predictors.dummy, y=ext)
predictors.dummy.current <- stack(predictors.dummy.current)

novel.levels <- ensemble.novel.object(predictors.dummy.current, name="novellevels")
novel.levels
novel.levels.raster <- ensemble.novel(x=predictors.dummy, novel.object=novel.levels,
    KML.out=T)
```

```
novel.levels.raster

novel.levels.quantiles <- ensemble.novel.object(predictors.dummy.current, quantiles=TRUE,
    name="novellevels_quantiles")
novel.levels.quantiles
novel.levels.quantiles.raster <- ensemble.novel(x=predictors.dummy,
    novel.object=novel.levels.quantiles, KML.out=T)
novel.levels.quantiles.raster

# difference in ranges for variables with low frequencies
background <- dismo::randomPoints(predictors.dummy.current, n=10000, p=NULL, excludep=F)
extract.data <- extract(predictors.dummy.current, y=background)
colSums(extract.data)/sum(extract.data)*100
novel.levels
novel.levels.quantiles

par.old <- graphics::par(no.readonly=T)
graphics::par(mfrow=c(1,2))
raster::plot(novel.levels.raster, breaks=c(-0.1, 0, 1), col=c("grey", "green"),
    main="novel outside minimum to maximum range")
rect(extent.values2[1], extent.values2[3], extent.values2[2], extent.values2[4])
raster::plot(novel.levels.quantiles.raster, breaks=c(-0.1, 0, 1), col=c("grey", "green"),
    main="novel outside quantile range")
rect(extent.values2[1], extent.values2[3], extent.values2[2], extent.values2[4])
graphics::par(par.old)


## End(Not run)
```

`ensemble.PET.season` *Calculate the balance between precipitation and potential evapotranspiration for the dry season with the largest balance (maximum climatological water deficit, accumulated aridity).*

Description

Internally, the function first determines different dry seasons, defined by consecutive months where precipitation is smaller than potential evapotranspiration. The function then returns the summation of monthly balances of precipitation minus potential evapotranspiration that is largest (most negative) of the different dry seasons.

Usage

```
ensemble.PET.season(PREC.stack = NULL, PET.stack = NULL,
    filename = NULL, overwrite = TRUE,
    CATCH.OFF = FALSE, ...)
```

Arguments

PREC.stack	stack object (stack) with monthly precipitation values.
PET.stack	stack object (stack) with monthly potential evapotranspiration values.
filename	Name for writing the resulting raster layer (as in writeRaster).
overwrite	Replace a previous version of the same file.
CATCH.OFF	Disable calls to function tryCatch.
...	Additional arguments for writeRaster.

Details

Unlike the methodology described by Chave et al. (2014), the assumption is not made that there is a single drought season. Internally, the function first identifies dry months as months where the balance of precipitation minus potential evapotranspiration is negative. Then dry seasons are identified as consecutive dry months. For each dry season, the total sum of balances is calculated. The function finally identifies and returns the largest of these balances.

The algorithm of the function should obtain the same values of the Maximum Cumulative Water Deficit as from rules described by Aragao et al. 2007 (section 2.2), when using fixed monthly PET values of 100 mm instead of calculated monthly PET values (calculated, for example, from monthly mean temperatures and extraterrestrial solar radiation through the Hargreaves method).

Note that calculation may take a while for larger raster data sets.

Value

The function returns and writes a raster layer

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Chave J et al. 2014. Improved allometric models to estimate the aboveground biomass of tropical trees. Global Change Biology https://doi.org/10.1111/gcb.12629

Aragao LZ et al. 2007. Spatial patterns and fire response of recent Amazonian droughts. Geophysical Research Letters 34(7) https://doi.org/10.1029/2006GL028946

See Also

ensemble.batch

Examples

```
## Not run:

## Not run:
```

```
library(raster)
stack1 <- stack(monthly.prec.files)
stack2 <- stack(monthly.PET.files)
# note that the stacks should be of the same extend and resolution
ENSEMBLE.PET.season(PREC.stack=stack1, PET.stack=stack2,
    filename=paste(getwd(), '//Aridity.deficit.tif', sep=""))


## End(Not run)
```

---

ensemble.raster *Suitability mapping based on ensembles of modelling algorithms: consensus mapping*

Description

The basic function ensemble.raster creates two consensus raster layers, one based on a (weighted) average of different suitability modelling algorithms, and a second one documenting the number of modelling algorithms that predict presence of the focal organisms. Modelling algorithms include maximum entropy (MAXENT), boosted regression trees, random forests, generalized linear models (including stepwise selection of explanatory variables), generalized additive models (including stepwise selection of explanatory variables), multivariate adaptive regression splines, regression trees, artificial neural networks, flexible discriminant analysis, support vector machines, the BIOCLIM algorithm, the DOMAIN algorithm and the Mahalonobis algorithm. These sets of functions were developed in parallel with the biomod2 package, especially for inclusion of the maximum entropy algorithm, but also to allow for a more direct integration with the BiodiversityR package, more direct handling of model formulae and greater focus on mapping. Researchers and students of species distribution are strongly encouraged to familiarize themselves with all the options of the biomod2 and dismo packages.

Usage

```
ensemble.raster(xn = NULL,
    models.list = NULL,
    input.weights = models.list$output.weights,
    thresholds = models.list$thresholds,
    RASTER.species.name = models.list$species.name,
    RASTER.stack.name = xn@title,
    RASTER.format = "raster", RASTER.datatype = "INT2S", RASTER.NAflag = -32767,
    RASTER.models.overwrite = TRUE,
    KML.out = FALSE, KML.maxpixels = 100000, KML.blur = 10,
    evaluate = FALSE, SINK = FALSE,
    p = models.list$p, a = models.list$a,
    pt = models.list$pt, at = models.list$at,
    CATCH.OFF = FALSE)

ensemble.habitat.change(base.map = file.choose(),
    other.maps = utils::choose.files(),
```

```
    change.folder = "ensembles/change",
    RASTER.format = "raster", RASTER.datatype = "INT1U", RASTER.NAflag = 255,
    KML.out = FALSE, KML.folder = "kml/change",
    KML.maxpixels = 100000, KML.blur = 10)

ensemble.area(x=NULL, km2=TRUE)
```

Arguments

xn	RasterStack object (stack) containing all layers that correspond to explanatory variables of an ensemble calibrated earlier with ensemble.calibrate.models. See also predict.
models.list	list with 'old' model objects such as MAXENT or RF.
input.weights	array with numeric values for the different modelling algorithms; if NULL then values provided by parameters such as MAXENT and GBM will be used. As an alternative, the output from ensemble.calibrate.weights can be used.
thresholds	array with the threshold values separating predicted presence for each of the algorithms.
RASTER.species.name	First part of the names of the raster files that will be generated, expected to identify the modelled species (or organism).
RASTER.stack.name	Last part of the names of the raster files that will be generated, expected to identify the predictor stack used.
RASTER.format	Format of the raster files that will be generated. See writeFormats and writeRaster.
RASTER.datatype	Format of the raster files that will be generated. See dataType and writeRaster.
RASTER.NAflag	Value that is used to store missing data. See writeRaster.
RASTER.models.overwrite	Overwrite the raster files that correspond to each suitability modelling algorithm (if TRUE). (Overwriting actually implies that raster files are created or overwritten that start with "working_").
KML.out	if FALSE, then no kml layers (layers that can be shown in Google Earth) are produced. If TRUE, then kml files will be saved in a subfolder 'kml'.
KML.maxpixels	Maximum number of pixels for the PNG image that will be displayed in Google Earth. See also KML.
KML.blur	Integer that results in increasing the size of the PNG image by KML.blur^2, which may help avoid blurring of isolated pixels. See also KML.
evaluate	if TRUE, then evaluate the created raster layers at locations p, a, pt and at (if provided). See also evaluate
SINK	Append the results to a text file in subfolder 'outputs' (if TRUE). The name of file is based on argument RASTER.species.name. In case the file already exists, then results are appended. See also sink.

p	presence points used for calibrating the suitability models, typically available in 2-column (x, y) or (lon, lat) dataframe; see also prepareData and extract
a	background points used for calibrating the suitability models, typically available in 2-column (x, y) or (lon, lat) dataframe; see also prepareData and extract
pt	presence points used for evaluating the suitability models, typically available in 2-column (lon, lat) dataframe; see also prepareData
at	background points used for calibrating the suitability models, typicall available in 2-column (lon, lat) dataframe; see also prepareData and extract
CATCH.OFF	Disable calls to function tryCatch.
base.map	filename with baseline map used to produce maps that show changes in suitable habitat
other.maps	files with other maps used to produce maps that show changes in suitable habitat from a defined base.map
change.folder	folder where new maps documenting changes in suitable habitat will be stored. NOTE: please ensure that the base folder (eg: ../ensembles) exists already.
KML.folder	folder where new maps (in Google Earth format) documenting changes in suitable habitat will be stored. NOTE: please ensure that the base folder (eg: ../kml) exists already.
x	RasterLayer object (raster) in a longitude-latitude coordinate system
km2	Provide results in square km rather than square m. See also areaPolygon

Details

The basic function ensemble.raster fits individual suitability models for all models with positive input weights. In subfolder "models" of the working directory, suitability maps for the individual suitability modelling algorithms are stored. In subfolder "ensembles", a consensus suitability map based on a weighted average of individual suitability models is stored. In subfolder "ensembles/presence", a presence-absence (1-0) map will be provided. In subfolder "ensembles/count", a consensus suitability map based on the number of individual suitability models that predict presence of the focal organism is stored.

Several of the features of ensemble.raster are also available from ensemble.calibrate.models. The main difference between the two functions is that ensemble.raster generates raster layers for individual suitability models, whereas the purpose of ensemble.calibrate.models is specifically to test different suitability modelling algorithms.

Note that values in suitability maps are integer values that were calculated by multiplying probabilities by 1000 (see also trunc).

As the Mahalanobis function (mahal) does not always provide values within a range of 0 - 1, the output values are rescaled by first subtracting the value of 1 -MAHAL.shape from each prediction, followed by calculating the absolute value, followed by calculating the reciprocal value and finally multiplying this reciprocal value with MAHAL.shape. As this rescaling method does not estimate probabilities, inclusion in the calculation of a (weighted) average of ensemble probabilities may be problematic (the same applies to other distance-based methods).

The ensemble.habitat.change function produces new raster layers that show changes in suitable and not suitable habitat between a base raster and a list of other rasters. The output uses the following coding: 0 = areas that remain unsuitable, 11 = areas that remain suitable, 10 = areas of lost

habitat, 1 = areas of new habitat. (Codes are inspired on a binary classification of habitat suitability in base [1- or 0-] and other layer [-1 or -0], eg new habitat is coded 01 = 1).

With KML.out = TRUE, kml files are created in a subfolder named "KML". The colouring of the consensus suitability PNG is based on 20 intervals of size 50 between 0 and 1000. The colouring of the presence-absence PNG uses green for presence and red for absence. The colouring of the count suitability PNG uses black for zero (no models predict presence) and blue for the theoretical maximum number of models to predict presence (i.e. the count of all final weights), whereas intermediate numbers (1 to theoretical maximum - 1) are ranged from red to green. The colouring of the habitat change maps are: black (cells that are never suitable [value: 0]), green (cells that are always suitable [value: 11]), red (cells that are lost habitat [value: 10] and blue (cells that are new habitat [value: 1]).

The ensemble.area function calculates the area of different categories with areaPolygon

Value

The basic function ensemble.raster mainly results in the creation of raster layers that correspond to fitted probabilities of presence of individual suitability models (in folder "models") and consensus models (in folder "ensembles"), and the number of suitability models that predict presence (in folder "ensembles"). Prediction of presence is based on a threshold usually defined by maximizing the sum of the true presence and true absence rates (see threshold.method and also ModelEvaluation).

If desired by the user, the ensemble.raster function also saves details of fitted suitability models or data that can be plotted with the evaluation.strip.plot function.

Author(s)

Roeland Kindt (World Agroforestry Centre), Eike Luedeling (World Agroforestry Centre) and Evert Thomas (Bioversity International)

References

Kindt R. 2018. Ensemble species distribution modelling with transformed suitability values. Environmental Modelling & Software 100: 136-145. https://doi.org/10.1016/j.envsoft.2017.11.009 Buisson L, Thuiller W, Casajus N, Lek S and Grenouillet G. 2010. Uncertainty in ensemble forecasting of species distribution. Global Change Biology 16: 1145-1157

See Also

evaluation.strip.plot, ensemble.calibrate.models, ensemble.calibrate.weights, ensemble.batch

Examples

```
## Not run:
# based on examples in the dismo package

# get predictor variables
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
```

```
# subset based on Variance Inflation Factors
predictors <- subset(predictors, subset=c("bio5", "bio6",
    "bio16", "bio17"))
predictors
predictors@title <- "base"

# presence points
# presence points
presence_file <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
pres <- read.table(presence_file, header=TRUE, sep=',')[,-1]

# choose background points
background <- randomPoints(predictors, n=1000, extf = 1.00)

# if desired, change working directory where subfolders of "models" and
# "ensembles" will be created
# raster layers will be saved in subfolders of /models and /ensembles:
getwd()

# first calibrate the ensemble
# calibration is done in two steps
# in step 1, a k-fold procedure is used to determine the weights
# in step 2, models are calibrated for all presence and background locations
# factor is not used as it is not certain whether correct levels will be used
# it may therefore be better to use dummy variables

# step 1: determine weights through 4-fold cross-validation
ensemble.calibrate.step1 <- ensemble.calibrate.weights(
    x=predictors, p=pres, a=background, k=4,
    SINK=TRUE, species.name="Bradypus",
    MAXENT=0, MAXNET=1, MAXLIKE=1, GBM=1, GBMSTEP=0, RF=1, CF=1,
    GLM=1, GLMSTEP=1, GAM=1, GAMSTEP=1, MGCV=1, MGCVFIX=1,
    EARTH=1, RPART=1, NNET=1, FDA=1, SVM=1, SVME=1, GLMNET=1,
    BIOCLIM.O=1, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=1,
    ENSEMBLE.tune=TRUE, PROBIT=TRUE,
    ENSEMBLE.best=0, ENSEMBLE.exponent=c(1, 2, 3),
    ENSEMBLE.min=c(0.65, 0.7),
    Yweights="BIOMOD",
    PLOTS=FALSE, formulae.defaults=TRUE)

# step 1 generated the weights for each algorithm
model.weights <- ensemble.calibrate.step1$output.weights
x.batch <- ensemble.calibrate.step1$x
p.batch <- ensemble.calibrate.step1$p
a.batch <- ensemble.calibrate.step1$a
MAXENT.a.batch <- ensemble.calibrate.step1$MAXENT.a
factors.batch <- ensemble.calibrate.step1$factors
dummy.vars.batch <- ensemble.calibrate.step1$dummy.vars

# step 2: calibrate models with all available presence locations
# weights determined in step 1 calculate ensemble in step 2
ensemble.calibrate.step2 <- ensemble.calibrate.models(
    x=x.batch, p=p.batch, a=a.batch, MAXENT.a=MAXENT.a.batch,
```

```
    factors=factors.batch, dummy.vars=dummy.vars.batch,
    SINK=TRUE, species.name="Bradypus",
    models.keep=TRUE,
    input.weights=model.weights,
    ENSEMBLE.tune=FALSE, PROBIT=TRUE,
    Yweights="BIOMOD",
    PLOTS=FALSE, formulae.defaults=TRUE)

# step 3: use previously calibrated models to create ensemble raster layers
# re-evaluate the created maps at presence and background locations
# (note that re-evaluation will be different due to truncation of raster layers
# as they wered saved as integer values ranged 0 to 1000)
ensemble.raster.results <- ensemble.raster(xn=predictors,
    models.list=ensemble.calibrate.step2$models,
    input.weights=model.weights,
    SINK=TRUE, evaluate=TRUE,
    RASTER.species.name="Bradypus", RASTER.stack.name="base")

# use the base map to check for changes in suitable habitat
# this type of analysis is typically done with different predictor layers
# (for example, predictor layers representing different possible future climates)
# In this example, changes from a previous model (ensemble.raster.results)
# are contrasted with a newly calibrated model (ensemble.raster.results2)
# step 1: 4-fold cross-validation
ensemble.calibrate2.step1 <- ensemble.calibrate.weights(
    x=x.batch, p=p.batch, a=a.batch, MAXENT.a=MAXENT.a.batch,
    factors=factors.batch, dummy.vars=dummy.vars.batch,
    k=4,
    SINK=TRUE, species.name="Bradypus",
    MAXENT=0, MAXNET=1, MAXLIKE=1, GBM=1, GBMSTEP=0, RF=1, CF=1,
    GLM=1, GLMSTEP=1, GAM=1, GAMSTEP=1, MGCV=1, MGCVFIX=1,
    EARTH=1, RPART=1, NNET=1, FDA=1, SVM=1, SVME=1, GLMNET=1,
    BIOCLIM.O=1, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=1,
    ENSEMBLE.tune=TRUE, PROBIT=TRUE,
    ENSEMBLE.best=0, ENSEMBLE.exponent=c(1, 2, 3),
    ENSEMBLE.min=c(0.65, 0.7),
    Yweights="BIOMOD",
    PLOTS=FALSE, formulae.defaults=TRUE)

model.weights2 <- ensemble.calibrate2.step1$output.weights

ensemble.calibrate2.step2 <- ensemble.calibrate.models(
    x=x.batch, p=p.batch, a=a.batch, MAXENT.a=MAXENT.a.batch,
    factors=factors.batch, dummy.vars=dummy.vars.batch,
    SINK=TRUE, species.name="Bradypus",
    models.keep=TRUE,
    input.weights=model.weights2,
    ENSEMBLE.tune=FALSE, PROBIT=TRUE,
    Yweights="BIOMOD",
    PLOTS=FALSE, formulae.defaults=TRUE)

ensemble.raster.results2 <- ensemble.raster(
    xn=predictors,
```

```
    models.list=ensemble.calibrate2.step2$models,
    input.weights=model.weights2,
    SINK=TRUE, evaluate=TRUE,
    RASTER.species.name="Bradypus", RASTER.stack.name="recalibrated")

base.file <- paste(getwd(), "/ensembles/presence/Bradypus_base.grd", sep="")
other.file <- paste(getwd(), "/ensembles/presence/Bradypus_recalibrated.grd", sep="")

changed.habitat <- ensemble.habitat.change(base.map=base.file,
    other.maps=c(other.file),
    change.folder="ensembles/change")

change.file <- paste(getwd(), "/ensembles/change/Bradypus_recalibrated_presence.grd", sep="")

par.old <- graphics::par(no.readonly=T)
dev.new()
par(mfrow=c(2,2))
raster::plot(raster(base.file), breaks=c(-1, 0, 1), col=c("grey", "green"),
    legend.shrink=0.8, main="base presence")
raster::plot(raster(other.file), breaks=c(-1, 0, 1), col=c("grey", "green"),
    legend.shrink=0.8, main="other presence")
raster::plot(raster(change.file), breaks=c(-1, 0, 1, 10, 11),
    col=c("grey", "blue", "red", "green"),
    legend.shrink=0.8, main="habitat change", sub="11 remaining, 10 lost, 1 new")
graphics::par(par.old)

areas <- ensemble.area(raster(change.file))
areas

## End(Not run)
```

`ensemble.red` *Area of Occupancy (AOO) and Extent of Occurrence (EOO) via the* **red** *library.*

Description

Function `ensemble.red` is a wrapper function for estimation of AOO and EOO computed for redlisting of species based on IUCN criteria (https://www.iucnredlist.org/about/regional). Function `ensemble.chull.create` creates a mask layer based on a convex hull around known presence locations, inspired by `mcp` argument of the `map.sdm` function.

Usage

```
ensemble.red(x)

ensemble.chull.create(x.pres = NULL, p = NULL, buffer.width = 0.2,
    buffer.maxmins = FALSE, lonlat.dist = FALSE,
```

```
    RASTER.format = "raster", RASTER.datatype = "INT1U", RASTER.NAflag = 255,
    overwrite = TRUE, ...)

ensemble.chull.apply(x.spec = NULL, mask.layer=NULL, keep.old=T,
    RASTER.format="raster", RASTER.datatype="INT1U", RASTER.NAflag=255,
    overwrite=TRUE, ...)

ensemble.chull.buffer.distances(p = NULL,
    buffer.maxmins = FALSE, lonlat.dist = FALSE)

ensemble.chull.MSDM(p = NULL, a = NULL, species.name = NULL,
    suit.file = NULL, suit.divide = 1000, MSDM.dir = NULL,
    method = "BMCP", threshold = "spec_sens",
    buffer = "species_specific")
```

Arguments

x	RasterLayer object (raster), representing 'count' suitability layers (available from the 'count' and 'consensuscount' subdirectories of the 'ensembles' directory)
x.pres	RasterLayer object (raster), representing 'presence' suitability layers (available from the 'presence' and 'consensuspresence' subdirectories of the 'ensembles' directory)
p	known presence locations, available in 2-column (lon, lat) dataframe; see also prepareData and extract
buffer.width	multiplier to create buffer (via gBuffer) by multiplying the maximum distance among the presence locations (calculated via pointDistance)
buffer.maxmins	Calculate the buffer width based on the two neighbouring locations that are furthest apart (maximum of minimum distances from each location).
lonlat.dist	Estimate the distance in km for longitude latitude data.
RASTER.format	Format of the raster files that will be generated. See writeFormats and writeRaster.
RASTER.datatype	Format of the raster files that will be generated. See dataType and writeRaster.
RASTER.NAflag	Value that is used to store missing data. See writeRaster.
overwrite	Overwrite existing raster files. See writeRaster.
...	Additional arguments for writeRaster.
x.spec	RasterLayer object (raster), representing any suitability layer for the species under investigation)
mask.layer	RasterLayer object (raster), representing the mask based on the convex hull around known presence locations. The function will replace all values in x.spec to zero where corresponding values in the mask.layer are zero.
keep.old	keep a copy of the RasterLayer before the mask is applied.
a	absence of background locations, available in 2-column (lon, lat) dataframe.

species.name	name of the species, ideally without spaces.
suit.file	file with raster data corresponding to suitability values of the focal species.
suit.divide	number by which values in the suitability raster should be divided to result in probabilities (BiodiversityR saves data as 1000 * suitability, hence these values need to be divided by 1000).
MSDM.dir	name of the directory where input and processed raster files will be saved.
method	method for MSDM_Posteriori function from c("OBR", "PRES", "LQ", "MCP", "BMCP").
threshold	threshold for MSDM_Posteriori function from c("kappa", "spec_sens", "no_omission", "prevalence", "equal_sens_spec", "sensitivty").
buffer	buffer for MSDM_Posteriori function.

Details

Function ensemble.red calculates AOO (aoo) and EOO (aoo) statistics calculated for areas with different consensus levels on species presence (1 model predicting presence, 2 models predicting presence, ...). In case that these statistics are within IUCN criteria for Critically Endangered (CR), Endangered (EN) or Vulnerable (VU), then this information is added in columns documenting the types of AOO and EOO.

Function ensemble.chull.create first creates a convex hull around known presence locations. Next, a buffer is created around the convex hull where the width of this buffer is calculated as the maximum distance among presence locations (pointDistance) multiplied by argument buffer.width. Finally, the mask is created by including all polygons of predicted species presence that are partially covered by the convex hull and its buffer.

Value

Function ensemble.red returns an array with AOO and EOO Function ensemble.chull.create creates a mask layer based on a convex hull around known presence locations. Function ensemble.chull.MSDM prepares the input data and script for the MSDM_Posteriori function of the MSDM package.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Cardoso P. 2017. red - an R package to facilitate species red list assessments according to the IUCN criteria. Biodiversity Data Journal 5:e20530. https://doi.org/10.3897/BDJ.5.e20530

Mendes, P.; Velazco S.J.E.; Andrade, A.F.A.; De Marco, P. (2020) Dealing with overprediction in species distribution models: how adding distance constraints can improve model accuracy, Ecological Modelling, in press. https://doi.org/10.1016/j.ecolmodel.2020.109180

Kindt R. 2018. Ensemble species distribution modelling with transformed suitability values. Environmental Modelling & Software 100: 136-145. https://doi.org/10.1016/j.envsoft.2017.11.009

See Also

ensemble.batch

Examples

```
## Not run:

## Not run:
# based on examples in the dismo package

# get predictor variables
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
# subset based on Variance Inflation Factors
predictors <- subset(predictors, subset=c("bio5", "bio6",
    "bio16", "bio17"))
predictors
predictors@title <- "red"

# presence points
presence_file <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
pres <- read.table(presence_file, header=TRUE, sep=',')

# fit 5 ensemble models (could take some time!)
# (examples for the red package use 100 models)
ensembles <- ensemble.batch(x=predictors,
    xn=c(predictors),
    species.presence=pres,
    thin.km=100,
    k.splits=4, k.test=0,
    n.ensembles=5,
    SINK=TRUE,
    ENSEMBLE.best=10, ENSEMBLE.exponent=c(1, 2, 3),
    ENSEMBLE.min=0.6,
    MAXENT=0, MAXNET=1, MAXLIKE=1, GBM=1, GBMSTEP=0, RF=1, CF=1,
    GLM=1, GLMSTEP=1, GAM=1, GAMSTEP=1, MGCV=1, MGCVFIX=1,
    EARTH=1, RPART=1, NNET=1, FDA=1, SVM=1, SVME=1,
    BIOCLIM.O=1, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=1,
    PROBIT=TRUE,
    Yweights="BIOMOD",
    formulae.defaults=TRUE)

# first application of ensemble.red before applying the convex hull mask
# AOO and EOO are determined for each count level
library(red)
count.file <- paste(getwd(),
    "/ensembles/consensuscount/Bradypus variegatus_red.grd", sep="")
count.raster <- raster(count.file)
ensemble.red(count.raster)
```

```
# do not predict presence in polygons completely outside convex hull
# of known presence locations
pres.file <- paste(getwd(),
    "/ensembles/consensuspresence/Bradypus variegatus_red.grd", sep="")
pres.raster <- raster(pres.file)
pres1 <- pres[, -1]
chull.created <- ensemble.chull.create(x.pres=pres.raster, p=pres1)

mask.raster <- chull.created$mask.layer
mask.poly <- chull.created$convex.hull

pres.chull <- ensemble.chull.apply(pres.raster, mask=mask.raster, keep.old=T)

# load previous for plotting
pres.file.old <- paste(getwd(),
    "/ensembles/consensuspresence/Bradypus variegatus_red_old.grd", sep="")
pres.raster.old <- raster(pres.file.old)

par.old <- graphics::par(no.readonly=T)
par(mfrow=c(1,2))
plot(pres.raster.old, breaks=c(-1, 0, 1), col=c("grey", "green"),
    main="before convex hull")
points(pres1, col="blue")

# load new
pres.file <- paste(getwd(),
    "/ensembles/consensuspresence/Bradypus variegatus_red.grd", sep="")
pres.raster <- raster(pres.file)
plot(pres.raster, breaks=c(-1, 0, 1), col=c("grey", "green"),
    main="after convex hull")
plot(mask.poly, add=T, border="blue")

# new application of ensemble.red
dev.new()
plot(count.raster, main="before convex hull")
ensemble.red(count.raster)
# all cells where species is predicted not to be present according to the mask layer
# will be modified to a count of zero
count.chull <- ensemble.chull.apply(count.raster, mask=mask.raster, keep.old=T)
# load new
count.file <- paste(getwd(),
    "/ensembles/consensuscount/Bradypus variegatus_red.grd", sep="")
count.raster <- raster(count.file)
ensemble.red(count.raster)
dev.new()
plot(count.raster, main="after convex hull")
# par.old <- graphics::par(no.readonly=T)

# create a smaller hull (0.05 * largest distance)
# First write back the original absence-presence file
pres.file.original <- paste(getwd(),
    "/ensembles/consensuspresence/Bradypus variegatus_red_old.grd", sep="")
```

```
pres.file <- paste(getwd(),
    "/ensembles/consensuspresence/Bradypus variegatus_red.grd", sep="")
pres.raster <- raster(pres.file.original)
# save as the original file
writeRaster(pres.raster, filename=pres.file, overwrite=T)
pres.raster <- raster(pres.file)

chull.created <- ensemble.chull.create(x.pres=pres.raster, p=pres1,
    buffer.width=0.05, lonlat.dist=TRUE)
mask.raster <- chull.created$mask.layer
mask.poly <- chull.created$convex.hull
pres.chull <- ensemble.chull.apply(pres.raster, mask=mask.raster, keep.old=T)

# load previous for plotting
pres.file.old <- paste(getwd(),
    "/ensembles/consensuspresence/Bradypus variegatus_red_old.grd", sep="")
pres.raster.old <- raster(pres.file.old)

par(mfrow=c(1,2))
plot(pres.raster.old, breaks=c(-1, 0, 1), col=c("grey", "green"),
    main="before convex hull")
points(pres1, col="blue")

# load new
pres.file <- paste(getwd(),
    "/ensembles/consensuspresence/Bradypus variegatus_red.grd", sep="")
pres.raster <- raster(pres.file)
plot(pres.raster, breaks=c(-1, 0, 1), col=c("grey", "green"),
    main="after convex hull")
plot(mask.poly, add=T, border="blue")


# create a hull based on the distance to the location with the farthest neighbour
# First write back the original absence-presence file
pres.file.original <- paste(getwd(),
    "/ensembles/consensuspresence/Bradypus variegatus_red_old.grd", sep="")
pres.file <- paste(getwd(),
    "/ensembles/consensuspresence/Bradypus variegatus_red.grd", sep="")
pres.raster <- raster(pres.file.original)
# save as the original file
writeRaster(pres.raster, filename=pres.file, overwrite=T)
pres.raster <- raster(pres.file)

chull.created <- ensemble.chull.create(x.pres=pres.raster, p=pres1,
    buffer.maxmins=TRUE, buffer.width=0.9, lonlat.dist=TRUE)
mask.raster <- chull.created$mask.layer
mask.poly <- chull.created$convex.hull
pres.chull <- ensemble.chull.apply(pres.raster, mask=mask.raster, keep.old=T)

# load previous for plotting
pres.file.old <- paste(getwd(),
    "/ensembles/consensuspresence/Bradypus variegatus_red_old.grd", sep="")
pres.raster.old <- raster(pres.file.old)
```

```
par(mfrow=c(1,2))
plot(pres.raster.old, breaks=c(-1, 0, 1), col=c("grey", "green"),
    main="before convex hull")
points(pres1, col="blue")

# load new
pres.file <- paste(getwd(),
    "/ensembles/consensuspresence/Bradypus variegatus_red.grd", sep="")
pres.raster <- raster(pres.file)
plot(pres.raster, breaks=c(-1, 0, 1), col=c("grey", "green"),
    main="after convex hull")
plot(mask.poly, add=T, border="blue")

par.old <- graphics::par(no.readonly=T)

# how distances were derived
# maximum distance between observations
ensemble.chull.buffer.distances(pres1, lonlat.dist=TRUE)
# the closest neigbhour that is farthest away from each observation
# this is the distance calculated by MSDM_posteriori for buffer="species_specific"
ensemble.chull.buffer.distances(pres1, buffer.maxmins=TRUE, lonlat.dist=TRUE)


## End(Not run)
```

`ensemble.spatialThin` *Thinning of presence point coordinates in geographical or environmental space*

Description

Function `ensemble.spatialThin` creates a randomly selected subset of point coordinates where the shortest distance (geodesic) is above a predefined minimum. The geodesic is calculated more accurately (via `distGeo`) than in the `spThin` or `red` packages.

Usage

```
ensemble.spatialThin(x, thin.km = 0.1,
    runs = 100, silent = FALSE, verbose = FALSE,
    return.notRetained = FALSE)

ensemble.spatialThin.quant(x, thin.km = 0.1,
    runs = 100, silent = FALSE, verbose = FALSE,
    LON.length = 21, LAT.length = 21)

ensemble.environmentalThin(x, predictors.stack = NULL, thin.n = 50,
    runs = 100, pca.var = 0.95, silent = FALSE, verbose = FALSE,
    return.notRetained = FALSE)
```

```
ensemble.environmentalThin.clara(x, predictors.stack = NULL, thin.n = 20,
    runs = 100, pca.var = 0.95, silent = FALSE, verbose = FALSE,
    clara.k = 100)

ensemble.outlierThin(x, predictors.stack = NULL, k = 10,
    quant = 0.95, pca.var = 0.95,
    return.outliers = FALSE)
```

Arguments

x	Point locations provided in 2-column (lon, lat) format.
thin.km	Threshold for minimum distance (km) in final point location data set.
runs	Number of runs to maximize the retained number of point coordinates.
silent	Do not provide any details on the process.
verbose	Provide some details on each run.
return.notRetained	Return in an additional data set the point coordinates that were thinned out.
LON.length	Number of quantile limits to be calculated from longitudes; see also quantile
LAT.length	Number of quantile limits to be calculated from latitudes; see also quantile
predictors.stack	RasterStack object (stack) containing environmental layers that define the environmental space of point observations.
thin.n	Target number of environmentally thinned points.
pca.var	Minimum number of axes based on the fraction of variance explained (default value of 0.95 indicates that at least 95 percent of variance will be explained on the selected number of axes). Axes and coordinates are obtained from Principal Components Analysis (scores).
clara.k	The number of clusters in which the point coordinates will be divided by clara. Clustering is done in environmental space with point coordinates determined from Principal Components Analysis.
k	The number of neighbours for the Local Outlier Factor analysis; see lof
quant	The quantile probability above with local outlier factors are classified as outliers; see also quantile
return.outliers	Return in an additional data set the point coordinates that were flagged as outliers.

Details

Locations with distances smaller than the threshold distance are randomly removed from the data set until no distance is smaller than the threshold. The function uses a similar algorithm as functions in the spThin or red packages, but the geodesic is more accurately calculated via distGeo.

With several runs (default of 100 as in the red package or some spThin examples), the (first) data set with the maximum number of records is retained.

Function `ensemble.spatialThin.quant` was designed to be used with large data sets where the size of the object with pairwise geographical distances could create memory problems. With this function, spatial thinning is only done within geographical areas defined by quantile limits of geographical coordinates.

Function `ensemble.environmentalThin` performs an analysis in environmental space similar to the analysis in geographical space by `ensemble.spatialThin`. However, the target number of retained point coordinates needs to be defined by the user. Coordinates are obtained in environmental space by a principal components analysis (function `rda`). Internally, first points are randomly selected from the pair with the smallest environmental distance until the selected target number of retained point coordinates is reached. From the retained point coordinates, the minimum environmental distance is determined. In a second step (more similar to spatial thinning), locations are randomly removed from all pairs that have a distance larger than the minimum distance calculated in step 1.

Function `ensemble.environmentalThin.clara` was designed to be used with large data sets where the size of the object with pairwise environmental distances could create memory problems. With this function, environmental thinning is done sequentially for each of the clusters defined by `clara`. Environmental space is obtained by by a principal components analysis (function `rda`). Environmental distances are calculated as the pairwise Euclidean distances between the point locations in the environmental space.

Function `ensemble.outlierThin` selects point coordinates that are less likely to be local outliers based on a Local Outlier Factor analysis (`lof`). Since LOF does not result in strict classification of outliers, a user-defined quantile probability is used to identify outliers.

Value

The function returns a spatially or environmentally thinned point location data set.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Aiello-Lammens ME, Boria RA, Radosavljevic A, Vilela B and Anderson RP. 2015. spThin: an R package for spatial thinning of species occurrence records for use in ecological niche models. Ecography 38: 541-545

See Also

`ensemble.batch`

Examples

```
## Not run:
# get predictor variables, only needed for plotting
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
```

```
# subset based on Variance Inflation Factors
predictors <- subset(predictors, subset=c("bio5", "bio6",
    "bio16", "bio17", "biome"))
predictors
predictors@title <- "base"

# presence points
presence_file <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
pres <- read.table(presence_file, header=TRUE, sep=',')[, -1]

# number of locations
nrow(pres)

par.old <- graphics::par(no.readonly=T)
par(mfrow=c(2,2))

pres.thin1 <- ensemble.spatialThin(pres, thin.km=100, runs=10, verbose=T)
plot(predictors[[1]], main="5 runs", ext=extent(SpatialPoints(pres.thin1)))
points(pres, pch=20, col="black")
points(pres.thin1, pch=20, col="red")

pres.thin2 <- ensemble.spatialThin(pres, thin.km=100, runs=10, verbose=T)
plot(predictors[[1]], main="5 runs (after fresh start)", ext=extent(SpatialPoints(pres.thin2)))
points(pres, pch=20, col="black")
points(pres.thin2, pch=20, col="red")

pres.thin3 <- ensemble.spatialThin(pres, thin.km=100, runs=100, verbose=T)
plot(predictors[[1]], main="100 runs", ext=extent(SpatialPoints(pres.thin3)))
points(pres, pch=20, col="black")
points(pres.thin3, pch=20, col="red")

pres.thin4 <- ensemble.spatialThin(pres, thin.km=100, runs=100, verbose=T)
plot(predictors[[1]], main="100 runs (after fresh start)", ext=extent(SpatialPoints(pres.thin4)))
points(pres, pch=20, col="black")
points(pres.thin4, pch=20, col="red")

graphics::par(par.old)

## thinning in environmental space

env.thin <- ensemble.environmentalThin(pres, predictors.stack=predictors, thin.n=60,
    return.notRetained=T)
pres.env1 <- env.thin$retained
pres.env2 <- env.thin$not.retained

# plot in geographical space
par.old <- graphics::par(no.readonly=T)
par(mfrow=c(1, 2))

plot(predictors[[1]], main="black = not retained", ext=extent(SpatialPoints(pres.thin3)))
points(pres.env2, pch=20, col="black")
points(pres.env1, pch=20, col="red")
```

```
# plot in environmental space
background.data <- data.frame(raster::extract(predictors, pres))
rda.result <- vegan::rda(X=background.data, scale=T)
# select number of axes
ax <- 2
while ( (sum(vegan::eigenvals(rda.result)[c(1:ax)])/
    sum(vegan::eigenvals(rda.result))) < 0.95 ) {ax <- ax+1}
rda.scores <- data.frame(vegan::scores(rda.result, display="sites", scaling=1, choices=c(1:ax)))
rownames(rda.scores) <- rownames(pres)
points.in <- rda.scores[which(rownames(rda.scores) %in% rownames(pres.env1)), c(1:2)]
points.out <- rda.scores[which(rownames(rda.scores) %in% rownames(pres.env2)), c(1:2)]
plot(points.out, main="black = not retained", pch=20, col="black",
    xlim=range(rda.scores[, 1]), ylim=range(rda.scores[, 2]))
points(points.in, pch=20, col="red")

graphics::par(par.old)

## removing outliers
out.thin <- ensemble.outlierThin(pres, predictors.stack=predictors, k=10,
    return.outliers=T)
pres.out1 <- out.thin$inliers
pres.out2 <- out.thin$outliers

# plot in geographical space
par.old <- graphics::par(no.readonly=T)
par(mfrow=c(1, 2))

plot(predictors[[1]], main="black = outliers", ext=extent(SpatialPoints(pres.thin3)))
points(pres.out2, pch=20, col="black")
points(pres.out1, pch=20, col="red")

# plot in environmental space
background.data <- data.frame(raster::extract(predictors, pres))
rda.result <- vegan::rda(X=background.data, scale=T)
# select number of axes
ax <- 2
while ( (sum(vegan::eigenvals(rda.result)[c(1:ax)])/
    sum(vegan::eigenvals(rda.result))) < 0.95 ) {ax <- ax+1}
rda.scores <- data.frame(vegan::scores(rda.result, display="sites", scaling=1, choices=c(1:ax)))
rownames(rda.scores) <- rownames(pres)
points.in <- rda.scores[which(rownames(rda.scores) %in% rownames(pres.out1)), c(1:2)]
points.out <- rda.scores[which(rownames(rda.scores) %in% rownames(pres.out2)), c(1:2)]
plot(points.out, main="black = outliers", pch=20, col="black",
    xlim=range(rda.scores[, 1]), ylim=range(rda.scores[, 2]))
points(points.in, pch=20, col="red")

graphics::par(par.old)


## End(Not run)
```

ensemble.zones *Mapping of environmental zones based on the Mahalanobis distance from centroids in environmental space.*

Description

Function ensemble.zones maps the zone of each raster cell within a presence map based on the minimum Mahalanobis distance (via mahalanobis) to different centroids. Function ensemble.centroids defines centroids within a presence map based on Principal Components Analysis (via rda) and K-means clustering (via kmeans).

Usage

```
ensemble.zones(presence.raster = NULL, centroid.object = NULL,
    x = NULL, ext = NULL,
    RASTER.species.name = centroid.object$name, RASTER.stack.name = x@title,
    RASTER.format = "raster", RASTER.datatype = "INT1S", RASTER.NAflag = -127,
    KML.out = FALSE, KML.maxpixels = 100000, KML.blur = 10,
    CATCH.OFF = FALSE)

ensemble.centroids(presence.raster = NULL, x = NULL, categories.raster = NULL,
    an = 10000, ext = NULL, name = "Species001",
    pca.var = 0.95, centers = 0, use.silhouette = TRUE,
    plotit = FALSE, dev.new.width = 7, dev.new.height = 7)
```

Arguments

presence.raster	RasterLayer object (raster) documenting presence (coded 1) of an organism
centroid.object	Object listing values for centroids and covariance to be used with the mahalanobis distance (used internally by the prediction function called from predict).
x	RasterStack object (stack) containing all environmental layers that correspond to explanatory variables
ext	an Extent object to limit the predictions and selection of background points to a sub-region of presence.raster and x, typically provided as c(lonmin, lonmax, latmin, latmax). See also randomPoints and extent.
RASTER.species.name	First part of the names of the raster file that will be generated, expected to identify the modelled species (or organism)
RASTER.stack.name	Last part of the names of the raster file that will be generated, expected to identify the predictor stack used
RASTER.format	Format of the raster files that will be generated. See writeFormats and writeRaster.

RASTER.datatype
: Format of the raster files that will be generated. See dataType and writeRaster.

RASTER.NAflag
: Value that is used to store missing data. See writeRaster.

KML.out
: If TRUE, then kml files will be saved in a subfolder 'kml/zones'.

KML.maxpixels
: Maximum number of pixels for the PNG image that will be displayed in Google Earth. See also KML.

KML.blur
: Integer that results in increasing the size of the PNG image by KML.blur^2, which may help avoid blurring of isolated pixels. See also KML.

CATCH.OFF
: Disable calls to function tryCatch.

categories.raster
: RasterLayer object (raster) documenting predefined zones such as vegetation types. In case this object is provided, then centroids will be calculated for each zone.

an
: Number of presence points to be used for Principal Components Analysis (via rda); see also prepareData and extract

name
: Name for the centroid object, for example identifying the species and area for which centroids are calculated

pca.var
: Minimum number of axes based on the fraction of variance explained (default value of 0.95 indicates that at least 95 percent of variance will be explained on the selected number of axes). Axes and coordinates are obtained from Principal Components Analysis (scores).

centers
: Number of centers (clusters) to be used for K-means clustering (kmeans). In case a value smaller than 1 is provided, function cascadeKM is called to determine the optimal number of centers via the Calinski-Harabasz criterion.

use.silhouette
: If TRUE, then centroid values are only based on presence points that have silhouette values (silhouette) larger than 0.

plotit
: If TRUE, then a plot is provided that shows the locations of centroids in geographical and environmental space. Plotting in geographical space is based on determination of the presence location (analogue) with smallest Mahalanobis distance to the centroid in environmental space.

dev.new.width
: Width for new graphics device (dev.new). If < 0, then no new graphics device is opened.

dev.new.height
: Heigth for new graphics device (dev.new). If < 0, then no new graphics device is opened.

Details

Function ensemble.zones maps the zone of each raster cell of a predefined presence map, whereby the zone is defined as the centroid with the smallest Mahalanobis distance. The function returns a RasterLayer object (raster) and possibly a KML layer.

Function ensemble.centroid provides the centroid locations in environmental space and a covariance matrix (cov) to be used with mahalanobis. Also provided is information on the analogue presence location that is closest to the centroid in environmental space.

Value

Function `ensemble.centroid` returns a list with following objects:

`centroids`	Location of centroids in environmental space
`centroid.analogs`	Location of best analogs to centroids in environmental space
`cov.mahal`	Covariance matrix

Author(s)

Roeland Kindt (World Agroforestry Centre)

See Also

`ensemble.raster`

Examples

```
## Not run:
# get predictor variables
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
predictors <- subset(predictors, subset=c("bio1", "bio5", "bio6", "bio7", "bio8",
    "bio12", "bio16", "bio17"))
predictors
predictors@title <- "base"

# choose background points
background <- randomPoints(predictors, n=1000, extf=1.00)

# predicted presence from GLM
ensemble.calibrate.step1 <- ensemble.calibrate.models(
    x=predictors, p=pres, a=background,
    species.name="Bradypus",
    MAXENT=0, MAXLIKE=0, GBM=0, GBMSTEP=0, RF=0, GLM=1, GLMSTEP=0,
    GAM=0, GAMSTEP=0, MGCV=0, MGCVFIX=0,
    EARTH=0, RPART=0, NNET=0, FDA=0, SVM=0, SVME=0, GLMNET=0,
    BIOCLIM.O=0, BIOCLIM=0, DOMAIN=0, MAHAL=0, MAHAL01=0,
    Yweights="BIOMOD",
    models.keep=TRUE)

ensemble.raster.results <- ensemble.raster(xn=predictors,
    models.list=ensemble.calibrate.step1$models,
    RASTER.species.name="Bradypus", RASTER.stack.name="base")

# get presence map as for example created with ensemble.raster in subfolder 'ensemble/presence'
# presence values are values equal to 1
presence.file <- paste("ensembles//presence//Bradypus_base.grd", sep="")
```

```
presence.raster <- raster(presence.file)

# let cascadeKM decide on the number of clusters
dev.new()
centroids <- ensemble.centroids(presence.raster=presence.raster,
    x=predictors, an=1000, plotit=T)
ensemble.zones(presence.raster=presence.raster, centroid.object=centroids,
    x=predictors, RASTER.species.name="Bradypus", KML.out=T)

dev.new()
zones.file <- paste("ensembles//zones//Bradypus_base.grd", sep="")
zones.raster <- raster(zones.file)
max.zones <- maxValue(zones.raster)
plot(zones.raster, breaks=c(0, c(1:max.zones)),
    col = grDevices::rainbow(n=max.zones), main="zones")
ensemble.zones(presence.raster=presence.raster, centroid.object=centroids,
    x=predictors, RASTER.species.name="Bradypus", KML.out=T)

# manually choose 6 zones
dev.new()
centroids6 <- ensemble.centroids(presence.raster=presence.raster,
    x=predictors, an=1000, plotit=T, centers=6)
ensemble.zones(presence.raster=presence.raster, centroid.object=centroids6,
    x=predictors, RASTER.species.name="Bradypus6", KML.out=T)

dev.new()
zones.file <- paste("ensembles//zones//Bradypus6_base.grd", sep="")
zones.raster <- raster(zones.file)
max.zones <- maxValue(zones.raster)
plot(zones.raster, breaks=c(0, c(1:max.zones)),
    col = grDevices::rainbow(n=max.zones), main="six zones")


## End(Not run)
```

`evaluation.strip.data` *Evaluation strips for ensemble suitability mapping*

Description

These functions provide a dataframe which can subsequently be used to evaluate the relationship between environmental variables and the fitted probability of occurrence of individual or ensemble suitability modelling algorithms. The `biomod2` package provides an alternative implementation of this approach (`response.plot2`).

Usage

```
evaluation.strip.data(xn = NULL, ext = NULL,
    models.list = NULL,
    input.weights = models.list$output.weights,
```

```
    steps=200, CATCH.OFF = FALSE
)

evaluation.strip.plot(data, TrainData=NULL,
    variable.focal = NULL, model.focal = NULL,
    ylim=c(0, 1.25),
    dev.new.width = 7, dev.new.height = 7, ...
)
```

Arguments

xn	RasterStack object (stack) containing all layers that correspond to explanatory variables of an ensemble calibrated earlier with ensemble.calibrate.models. See also predict.
ext	an Extent object to limit the prediction to a sub-region of xn and the selection of background points to a sub-region of x, typically provided as c(lonmin, lonmax, latmin, latmax); see also predict, randomPoints and extent
models.list	list with 'old' model objects such as MAXENT or RF.
input.weights	array with numeric values for the different modelling algorithms; if NULL then values provided by parameters such as MAXENT and GBM will be used. As an alternative, the output from ensemble.calibrate.weights can be used.
steps	number of steps within the range of a continuous explanatory variable
CATCH.OFF	Disable calls to function tryCatch.
data	data set with ranges of environmental variables and fitted suitability models, typically returned by evaluation.strip.data
TrainData	Data set representing the calibration data set. If provided, then a boxplot will be added for presence locations via boxplot
variable.focal	focal explanatory variable for plots with evaluation strips
model.focal	focal model for plots with evaluation strips
ylim	range of Y-axis
dev.new.width	Width for new graphics device (dev.new). If < 0, then no new graphics device is opened.
dev.new.height	Heigth for new graphics device (dev.new). If < 0, then no new graphics device is opened.
...	Other arguments passed to plot

Details

These functions are mainly intended to be used internally by the ensemble.raster function.

evaluation.strip.data creates a data frame with variables (columns) corresponding to the environmental variables encountered in the RasterStack object (x) and the suitability modelling approaches that were defined. The variable of focal.var is an index of the variable for which values are ranged. The variable of categorical is an index for categorical (factor) variables.

A continuous (numeric) variable is ranged between its minimum and maximum values in the number of steps defined by argument `steps`. When a continuous variable is not the focal variable, then the average (`mean`) is used.

A categorical (factor) variable is ranged for all the encountered levels (`levels`) for this variable. When a categorical variable is not the focal variable, then the most frequent level is used.

Value

function `evaluation.strip.data` creates a data frame, function codeevaluation.strip.data allows for plotting.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt R. 2018. Ensemble species distribution modelling with transformed suitability values. Environmental Modelling & Software 100: 136-145. https://doi.org/10.1016/j.envsoft.2017.11.009 Elith J, Ferrier S, Huettmann F & Leathwick J. 2005. The evaluation strip: A new and robust method for plotting predicted responses from species distribution models. Ecological Modelling 186: 280-289

See Also

`ensemble.calibrate.models` and `ensemble.raster`

Examples

```
## Not run:

# get predictor variables
library(dismo)
predictor.files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
    pattern='grd', full.names=TRUE)
predictors <- stack(predictor.files)
# subset based on Variance Inflation Factors
predictors <- subset(predictors, subset=c("bio5", "bio6",
    "bio16", "bio17"))
predictors <- stack(predictors)
predictors
predictors@title <- "base"

# presence points
presence_file <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
pres <- read.table(presence_file, header=TRUE, sep=',')[,-1]

# the kfold function randomly assigns data to groups;
# groups are used as calibration (1/5) and training (4/5) data
groupp <- kfold(pres, 5)
pres_train <- pres[groupp !=  1, ]
```

```
pres_test <- pres[groupp ==  1, ]

# choose background points
background <- randomPoints(predictors, n=1000, extf=1.00)
colnames(background)=c('lon', 'lat')
groupa <- kfold(background, 5)
backg_train <- background[groupa != 1, ]
backg_test <- background[groupa == 1, ]

# calibrate the models
# MAXLIKE not included as does not allow predictions for data.frames
# ENSEMBLE.min and ENSEMBLE.weight.min set very low to explore all
# algorithms.
# If focus is on actual ensemble, then set ENSEMBLE.min and
# ENSEMBLE.weight.min to more usual values
ensemble.calibrate <- ensemble.calibrate.models(x=predictors,
    p=pres_train, a=backg_train,
    pt=pres_test, at=backg_test,
    ENSEMBLE.min=0.5, ENSEMBLE.weight.min = 0.001,
    MAXENT=0, MAXNET=1, MAXLIKE=1, GBM=1, GBMSTEP=0, RF=1, CF=1,
    GLM=1, GLMSTEP=1, GAM=1, GAMSTEP=1, MGCV=1, MGCVFIX=1,
    EARTH=1, RPART=1, NNET=1, FDA=1, SVM=1, SVME=1,
    BIOCLIM.O=1, BIOCLIM=1, DOMAIN=1, MAHAL=0, MAHAL01=1,
    Yweights="BIOMOD",
    PLOTS=FALSE, models.keep=TRUE)

# obtain data for plotting the evaluation strip
strip.data <- evaluation.strip.data(xn=predictors, steps=500,
    models.list=ensemble.calibrate$models)

# in case predictions for DOMAIN failed
# however, ENSEMBLE should also be recalculated
DOMAIN.model <- ensemble.calibrate$models$DOMAIN
strip.data$plot.data[, "DOMAIN"] <- dismo::predict(object=DOMAIN.model,
    x=strip.data$plot.data)

# in case predictions for MAHAL01 failed
predict.MAHAL01 <- function(model, newdata, MAHAL.shape) {
    p <- dismo::predict(object=model, x=newdata)
    p <- p - 1 - MAHAL.shape
    p <- abs(p)
    p <- MAHAL.shape / p
    return(as.numeric(p))
}

MAHAL01.model <- ensemble.calibrate$models$MAHAL01
MAHAL.shape1 <- ensemble.calibrate$models$formulae$MAHAL.shape
strip.data$plot.data[, "MAHAL01"] <- predict.MAHAL01(model=MAHAL01.model,
    newdata=strip.data$plot.data, MAHAL.shape=MAHAL.shape1)

# create graphs
evaluation.strip.plot(data=strip.data$plot.data, variable.focal="bio6",
    TrainData=strip.data$TrainData,
```

```
    type="o", col="red")
evaluation.strip.plot(data=strip.data$plot.data, model.focal="ENSEMBLE",
    TrainData=strip.data$TrainData,
    type="o", col="red")


## End(Not run)
```

`faramea` *Faramea occidentalis abundance in Panama*

Description

This dataset describes the abundance (number of trees with diameter at breast height equal or larger than 10 cm) of the tree species Faramea occidentalis as observed in a 1-ha quadrat survey from the Barro Colorada Island of Panama. For each quadrat, some environmental characteristics are also provided.

Usage

```
data(faramea)
```

Format

A data frame with 45 observations on the following 8 variables.

`UTM.EW` a numeric vector

`UTM.NS` a numeric vector

`Precipitation` a numeric vector

`Elevation` a numeric vector

`Age` a numeric vector

`Age.cat` a factor with levels `c1` `c2` `c3`

`Geology` a factor with levels `pT` `Tb` `Tbo` `Tc` `Tcm` `Tgo` `Tl`

`Faramea.occidentalis` a numeric vector

Details

Although the original survey documented tree species composition of all 1-ha subplots of larger (over 1 ha) sample plot, only the first (and sometimes the last) quadrats of the larger plots were included. This selection was made to avoid that larger sample plots dominated the analysis. This selection of sites is therefore different from the selection of the 50 1-ha quadrats of the largest sample plot of the same survey (`BCI` and `BCI.env`)

This dataset is the main dataset used for the examples provided in chapters 6 and 7 of the Tree Diversity Analysis manual (Kindt & Coe, 2005).

Source

http://www.sciencemag.org/cgi/content/full/295/5555/666/DC1

References

Pyke CR, Condit R, Aguilar S and Lao S. (2001). Floristic composition across a climatic gradient in a neotropical lowland forest. Journal of Vegetation Science 12: 553-566.

Condit, R, Pitman, N, Leigh, E.G., Chave, J., Terborgh, J., Foster, R.B., Nunez, P., Aguilar, S., Valencia, R., Villa, G., Muller-Landau, H.C., Losos, E. & Hubbell, S.P. (2002). Beta-diversity in tropical forest trees. *Science* 295: 666-669.

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
data(faramea)
```

---

ifri *Example data from the International Forestry Resources and Institutions (IFRI) research network*

Description

This data set contains information on the number of stems (individuals) and basal areas for 34 vegetation plots inventoried in February 1997 in Lothlorien forest, 37 vegetation plots inventoried in February 1996 in May Creek Forest and 36 vegetation plots inventoried in May 1995 in Yellowwood State Forest. All three sites are in Indiana, USA. Data were gathered through IFRI inventory protocols to record any tree, palm and woody climber with diameter at breast height greater than or equal to 10 cm in 10-m radius circular plots; only tree species data were kept in the example data sets (IFRI research instruments and IFRI manual section P: Forest Plot Form, section D1: Tree, Palm and Woody Climber Information).

Usage

```
data(ifri)
```

Format

A data frame with 486 observations on the following 5 variables.

`forest` a factor with 3 levels: "LOT" (Lothlorien forest), "MCF" (May Creek Forest) and "YSF" (Yellowwood State Forest)

`plotID` a factor with 107 levels providing an identification code for a 314.16 square metres (10 m radius) vegetation plot

`species` a factor with 50 levels providing an 8 character code for a tree species

`count` a numeric vector providing the number of stems (individuals) for each species in each vegetation plot

`basal` a numeric vector providing the basal area (calculated from the diameter at breast height) in square cm for each species in each vegetation plot

Source

IFRI (2014) Data from the International Forestry Resources and Institutions (IFRI) research network. http://ifri.forgov.org/

Examples

```
data(ifri)
```

`importancevalue` *Importance Value*

Description

Calculates the importance values of tree species based on frequency (calculated from number of plots), density (calculated from number of individuals) and dominance (calculated from basal area). See details.

Usage

```
importancevalue(x, site="plotID", species="species",
    count="count", basal="basal",
    factor="forest", level="")

importancevalue.comp(x, site="plotID", species="species",
    count="count", basal="basal",
    factor="forest")
```

Arguments

`x`	data frame with information on plot identities, species identities, number of individuals and basal areas
`site`	factor variable providing the identities of survey plots
`species`	factor variable providing the identities of tree species
`count`	number of individuals for each tree species in each survey plot
`basal`	basal area for each tree species in each survey plot
`factor`	factor variable used to define subsets (typically different forest reserves)
`level`	level of the factor variable used to create a subset from the original data

Details

The importance value is calculated as the sum from (i) the relative frequency; (ii) the relative density; and (iii) the relative dominance. The importance value ranges between 0 and 300.

Frequency is calculated as the number of plots where a species is observed divided by the total number of survey plots. Relative frequency is calculated by dividing the frequency by the sum of the frequencies of all species, multiplied by 100 (to obtain a percentage).

Density is calculated as the total number of individuals of a species. Relative density is calculated by dividing the density by the sum of the densities of all species, multiplied by 100 (to obtain a percentage).

Dominance is calculated as the total basal area of a species. Relative dominance is calculated by dividing the dominance by the sum of the dominance of all species, multiplied by 100 (to obtain a percentage).

Functions `importancevalue.comp` applies function `importancevalue` to all available levels of a factor variable.

Value

Provides information on the importance value for all tree species

Author(s)

Roeland Kindt (World Agroforestry Centre), Peter Newton (University of Michigan)

References

Curtis, J.T. & McIntosh, R. P. (1951) An Upland Forest Continuum in the Prairie-Forest Border Region of Wisconsin. Ecology 32: 476-496.

Kent, M. (2011) Vegetation Description and Data Analysis: A Practical Approach. Second edition. 428 pages.

See Also

`ifri`

Examples

```
data(ifri)
importancevalue(ifri, site='plotID', species='species', count='count',
    basal='basal', factor='forest', level='YSF')
importancevalue.comp(ifri, site='plotID', species='species', count='count',
    basal='basal', factor='forest')

# When all survey plots are the same size, importance value
# is not affected. Counts and basal areas now calculated per square metre
ifri$count <- ifri$count/314.16
ifri$basal <- ifri$basal/314.16

importancevalue(ifri, site='plotID', species='species', count='count',
```

```
    basal='basal', factor='forest', level='YSF')
importancevalue.comp(ifri, site='plotID', species='species', count='count',
    basal='basal', factor='forest')

# Calculate diversity profiles from importance values
imp <- importancevalue.comp(ifri, site='plotID', species='species',
    count='count', basal='basal', factor='forest')
vals <- imp[["values"]]
for (i in 1:length(vals)) {
    imp.i <- data.frame(imp[[vals[i]]])
    name.i <- paste(vals[[i]], ".Renyi", sep="")
    imp[[name.i]] <- renyi(imp.i$importance.value)
}

# LOT more diverse
imp$LOT.Renyi - imp$MCF.Renyi
imp$LOT.Renyi - imp$YSF.Renyi

# YSF and MCF different richness and evenness
imp$YSF.Renyi - imp$MCF.Renyi
```

`loaded.citations` *Give Citation Information for all Loaded Packages*

Description

This function provides citation information for all loaded packages.

Usage

```
loaded.citations()
```

Details

The function checks for the loaded packages via `.packages`. Citation information is provided for the base package and for all the non-standard packages via `citation`.

Value

The function provides a list of all loaded packages and the relevant citation information.

Author(s)

Roeland Kindt (World Agroforestry Centre)

`makecommunitydataset` *Make a Community Dataset from a Stacked Dataset*

Description

Makes a community data set from a stacked dataset (with separate variables for the site identities, the species identities and the abundance).

Usage

```
makecommunitydataset(x, row, column, value, factor="", level="", drop=F)
stackcommunitydataset(comm, remove.zeroes=FALSE, order.sites=FALSE, order.species=FALSE)
```

Arguments

`x`	Data frame.
`row`	Name of the categorical variable for the rows of the crosstabulation (typically indicating sites)
`column`	Name of the categorical variable for the columns of the crosstabulation (typically indicating species)
`value`	Name of numerical variable for the cells of the crosstabulation (typically indicating abundance). The cells provide the sum of all values in the data frame.
`factor`	Name of the variable to calculate a subset of the data frame.
`level`	Value of the subset of the factor variable to calculate a subset of the data frame.
`drop`	Drop rows without species (species with total abundance of zero are always dropped)
`comm`	Community data set
`remove.zeroes`	Should rows with zero abundance be removed?
`order.sites`	Should sites be ordered alphabetically?
`order.species`	Should species be ordered alphabetically?

Details

`makecommunitydataset` calculates a cross-tabulation from a data frame, summing up all the values of the numerical variable identified as variable for the cell values. If factor="", then no subset is calculated from the data frame in the first step.

`stackcommunitydataset` reverses the actions of `makecommunitydataset` and recreates the data in stacked format.

Value

The function provides a community dataset from another data frame.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
## Not run:
dune.file <- normalizePath(paste(system.file(package="BiodiversityR"),
    '/etc/dunestacked.csv', sep=''))
dune.stacked <- read.csv(dune.file)

# dune.stacked has different variables for sites, species and abundance
head(dune.stacked)
dune.comm2 <- makecommunitydataset(dune.stacked, row='sites', column='species',
    value='abundance')

# recreate the original stack
dune.stacked2 <- stackcommunitydataset(dune.comm2, remove.zeroes=T)


## End(Not run)
```

---

multiconstrained *Pairwise Comparisons for All Levels of a Categorical Variable by RDA, CCA or Capscale*

Description

This function implements pairwise comparisons for categorical variable through capscale, cca, dbrda or rda followed by anova.cca. The function simply repeats constrained ordination analysis by selecting subsets of data that correspond to two factor levels.

Usage

```
multiconstrained(method="capscale", formula, data, distance = "bray"
    , comm = NULL, add = FALSE, multicomp="", contrast=0, ...)
```

Arguments

method	Method for constrained ordination analysis; one of "rda", "cca", "dbrda" or "capscale".
formula	Model formula as in capscale, cca or rda. The LHS can be a community data matrix or a distance matrix for capscale.
data	Data frame containing the variables on the right hand side of the model formula as in capscale, cca or rda.
distance	Dissimilarity (or distance) index in vegdist used if the LHS of the formula is a data frame instead of dissimilarity matrix; used only with function vegdist and partial match to "manhattan", "euclidean", "canberra", "bray", "kulczynski", "jaccard", "gower", "morisita", "horn" or "mountford". This argument is only used for capscale in case that the LHS of the formula is a community matrix.
comm	Community data frame which will be used for finding species scores when the LHS of the formula was a dissimilarity matrix as only allowed for capscale. This is not used if the LHS is a data frame.
add	Logical indicating if an additive constant should be computed, and added to the non-diagonal dissimilarities such that all eigenvalues are non-negative in underlying Principal Co-ordinates Analysis; only applicable in capscale.
multicomp	Categorical variable used to construct the contrasts from. In case that this variable is missing, then the first explanatory variable of the formula will be used.
contrast	Return the ordination results for the particular contrast indicated by this number (e.g. with 5 levels, one can choose in between contrast 1-10). In case=0, then the first row of the anova.cca results for all contrasts is provided.
...	Other parameters passed to anova.cca.

Details

This function provides a simple expansion of capscale, cca and rda by conducting the analysis for subsets of the community and environmental datasets that only contain two levels of a categoricl variable.

When the choice is made to return results from all contrasts (contrast=0), then the first row of the anova.cca tables for each contrast are provided. It is therefore possible to compare differences in results by modifying the "by" argument of this function (i.e. obtain the total of explained variance, the variance explained on the first axis or the variance explained by the variable alone).

When the choice is made to return results from a particular contrast (contrast>0), then the ordination result is returned and two new datasets ("newcommunity" and "newenvdata") are created that only contain data for the two selected contrasts.

Value

The function returns an ANOVA table that contains the first rows of the ANOVA tables obtained for all possible combinations of levels of the first variable. Alternatively, it returns an ordination result for the selected contrast and creates two new datasets ("newcommunity" and "newenvdata")

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Legendre, P. & Anderson, M.J. (1999). Distance-based redundancy analysis: testing multispecies responses in multifactorial ecological experiments. Ecological Monographs 69: 1-24.

Anderson, M.J. & Willis, T.J. (2003). Canonical analysis of principal coordinates: a useful method of constrained ordination for ecology. Ecology 84: 511-525.

Examples

```
## Not run:
library(vegan)
library(MASS)
data(dune)
data(dune.env)
multiconstrained(method="capscale", dune~Management, data=dune.env,
    distance="bray",add=TRUE)
multiconstrained(method="capscale", dune~Management, data=dune.env,
    distance="bray", add=TRUE, contrast=3)

## End(Not run)
```

`nested.anova.dbrda` *Nested Analysis of Variance via Distance-based Redundancy Analysis or Non-parametric Multivariate Analysis of Variance*

Description

The functions provide nested analysis of variance for a two-level hierarchical model. The functions are implemented by estimating the correct F-ratio for the main and nested factors (assuming the nested factor is random) and using the recommended permutation procedures to test the significance of these F-ratios. F-ratios are estimated from variance estimates that are provided by distance-based redundancy analysis (`capscale`) or non-parametric multivariate analysis of variance (`adonis`).

Usage

```
nested.anova.dbrda(formula, data, method="euc", add=FALSE,
    permutations=100, warnings=FALSE)
nested.npmanova(formula, data, method="euc", permutations=100, warnings=FALSE)
```

Arguments

`formula`	Formula with a community data frame (with sites as rows, species as columns and species abundance as cell values) or (for `nested.anova.dbrda` only) distance matrix on the left-hand side and two categorical variables on the right-hand side (with the second variable assumed to be nested within the first).

data	Environmental data set.
method	Method for calculating ecological distance with function vegdist: partial match to "manhattan", "euclidean", "canberra", "bray", "kulczynski", "jaccard", "gower", "morisita", "horn" or "mountford". This argument is ignored in case that the left-hand side of the formula already is a distance matrix.
add	Should a constant be added to the off-diagonal elements of the distance-matrix (TRUE) or not.
permutations	The number of permutations for significance testing.
warnings	Should warnings be suppressed (TRUE) or not.

Details

The functions provide two alternative procedures for multivariate analysis of variance on the basis of any distance measure. Function nested.anova.dbrda proceeds via capscale, whereas nested.npmanova proceeds via adonis. Both methods are complementary to each other as nested.npmanova always provides correct F-ratios and estimations of significance, whereas nested.anova.dbrda does not provide correct F-ratios and estimations of significance when negative eigenvalues are encountered or constants are added to the distance matrix, but always provides an ordination diagram.

The F-ratio for the main factor is estimated as the mean square of the main factor divided by the mean square of the nested factor. The significance of the F-ratio of the main factor is tested by permuting entire blocks belonging to levels of the nested factor. The significance of the F-ratio of the nested factor is tested by permuting sample units within strata defined by levels of the main factor.

Value

The functions provide an ANOVA table.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Legendre, P. & Anderson, M. J. (1999). Distance-based redundancy analysis: testing multispecies responses in multifactorial ecological experiments. Ecological Monographs 69, 1-24.

Anderson, M.J. (2001). A new method for non-parametric multivariate analysis of variance. Austral Ecology, 26: 32-46.

McArdle, B.H. and M.J. Anderson. (2001). Fitting multivariate models to community data: A comment on distance-based redundancy analysis. Ecology, 82: 290-297.

Examples

```
## Not run:
library(vegan)
data(warcom)
data(warenv)
# use larger number of permutations for real studies
```

```
nested.npmanova(warcom~rift.valley+popshort, data=warenv, method="jac",
    permutations=5)
nested.anova.dbrda(warcom~rift.valley+popshort, data=warenv, method="jac",
    permutations=5)

## End(Not run)
```

NMSrandom *Calculate the NMS Result with the Smallest Stress from Various Random Starts*

Description

This function provides a simplified version of the method of calculating NMS results implemented by the function metaMDS (**vegan**).

Usage

```
NMSrandom(x,perm=100,k=2,stressresult=F,method="isoMDS")
```

Arguments

x	Distance matrix.
perm	Number of permutations to select the configuration with the lowest stress.
k	Number of dimensions for the non metric scaling result; passed to isoMDS or sammon.
stressresult	Provide the calculated stress for each permutation.
method	Method for calculating the NMS: isoMDS or sammon.

Details

This function is an easier method of calculating the best NMS configuration after various random starts than implemented in the metaMDS function (**vegan**). The function uses a distance matrix (as calculated for example by function vegdist from a community data set) and calculates random starting positions by function initMDS (**vegan**) analogous to metaMDS.

Value

The function returns the NMS ordination result with the lowest stress (calculated by isoMDS or sammon.), or the stress of each NMS ordination.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
library(MASS)
data(dune)
distmatrix <- vegdist(dune)
Ordination.model1 <- NMSrandom(distmatrix,perm=100,k=2)
Ordination.model1 <- add.spec.scores(Ordination.model1,dune,
    method='wa.scores')
Ordination.model1
```

`nnetrandom` *Calculate the NNET Result with the Smallest Value from Various Random Starts*

Description

This function provides the best solution from various calls to the `nnet` feed-forward artificial neural networks function (**nnet**).

Usage

```
nnetrandom(formula,data,tries=10,leave.one.out=F,...)
```

Arguments

`formula`	Formula as passed to `nnet`.
`data`	Data as passed to `nnet`.
`tries`	Number of calls to `nnet` to obtain the best solution.
`leave.one.out`	Calculate leave-one-out predictions.
`...`	Other arguments passed to `nnet`.

Details

This function makes various calls to `nnet`. If desired by the user, leave-one-out statistics are provided that report the prediction if one particular sample unit was not used for iterating the networks.

Value

The function returns the same components as nnet, but adds the following components:

range	Summary of the observed "values".
tries	Number of different attempts to iterate an ANN.
CV	Predicted class when not using the respective sample unit for iterating ANN.
succesful	Test whether leave-one-out statistics provided the same class as the original class.

Author(s)

Roeland Kindt (World Agroforestry Centre)

Examples

```
## Not run:
data(faramea)
faramea <- na.omit(faramea)
faramea$presence <- as.numeric(faramea$Faramea.occidentalis > 0)
attach(faramea)
library(nnet)
result <- nnetrandom(presence ~ Elevation, data=faramea, size=2,
    skip=FALSE, entropy=TRUE, trace=FALSE, maxit=1000, tries=100,
    leave.one.out=FALSE)
summary(result)
result$fitted.values
result$value
result2 <- nnetrandom(presence ~ Elevation, data=faramea, size=2,
    skip=FALSE, entropy=TRUE, trace=FALSE, maxit=1000, tries=50,
    leave.one.out=TRUE)
result2$range
result2$CV
result2$successful

## End(Not run)
```

---

ordicoeno *Coenoclines for an Ordination Axis*

Description

A graph is produced that summarizes (through GAM as implemented by gam) how the abundance of all species of the community data set change along an ordination axis (based on the position of sites along the axis and the information from the community data set).

Usage

```
ordicoeno(x, ordiplot, axis = 1, legend = FALSE, cex = 0.8, ncol = 4, ...)
```

Arguments

x	Community data frame with sites as rows, species as columns and species abundance as cell values.
ordiplot	Ordination plot created by ordiplot.
axis	Axis of the ordination graph (1: horizontal, 2: vertical).
legend	if TRUE, then add a legend to the plot.
cex	the amount by which plotting text and symbols should be magnified relative to the default; see also par
ncol	the number of columns in which to set the legend items; see also legend
...	Other arguments passed to functions plot and points.

Details

This functions investigates the relationship between the species vectors and the position of sites on an ordination axis. A GAM (gam) investigates the relationship by using the species abundances of each species as response variable, and the site position as the explanatory variable. The graph shows how the abundance of each species changes over the gradient of the ordination axis.

Value

The function plots coenoclines and provides the expected degrees of freedom (complexity of the relationship) estimated for each species by GAM.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
library(mgcv)
data(dune)
Ordination.model1 <- rda(dune)
plot1 <- ordiplot(Ordination.model1, choices=c(1,2), scaling=1)
ordicoeno(dune, ordiplot=plot1, legend=TRUE)
```

ordisymbol *Add Other Graphical Items to Ordination Diagrams*

Description

Functions to add some other graphical itmes to ordination diagrams than provided within **vegan** by ordihull, ordispider, ordiarrows, ordisegments, ordigrid, ordiellipse, ordicluster and lines.spantree.

Usage

```
ordisymbol(ordiplot, y, factor, col = 1, colors = TRUE, pchs = TRUE,
    rainbow_hcl = TRUE, rainbow_hcl.c = 90, rainbow_hcl.l = 50,
    rainbow = TRUE, heat.colors = FALSE, terrain.colors = FALSE,
    topo.colors = FALSE, cm.colors = FALSE,
    legend = TRUE, legend.x = "topleft", legend.ncol = 1, ...)
ordibubble(ordiplot,var,...)
ordicluster2(ordiplot, cluster, mingroups = 1, maxgroups = nrow(ordiplot$sites), ...)
ordinearest(ordiplot, dist,...)
ordivector(ordiplot, spec, lty=2,...)
```

Arguments

ordiplot	An ordination graph created by ordiplot (**vegan**).
y	Environmental data frame.
factor	Variable of the environmental data frame that defines subsets to be given different symbols.
var	Continous variable of the environmental dataset or species from the community dataset.
col	Colour (as points).
colors	Apply different colours to different factor levels
pchs	Apply different symbols (plotting characters) to different factor levels (as in points))
rainbow_hcl	Use rainbow_hcl colours (rainbow_hcl)
rainbow_hcl.c	Set the chroma value
rainbow_hcl.l	Set the luminance value
rainbow	Use rainbow colours
heat.colors	Use heat colours
terrain.colors	Use terrain colours
topo.colors	Use topo colours
cm.colors	Use cm colours
legend	Add the legend.

legend.x	Location of the legend; see also legend.
legend.ncol	the number of columns in which to set the legend items; see also legend
cluster	Cluster object.
mingroups	Minimum of clusters to be plotted.
maxgroups	Maximum of clusters to be plotted..
dist	Distance matrix.
spec	Species name from the community dataset.
lty	Line type as specified for par.
...	Other arguments passed to functions points, symbols, ordihull or arrows.

Details

Function ordisymbol plots different levels of the specified variable in different symbols and different colours. In case more than one colour palettes are selected, the last palette selected will be used.

Function ordibubble draws bubble diagrams indicating the value of the specified continuous variable. Circles indicate positive values, squares indicate negative values.

Function ordicluster2 provides an alternative method of overlaying information from hierarchical clustering on an ordination diagram than provided by function ordicluster. The method draws convex hulls around sites that are grouped into the same cluster. You can select the minimum and maximum number of clusters that are plotted (i.e. the range of clustering steps to be shown).

Function ordinearest draws a vector from each site to the site that is nearest to it as determined from a distance matrix. When you combine the method with lines.spantree using the same distance measure, then you can evaluate in part how the minimum spanning tree was constructed.

Function ordivector draws a vector for the specified species on the ordination diagramme and draws perpendicular lines from each site to a line that connects the origin and the head of species vector. This method helps in the biplot interpretation of a species vector as described by Jongman, ter Braak and van Tongeren (1995).

Value

These functions add graphical items to an existing ordination diagram.

Author(s)

Roeland Kindt (World Agroforestry Centre) and Jari Oksanen (ordinearest)

References

Jongman, R.H.G, ter Braak, C.J.F & van Tongeren, O.F.R. (1987). Data Analysis in Community and Landscape Ecology. Pudog, Wageningen.

Kindt, R. & Coe, R. (2005). Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(dune)
data(dune.env)
Ordination.model1 <- rda(dune)
plot1 <- ordiplot(Ordination.model1, choices=c(1,2), scaling=2)
ordisymbol(plot1, dune.env, "Management", legend=TRUE,
    legend.x="topleft", legend.ncol=1)
plot2 <- ordiplot(Ordination.model1, choices=c(1,2), scaling=1)
distmatrix <- vegdist(dune, method='bray')
cluster <- hclust(distmatrix, method='single')
ordicluster2(plot2, cluster)
ordinearest(plot2, distmatrix, col=2)
ordivector(plot2, "Agrostol", lty=2)
```

PCAsignificance *PCA Significance*

Description

Calculates the number of significant axes from a Principal Components Analysis based on the broken-stick criterion, or adds an equilibrium circle to an ordination diagram.

Usage

```
PCAsignificance(pca,axes=8)
ordiequilibriumcircle(pca,ordiplot,...)
```

Arguments

pca	Principal Components Analysis result as calculated by rda (**vegan**).
axes	Number of axes to calculate results for.
ordiplot	Ordination plot created by ordiplot (**vegan**)
...	Other arguments passed to function arrows.

Details

These functions provide two methods of providing some information on significance for a Principal Components Analysis (PCA).

Function PCAsignificance uses the broken-stick distribution to evaluate how many PCA axes are significant. This criterion is one of the most reliable to check how many axes are significant. PCA axes with larger percentages of (accumulated) variance than the broken-stick variances are significant (Legendre and Legendre, 1998).

Function ordiequilibriumcircle draws an equilibirum circle to a PCA ordination diagram. Only species vectors with heads outside of the equilibrium circle significantly contribute to the ordination diagram (Legendre and Legendre, 1998). Vectors are drawn for these species. The function considers the scaling methods used by rda for scaling=1. The method should only be used for scaling=1 and PCA calculated by function rda.

Value

Function PCAsignificance returns a matrix with the variances that are explained by the PCA axes and by the broken-stick criterion.

Function ordiequilibriumcircle plots an equilibirum circle and returns a list with the radius and the scaling constant used by rda.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Legendre, P. & Legendre, L. (1998). Numerical Ecology. 2nd English Edition. Elsevier.

Kindt, R. & Coe, R. (2005). Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(dune)
Ordination.model1 <- rda(dune)
PCAsignificance(Ordination.model1)
plot1 <- ordiplot(Ordination.model1, choices=c(1,2), scaling=1)
ordiequilibriumcircle(Ordination.model1,plot1)
```

---

radfitresult *Alternative Rank Abundance Fitting Results*

Description

Provides alternative methods of obtaining rank abundance curves than provided by functions radfit, fisherfit and prestonfit (**vegan**), although these same functions are called.

Usage

```
radfitresult(x,y="",factor="",level,plotit=T)
```

Arguments

x	Community data frame with sites as rows, species as columns and species abundance as cell values.
y	Environmental data frame.
factor	Variable of the environmental data frame that defines subsets to calculate fitted rank-abundance curves for.
level	Level of the variable to create the subset to calculate fitted rank-abundance curves.
plotit	Plot the results obtained by plot.radfit .

Details

These functions provide some alternative methods of obtaining fitted rank-abundance curves, although functions radfit, fisherfit and prestonfit (**vegan**) are called to calculate the actual results.

Value

The function returns the results from three methods of fitting rank-abundance curves:

radfit	results of radfit.
fisherfit	results of fisherfit.
prestonfit	results of prestonfit.

Optionally, a plot is provided of the radfit results by plot.radfit.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(BCI)
BCIall <- t(as.matrix(colSums(BCI)))
radfitresult(BCIall)
```

---

rankabundance *Rank Abundance Curves*

Description

Provides methods of calculating rank-abundance curves.

Usage

```
rankabundance(x, y="", factor="", level, digits=1, t=qt(0.975, df=n-1))

rankabunplot(xr, addit=F, labels="", scale="abundance", scaledx=F, type="o",
    xlim=c(min(xpos), max(xpos)),
    ylim=c(0, max(x[,scale])),
    specnames=c(1:5), srt=0, ...)
```

```
rankabuncomp(x, y="", factor, scale="abundance",
    scaledx=F, type="o", rainbow=T,
    legend=T, xlim=c(1, max1), ylim=c(0, max2), ...)
```

Arguments

x	Community data frame with sites as rows, species as columns and species abundance as cell values.
y	Environmental data frame.
factor	Variable of the environmental data frame that defines subsets to calculate rank abundance curves for.
level	Level of the variable to create the subset to calculate rank abundance curves.
digits	Number of digits in the results.
t	t-value to calculate confidence interval limits for the species proportion for cluster sampling (following Hayek and Buzas 1997).
xr	Result from rankabundance.
addit	Add rank abundance curve to an existing graph.
labels	Labels to plot at left of the rank abundance curves.
scale	Method of scaling the vertical axis. Method "abundance" uses abundance, "proportion" uses proportional abundance (species abundance / total abundance), "logabun" calculates the logarithm of abundance using base 10 and "accumfreq" accumulates the proportional abundance.
scaledx	Scale the horizontal axis to 100 percent of total number of species.
type	Type of plot (as in function plot)
xlim	Limits for the horizontal axis.
ylim	Limits for the vertical axis.
specnames	Vector positions of species names to add to the rank-abundance curve.
srt	The string rotation in degrees of the species names (as in par).
rainbow	Use rainbow colouring for the different curves.
legend	Add the legend (you need to click in the graph where the legend needs to be plotted).
...	Other arguments to be passed to functions plot or points.

Details

These functions provide methods of calculating and plotting rank-abundance curves.

The vertical axis can be scaled by various methods. Method "abundance" uses abundance, "proportion" uses proportional abundance (species abundance / total abundance), "logabun" calculates the logarithm of abundance using base 10 and "accumfreq" accumulates the proportional abundance.

The horizontal axis can be scaled by the total number of species, or by 100 percent of all species by option "scaledx".

The method of calculating the confidence interval for species proportion is described in Hayek and Buzas (1997).

Functions rankabundance and rankabuncomp allow to calculate rank abundance curves for subsets of the community and environmental data sets. Function rankabundance calculates the rank abundance curve for the specified level of a selected environmental variable. Method rankabuncomp calculates the rank abundance curve for all levels of a selected environmental variable separatedly.

Value

The functions provide information on rankabundance curves. Function rankabundance provides information on abundance, proportional abundance, logarithmic abundance and accumulated proportional abundance. The function also provides confidence interval limits for the proportion of each species (plower, pupper) and the proportion of species ranks (in percentage).

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Hayek, L.-A. C. & Buzas, M.A. (1997). Surveying Natural Populations. Columbia University Press.

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(dune.env)
data(dune)
RankAbun.1 <- rankabundance(dune)
RankAbun.1
rankabunplot(RankAbun.1, scale='abundance', addit=FALSE, specnames=c(1,2,3))
rankabunplot(RankAbun.1, scale='logabun', addit=FALSE, specnames=c(1:30),
    srt=45, ylim=c(1,100))
rankabuncomp(dune, y=dune.env, factor='Management',
    scale='proportion', legend=FALSE)
## CLICK IN THE GRAPH TO INDICATE WHERE THE LEGEND NEEDS TO BE PLACED
## IF YOU OPT FOR LEGEND=TRUE.
```

---

removeNAcomm *Synchronize Community and Environmental Datasets*

Description

These functions may assist to ensure that the sites of the community dataset are the same sites as those from the environmental dataset, something that is assumed to be the case for the **BiodiversityR** and **vegan** packages.

Usage

```
same.sites(x, y)
check.datasets(x, y)
check.ordiscores(x, ord, check.species = TRUE)
removeNAcomm(x, y, variable)
removeNAenv(x, variable)
removezerospecies(x)
subsetcomm(x, y, factor, level, returncomm = TRUE)

import.with.readxl(file = file.choose(), data.type = "community", sheet = NULL,
    sitenames = "sites", column = "species", value = "abundance",
    factor = "", level = "", cepnames = FALSE,
    write.csv = FALSE, csv.file = paste(data.type, ".csv", sep=""))
```

Arguments

x	Data frame assumed to be the community dataset with variables corresponding to species.
y	Data frame assumed to be the environmental dataset with variables corresponding to descriptors of sites.
ord	Ordination result.
check.species	Should the species scores be checked (TRUE) or not.
variable	Name of the variable from the environmental dataset with NA values that indicate those sites that should be removed.
factor	Variable of the environmental data frame that defines subsets for the data frame.
level	Level of the variable to create the subsets for the data frame.
returncomm	For the selected sites, return the community dataset (TRUE) or the environmental dataset.
file	Location of the Excel (or Access) file.
data.type	Type of the data set to be imported: one of "community", "environmental" or "stacked".
sheet	Name of the sheet of the Excel file to import from (if missing, then data.type is used)
sitenames	Name of categorical variable that provides the names for the sites.
column	Name of the categorical variable for the columns of the crosstabulation (typically indicating species); passed to makecommunitydataset.
value	Name of numerical variable for the cells of the crosstabulation (typically indicating abundance). The cells provide the sum of all values in the data frame; passed to makecommunitydataset.
cepnames	Should the names of columns be abbreviated via make.cepnames (TRUE) or not (FALSE).
write.csv	Create a comma-delimited text file in the working directory (if TRUE).
csv.file	Name of the comma-delimited text file to be created.

Details

Function `same.sites` provides a new data frame that has the same row names as the row names of the environmental data set and the same (species) variables as the original community data set. Sites from the original community data set that have no corresponding sites in the environmental data set are not included in the new community data set. (Hint: this function can be especially useful when some sites do not contain any species and where a community dataset was generated by the `makecommunitydataset` function.)

Function `check.datasets` checks whether the community and environmental data sets have the same number of rows, and (if this was the case) whether the rownames of both data sets are the same. The function also returns the dimensions of both data sets.

Function `check.ordiscores` checks whether the community data set and the ordination result have the same number of rows (sites) and columns (species, optional for `check.species==TRUE`), and (if this was the case) whether the row and column names of both data sets are the same. Site and species scores for the ordination result are obtained via function `scores` (**vegan**).

Functions `removeNAcomm` and `removeNAenv` provide a new data frame that does not contain `NA` for the specified variable. The specifed variable is part of the environmental data set. These functions are particularly useful when using community and environmental datasets, as new community and environmental datasets can be calculated that contain information from the same sample plots (sites). An additional result of `removeNAenv` is that factor levels of any categorical variable that do not occur any longer in the new data set are removed from the levels of the categorical variable.

Function `replaceNAcomm` substitutes cells containing NA with 0 in the community data set.

Function `removezerospecies` removes species from a community dataset that have total abundance that is smaller or equal to zero.

Function `subsetcomm` makes a subset of sites that contain a specified level of a categorical variable from the environmental data set. The same functionality of selecting subsets of the community or environmental data sets are implemented in various functions of **BiodiversityR** (for example `diversityresult`, `renyiresult` and `accumresult`) and have the advantage that it is not necessary to create a new data set. If a community dataset is returned, species that did not contain any individuals were removed from the data set. If an environmental dataset is returned, factor levels that did not occur were removed from the data set.

Function `import.with.readxl` provides methods of importing community or environmental datasets through `read_excel`.

For stacked datasets, a community data set is created with function `makecommunitydataset`. For community data with more species than the limited number of columns in Excel, this may be the only option of importing a community dataset.

An additional advantage of the function is that the community and environmental data can be stored in the same file.

You may want to check compatibility of the community and environmental datasets with functions `check.datasets` and modify the community dataset through `same.sites`.

Value

The functions return a data frame or results of tests on the correspondence between community and environmental data sets.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(dune.env)
data(dune)
dune.env2 <- dune.env
dune.env2[1:4,"Moisture"] <- NA
dune2 <- removeNAcomm(dune,dune.env2,"Moisture")
dune.env2 <- removeNAenv(dune.env2,"Moisture")
dune3 <- same.sites(dune,dune.env2)
check.datasets(dune,dune.env2)
check.datasets(dune2,dune.env2)
check.datasets(dune3,dune.env2)
dune4 <- subsetcomm(dune,dune.env,"Management","NM",returncomm=TRUE)
dune.env4 <- subsetcomm(dune,dune.env,"Management","NM",returncomm=FALSE)
dune5 <- same.sites(dune,dune.env4)
check.datasets(dune4,dune5)
```

---

renyiresult *Alternative Renyi Diversity Results*

Description

Provides some alternative methods of obtaining results on Renyi diversity profile values than provided by `renyi` (**vegan**).

Usage

```
renyiresult(x, y=NULL, factor, level, method = "all",
    scales = c(0, 0.25, 0.5, 1, 2, 4, 8, Inf), evenness = FALSE ,...)

renyiplot(xr, addit=FALSE, pch = 1,
    xlab = "alpha", ylab = "H-alpha", ylim = NULL,
    labelit = TRUE, legend = TRUE, legend.x="topleft", legend.ncol = 8,
    col = 1, cex = 1, rainbow = TRUE, evenness = FALSE, ...)

renyiaccumresult(x, y=NULL, factor, level,
    scales=c(0, 0.25, 0.5, 1, 2, 4, 8, Inf), permutations = 100,...)
```

```
renyicomp(x, y, factor, sites=Inf,
   scales = c(0, 0.25, 0.5, 1, 2, 4, 8, Inf), permutations = 100, plotit = FALSE, ...)
```

Arguments

x	Community data frame with sites as rows, species as columns and species abundance as cell values.
y	Environmental data frame.
factor	Variable of the environmental data frame that defines subsets to calculate diversity profiles for.
level	Level of the variable to create the subset to calculate diversity profiles.
method	Method of calculating the diversity profiles: "all" calculates the diversity of the entire community (all sites pooled together), "s" calculates the diversity of each site separatedly.
scales	Scale parameter values as in function renyi (**vegan**).
evenness	Calculate or plot the evenness profile.
xr	Result from renyi or renyiresult.
addit	Add diversity profile to an existing graph.
pch	Symbol used for drawing the diversity profiles (as in function points).
xlab	Label for the horizontal axis.
ylab	Label for the vertical axis.
ylim	Limits of the vertical axis.
labelit	Provide site labels (site names) at beginning and end of the diversity profiles.
legend	Add the legend (you need to click in the graph where the legend needs to be plotted).
legend.x	Location of the legend; see also legend.
legend.ncol	number of columns for the legend (as in function legend).
col	Colour for the diversity profile (as in function points).
cex	Character expansion factor (as in function points).
rainbow	Use rainbow colours for the diversity profiles.
sites	Number of accumulated sites to provide profile values.
permutations	Number of permutations for the Monte-Carlo simulations for accumulated renyi diversity profiles (estimated by renyiaccum).
plotit	Plot the results (you need to click in the graph where the legend should be plotted).
...	Other arguments to be passed to functions renyi or plot.

Details

These functions provide some alternative methods of obtaining results with diversity profiles, although function renyi is always used to calculate the diversity profiles.

The method of calculating the diversity profiles: "all" calculates the diversity profile of the entire community (all sites pooled together), whereas "s" calculates the diversity profile of each site separatedly. The evenness profile is calculated by subtracting the profile value at scale 0 from all the profile values.

Functions renyiresult, renyiaccumresult and renyicomp allow to calculate diversity profiles for subsets of the community and environmental data sets. functions renyiresult and renyiaccumresult calculate the diversity profiles for the specified level of a selected environmental variable. Method renyicomp calculates the diversity profile for all levels of a selected environmental variable separatedly.

Functions renyicomp and renyiaccumresult calculate accumulation curves for the Renyi diversity profile by randomised pooling of sites and calculating diversity profiles for the pooled sites as implemented in renyiaccum. The method is similar to the random method of species accumulation (specaccum). If the number of "sites" is not changed from the default, it is replaced by the sample size of the level with the fewest number of sites.

Value

The functions provide alternative methods of obtaining Renyi diversity profiles.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt R., Degrande A., Turyomurugyendo L., Mbosso C., Van Damme P., Simons A.J. (2001). Comparing species richness and evenness contributions to on-farm tree diversity for data sets with varying sample sizes from Kenya, Uganda, Cameroon and Nigeria with randomised diversity profiles. Paper presented at IUFRO conference on forest biometry, modeling and information science, 26-29 June, University of Greenwich, UK

Kindt R. (2002). Methodology for tree species diversification planning for African agroecosystems. Thesis submitted in fulfilment of the requirement of the degree of doctor (PhD) in applied biological sciences. Faculty of agricultural and applied biological sciences, Ghent University, Ghent (Belgium), 332+xi pp.

Kindt R., Van Damme P. & Simons A.J. (2006). Tree diversity in western Kenya: using diversity profiles to characterise richness and evenness. Biodiversity and Conservation 15: 1253-1270.

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
data(dune.env)
```

```
data(dune)
Renyi.1 <- renyiresult(dune, y=dune.env, factor='Management', level='NM',
    method='s')
Renyi.1
renyiplot(Renyi.1, evenness=FALSE, addit=FALSE, pch=1,col='1', cex=1,
    legend=FALSE)
## CLICK IN THE GRAPH TO INDICATE WHERE THE LEGEND NEEDS TO BE PLACED
## IN CASE THAT YOU OPT FOR LEGEND=TRUE
```

`residualssurface` *Show and Interpolate Two Dimensional Distribution of Residuals*

Description

This function interpolates the spatial structure of residuals of a GLM through `gam` or `surf.ls` and optionally provides a graph.

Usage

```
residualssurface(model, data, x, y, gam = F, npol = 2, plotit = T, filled = F, bubble = F)
```

Arguments

`model`	Result of GLM as calculated by `glm` or `glm.nb`.
`data`	Data set that contains the spatial coordinates of the sample units used for the original model (specified as "x" and "y").
`x`	Horizontal position of the sample units.
`y`	Vertical position of the sample units.
`gam`	Interpolate the spatial structure by `gam` (if "TRUE") or by `surf.ls` (if "FALSE").
`npol`	Degree of polynomial surface as passed to `surf.ls`.
`plotit`	Plot the interpolated surface (through `interp` and the residuals) .
`filled`	Fill the contours by `filled.contour`.
`bubble`	Provide a bubble graph of the residuals: circles indicate positive residuals, whereas squares indicate negative residuals.

Details

The function reports the results of a GAM or least-squares trend surface analysis of the spatial distribution of residuals of a model (through `residuals`).

Optionally, a graph is produced that can contain the trend surface, filled contours and bubble graphs in addition to the spatial location of the sample units.

Value

The function reports the results of a GAM or least-squares trend surface analysis of the spatial distribution of residuals. Optionally, a graph is provided.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(vegan)
library(mgcv)
library(akima)
data(faramea)
Count.model1 <- lm(Faramea.occidentalis ~ Precipitation,
    data=faramea, na.action=na.exclude)
surface.1 <- residualssurface(Count.model1, na.omit(faramea),
    'UTM.EW', 'UTM.NS', gam=TRUE, plotit=TRUE, bubble=TRUE)
```

---

spatialsample *Spatial Sampling within a Polygon*

Description

Spatial sampling within a polygon provides several methods of selecting rectangular sample plots within a polygon. Using a GIS package may be preferred for actual survey design.

Usage

```
spatialsample(x,method="random",n=5,xwidth=0.5,ywidth=0.5,xleft=0,
    ylower=0,xdist=0,ydist=0,plotit=T,plothull=F)
```

Arguments

x	2-column matrix with the coordinates of the vertices of the polygon. The first column contains the horizontal (x) position, the second column contains the vertical (y) position.
method	Method of sampling, any of "random", "grid" or "random grid".
n	Number of sample plots to be selected, or number of horizontal and vertical grid positions.
xwidth	Horizontal width of the sample plots.
ywidth	Vertical width of the sample plots.
xleft	Horizontal starting position of the grid.
ylower	Vertical starting position of the grid.

xdist	Horizontal distance between grid locations.
ydist	Vertical distance between grid locations.
plotit	Plot the sample plots on the current graph.
plothull	Plot a convex hull around the sample plots.

Details

Spatial sampling within a polygon provides several methods of selecting the position of sample plots.

Method "random" selects random positions of the sample plots using simple random sampling.

Method "grid" selects sample plots from a grid defined by "xleft", "ylower", "xdist" and "ydist". In case `xdist=0` or `ydist=0`, then the number of grid positions are defined by "n". In case "xleft" or "ylower" are below the minimum position of any vertix of the polygon, then a random starting position is selected for the grid.

Method "random grid" selects sample plots at random from the sampling grid using the same methods of defining the grid as for method "grid".

Value

The function returns a list of centres of rectangular sample plots.

Author(s)

Roeland Kindt (World Agroforestry Centre)

References

Kindt, R. & Coe, R. (2005) Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies.

http://www.worldagroforestry.org/output/tree-diversity-analysis

Examples

```
library(splancs)
area <- array(c(10,10,15,35,40,35,5,35,35,30,30,10), dim=c(6,2))
landuse1 <- array(c(10,10,15,15,30,35,35,30), dim=c(4,2))
landuse2 <- array(c(10,10,15,15,35,30,10,30,30,35,30,15), dim=c(6,2))
landuse3 <- array(c(10,10,30,35,40,35,5,10,15,30,30,10), dim=c(6,2))
plot(area[,1], area[,2], type="n", xlab="horizontal position",
    ylab="vertical position", lwd=2, bty="l")
polygon(landuse1)
polygon(landuse2)
polygon(landuse3)
spatialsample(area, method="random", n=20, xwidth=1, ywidth=1, plotit=TRUE,
    plothull=FALSE)
spatialsample(area, method="grid", xwidth=1, ywidth=1, plotit=TRUE, xleft=12,
    ylower=7, xdist=4, ydist=4)
spatialsample(area, method="random grid", n=20, xwidth=1, ywidth=1,
    plotit=TRUE, xleft=12, ylower=7, xdist=4, ydist=4)
```

transfgradient *Gradient for Hypothetical Example of Turover of Species Composition*

Description

This dataset documents the site sequence of 19 sites on a gradient determined from unimodal species distributions. The dataset is accompanied by transfspecies that documents the species composition of the sites. This is a hypothetical example that allows to investigate how well ecological distance measures or ordination methods recover the expected best sequence of sites.

Usage

```
data(transfgradient)
```

Format

A data frame with 19 observations on the following variable.

`gradient` a numeric vector

Source

Legendre, P. & Gallagher, E.D. (2001) Ecologically meaningful transformations for ordination of species data. Oecologia 129: 271-280.

References

Figure 3a.

Examples

```
data(transfspecies)
data(transfgradient)
plot(transfspecies[,1]~transfgradient[,1],xlab="gradient",
    ylab="species abundance",type="n",ylim=c(0.5,8.5))
for (i in 1:9) {points(transfgradient[,1],transfspecies[,i],type="o",pch=i)}
```

transfspecies *Hypothetical Example of Turover of Species Composition*

Description

This dataset documents the species composition of 19 sites that follow a specific sequence of sites as determined from unimodal species distributions. The dataset is accompanied by transfgradient that documents the gradient in species turnover. This is a hypothetical example that allows to investigate how well ecological distance measures or ordination methods recover the expected best sequence of sites.

Usage

```
data(transfspecies)
```

Format

A data frame with 19 observations on the following 9 variables.

`species1` a numeric vector

`species2` a numeric vector

`species3` a numeric vector

`species4` a numeric vector

`species5` a numeric vector

`species6` a numeric vector

`species7` a numeric vector

`species8` a numeric vector

`species9` a numeric vector

Details

The example in the Tree Diversity Analysis manual only looks at the ecological distance from the first site. Hence, only the first 10 sites that share some species with this site should be selected.

This dataset enables investigations of how well ecological distance measures and ordination diagrams reconstruct the gradient (sequence of sites). The gradient expresses how the sites would be arranged based on their species composition.

Source

Legendre, P. & Gallagher, E.D. (2001) Ecologically meaningful transformations for ordination of species data. Oecologia 129: 271-280.

References

Figure 3a.

Examples

```
data(transfspecies)
data(transfgradient)
plot(transfspecies[,1]~transfgradient[,1],xlab="gradient",
    ylab="species abundance",type="n",ylim=c(0.5,8.5))
for (i in 1:9) {points(transfgradient[,1],transfspecies[,i],type="o",pch=i)}
```

warcom *Warburgia ugandensis AFLP Scores*

Description

This data set contains scores for 185 loci for 100 individuals of the Warburgia ugandensis tree species (a medicinal tree species native to Eastern Africa). Since the data set is a subset of a larger data set that originated from a study of several Warburgia species, some of the loci did not produce bands for W. ugandensis (i.e. some loci only contain zeroes). This data set is accompanied by warenv that describes population and regional structure of the 100 individuals.

Usage

```
data(warcom)
```

Format

A data frame with 100 observations on the following 185 variables.

locus001 a numeric vector

locus002 a numeric vector

locus003 a numeric vector

locus004 a numeric vector

locus005 a numeric vector

locus006 a numeric vector

locus007 a numeric vector

locus008 a numeric vector

locus009 a numeric vector

locus010 a numeric vector

locus011 a numeric vector

locus012 a numeric vector

locus013 a numeric vector

locus014 a numeric vector

locus015 a numeric vector

locus016 a numeric vector

locus017 a numeric vector

locus018 a numeric vector

locus019 a numeric vector

locus020 a numeric vector

locus021 a numeric vector

locus022 a numeric vector

`locus023` a numeric vector
`locus024` a numeric vector
`locus025` a numeric vector
`locus026` a numeric vector
`locus027` a numeric vector
`locus028` a numeric vector
`locus029` a numeric vector
`locus030` a numeric vector
`locus031` a numeric vector
`locus032` a numeric vector
`locus033` a numeric vector
`locus034` a numeric vector
`locus035` a numeric vector
`locus036` a numeric vector
`locus037` a numeric vector
`locus038` a numeric vector
`locus039` a numeric vector
`locus040` a numeric vector
`locus041` a numeric vector
`locus042` a numeric vector
`locus043` a numeric vector
`locus044` a numeric vector
`locus045` a numeric vector
`locus046` a numeric vector
`locus047` a numeric vector
`locus048` a numeric vector
`locus049` a numeric vector
`locus050` a numeric vector
`locus051` a numeric vector
`locus052` a numeric vector
`locus053` a numeric vector
`locus054` a numeric vector
`locus055` a numeric vector
`locus056` a numeric vector
`locus057` a numeric vector
`locus058` a numeric vector
`locus059` a numeric vector

`locus060` a numeric vector

`locus061` a numeric vector

`locus062` a numeric vector

`locus063` a numeric vector

`locus064` a numeric vector

`locus065` a numeric vector

`locus066` a numeric vector

`locus067` a numeric vector

`locus068` a numeric vector

`locus069` a numeric vector

`locus070` a numeric vector

`locus071` a numeric vector

`locus072` a numeric vector

`locus073` a numeric vector

`locus074` a numeric vector

`locus075` a numeric vector

`locus076` a numeric vector

`locus077` a numeric vector

`locus078` a numeric vector

`locus079` a numeric vector

`locus080` a numeric vector

`locus081` a numeric vector

`locus082` a numeric vector

`locus083` a numeric vector

`locus084` a numeric vector

`locus085` a numeric vector

`locus086` a numeric vector

`locus087` a numeric vector

`locus088` a numeric vector

`locus089` a numeric vector

`locus090` a numeric vector

`locus091` a numeric vector

`locus092` a numeric vector

`locus093` a numeric vector

`locus094` a numeric vector

`locus095` a numeric vector

`locus096` a numeric vector

locus097 a numeric vector
locus098 a numeric vector
locus099 a numeric vector
locus100 a numeric vector
locus101 a numeric vector
locus102 a numeric vector
locus103 a numeric vector
locus104 a numeric vector
locus105 a numeric vector
locus106 a numeric vector
locus107 a numeric vector
locus108 a numeric vector
locus109 a numeric vector
locus110 a numeric vector
locus111 a numeric vector
locus112 a numeric vector
locus113 a numeric vector
locus114 a numeric vector
locus115 a numeric vector
locus116 a numeric vector
locus117 a numeric vector
locus118 a numeric vector
locus119 a numeric vector
locus120 a numeric vector
locus121 a numeric vector
locus122 a numeric vector
locus123 a numeric vector
locus124 a numeric vector
locus125 a numeric vector
locus126 a numeric vector
locus127 a numeric vector
locus128 a numeric vector
locus129 a numeric vector
locus130 a numeric vector
locus131 a numeric vector
locus132 a numeric vector
locus133 a numeric vector

locus134 a numeric vector
locus135 a numeric vector
locus136 a numeric vector
locus137 a numeric vector
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locus141 a numeric vector
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locus143 a numeric vector
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locus145 a numeric vector
locus146 a numeric vector
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locus148 a numeric vector
locus149 a numeric vector
locus150 a numeric vector
locus151 a numeric vector
locus152 a numeric vector
locus153 a numeric vector
locus154 a numeric vector
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locus156 a numeric vector
locus157 a numeric vector
locus158 a numeric vector
locus159 a numeric vector
locus160 a numeric vector
locus161 a numeric vector
locus162 a numeric vector
locus163 a numeric vector
locus164 a numeric vector
locus165 a numeric vector
locus166 a numeric vector
locus167 a numeric vector
locus168 a numeric vector
locus169 a numeric vector
locus170 a numeric vector

locus171 a numeric vector

locus172 a numeric vector

locus173 a numeric vector

locus174 a numeric vector

locus175 a numeric vector

locus176 a numeric vector

locus177 a numeric vector

locus178 a numeric vector

locus179 a numeric vector

locus180 a numeric vector

locus181 a numeric vector

locus182 a numeric vector

locus183 a numeric vector

locus184 a numeric vector

locus185 a numeric vector

Source

Muchugi, A.N. (2007) Population genetics and taxonomy of important medicinal tree species of the genus Warburgia. PhD Thesis. Kenyatta University, Kenya.

Examples

```
data(warcom)
```

---

warenv *Warburgia ugandensis Population Structure*

Description

This data set contains population and regional locations for 100 individuals of the Warburgia ugandensis tree species (a medicinal tree species native to Eastern Africa). This data set is associated with warcom that contains scores for 185 AFLP loci.

Usage

```
data(warenv)
```

Format

A data frame with 100 observations on the following 4 variables.

population a factor with levels Kibale Kitale Laikipia Lushoto Mara

popshort a factor with levels KKIT KLAI KMAR TLUS UKIB

country a factor with levels Kenya Tanzania Uganda

rift.valley a factor with levels east west

Source

Muchugi, A.N. (2007) Population genetics and taxonomy of important medicinal tree species of the genus Warburgia. PhD Thesis. Kenyatta University, Kenya.

Examples

```
data(warenv)
```

Index