

Package ‘ENMeval’

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Type Package

Title Automated runs and evaluations of ecological niche models

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Description Automatically partitions data into evaluation bins, executes ecological niche models across a range of settings, and calculates a variety of evaluation statistics. Current version only implements ENMs with Maxent (Phillips et al. 2006).

License GPL

Depends dismo, raster, rJava (>= 0.5-0), methods, R (>= 2.10)

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Description

Automatically partitions data into bins for model training and testing, executes ecological niche models (ENMs) across a range of user-defined settings, and calculates evaluation metrics to help achieve a balance between goodness-of-fit and model complexity.

Details

Package: ENMeval
Type: Package
Version: 0.1.0
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License: GNU 3.0

The **ENMeval** package (1) automatically partitions data into training and testing bins using one of six methods (including several options for spatially independent partitions as well as user-defined bins), (2) executes a series of ENMs using Maxent (Phillips *et al.* 2006) with a variety of user-defined settings (i.e., feature classes and regularization multipliers), conducting k -fold cross validation, and (3) calculates multiple evaluation metrics to aid in selecting model settings that balance model goodness-of-fit and complexity (i.e., "model tuning" or "smoothing").

`ENMevaluate` is the primary function of the **ENMeval** package, and multiple other functions highlighted below are called when it is run. The six options for partitioning occurrence data into training and testing (i.e., calibration and evaluation) bins are: $n-1$ jackknife, random k -fold, user-specified bins, and three explicit methods of masked geographically structured k -fold partitioning (see: `get.evaluation.bins`). After model training, these bins are used to calculate five metrics of model performance for each combination of settings: model discrimination (AUC of test localities), the difference between training and testing AUC, two different threshold-based omission rates, and the small sample-size corrected version of the Akaike information criterion (AICc), the latter using the unpartitioned dataset. A model prediction (as a raster layer) using the full (unpartitioned) dataset is generated for each combination of feature class and regularization multiplier settings. Similarity of these models in geographic space (i.e., "niche overlap") can be calculated to better understand how model settings change predictions (see `calc.niche.overlap`). The results of `ENMevaluate` are returned as an object of class `ENMevaluation-class`. A basic plotting function (`eval.plot`) can be used to visualize how evaluation metrics depend on model settings.

Note

Currently, **ENMeval** only implements the Maxent algorithm, but we eventually plan to expand it to work with other algorithms. All calculations are based on the raw Maxent output (i.e., *not* logistic or cumulative transformations) and users can choose whether to use 'clamping' (see Maxent documentation for details on this option). Additionally, Maxent models are run with the arguments:

noaddsamplestobackground and noremoveDuplicates. Users should consult Maxent documentation (Phillips *et al.* 2006) and other references (e.g., Phillips and Dudik 2008) for more information on these options. We note that interested users can edit the source code of ENMeval (in particular, the `make.args` and `tuning` functions) if they desire to change these or other options.

ENMevaluate directly uses several functions from the **dismo** package (Hijmans *et al.* 2011), the most important of which is the `maxent` function that runs the Maxent algorithm (Phillips *et al.* 2006) in Java. Before running this command, the user must first download Maxent from [this website](#). Then, place the file 'maxent.jar' in the 'java' folder of the **dismo** package. The user can locate that folder by typing: `system.file("java", package="dismo")`. For additional details, users should consult the documentation of the **dismo** package.

Author(s)

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References

Hijmans, R. J., Phillips, S., Leathwick, J. and Elith, J. 2011. dismo package for R. Available online at: <http://cran.r-project.org/web/packages/dismo/index.html>.

Phillips, S. J., Anderson, R. P., and Schapire, R. E. 2006. Maximum entropy modeling of species geographic distributions. *Ecological Modelling*, **190**: 231-259.

Phillips, S. J., and Dudik, M. 2008. Modeling of species distributions with Maxent: new extensions and a comprehensive evaluation. *Ecography*, **31**: 161-175.

See Also

maxent in the **dismo** package

calc.aicc

Calculate AICc from Maxent model prediction

Description

This function calculates AICc for Maxent models based on Warren and Seifert (2011).

Usage

```
calc.aicc(nparam, occ, predictive.maps)
```

```
get.params(model)
```

Arguments

nparam	The number of parameters in a model calculated with the <code>get.params</code> function.
occ	A <code>data.frame</code> of occurrence localities.
predictive.maps	A raster layer or <code>RasterStack</code> of predicted model surface(s).
model	A Maxent model object generated by the <code>maxent</code> function in the dismo package.

Details

As motivated by Warren and Seifert (2011) and implemented in ENMTools (Warren *et al.* 2010), this function calculates the small sample size version of Akaike Information Criterion for ENMs (Akaike 1974). We use AICc (instead of AIC) regardless of sample size based on the recommendation of Burnham and Anderson (1998, 2004). The number of parameters is determined by counting the number of non-zero parameters in the `maxent` lambda file. See Warren *et al.* (2014) for limitations of this approach, namely that the number of parameters is an estimate of the true degrees of freedom. For Maxent ENMs, AICc is calculated by standardizing the raw output such that all cells in the study extent sum to 1. The likelihood of the data for a given model is then calculated by taking the product of the raw output values for all grid cells that contain an occurrence locality (Warren and Seifert 2011).

Value

A `data.frame` with four columns:

AICc is the Akaike Information Criterion corrected for small sample sizes calculated as:

$$(2 * K - 2 * \logLikelihood) + (2 * K) * (K + 1) / (n - K - 1)$$

where K is the number of parameters in the model (i.e., number of non-zero parameters in Maxent lambda file) and n is the number of occurrence localities. The *logLikelihood* is calculated as:

$$\text{sum}(\log(\text{vals}/\text{total}))$$

where *vals* is a vector of Maxent raw values at occurrence localities and *total* is the sum of Maxent raw values across the entire study area.

`delta.AICc` is the difference between the AICc of a given model and the AICc of the model with the lowest AICc.

`w.AICc` is the Akaike weight (calculated as the relative likelihood of a model ($\exp(-0.5 * \text{delta.AICc})$) divided by the sum of the likelihood values of all models included in a run. These can be used for model averaging (Burnham and Anderson 2002).

`nparam` is the number of parameters in a Maxent model (number of non-zero parameters in the lambda file) and is used internally during a call of `calc.aicc` by `get.params`.

Note

Returns all NAs if the number of parameters is larger than the number of observations (occurrence localities).

This function could produce erroneous results in version 0.1.0. when calculating AICc on multiple models simultaneously. This problem has been addressed in version 0.1.1.

Author(s)

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References

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- Warren, D. L., Glor, R. E, and Turelli, M. (2010) ENMTools: a toolbox for comparative studies of environmental niche models. *Ecography*, **33**: 607-611.
- Warren, D. L. and Seifert, S. N. (2011) Ecological niche modeling in Maxent: the importance of model complexity and the performance of model selection criteria. *Ecological Applications*, **21**: 335-342.
- Warren, D. L., Wright, A. N., Seifert, S. N., and Shaffer, H. B. (2014) Incorporating model complexity and sampling bias into ecological niche models of climate change risks faced by 90 California vertebrate species of concern. *Diversity and Distributions*, **20**: 334-343.

See Also

maxent in the **dismo** package.

calc.niche.overlap *Calculate Similarity of ENMs in Geographic Space*

Description

Compute pairwise "niche overlap" in geographic space for Maxent predictions. The value ranges from 0 (no overlap) to 1 (identical predictions). The function uses the nicheOverlap function of the **dismo** package (Hijmans *et al.* 2011).

Usage

```
calc.niche.overlap(predictive.maps, stat = "D", maxent.args)
```

Arguments

- | | |
|-----------------|---|
| predictive.maps | A rasterStack of at least 2 Maxent predictive raster layers. |
| stat | The statistic calculated by the nicheOverlap function of the dismo package. Defaults to Schoener's <i>D</i> (Schoener 1968) but can also accept "I" to calculate the <i>I</i> similarity statistic from Warren <i>et al.</i> (2008). |
| maxent.args | A list of (1) feature classes, and (2) regularization multiplier values that describe model settings for each predictive map provided in predictive.maps. This is generated by the function <code>make.args(..., labels=TRUE)</code> . |

Value

A matrix with the lower triangle giving values of pairwise "niche overlap" in geographic space. Row and column names are given by the `make.args` argument when run by the `ENMevaluate` function.

Author(s)

Based on `dismo::nicheOverlap`, which is based on `SDMTools::Istat`
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References

Hijmans, R. J., Phillips, S., Leathwick, J. and Elith, J. (2011) `dismo` package for R. Available online at: <http://cran.r-project.org/web/packages/dismo/index.html>.

Schoener, T. W. (1968) The *Anolis* lizards of Bimini: resource partitioning in a complex fauna. *Ecology*, **49**: 704-726.

Warren, D. L., Glor, R. E., Turelli, M. and Funk, D. (2008) Environmental niche equivalency versus conservatism: quantitative approaches to niche evolution. *Evolution*, **62**: 2868-2883.

See Also

[make.args](#); `nicheOverlap` in the `dismo` package

corrected.var	<i>Calculate variance corrected for non-independence of k-fold iterations</i>
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Description

This function calculates variance corrected for non-independence of k -fold iterations. See Appendix of Shcheglovitova & Anderson (2013) and other references (Miller 1974; Parr 1985; Shao and Wu 1989) for additional details.

Usage

```
corrected.var(x, nk)
```

Arguments

<code>x</code>	A numeric vector.
<code>nk</code>	Number of k -fold iterations.

Details

This function calculates variance that is corrected for the non-independence of k cross-validation iterations. Following Shao and Wu (1989):

$$SumOfSquares * ((n - 1)/n)$$

where n = the number of k -fold iterations.

Value

A numeric value of the corrected variance.

Author(s)

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References

Miller, R. G. (1974) The jackknife - a review. *Biometrika*, **61**: 1-15.

Parr, W. C. (1985) Jackknifing differentiable statistical functionals. *Journal of the Royal Statistics Society, Series B*, **47**: 56-66.

Shao J. and Wu, C. F. J. (1989) A general theory for jackknife variance estimation. *Annals of Statistics*, **17**: 1176-1197.

Shcheglovitova, M. and Anderson, R. P. (2013) Estimating optimal complexity for ecological niche models: a jackknife approach for species with small sample sizes. *Ecological Modelling*, **269**: 9-17.

ENMevaluate

Tuning and evaluation of ENMs with Maxent

Description

ENMevaluate automatically executes Maxent (Phillips *et al.* 2006; Phillips and Dudik 2008) across a range of settings, returning a data.frame of evaluation metrics to aid in identifying settings that balance model fit and predictive ability. The function calls Maxent using the maxent function in the **dismo** package (Hijmans *et al.* 2011). Users should consult [ENMeval-package](#) and help documentation of the **dismo** package for guidelines on how to run Maxent in R.

Usage

```
ENMevaluate(occ, env, bg.coords = NULL, occ.grp = NULL,
            bg.grp = NULL, RMvalues = seq(0.5, 4, 0.5),
            fc = c("L", "LQ", "H", "LQH", "LQHP", "LQHPT"),
            categoricals = NULL, n.bg = 10000, method = NULL,
            overlap = FALSE, aggregation.factor = c(2, 2),
            kfolds = NA, bin.output = FALSE, clamp = TRUE)
```

```
tuning(occ, env, bg.coords, occ.grp, bg.grp, method,
      maxent.args, args.lab, categoricals, aggregation.factor,
      kfolds, bin.output, clamp)
```

Arguments

<code>occ</code>	Two-column matrix or data.frame of longitude and latitude (in that order) of occurrence localities.
<code>env</code>	RasterStack of model predictor variables (environmental layers).
<code>bg.coords</code>	Two-column matrix or data.frame of longitude and latitude (in that order) of background localities (required for 'user' method).
<code>occ.grp</code>	Vector of bins of occurrence localities (required for 'user' method).
<code>bg.grp</code>	Vector of bins of background localities (required for 'user' method).
<code>RMvalues</code>	Vector of (non-negative) values to use for the regularization multiplier.
<code>fc</code>	Character vector of feature class combinations to be included in analysis.
<code>categoricals</code>	Vector indicating which (if any) of the input environmental layers are categorical.
<code>n.bg</code>	The number of random background localities to draw from the study extent.
<code>method</code>	Character string designating the method used for data partitioning. Choices are: "jackknife", "randomkfold", "user", "block", "checkerboard1", "checkerboard2". See details and get.evaluation.bins for more information.
<code>overlap</code>	logical; If TRUE, provides pairwise metric of niche overlap (see details and calc.niche.overlap).
<code>aggregation.factor</code>	List giving the factor by which the original input grid should be aggregated for checkerboard partitioning methods (see details and get.evaluation.bins).
<code>kfolds</code>	Number of bins to use in the <i>k</i> -fold random method of data partitioning.
<code>bin.output</code>	logical; If TRUE, appends evaluations metrics for each evaluation bin to results table (i.e., in addition to the average values across bins).
<code>maxent.args</code>	Arguments to pass to Maxent that are generated by the <code>make.args</code> function
<code>args.lab</code>	Character labels describing feature classes and regularization multiplier values for Maxent runs provided by the <code>make.args</code> function.
<code>clamp</code>	logical; If TRUE, 'clamping' is used (see Maxent documentation and tutorial for more details).

Details

ENMevaluate is the primary function for general use in the **ENMeval** package; the tuning function is used internally.

Maxent settings: In the current default implementation of Maxent, the combination of feature classes (*fcs*) allowed depends on the number of occurrence localities, and the value for the regularization multiplier (*RM*) is 1.0. ENMevaluate provides an automated way to execute ecological niche models in Maxent across a user-specified range of (*RM*) values and (*fc*) combinations, regardless of sample size. Acceptable values for the *fc* argument include: L=linear, Q=quadratic, P=product, T=threshold, and H=hinge (see Maxent help documentation, Phillips *et al.* (2006), Phillips and Dudik (2008), Elith *et al.* (2011), and Merow *et al.* (2013) for additional details on *RM* and *fcs*). Categorical feature classes (*C*) are specified by the `categoricals` argument.

Methods for partitioning data: ENMevaluate includes six methods to partition occurrence and background localities into bins for training and testing ('jackknife', 'randomkfold', 'user', 'block', 'checkerboard1', 'checkerboard2'). The jackknife method is a special case of k -fold cross validation where the number of folds (k) is equal to the number of occurrence localities (n) in the dataset. The randomkfold method partitions occurrence localities randomly into a user-specified number of (k) bins - this is equivalent to the method of k -fold cross validation currently provided by Maxent. The user method enables users to define bins *a priori*. For this method, the user is required to provide background coordinates (bg.coords) and bin designations for both occurrence localities (occ.grp) and background localities (bg.grp). The block method partitions the data into four bins according to the lines of latitude and longitude that divide the occurrence localities into bins of as equal number as possible. The checkerboard1 (and checkerboard2) methods partition data into two (or four) bins based on one (or two) checkerboard patterns with grain size defined as one (or two) aggregation factor(s) of the original environmental layers. Although the checkerboard1 (and checkerboard2) methods are designed to partition occurrence localities into two (and four) evaluation bins, they may give fewer bins depending on the location of occurrence localities with respect to the checkerboard grid(s) (e.g., all records happen to fall in the "black" squares). A warning is given if the number of bins is < 4 for the checkerboard2 method, and an error is given if all localities fall in a single evaluation bin. Additional details can be found in `get.evaluation.bins`.

Evaluation metrics: Four evaluation metrics are calculated using the partitioned dataset, and one additional metric is provided based on the full dataset. ENMevaluate uses the same background localities and evaluation bin designations for each of the k iterations (for each unique combination of RM and fc) to facilitate valid comparisons among model settings.

Mean.AUC is the area under the curve of the receiver operating characteristic plot made based on the testing data (i.e., AUCtest), averaged across k bins. In each iteration, as currently implemented, the AUCtest value is calculated with respect to the full set of background localities to enable comparisons across the k iterations (Radosavljevic and Anderson 2014). As a relative measure for a given study species and region, high values of Mean.AUC are associated with the degree to which a model can successfully discriminate occurrence from background localities. This rank-based non-parametric metric, however, does not reveal the model goodness-of-fit (Lobo *et al.* 2008; Peterson *et al.* 2011).

To quantify the degree of overfitting, ENMevaluate calculates three metrics. The first is the difference between training and testing AUC, averaged across k bins (Mean.AUC.DIFF) (Warren and Seifert 2011). Mean.AUC.DIFF is expected to be high for models overfit to the training data. ENMevaluate also calculates two threshold-dependent omission rates that quantify overfitting when compared with the omission rate expected by the threshold employed: the proportion of testing localities with Maxent output values lower than the value associated with (1) the training locality with the lowest value (i.e., the minimum training presence, MTP; = 0 percent training omission) (Mean.ORmin) and (2) the value that excludes the 10 percent of training localities with the lowest predicted suitability (Mean.OR10) (Pearson *et al.* 2007). ENMevaluate uses `corrected.var` to calculate the variance for each of these metrics across k bins (i.e., variances are corrected for non-independence of cross-validation iterations; see Shcheglovitova and Anderson 2013). The value of these metrics for each of the individual k bins is returned if `bin.output = TRUE`.

Based on the unpartitioned (full) dataset, ENMevaluate uses `calc.aicc` to calculate the AICc value for each model run and provides delta.AIC, AICc weights, as well as the number of parameters for each model (Warren and Seifert 2011). The AUCtrain value for the full model is also returned (`full.AUC`).

To quantify how resulting predictions differ in geographic space depending on the settings used,

ENMevaluate includes an option to compute pairwise niche overlap between all pairs of full models (i.e., using the unpartitioned dataset) with Schoener's D statistic (Schoener 1968; Warren *et al.* 2009).

Value

An object of class ENMevaluation with named slots:

@results data.frame of evaluation metrics. If bin.output=TRUE, evaluation metrics calculated separately for each evaluation bin are included in addition to the averages across k bins.

@predictions RasterStack of full model predictions with each layer named as: fc_RM (e.g., L_1).

@partition.method character vector with the method used for data partitioning.

@occ.pts data.frame of the latitude/longitude of input occurrence localities.

@occ.grp vector identifying the bin for each occurrence locality.

@bg.pts data.frame of the latitude/longitude of input background localities.

@bg.grp vector identifying the bin for each background locality.

@overlap matrix of pairwise niche overlap (blank if overlap = FALSE).

Author(s)

Uses the maxent function in the **dismo** package (Hijmans *et al.* 2011, Phillips *et al.* 2006)

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References

- Elith, J., Phillips, S. J., Hastie, T., Dudik, M., Chee, Y. E., and Yates, C. J. (2011) A statistical explanation of MaxEnt for ecologists. *Diversity and Distributions*, **17**: 43-57.
- Hijmans, R. J., Phillips, S., Leathwick, J. and Elith, J. (2011) dismo package for R. Available online at: <http://cran.r-project.org/web/packages/dismo/index.html>.
- Lobo, J. M., Jimenez-Valverde, A., and Real, R. (2008) AUC: A misleading measure of the performance of predictive distribution models. *Global Ecology and Biogeography*, **17**: 145-151.
- Pearson, R. G., Raxworthy, C. J., Nakamura, M. and Peterson, A. T. 2007. Predicting species distributions from small numbers of occurrence records: a test case using cryptic geckos in Madagascar. *Journal of Biogeography*, **34**: 102-117.
- Peterson, A. T., Soberon, J., Pearson, R. G., Anderson, R. P., Martinez-Meyer, E., Nakamura, M. and Araujo, M. B. (2011) *Ecological Niches and Geographic Distributions*. Monographs in Population Biology, 49. Princeton University Press, Princeton, NJ.
- Phillips, S. J., Anderson, R. P., and Schapire, R. E. (2006) Maximum entropy modeling of species geographic distributions. *Ecological Modelling*, **190**: 231-259.
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- Merow, C., Smith, M., and Silander, J. A. (2013) A practical guide to Maxent: what it does, and why inputs and settings matter. *Ecography*, **36**: 1-12.
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Schoener, T. W. (1968) The *Anolis* lizards of Bimini: resource partitioning in a complex fauna. *Ecology*, **49**: 704-726.

Shcheglovitova, M. and Anderson, R. P. (2013) Estimating optimal complexity for ecological niche models: A jackknife approach for species with small sample sizes. *Ecological Modelling*, **269**: 9-17.

Warren, D. L., Glor, R. E., Turelli, M. and Funk, D. (2009) Environmental niche equivalency versus conservatism: quantitative approaches to niche evolution. *Evolution*, **62**: 2868-2883; *Erratum: Evolution*, **65**: 1215.

Warren, D.L. and Seifert, S.N. (2011) Ecological niche modeling in Maxent: the importance of model complexity and the performance of model selection criteria. *Ecological Applications*, **21**: 335-342.

See Also

maxent in the **dismo** package

Examples

```
### Simulated data environmental covariates
set.seed(1)
r1 <- raster(matrix(nrow=50, ncol=50, data=runif(10000, 0, 25)))
r2 <- raster(matrix(nrow=50, ncol=50, data=rep(1:100, each=100), byrow=TRUE))
r3 <- raster(matrix(nrow=50, ncol=50, data=rep(1:100, each=100)))
r4 <- raster(matrix(nrow=50, ncol=50, data=c(rep(1,1000),rep(2,500)),byrow=TRUE))
values(r4) <- as.factor(values(r4))
env <- stack(r1,r2,r3,r4)

### Simulate occurrence localities
nocc <- 50
x <- (rpois(nocc, 2) + abs(rnorm(nocc)))/11
y <- runif(nocc, 0, .99)
occ <- cbind(x,y)

## Not run:
### This call gives the results loaded below
enmeval_results <- ENMevaluate(occ, env, method="block", n.bg=500, overlap=TRUE,
bin.output=TRUE, clamp=TRUE)

## End(Not run)

data(enmeval_results)
enmeval_results

### See table of evaluation metrics
enmeval_results@results

### Plot prediction with lowest AICc
plot(enmeval_results@predictions[[which (enmeval_results@results$delta.AICc == 0) ]])
points(enmeval_results@occ.pts, pch=21, bg=enmeval_results@occ.grp)

### Niche overlap statistics between model predictions
```

enmeval_results@overlap

ENMevaluation-class *Class "ENMevaluation"*

Description

Objects of this class are generated by a call of [ENMevaluate](#).

Objects from the Class

Objects can be created by calls of the form `new("ENMevaluation", ...)`.

Slots

results: Object of class "data.frame" ~~
predictions: Object of class "RasterStack" ~~
partition.method: Object of class "character" ~~
occ.pts: Object of class "data.frame" ~~
occ.grp: Object of class "numeric" ~~
bg.pts: Object of class "data.frame" ~~
bg.grp: Object of class "numeric" ~~
overlap: Object of class "matrix" ~~

Author(s)

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Examples

```
showClass("ENMevaluation")
```

enmeval_results *An object of class "ENMEvaluation"*

Description

An example results file based on a call of ENMEvaluate (see example).

Usage

```
data(enmeval_results)
```

Format

An object of class 'ENMEvaluation' with eight slots:

- @ results : data.frame of evaluation metrics
- @ predictions : RasterStack of model predictions
- @ partition.method: character giving method of data partitioning
- @ occ.pts : data.frame of latitude and longitude of occurrence localities
- @ occ.grp : data.frame of bins for occurrence localities
- @ bg.pts : data.frame of latitude and longitude of background localities
- @ bg.grp : data.frame of bins for background localities
- @ overlap : matrix of pairwise niche overlap

Details

The dataset is based on the simulated dataset and call of [ENMEvaluate](#) shown in the example section below.

Examples

```
### Simulated data environmental covariates
set.seed(1)
r1 <- raster(matrix(nrow=50, ncol=50, data=runif(10000, 0, 25)))
r2 <- raster(matrix(nrow=50, ncol=50, data=rep(1:100, each=100), byrow=TRUE))
r3 <- raster(matrix(nrow=50, ncol=50, data=rep(1:100, each=100)))
r4 <- raster(matrix(nrow=50, ncol=50, data=c(rep(1,1000),rep(2,500)),byrow=TRUE))
values(r4) <- as.factor(values(r4))
env <- stack(r1,r2,r3,r4)

### Simulate occurrence localities
nocc <- 50
x <- (rpois(nocc, 2) + abs(rnorm(nocc)))/11
y <- runif(nocc, 0, .99)
occ <- cbind(x,y)

## Not run:
```

```

### This gives the results that are loaded below:

enmeval_results <- ENMevaluate(occ, env, method='block', n.bg=500,
RMvalues=c(0.1, 1, 5), fc=c('L','LQ','LQP'), overlap=TRUE, clamp=T)
## End(Not run)

data(enmeval_results)
enmeval_results

### See table of evaluation metrics
enmeval_results@results

### Plot prediction with lowest AICc
plot(enmeval_results@predictions[[which (enmeval_results@results$delta.AICc == 0) ]])
points(enmeval_results@occ.pts, pch=21, bg= enmeval_results@occ.grp)

### Niche overlap statistics between model predictions
enmeval_results@overlap

```

eval.plot

Generate Basic Plot for ENMevaluate Output

Description

This function can be used to generate a basic plot of evaluation metrics generated by a call of [ENMevaluate](#).

Usage

```
eval.plot(results, value = "delta.AICc", variance = NULL, legend = TRUE,
legend.position = "topright")
```

Arguments

results	A data.frame of results from ENMevaluate .
value	Character string of the column of results to use for plotting.
variance	Character string of the column of results to be used for error bars.
legend	logical; If TRUE (default), includes legend in plot with fcs.
legend.position	Character string for the placement of the legend.

Author(s)

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Examples

```

data(enmeval_results)

par(mfrow=c(2,2))
eval.plot(enmeval_results@results, legend.position="topright")
eval.plot(enmeval_results@results, "Mean.AUC", )
eval.plot(enmeval_results@results, "Mean.AUC.DIFF", variance="Var.AUC.DIFF")
eval.plot(enmeval_results@results, "Mean.ORmin")

```

get.evaluation.bins *Methods to partition data for evaluation*

Description

ENMeval provides six methods to partition occurrence and background localities into bins for training and testing (or, evaluation and calibration). Users should carefully consider the objectives of their study and the influence of spatial bias when deciding on a method of data partitioning.

Usage

```

get.block(occ, bg.coords)
get.checkerboard1(occ, env, bg.coords, aggregation.factor)
get.checkerboard2(occ, env, bg.coords, aggregation.factor)
get.jackknife(occ, bg.coords)
get.randomkfold(occ, bg.coords, kfolds)
get.user(occ.grp, bg.grp)

```

Arguments

occ	Two-column matrix or data.frame of longitude and latitude (in that order) of occurrence localities.
bg.coords	Two-column matrix or data.frame of longitude and latitude (in that order) of background localities.
env	RasterStack of environmental predictor variables.
aggregation.factor	A vector or list of 1 or 2 numbers giving the scale for aggregation used for the get.checkerboard1 and get.checkerboard2 methods. If a single number is given and get.checkerboard2 partitioning method is used, the single value is used for both scales of aggregation.
kfolds	Number of random <i>k</i> -folds for get.randomkfold method.
occ.grp	Vector of user-defined bins for occurrence localities for get.user method.
bg.grp	Vector of user-defined bins for background localities for get.user method.

Details

These functions are used internally to partition data during a call of `ENMevaluate`.

The `get.block` method partitions occurrence localities by finding the latitude and longitude that divide the occurrence localities into four groups of (insofar as possible) equal numbers. Background localities are assigned to each of the four groups based on their position with respect to these lines. While the `get.block` method results in (approximately) equal division of occurrence localities among four groups, the number of background localities (and, consequently, environmental and geographic space) in each group depends on the distribution of occurrence localities across the study area.

The `get.checkerboard1` and `get.checkerboard2` methods are variants of a checkerboard approach to partition occurrence localities. These methods use the `gridSample` function of the **dismo** package (Hijmans *et al.* 2011) to partition records according to checkerboard grids across the study extent. The spatial grain of these grids is determined by resampling (or aggregating) the original environmental input grids based on the user-defined aggregation factor (e.g., an aggregation factor of 2 results in a checkerboard with grid cells four times as large in area as the original input grids). The `get.checkerboard1` method partitions data into two groups according to a single checkerboard pattern, and the `get.checkerboard2` method partitions data into four groups according to two nested checkerboard grids. In contrast to the `get.block` method, both the `get.checkerboard1` and `get.checkerboard2` methods subdivide geographic space equally but do not ensure a balanced number of occurrence localities in each group.

The `get.jackknife` method is a special case of k -fold cross validation where the number of bins (k) is equal to the number of occurrence localities (n) in the dataset. It is suggested for datasets of relatively small sample size (generally < 25 localities) (Pearson *et al.* 2007; Shcheglovitova and Anderson 2013).

The `get.randomkfold` method partitions occurrence localities randomly into a user-specified number of (k) bins. This is equivalent to the method of k -fold cross validation currently provided by Maxent.

The `get.user` method is flexible and enables users to define evaluation bins *a priori*. With this method, occurrence and background localities, as well as evaluation bin designation for each locality, are supplied by the user.

Value

A named list of two items:

<code>\$occ.grp</code>	A vector of bin designation for occurrence localities in the same order they were provided.
<code>\$bg.grp</code>	A vector of bin designation for background localities in the same order they were provided.

Note

The `checkerboard1` and `checkerboard2` methods are designed to partition occurrence localities into two and four evaluation bins, respectively. They may give fewer bins, however, depending on where the occurrence localities fall with respect to the grid cells (e.g., all records happen to fall in the "black" squares). A warning is given if the number of bins is < 4 for the `checkerboard2` method, and an error is given if all localities fall into a single evaluation bin.

Author(s)

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References

Hijmans, R. J., Phillips, S., Leathwick, J. and Elith, J. 2011. dismo package for R. Available online at: <http://cran.r-project.org/web/packages/dismo/index.html>.

Pearson, R. G., Raxworthy, C. J., Nakamura, M. and Peterson, A. T. 2007. Predicting species distributions from small numbers of occurrence records: a test case using cryptic geckos in Madagascar. *Journal of Biogeography*, **34**: 102-117.

Shcheglovitova, M. and Anderson, R. P. (2013) Estimating optimal complexity for ecological niche models: a jackknife approach for species with small sample sizes. *Ecological Modelling*, **269**: 9-17.

Examples

```
set.seed(1)

### Create environmental extent (raster)
env <- raster(matrix(nrow=25, ncol=25))

### Create presence localities
set.seed(1)
nocc <- 25
xocc <- rnorm(nocc, sd=0.25) + 0.5
yocc <- runif(nocc, 0, 1)
occ.pts <- as.data.frame(cbind(xocc, yocc))

### Create background points
nbg <- 500
xbg <- runif(nbg, 0, 1)
ybg <- runif(nbg, 0, 1)
bg.pts <- as.data.frame(cbind(xbg, ybg))

### Show points
plot(env)
points(bg.pts)
points(occ.pts, pch=21, bg=2)

### Block partitioning method
blk.pts <- get.block(occ.pts, bg.pts)
plot(env)
points(occ.pts, pch=23, bg=blk.pts$occ.grp)
plot(env)
points(bg.pts, pch=21, bg=blk.pts$bg.grp)

### Checkerboard1 partitioning method
chk1.pts <- get.checkerboard1(occ.pts, env, bg.pts, 4)
plot(env)
points(occ.pts, pch=23, bg=chk1.pts$occ.grp)
plot(env)
```

```

points(bg.pts, pch=21, bg=chk1.pts$bg.grp)

### Checkerboard2 partitioning method
chk2.pts <- get.checkerboard2(occ.pts, env, bg.pts, c(2,2))
plot(env)
points(occ.pts, pch=23, bg=chk2.pts$occ.grp)
plot(env)
points(bg.pts, pch=21, bg=chk2.pts$bg.grp)

### Random k-fold partitions
# Note that k random does not partition the background
krandom.pts <- get.randomkfold(occ.pts, bg.pts, 4)
plot(env)
points(occ.pts, pch=23, bg=krandom.pts$occ.grp)
plot(env)
points(bg.pts, pch=21, bg=krandom.pts$bg.grp)

### k-1 jackknife partitions
# Note background is not partitioned
jack.pts <- get.jackknife(occ.pts, bg.pts)
plot(env)
points(occ.pts, pch=23, bg=rainbow(length(jack.pts$occ.grp)))
plot(env)
points(bg.pts, pch=21, bg=jack.pts$bg.grp)

### User-defined partitions
# Note background is not partitioned
occ.grp <- c(rep(1, 10), rep(2, 5), rep(3, 10))
bg.grp <- c(rep(1, 200), rep(2, 100), rep(3, 200))
user.pts <- get.user(occ.grp, bg.grp)
plot(env)
points(occ.pts, pch=23, bg=user.pts$occ.grp)
plot(env)
points(bg.pts, pch=21, bg=user.pts$bg.grp)

```

make.args

Generate arguments for Maxent

Description

This function generates a list of arguments to pass to Maxent or to use as convenient labels for plotting.

Usage

```

make.args(RMvalues = seq(0.5, 4, 0.5),
fc = c("L", "LQ", "H", "LQH", "LQHP", "LQHPT"),
labels = FALSE)

```

Arguments

RMvalues	Vector of (non-negative) values to use for the regularization multiplier.
fc	Character vector of feature class combinations to be included in analysis.
labels	logical; If FALSE (default), provides arguments to pass directly to Maxent; if TRUE, provides more intuitive labels to use, for example, in plotting.

Details

When labels = FALSE, the following additional arguments are added:

noaddsamplestobackground, noremoveDuplicates, noautofeature.

For details on these arguments, see Phillips *et al.* (2006) and the help documentation and tutorial of the Maxent software and the tutorial that can be downloaded from [this website](#).

Value

If labels = FALSE, a list the length of the total number of unique combinations of feature class(es) and regularization multiplier(s).

If labels = TRUE, a list of two items:

\$	character vector of feature class combinations in the same order they were provided.
\$	numeric vector of regularization multiplier values in the same order they were provided.

Author(s)

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References

Phillips, S. J., Anderson, R. P. and Schapire, R. E. 2006. Maximum entropy modeling of species geographic distributions. *Ecological Modelling*, **190**: 231-259.

See Also

maxent in the **dismo** package.

Examples

```
make.args(RMvalues=c(1:3), fc=c("L", "LQ"))
```

```
make.args(RMvalues=c(1:3), fc=c("L", "LQ"), labels=TRUE)
```

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