Package ‘maxlike’

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Type Package

Title Model Species Distributions by Estimating the Probability of Occurrence Using Presence-Only Data

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Depends R (>= 2.10.0), raster

Suggests dismo

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Description Provides a likelihood-based approach to modeling species distributions using presence-only data. In contrast to the popular software program MAXENT, this approach yields estimates of the probability of occurrence, which is a natural descriptor of a species' distribution.

License GPL (>= 3)

LazyLoad yes

NeedsCompilation no

Repository CRAN

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maxlike-package

Description

A species’ distribution can be characterized by the probability that it occurs at some location in space. Estimating occurrence probability can be easily accomplished using presence-absence data, but often researchers only have presence locations and environmental data for the study area. MAX-ENT is a popular software program for modeling species distributions, but it does not estimate the probability of occurrence. Rather, it returns various indices that are not easy to interpret (see Royle et al. 2012). Package "maxlike" provides a simple likelihood-based alternative.

Details

Package: maxlike
Type: Package
Version: 0.1-5
Date: 2013-12-17
License: GPL (>=3)
LazyLoad: yes

Note

All presence-only models require a random sample of data from locations where the species is present. Unfortunately, random sampling is not a feature of most presence-only datasets, and bias in the estimated probability surface should be expected in such cases. This assumption can be greatly relaxed if one has presence-absence data, which will always contain more information about a species’ distribution.

References


See Also

maxlike, raster
The Carolina Wren data used by Royle et al. (2012)

Description

These data come from the North American Breeding Bird Survey. They include presence-only and presence-absence data for all 25 square-kilometer covering the contiguous United States. See Royle et al. (2012) for details.

Usage

data(carw)

Format

The format is: List of 5 $ raster.data:’data.frame’: 31980 obs. of 6 variables:
$ pa.data ‘data.frame’: 4615 obs. of 9 variables:
$ xy1 ‘data.frame’: 12082 obs. of 2 variables:
$ dim : num [1:2] 130 246

Details

The component raster.data contains the spatially-referenced covariate data that can be converted to a raster object. pa.data is a data.frame of presence-absence data. xy1 is a data.frame of coordinates of routes where Carolina Wrens were detected. The other components are attributes necessary for formatting raster.data as a raster object.

Source


References


Examples

data(carw)

# Convert data frame to a list of rasters
r1 <- lapply(carw$data$raster.data, function(x) {
m <- matrix(x, nrow=carw$data$dim[1], ncol=carw$data$dim[2], byrow=TRUE)
r <- raster(m)
Fake data for the Maunga Whau volcano

Description

Based upon volcano in the datasets package.

Usage

data(MaungaWhau)

Format

The format is: List of 3

$ elev : num [1:87, 1:61] -1.17 -1.13 -1.09 -1.05 -1.01 ...

$ precip: num [1:87, 1:61] -2.27 -2.25 -2.24 -2.22 -2.2 ...

$ xy : num [1:1000, 1:2] 38.5 42.5 30.5 25.5 16.5 36.5 22.5 56.5 49.5 18.5 ...

Details

No coordinate system attributes are included

Examples

data(MaungaWhau)
elev <- raster(MaungaWhau$elev, xmn=0, xmx=61, ymn=0, ymx=87)
precip <- raster(MaungaWhau$precip, xmn=0, xmx=61, ymn=0, ymx=87)
maxlike

Model occurrence probability using presence-only data

Description

This function estimates the probability of occurrence using presence-only data and spatially-referenced
covariates. Species distribution maps can be created by plotting the expected values of occurrence
probability. The model is described by Royle et al. (2012).

Usage

maxlike(formula, rasters, points, x=NULL, z=NULL,
link=c("logit", "cloglog"),
starts, hessian = TRUE, fixed, removeDuplicates=FALSE,
savedata=FALSE, na.action = "na.omit", ...)

Arguments

formula A right-hand side formula describing the model. At least 1 continuous covariate
must be present in the formula.
rasters The spatially-referenced covariate data formatted as a ‘raster stack’ created by
the stack function in the raster-package. It’s a good idea to standardize these
by subtracting the mean and dividing by the standard deviation. This will make
it easier for optim to find the maximum-likelihood estimates.
points A matrix or data.frame with the X and Y coordinates of the presence loca-
tions.
x A matrix or data.frame with the explanatory data for presence locations. In
case data is provided for x and z, arguments rasters and points will be ignored
z A matrix or data.frame with the explanatory data for background locations.
In case data is provided for x and z, arguments rasters and points will be ignored
link The link function. Either "logit" (the default) or "cloglog".
starts Starting values for the parameters. This should be a vector with as many ele-
ments as there are parameters. By default, all starting values are 0, which should
be adequate if covariates are standardized.
hessian Logical. Should the hessian be computed and the variance-covariance matrix
returned?
fixed Optional vector for fixing parameters. It must be of length equal to the number
of parameters in the model. If an element of fixed is NA, then the parameter is
estimated, otherwise if it is a real number, the parameter is fixed at this value.
removeDuplicates Logical. Should duplicate points be removed? Defaults to FALSE, but note that
the MAXENT default is TRUE.
savedata  Should the raster data be saved with the fitted model? Defaults to FALSE in order to reduce the size of the returned object. If you wish to make predictions, it is safer to set this to TRUE, otherwise the raster data are searched for in the working directory, and thus may not be the data used to fit the model.

na.action  See options for choices

Additional arguments passed to optim

Details

points and rasters should the same coordinate system. The program does not check this so it is up to the user.

Value

A list with 8 components

Est  data.frame containing the parameter estimates (Ests) and standard errors (SE).
vcov  variance-covariance matrix
AIC  AIC
call  the original call
pts.removed  The points removed due to missing values
pix.removed  The pixels removed due to missing values
optim  The object returned by optim
not.fixed  A logical vector indicating if a parameter was estimated or fixed.
link  The link function

Warnings

Maximizing the log-likelihood function is achieved using the optim function, which can fail to find the global optima if sensible starting values are not supplied. The default starting values are rep(0, npars), which will often be adequate if the covariates have been standardized. Standardizing covariates is thus recommended. Even when covariates are standardized, it is always a good idea to try various starting values to see if the log-likelihood can be increased. When fitting models with many parameters, good starting values can be found by fitting simpler models first.

Note

In general it is very hard to obtain a random sample of presence points, which is a requirement of both the Royle et al. (2012) method and of MAXENT. This is one of many reasons why presence-absence data are preferable to presence-only data. When presence-absence data are available, they can be modeled using functions such as glm. Creating species distribution maps from glm is easily accomplished using the predict method.

The MAXENT software assumes that species prevalence is known a priori. If the user does not specify a value for prevalence, prevalence is set to 0.5. MAXENT predictions of occurrence probability are highly sensitive to this setting. In contrast, maxlike directly estimates prevalence.
Another weakness of models for presence-only data is that they do not allow one to model detection probability, which is typically less than one in field conditions. If detection probability is affected by the same covariates that affect occurrence probability, then bias is inevitable. The R package unmarked (Fiske and Chandler 2011) offers numerous methods for jointly modeling both occurrence and detection probability when detection/non-detection data are available.

References


See Also

maxlike-package, raster, carw

Examples

# Carolina Wren data used in Royle et. al (2012)
data(carw)

# Covert data.frame to a list of rasters
rl <- lapply(carw$data$raster.data, function(x) {
  m <- matrix(x, nrow=carw$data$dim[1], ncol=carw$data$dim[2], byrow=TRUE)
  r <- raster(m)
  extent(r) <- carw$data$ext
  r
})

# Create a raster stack and add layer names
rs <- stack(rl[[1]], rl[[2]], rl[[3]], rl[[4]], rl[[5]], rl[[6]])
names(rs) <- names(carw$data$raster.data)

plot(rs)

# Fit a model
fm <- maxlike(~pcMix + I(pcMix^2) + pcDec + I(pcDec^2)+ pcCon + I(pcCon^2) + pcGr + I(pcGr^2) + Lat + I(Lat^2) + Lon + I(Lon^2), rs, carw$data$xy1, method="BFGS", removeDuplicates=TRUE, savedata=TRUE)

summary(fm)
confint(fm)
AIC(fm)
logLik(fm)
# Produce species distribution map (ie, expected probability of occurrence)
psi.hat <- predict(fm)  # Will warn if savedata=FALSE
plot(psi.hat)
points(carw.data$xy1, pch=16, cex=0.1)

# MAXENT sets "default prevalence" to an arbitrary value, 0.5.
# We could do something similar by fixing the intercept at logit(0.5)=0.
# However, it seems more appropriate to estimate this parameter.
fm.fix <- update(fm, fixed=c(0, rep(NA, length(coef(fm))-1)))

# Predict data.frame
presenceData <- as.data.frame(extract(rs, carw.data$xy1))
presenceData <- presenceData[complete.cases(presenceData),]
presence.predictions <- predict(fm, newdata=presenceData)
summary(presence.predictions)

# Calibrate with data.frames
PresenceUniqueCells <- unique(cellFromXY(rs, xy=carw.data$xy1))
PresenceUnique <- xyFromCell(rs, PresenceUniqueCells)
presenceData <- as.data.frame(extract(rs, PresenceUnique))
library(dismo)
background <- randomPoints(rs, n=ncell(rs), extf=1.00)
backgroundData <- as.data.frame(extract(rs, y=background))
backgroundData <- backgroundData[complete.cases(backgroundData),]
fm2 <- maxlike(~pcmix + 1(pcmix^2) + pcdec + 1(pcdec^2) + pccon +
   I(pcCon^2) + pcGr + I(pcGr^2) +
   Lat + I(Lat^2) + Lon + I(Lon^2),
   rasters=NULL, points=NULL,
   x=presenceData, z=backgroundData,
   method="BFGS", removeDuplicates=TRUE, savedata=TRUE)
summary(fm2)

fm2$rasters <- rs
psi.hat2 <- predict(fm2)

## Not run:

# Simulation example
set.seed(131)
x1 <- sort(rnorm(100))
x1 <- raster(outer(x1, x1), xmn=0, xmx=100, ymn=0, ymx=100)
x2 <- raster(matrix(runif(1e4), 100, 100), 0, 100, 0, 100)

# Code factors as dummy variables.
# Note, using asFactor(x3) will not help
x3 <- raster(matrix(c(0,1), 100, 100), 0, 100, 0, 100)

logit.psi <- -1 + 1*x1 + 0*x2
psi <- exp(logit.psi)/(1+exp(logit.psi))
plot(psi)

r <- stack(x1, x2, x3)
names(r) <- c("x1", "x2", "x3")
plot(r)

pa <- matrix(NA, 100, 100)
pa[] <- rbinom(1e4, 1, as.matrix(psi))
str(pa)
table(pa)

pa <- raster(pa, 0, 100, 0, 100)
plot(pa)

xy <- xyFromCell(pa, sample(Which(pa==1, cells=TRUE), 10000))
plot(x1)
points(xy)

fm2 <- maxlike(~x1 + x2 + x3, r, xy)

summary(fm2)
confint(fm2)
AIC(fm2)
logLik(fm2)

## End(Not run)
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