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maxent {dismo}

Maxent

Package: dismo
Version: 0.9-3

Description

Build a "MaxEnt" (Maximum Entropy) species distribution model (see references below). The function uses environmental data for locations of known presence and for a large number of 'background' locations. Environmental data can be extracted from raster files. The result is a model object that can be used to predict the suitability of other locations, for example, to predict the entire range of a species.

This function uses the MaxEnt species distribution model software, which is a java program that you can download http://www.cs.princeton.edu/~schapire/maxent/here. Put the file 'maxent.jar' in the 'java' folder of this package. That is the folder returned by **system.file**("java", package="dismo"). You need MaxEnt version 3.3.3b or higher. Please note that this program (maxent.jar) cannot be redistributed or used for commercial or for-profit purposes.

Usage

```
maxent(x, p, ...)
```

Arguments

x

    Predictors. Raster* object or SpatialGridDataFrame, containing grids with predictor variables. These will be used to extract values from for the point locations. x can also be a data.frame, in which case each column should be a predictor variable and each row a presence or background record.

p

    Occurrence data. This can be a data.frame, matrix, SpatialPoints* object, or a vector. If p is a data.frame or matrix it represents a set of point locations; and it must have two columns with the first being the x-coordinate (longitude) and the second the y-coordinate (latitude). Coordinates can also be specified with a SpatialPoints* object (defined in the sp package). Background points are sampled randomly from the cells that are not NA in the first predictor variable, unless background points are specified with an additional argument a (see Details). If x is a data.frame, p should be a vector with a length equal to **nrow**(x) and contain 0 (background) and 1 (presence) values, to indicate which records (rows) in data.frame x are presence records, and which are background records.

…

    Additional arguments. See Details

Details

Additional arguments:

a	Background points. Only used if 'p' is not missing, and not a vector.
factors	Which (if any) variables should be considered as categorical? Either by (layer)name or by index. Only used when argument 'x' is a Raster* object because it is not needed in other cases as you can set the appropriate class to the variables in the data.frame
args	Additional argument that can be passed to MaxEnt. See the MaxEnt help for more information. The R maxent function only uses the arguments relevant to model fitting. There is no point in using args='outputformat=raw' when *fitting* the model; but you can use arguments relevant for *prediction* when using the predict function. Some other arguments do not apply at all to the R implementation. An example is 'outputfiletype', because the 'predict' function has its own 'filename' argument for that

removeDuplicates	Boolean. If TRUE, duplicate presence points (that fall in the same grid cell) are removed.
path	Optional. Where do you want the MaxEnt output files to be stored. This allows you to permanently keep these files. If not supplied the MaxEnt files will be stored in a temporary file. These are the files that are shown in a browser when typing the model name or when you use "show(model)"

Values

An object of class 'MaxEnt' (inherits from DistModel-**class**). Or a 'MaxEntReplicates' object if you use 'replicates=' as part of the **args** argument.

References

http://www.cs.princeton.edu/~schapire/maxent/

Steven J. Phillips, Miroslav Dudik, Robert E. Schapire, 2004. A maximum entropy approach to species distribution modeling. Proceedings of the Twenty-First International Conference on Machine Learning. p. 655-662.

Steven J. Phillips, Robert P. Anderson, Robert E. Schapire, 2006. Maximum entropy modeling of species geographic distributions. Ecological Modelling 190:231-259.

Jane Elith, Steven J. Phillips, Trevor Hastie, Miroslav Dudik, Yung En Chee, Colin J. Yates, 2011. A statistical explanation of MaxEnt for ecologists. Diversity and Distributions 17:43-57. http://dx.doi.org/10.1111/j.1472-4642.2010.00725.x

Note

If you want to give MaxEnt (the Java virtual machine that runs it) more memory, you can do that by running something like this (for 1 GB) **before** you load the dismo library.

options(java.parameters = "-Xmx1g")

Some people have reported problems when using this function on a Mac (Apple) computer. Specifically, the following error message occurs:

Error **in** .jcall(mxe, "S", "fit", **c**("autorun", "-e", afn, "-o", dirout, : java.lang.InternalError: Can't start the AWT because Java was started on the first thread. Make sure StartOnFirstThread is not specified in your application's Info.plist or on the command line.

This is a known problem with certain Java applications on Macs. There are two work-arounds that we are aware of: 1) run **Sys.setenv**(NOAWT=**TRUE**) before running **library** rJava (this is what dismo does if rJava is not loaded).

2) use the JGR interface (a Java based R GUI). You can install JGR from here: http://www.rforge.net/JGR/

See Also

predict

Examples

```
# only run if the maxent.jar file is available, in the right folder
jar <- paste(system.file(package="dismo"), "/java/maxent.jar", sep=&rdquo;)

# checking if maxent can be run (normally not part of your script)
if (file.exists(jar) & require(rJava)) {

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

# file with presence points
occurence <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep=&rdquo;)
occ <- read.table(occurence, header=TRUE, sep=',')[,-1]

# witholding a 20% sample for testing
fold <- kfold(occ, k=5)
occtest <- occ[fold == 1, ]
occtrain <- occ[fold != 1, ]

# fit model, biome is a categorical variable
me <- maxent(predictors, occtrain, factors='biome')

# see the maxent results in a browser:
# me

# use "args"
```

```r
# me2 <- maxent(predictors, occtrain, factors='biome', args=c("-J", "-P"))

# plot showing importance of each variable
plot(me)

# response curves
# response(me)

# predict to entire dataset
r <- predict(me, predictors)

# with some options:
# r <- predict(me, predictors, args=c("outputformat=raw"), progress='text',
#       filename='maxent_prediction.grd')

plot(r)
points(occ)

#testing
# background data
bg <- randomPoints(predictors, 1000)

#simplest way to use 'evaluate'
e1 <- evaluate(me, p=occtest, a=bg, x=predictors)

# alternative 1
# extract values
pvtest <- data.frame(extract(predictors, occtest))
avtest <- data.frame(extract(predictors, bg))

e2 <- evaluate(me, p=pvtest, a=avtest)

# alternative 2
# predict to testing points
testp <- predict(me, pvtest)
head(testp)
testa <- predict(me, avtest)

e3 <- evaluate(p=testp, a=testa)
e3
threshold(e3)

plot(e3, 'ROC')
}
```

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