

Package ‘vandalico’

September 6, 2024

Type Package

Title Evaluation of Presence-Absence Models

Version 0.1.0

Date 2024-09-06

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Description Collection of functions to evaluate presence-absence models. It comprises functions to adjust discrimination statistics for the representativeness effect through case-weighting, along with functions for visualizing the outcomes. Originally outlined in: Jiménez-Valverde (2022) The uniform AUC: dealing with the representativeness effect in presence-absence models. *Methods Ecol. Evol.*, 13, 1224-1236.

License GPL-3

Imports ROCR (>= 1.0-7), stats, graphics

Depends R (>= 3.5.0)

RoxygenNote 7.1.0

Encoding UTF-8

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-09-06 16:20:02 UTC

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AUCuniform

*Calculates the uniform AUC and uniform Se**

Description

This function computes the uniform *AUC* (*uAUC*) and uniform *Se** (*uSe**) following Jiménez-Valverde (2022).

Usage

```
AUCuniform(
  mat,
  rep = 100,
  by = 0.1,
  deleteBins = NULL,
  plot = FALSE,
  plot.adds = FALSE
)
```

Arguments

<code>mat</code>	A matrix with two columns. The first column must contain the suitability values (i.e., the classification rule); the second column must contain the presences and absences.
<code>rep</code>	Number of sampling replications. By default, <code>rep = 100</code> .
<code>by</code>	Size of the suitability intervals (i.e., bins). By default, <code>by = 0.1</code> .
<code>deleteBins</code>	A vector (e.g., from 1 to 10 if <code>by = 0.1</code>) with the bins that have to be excluded (1 for [0,0.1), 10 for [0.9,1]) from the resampling procedure (trimming); NULL by default.
<code>plot</code>	Logical. Indicates whether or not the observed ROC curve is plotted.
<code>plot.adds</code>	Logical. Indicates whether or not the negative diagonal and the point of equivalence are added to the observed ROC plot.

Details

This function performs the stratified weighted bootstrap to calculate the uniform *AUC* (*uAUC*) and uniform *Se** (*uSe**) as suggested in Jiménez-Valverde (2022). A warning message will be shown if the sample size of any bin is zero. Another warning message will be shown if the sample size of any bin is lower than 15. In such case, trimming should be considered. The *AUC* (non-uniform) is estimated non-parametrically (Bamber 1975). *Se** is calculated by selecting the point that minimizes the absolute difference between sensitivity and specificity and by doing the mean of those values (Jiménez-Valverde 2020).

Value

A list with the following elements:

AUC: the *AUC* value (non-uniform), a numeric value between 0 and 1.

Se: the *Se** value (non-uniform), a numeric value between 0 and 1.

bins: a table with the sample size of each bin.

suit.sim: a matrix with the bootstrapped suitability values.

sp.sim: a matrix with the bootstrapped presence-absence data.

uAUC: a numeric vector with the (*uAUC*) values for each replication.

uAUC.95CI: a numeric vector with the sample (*uAUC*) quantiles corresponding to the probabilities 0.025, 0.5 and 0.975.

uSe: a numeric vector with the (*uSe**) values for each replication.

uSe.95CI: a numeric vector with the sample (*uSe**) quantiles corresponding to the probabilities 0.025, 0.5 and 0.975.

References

Bamber, D. (1975). The Area above the Ordinal Dominance Graph and the Area below the Receiver Operating Characteristic Graph. *J. Math. Psychol.*, 12, 387-415.

Jiménez-Valverde, A. (2020). Sample size for the evaluation of presence-absence models. *Ecol. Indic.*, 114, 106289.

Jiménez-Valverde, A. (2022). The uniform AUC: dealing with the representativeness effect in presence-absence models. *Methods Ecol. Evol.*, 13, 1224-1236.

Examples

```
suit<-rbeta(100, 2, 2) #Generate suitability values
random<-runif(100)
sp<-ifelse(random < suit, 1, 0) #Generate presence-absence data
result<-AUCuniform(cbind(suit, sp), plot = TRUE, plot.adds = TRUE)
result$uAUC.95CI[2] #Get the uAUC
```

AUCuniform_trap

Calculates the uniform AUC and uniform Se by the trapezoidal method.*

Description

This function computes the uniform *AUC* (*uAUC*) and uniform *Se** (*uSe**) using the weighted trapezoidal method instead of the weighted bootstrapping method used in *AUCuniform* and originally proposed in Jiménez-Valverde (2022). This procedure reduces bias and improves the coverage of confidence intervals (Jiménez-Valverde 2024). Additionally, the weights vector associated to each case can be customized. See Jiménez-Valverde (2024) for details.

Usage

```
AUCuniform_trap(
  mat,
  by = 0.1,
  deleteBins = NULL,
  w = NULL,
  plot = FALSE,
  plot.compare = FALSE,
  plot.adds = FALSE
)
```

Arguments

<code>mat</code>	A matrix with two columns. The first column must contain the suitability values (i.e., the classification rule); the second column must contain the presences and absences.
<code>by</code>	Size of the suitability intervals (i.e., bins). By default, <code>by = 0.1</code> .
<code>deleteBins</code>	A vector (e.g., from 1 to 10 if <code>by = 0.1</code>) with the bins that have to be excluded (1 for <code>[0,0.1)</code> , 10 for <code>[0.9,1)</code>) from the calculation of the uniform statistics; <code>NULL</code> by default.
<code>w</code>	A vector with the weights associated to each case. If <code>NULL</code> (default), then the uniform <i>AUC</i> (<i>uAUC</i>) and uniform <i>Se*</i> (<i>uSe*</i>) are calculated.
<code>plot</code>	Logical. Indicates whether or not the observed ROC curve is plotted (gray dots).
<code>plot.compare</code>	Logical. Indicates whether or not the weighed ROC curve is plotted (black line).
<code>plot.adds</code>	Logical. Indicates whether or not the negative diagonal and the points of equivalence (weighted and unweighted) are added to the ROC plot.

Details

This function calculates the uniform *AUC* (*uAUC*) and uniform *Se** (*uSe**) using the weighted trapezoidal method as suggested in Jiménez-Valverde (2024). A warning message will be shown if the sample size of any bin is zero. Another warning message will be shown if the sample size of any bin is lower than 15. In such case, trimming should be considered using `deleteBins` (Jiménez-Valverde 2022). Alternatively, the weights associated to each case can be fully customized with the `w` parameter (Jiménez-Valverde 2024). In this case, no warnings regarding sample size issues are raised, and `deleteBins` is not used. The *AUC* (non-uniform, unweighted) is estimated non-parametrically by the trapezoidal rule, which is equivalent to the Wilcoxon-based estimation (Hanley & McNeil 1982) used in `AUCuniform`. *Se** is calculated as in `AUCuniform`.

Value

A list with the following elements:

`AUC`: the *AUC* value (non-uniform, unweighted), a numeric value between 0 and 1.

`Se`: the *Se** value (non-uniform, unweighted), a numeric value between 0 and 1.

`bins`: a table with the sample size of each bin (only if `w = NULL`).

`uAUC`: the uniform *AUC* value (only if `w = NULL`).

uSe: the uniform Se^* value (only if $w = \text{NULL}$).
 wAUC: the weighted AUC estimated with the vector w
 wSe: the weighted Se^* estimated with the vector w

References

Hanley, J. A. & McNeil, B. J. (1982). The Meaning and Use of the Area under a Receiver Operating Characteristic (ROC) Curve. *Radiology.*, 143, 29-36.

Jiménez-Valverde, A. (2022). The uniform AUC: dealing with the representativeness effect in presence-absence models. *Methods Ecol. Evol.*, 13, 1224-1236.

Jiménez-Valverde, A. (2024). Improving the uniform AUC (uAUC): towards a case-by-case weighting evaluation in species distribution models. *In preparation.*

Examples

```
suit<-rbeta(100, 2, 2) #Generate suitability values
random<-runif(100)
sp<-ifelse(random < suit, 1, 0) #Generate presence-absence data
result<-AUCuniform_trap(cbind(suit, sp), plot = TRUE, plot.compare = TRUE)
result$AUC #Get the AUC
result$uAUC #Get the uAUC. Note how it is closer to the reference value of
#0.83 since the suitability values are simulated to be
#well-calibrated (see Jimenez-Valverde 2022).
```

CALplot

Calibration graph

Description

A function to plot a calibration graph.

Usage

```
CALplot(mat, by = 0.1)
```

Arguments

mat	A matrix with two columns. The first column must contain the suitability values (i.e., the classification rule); the second column must contain the presences and absences.
by	Size of the suitability intervals (bins). By default, by = 0.1.

Details

Dots for bins with 15 or more cases are shown in solid black; dots for bins with less than 15 cases are shown empty (see Jiménez-Valverde et al. 2013). This way, by plotting the calibration graph before running `AUCuniform`, one can get a glimpse of how reliable $uAUC$ or uSe^* can be expected to be.

Value

This function returns a calibration plot

References

Jiménez-Valverde, A., Acevedo, P., Barbosa, A. M., Lobo, J. M. & Real, R. (2013). Discrimination capacity in species distribution models depends on the representativeness of the environmental domain. *Global Ecol. Biogeogr.*, 22, 508-516.

Examples

```
suit<-rbeta(100, 2, 2) #Generate suitability values
random<-runif(100)
sp<-ifelse(random < suit,1 , 0) #Generate presence-absence data
CALplot(cbind(suit, sp))
```

HSgraph

Suitability values distribution graph

Description

A function to visualize the distribution of the suitability values associated to presences, absences, and all cases together.

Usage

```
HSgraph(mat, breaks = 10, hist.total = TRUE)
```

Arguments

mat	A matrix with two columns. The first column must contain the suitability values (i.e., the classification rule); the second column must contain the presences and absences.
breaks	Number of cells for the total histogram. By default, breaks = 10.
hist.total	Logical. Indicates whether or not the distribution of suitability values for all the cases together is graphed.

Details

In blue, the distribution of the suitability values associated to presences. In red, the distribution of the suitability values associated to absences. This graph helps to understand why the *AUC* (or *Se**) is greater, equal to, or less than the *uAUC* (or *uSe**) (see Jiménez-Valverde 2022).

Value

This function returns a multiple histogram.

References

Jiménez-Valverde, A. (2022). The uniform AUC: dealing with the representativeness effect in presence-absence models. *Methods Ecol. Evol.*, 13, 1224-1236.

Examples

```
suit<-rbeta(100, 2, 2) #Generate suitability values
random<-runif(100)
sp<-ifelse(random < suit, 1 , 0) #Generate presence-absence data
HSgraph(cbind(suit, sp), breaks = 20, hist.total = TRUE)
```

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