

Package ‘dismo’

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Description Functions for species distribution modeling, that is, predicting entire geographic distributions from occurrences at a number of sites.

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R topics documented:

dismo-package	3
acaule	3
Anguilla data	3
bioclim	4
biovars	6
boxplot	8
calc.deviance	8
Circles	9

Convex Hull	10
dcEvaluate	11
density	12
DistModel	13
domain	13
ecocrop	14
ecolim	15
evaluate	17
evaluateROCR	19
Evaluation plots	19
gbif	20
gbm.fixed	22
gbm.holdout	23
gbm.interactions	25
gbm.perspec	25
gbm.plot	27
gbm.plot.fits	28
gbm.simplify	28
gbm.step	29
geocode	32
Geographic Distance	33
gmap	34
gridSample	37
InvDistW	38
kfold	39
lookup	40
mahal	40
maxent	41
mess	45
ModelEvaluation	46
nicheEquivalency	47
nicheOverlap	48
pairs	49
plot	50
pointValues	50
predict	51
prepareData	52
pwdSample	53
Random null model	55
randomPoints	56
response	57
ssb	58
threshold	59
voronoi	60
Voronoi Hull	61

dismo-package

Species distribution modeling

Description

This package implements a few species distribution models, including an R link to the 'maxent' model, and native implementations of Bioclim and Domain. It also provides a number of functions that can assist in using Boosted Regression Trees.

A good place to start is the vignette, which you can access by typing `vignette('sdm', 'dismo')`

In addition there are a number of functions, such sampling background points, k-fold sampling, and for model evaluation (AUC) that are useful for these and for other species distribution modeling methods available in R (e.g. GLM, GAM, and RandomForest).

Author(s)

Robert J. Hijmans, Steven Phillips, John Leathwick and Jane Elith

acaule

Solanum acaule data

Description

Distribution data for *Solanum acaule* (a plant species that occurs in the high Andes of Peru and Bolivia). Downloaded from GBIF with the `gbif` function. For use in the 'species distribution modeling' vignette.

Usage

```
data(acaule)
```

References

<http://www.gbif.org>

Anguilla data

Anguilla australis distribution data

Description

A number of sites with presence or absence of the short-finned eel (*Anguilla australis*) in New Zealand, and environmental data at these sites; and gridded data of the environmental variables for the study area.

type	variable name	values
Reach	LocSed	weighted average of proportional cover of bed sediment
Segment	SegSumT	Summer air temperature (degrees C)
	SegTSeas	Winter air temperature (degrees C), normalised with respect to SegJanT
	SegLowFlow	segment low flow (m3/sec), fourth root transformed
Downstream	DSDist	distance to coast (km)
	DSDam	presence of known downstream obstructions, mostly dams
	DSMaxSlope	maximum downstream slope (degrees)
Upstream / catchment	USAvgT	average temperature in catchment (deg C) compared to segment, normalised with r
	USRainDays	days/month with rain greater than 25 mm
	USSlope	average slope in the upstream catchment (degrees)
	USNative	area with indigenous forest (proportion)
	Fishing method	fishing method in five classes: electric, net, spot, trap & mixture

Usage

```
data(Anguilla_train)
data(Anguilla_test)
data(Anguilla_grids)
```

Author(s)

John R. Leathwick and Jane Elith

References

Elith, J., J.R. Leathwick and T. Hastie, 2009. A working guide to boosted regression trees. *Journal of Animal Ecology* 77: 802-81

bioclim

Bioclim

Description

The Bioclim algorithm has been extensively used for species distribution modeling. Bioclim is the classic 'climate-envelope-model'. Although it generally does not perform as good as some other modeling methods (Elith et al. 2006) and is unsuited for predicting climate change effects (Hijmans and Graham, 2006). It is still used, however, among other reasons because the algorithm is easy to understand and thus useful in teaching species distribution modeling.

The BIOCLIM algorithm computes the similarity of a location by comparing the values of environmental variables at any location to a percentile distribution of the values at known locations of occurrence ('training sites'). The closer to the 50th percentile (the median), the more suitable the location is. The tails of the distribution are not distinguished, that is, 10 percentile is treated as equivalent to 90 percentile.

In this R implementation, percentile scores are between 0 and 1, but predicted values larger than 0.5 are subtracted from 1. Then, the minimum percentile score across all the environmental variables

is computed (i.e. this is like Liebig's law of the minimum, except that high values can also be limiting factors). The final value is subtracted from 1 and multiplied with 2 so that the results are between 0 and 1. The reason for this transformation is that the results become more like that of other distribution modeling methods and are thus easier to interpret. The value 1 will rarely be observed as it would require a location that has the median value of the training data for all the variables considered. The value 0 is very common as it is assigned to all cells with a value of an environmental variable that is outside the percentile distribution (the range of the training data) for at least one of the variables.

In the `predict` function, you can choose to ignore one of the tails of the distribution (e.g. to make low rainfall a limiting factor, but not high rainfall),

Usage

```
bioclim(x, p, ...)
```

Arguments

x	Raster* object or matrix
p	two column matrix or SpatialPoints* object
...	Additional arguments

Value

An object of class 'Bioclim' (inherits from `DistModel-class`)

Author(s)

Robert J. Hijmans

References

Nix, H.A., 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.

Elith, J., C.H. Graham, R.P. Anderson, M. Dudik, S. Ferrier, A. Guisan, R.J. Hijmans, F. Huettmann, J. Leathwick, A. Lehmann, J. Li, L.G. Lohmann, B. Loiselle, G. Manion, C. Moritz, M. Nakamura, Y. Nakazawa, J. McC. Overton, A.T. Peterson, S. Phillips, K. Richardson, R. Scachetti-Pereira, R. Schapire, J. Soberon, S. Williams, M. Wisz and N. Zimmerman, 2006. Novel methods improve prediction of species' distributions from occurrence data. *Ecography* 29: 129-151. <http://dx.doi.org/10.1111/j.2006.0906-7590.04596.x>

Hijmans R.J., and C.H. Graham, 2006. Testing the ability of climate envelope models to predict the effect of climate change on species distributions. *Global change biology* 12: 2272-2281. <http://dx.doi.org/10.1111/j.1365-2486.2006.01256.x>

See Also

`predict`, `maxent`, `domain`, `mahal`

Examples

```

logo <- stack(system.file("external/rlogo.grd", package="raster"))
#presence data
pts <- matrix(c(48.243420, 48.243420, 47.985820, 52.880230, 49.531423, 46.182616, 54.168232,
  69.624263, 83.792291, 85.337894, 74.261072, 83.792291, 95.126713, 84.565092, 66.275456, 41.803408,
  25.832176, 3.936132, 18.876962, 17.331359, 7.048974, 13.648543, 26.093446, 28.544714, 39.104026,
  44.572240, 51.171810, 56.262906, 46.269272, 38.161230, 30.618865, 21.945145, 34.390047, 59.656971,
  69.839163, 73.233228, 63.239594, 45.892154, 43.252326, 28.356155) , ncol=2)
bc <- bioclim(logo, pts)

#or
v <- extract(logo, pts)
bc <- bioclim(v)
p1 <- predict(logo, bc)
p2 <- predict(logo, bc, tails=c('both', 'low', 'high'))

#or
#sp <- SpatialPoints(pts)
#bc <- bioclim(logo, pts)

```

 biovars

bioclimatic variables

Description

Function to create 'bioclimatic variables' from monthly climate data.

Usage

```
biovars(prec, tmin, tmax, ...)
```

Arguments

prec	vector, matrix, or RasterStack/Brick of precipitation data
tmin	vector, matrix, or RasterStack/Brick of minimum temperature data
tmax	vector, matrix, or RasterStack/Brick of maximum temperature data
...	Additional arguments

Details

Input data is normally monthly. I.e. there should be 12 values (layers) for each variable, but the function should also work for e.g. weekly data (with some changes in the meaning of the output variables. E.g. #8 would then not be for a quarter (3 months), but for a 3 week period).

Value

Depending on the class of the input data, an object of class 'vector', 'matrix' or 'RasterBrick' with 19 variables (columns, layers)

bio1 = Mean annual temperature

bio2 = Mean diurnal range (mean of max temp - min temp)

bio3 = Isothermality (bio2/bio7) (* 100)

bio4 = Temperature seasonality (standard deviation *100)

bio5 = Max temperature of warmest month

bio6 = Min temperature of coldest month

bio7 = Temperature annual range (bio5-bio6)

bio8 = Mean temperature of the wettest quarter

bio9 = Mean temperature of driest quarter

bio10 = Mean temperature of warmest quarter

bio11 = Mean temperature of coldest quarter

bio12 = Total (annual) precipitation

bio13 = Precipitation of wettest month

bio14 = Precipitation of driest month

bio15 = Precipitation seasonality (coefficient of variation)

bio16 = Precipitation of wettest quarter

bio17 = Precipitation of driest quarter

bio18 = Precipitation of warmest quarter

Author(s)

Robert J. Hijmans

Examples

```
tmin <- c(10,12,14,16,18,20,22,21,19,17,15,12)
tmax <- tmin + 5
prec <- c(0,2,10,30,80,160,80,20,40,60,20,0)
biovars(prec, tmin, tmax)

tmn = tmx = prc = brick(nrow=1, ncol=1)
tmn <- setValues(tmn, t(matrix(c(10,12,14,16,18,20,22,21,19,17,15,12))))
tmx <- tmn + 5
prc <- setValues(prc, t(matrix(c(0,2,10,30,80,160,80,20,40,60,20,0))))
b <- biovars(prc, tmn, tmx)
as.matrix(b)
```

boxplot	<i>Box plot of model evaluation data</i>
---------	--

Description

Make a box plot of model evaluation data, i.e., the model predictions for known presence and absence points.

Details

Arguments:

x Object of class ModelEvaluation . . . Additional arguments that can be passed to [boxplot](#)

Author(s)

Robert J. Hijmans

See Also

[evaluate](#)

calc.deviance	<i>Calculate deviance</i>
---------------	---------------------------

Description

Function to calculate deviance given two vectors of observed and predicted values. Requires a family argument which is set to binomial by default

Usage

```
calc.deviance(obs, pred, weights = rep(1,length(obs)),
              family="binomial", calc.mean = TRUE)
```

Arguments

obs	a vector with observed values
pred	a vector with predicted values that correspond the the values in obs
weights	a vector of weight values
family	One of "binomial", "bernoulli", "poisson", "laplace", or "gaussian"
calc.mean	Logical. If TRUE, the mean deviance is returned

Author(s)

John R. Leathwick and Jane Elith

Circles *Circles range*

Description

The circles model predicts that a species is present at sites within a certain distance from a training point, and absent further away.

Usage

```
circles(p, ...)
```

Arguments

`p` point locations (presence). Two column matrix, data.frame or SpatialPoints* object

`...` Additional arguments. See Details

Details

The following additional arguments can be supplied to the circles function:

`d` The radius of each circle in meters. A single number or a vector with elements corresponding to rows in 'p'. If m

`n` How many vertices in the circle? Default is 360

`lonlat` Are these longitude/latitude data? Default value is FALSE

`r` Radius of the earth. Only relevant for longitude/latitude data. Default is 6378137 m

Value

An object of class 'CirclesRange' (inherits from [DistModel-class](#))

Author(s)

Robert J. Hijmans

See Also

[predict](#), [geoDist](#), [convHull](#), [maxent](#), [domain](#), [mahal](#), [convexHull](#)

Examples

```
r <- raster(system.file("external/rlogo.grd", package="raster"))
#presence data
pts <- matrix(c(17, 42, 85, 70, 19, 53, 26, 84, 84, 46, 48, 85, 4, 95, 48, 54, 66,
74, 50, 48, 28, 73, 38, 56, 43, 29, 63, 22, 46, 45, 7, 60, 46, 34, 14, 51, 70, 31, 39, 26), ncol=2)
train <- pts[1:12, ]
test <- pts[13:20, ]
```

```

cc <- circles(train, lonlat=FALSE)
predict(cc, test)

plot(r)
plot(cc@polygons, border='red', lwd=2, add=TRUE)
points(train, col='red', pch=20, cex=2)
points(test, col='black', pch=20, cex=2)

pr = predict(cc, r, progress='')
plot(r, legend=FALSE)
plot(pr, add=TRUE, col='blue')
points(test, col='black', pch=20, cex=2)
points(train, col='red', pch=20, cex=2)

```

Convex Hull

Convex hull model

Description

The Convex hull model predicts that a species is present at sites inside the convex hull of a set of training points, and absent outside that hull. I.e. this is the spatial convex hull, not an environmental hull.

Usage

```
convHull(p, ...)
```

Arguments

p	point locations (presence). Two column matrix, data.frame or SpatialPoints* object
...	Additional arguments. See details

Details

You can supply an argument n (≥ 1) to get n convex hulls around subset of the points. You can also set $n=1:x$, to get a set of overlapping polygons consisting of 1 to x parts. I.e. the first polygon has 1 part, the second has 2 parts, and x has x parts.

Value

An object of class 'ConvexHull' (inherits from [DistModel-class](#))

Author(s)

Robert J. Hijmans

See Also

[predict](#), [geoDist](#), [maxent](#), [domain](#), [mahal](#)

Examples

```
r <- raster(system.file("external/rlogo.grd", package="raster"))
#presence data
pts <- matrix(c(17, 42, 85, 70, 19, 53, 26, 84, 84, 46, 48, 85, 4, 95, 48, 54, 66,
74, 50, 48, 28, 73, 38, 56, 43, 29, 63, 22, 46, 45, 7, 60, 46, 34, 14, 51, 70, 31, 39, 26), ncol=2)
train <- pts[1:12, ]
test <- pts[13:20, ]

ch <- convHull(train)
predict(ch, test)

plot(r)
plot(ch@polygons, border='red', lwd=2, add=TRUE)
points(train, col='red', pch=20, cex=2)
points(test, col='black', pch=20, cex=2)

pr <- predict(ch, r, progress='')
plot(pr)
points(test, col='black', pch=20, cex=2)
points(train, col='red', pch=20, cex=2)
```

dcEvaluate

Evaluate by distance class

Description

Evaluate a model for intervals of distances to the nearest point in a reference dataset for presence data and a sample of the absence data selected to have a low spatial sorting bias (obtained with `pwdSample`).

Usage

```
dcEvaluate(p, a, reference, lonlat=TRUE, binsize=15, predp, preda, model,
predictors, fun=predict)
```

Arguments

<code>p</code>	two column matrix (x, y) or (longitude/latitude) or <code>SpatialPoints</code> object, for point locations
<code>a</code>	two column matrix (x, y) or (longitude/latitude) or <code>SpatialPoints</code> object, for point locations
<code>reference</code>	as above for reference point locations to which distances are computed
<code>lonlat</code>	Logical. Use <code>TRUE</code> if the coordinates are spherical (in degrees), and use <code>FALSE</code> if they are planar

binsize	positive integer. How many presence points in each distance bin?
predp	p
preda	a
model	m
predictors	pr
fun	function

Value

list with Evaluation objects

Author(s)

Robert J. Hijmans

See Also

[pwdSample](#), [ssb](#)

density	<i>density</i>
---------	----------------

Description

Create a density plots of presence and absence data

Value

A density plot. Presence data are in red, and absence data (if available) are in blue.

Methods

`density(x, ...)`

- x Object of class 'ModelEvaluation' or of a class that inherits from 'DistModel', (such as 'MaxEnt', 'Bioclim')
- ... Additional arguments that can be passed to plot

Author(s)

Robert J. Hijmans

See Also

[evaluate](#)

 DistModel

 Class "*DistModel*"

Description

Parent class for a number of distribution models defined in the `dismo` package (those created by `bioclim`, `domain`, `maxent` and `mahal`). This is a virtual Class, no objects may be directly created from it.

Slots

presence: presence data used

absence: absence or background data used

hasabsence: Logical indicating whether there is any absence data

Author(s)

Robert J. Hijmans

 domain

Domain

Description

The Domain algorithm (Carpenter et al. 1993) that has been extensively used for species distribution modeling. It is included here for that reason but please note that it generally does not perform very well in model comparison (Elith et al. 2006, Hijmans and Graham, 2006). The Domain algorithm computes the Gower distance between environmental variables at any location and those at any of the known locations of occurrence ('training sites'). For each variable the minimum distance between a site and any of the training points is taken. To integrate over environmental variables, the maximum distance to any of the variables is used. This distance is subtracted from one, and (in this R implementation) values below zero are truncated so that the scores are between 0 (low) and 1 (high).

Usage

```
domain(x, p, ...)
```

Arguments

x	Raster* object or matrix
p	two column matrix or SpatialPoints* object
...	Additional arguments

Value

An object of class 'Domain' (inherits from [DistModel-class](#))

Author(s)

Robert J. Hijmans

References

Carpenter G., A.N. Gillison and J. Winter, 1993. Domain: a flexible modelling procedure for mapping potential distributions of plants and animals. *Biodiversity Conservation* 2:667-680.

Elith, J., C.H. Graham, R.P. Anderson, M. Dudik, S. Ferrier, A. Guisan, R.J. Hijmans, F. Huettmann, J. Leathwick, A. Lehmann, J. Li, L.G. Lohmann, B. Loiselle, G. Manion, C. Moritz, M. Nakamura, Y. Nakazawa, J. McC. Overton, A.T. Peterson, S. Phillips, K. Richardson, R. Scachetti-Pereira, R. Schapire, J. Soberon, S. Williams, M. Wisz and N. Zimmerman, 2006. Novel methods improve prediction of species' distributions from occurrence data. *Ecography* 29: 129-151. <http://dx.doi.org/10.1111/j.2006.0906-7590.04596.x>

Hijmans R.J., and C.H. Graham, 2006. Testing the ability of climate envelope models to predict the effect of climate change on species distributions. *Global change biology* 12: 2272-2281. <http://dx.doi.org/10.1111/j.1365-2486.2006.01256.x>

See Also

[predict](#), [maxent](#), [bioclim](#), [mahal](#)

Examples

```
logo <- stack(system.file("external/rlogo.grd", package="raster"))
#presence data
pts <- matrix(c(48.243420, 48.243420, 47.985820, 52.880230, 49.531423, 46.182616, 54.168232,
  69.624263, 83.792291, 85.337894, 74.261072, 83.792291, 95.126713, 84.565092, 66.275456,
  41.803408, 25.832176, 3.936132, 18.876962, 17.331359, 7.048974, 13.648543, 26.093446,
  28.544714, 39.104026, 44.572240, 51.171810, 56.262906, 46.269272, 38.161230, 30.618865,
  21.945145, 34.390047, 59.656971, 69.839163, 73.233228, 63.239594, 45.892154, 43.252326,
  28.356155), ncol=2)
d <- domain(logo, pts)
p <- predict(d, logo)
```

ecocrop

Ecocrop model

Description

Very simple mechanistic model for plants.

Usage

```
ecocrop(crop, tmin, tavg, prec, rainfed=TRUE, ...)
getCrop(name)
data(ECOcrops)
```

Arguments

crop	An object of class 'ECOCROP', or the name of a crop as in getCrop
tmin	Vector of monthly minimum temperature (degrees C)
tavg	Vector of monthly average temperature (degrees C)
prec	Vector of monthly precipitation (mm)
rainfed	Logical. If FALSE, the crop is assumed to be irrigated
...	Additinal arguments
name	Name of a crop (character). If missing a data.frame with all crop names is returned

Value

Object of class ECOCROP

Author(s)

Robert J. Hijmans

Examples

```
ecocrop('potato', 5:16, 15:26, runif(12)*100)
getCrop('Acacia brachystachya Benth.')
crop <- getCrop('Hot pepper')
ecocrop(crop, 5:16, 15:26, rainfed=FALSE)
```

ecolim

Ecolim model

Description

Simple generic limiting factor based model, in the tradition of the PLANTGRO model (Hackett, 1991)

Usage

```
## S4 method for signature 'matrix,matrix'
ecolim(x, y, extrapolate=TRUE, ...)
```

Arguments

x	numeric matrix with driver variables (each column has values for the variables). Values have to be in ascending order
y	numeric matrix with responses (between 0 and 1), one column for each column in x
extrapolate	logical. Should the model extrapolate beyond the extremes of x? If TRUE the value of y at the closest data extreme in x is used, else NA is returned for such records
...	Additional arguments. None implemented

Author(s)

Robert J. Hijmans

References

Hackett, C., 1991. PLANTGRO, a software package for coarse prediction of plant growth. CSIRO, Melbourne, Australia

Examples

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

bio1 <- c(200,250,400,450)
bio12 <- c(0,1000, 3000, 4000)
r1 <- c(0, 1, 1, 0)
r2 <- c(0, 0, 1, 1)
x <- cbind(bio1, bio12)
y <- cbind(r1, r2)

e <- ecolim(x, y)
plot(e, lwd=2, col='red')
p <- predict(e, env)
plot(p)

# no extrapolation:
ef <- ecolim(x, y, extrapolate=FALSE)
pf <- predict(ef, env)
plot(pf)

occurrence <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
occ <- read.table(occurrence, header=TRUE, sep=',')[,-1]
fold <- kfold(occ, k=5)
occtest <- occ[fold == 1, ]
occtrain <- occ[fold != 1, ]
bg <- randomPoints(env, 1000)
```



```

## Not run:
# An approach to optimize the values based on
# some known presences and (here random) absences
# for the same species as in the maxent example

# initial parameters
v <- c(200, 250, 400, 450, 0, 1000, 3000, 4000)

# function to be minimized
f <- function(p) {
  x[] <- p
  # numbers must go up
  if ( any(x[-1,] < x[-nrow(x), ]) ) return(Inf)
  e <- ecolim(x, y)
  # we are minimizing, hence 1-AUC
  1-evaluate(e, p=occtrain, a=bg, x=env)@auc
}

# patience...
set.seed(0)
z <- optim(v, f)

x[] <- z$par
eco <- ecolim(x, y)
evaluate(eco, p=occtest, a=bg, x=env)

set.seed(0)
pwd <- pwdSample(occtest,bg,occtrain)
ptest <- occtest[!is.na(pwd),]
atest <- bg[na.omit(pwd),]
evaluate(eco, p=ptest, a=atest, x=env)

p2 <- predict(eco, env)
plot(p2)

## End(Not run)

```

evaluate

Model evaluation

Description

Cross-validation of models with presence/absence data. Given a vector of presence and a vector of absence values (or a model and presence and absence points and predictors), confusion matrices are computed (for varying thresholds), and model evaluation statistics are computed for each confusion matrix / threshold. See the description of class [ModelEvaluation-class](#) for more info.

Usage

```
evaluate(p, a, model, x, tr, ...)
```

Arguments

p	presence points (x and y coordinates or SpatialPoints* object). Or, if x is missing, values at presence points Or, a matrix with values to compute predictions for
a	absence points (x and y coordinates or SpatialPoints* object). Or, if x is missing, values at presence points. Or, a matrix with values to compute predictions for
model	any fitted model, including objects inheriting from 'DistModel'; not used when x is missing
x	Optional. Predictor variables (object of class Raster*). If present, p and a are interpreted as (spatial) points
tr	Optional. a vector of threshold values to use for computing the confusion matrices
...	Additional arguments for the predict function

Value

An object of [ModelEvaluation-class](#)

Author(s)

Robert J. Hijmans

References

Fielding, A.H. and J.F. Bell, 1997. A review of methods for the assessment of prediction errors in conservation presence/absence models. *Environmental Conservation* 24:38-49

See Also

[threshold](#)

Examples

```
## See ?maxent for an example with real data.
# this is a contrived example:
# p has the predicted values for 50 known cases (locations)
# with presence of the phenomenon (species)
p <- rnorm(50, mean=0.7, sd=0.3)
# b has the predicted values for 50 background locations (or absence)
a <- rnorm(50, mean=0.4, sd=0.4)
e <- evaluate(p=p, a=a)

threshold(e)
```

```

plot(e, 'ROC')
plot(e, 'TPR')
boxplot(e)
density(e)

str(e)

```

evaluateROCR

Model testing with the ROCR package

Description

Preparing data for model testing with the ROCR package.

Usage

```
evaluateROCR(model, p, a, x)
```

Arguments

model	any fitted model, including objects inheriting from 'DistModel'
p	presence points (x and y coordinates or SpatialPoints* object). Or, if x is missing, values at presence points Or, a matrix with values to compute predictions for
a	absence points (x and y coordinates or SpatialPoints* object). Or, if x is missing, values at presence points. Or, a matrix with values to compute predictions for
x	optional. predictor variables, if present, p and a are considered

Value

An object of class "prediction" (defined in the ROCR package)

Author(s)

Robert J. Hijmans

Evaluation plots

Plot model evaluation data

Description

Make a ROC curve, or a plot of a threshold dependent measure against threshold values

Methods

usage: plot(x, y, ...)

- x Object of class ModelEvaluation
- y Character. Either 'ROC' or a threshold dependent measure such as 'kappa', 'TPR'
- ... Additional arguments that can be passed to [plot](#)

Author(s)

Robert J. Hijmans

See Also

[ModelEvaluation-class](#), [density](#), [pairs](#), [plot](#)

Examples

```
# p = the predicted value for 50 known cases (locations) with presence of the phenomenon (species)
p = rnorm(50, mean=0.7, sd=0.3)
# b = the predicted value for 50 known cases (locations) with absence of the phenomenon (species)
a = rnorm(50, mean=0.4, sd=0.4)
e = evaluate(p=p, a=a)
plot(e, 'ROC')
plot(e, 'kappa')
plot(e, 'FPR')
plot(e, 'prevalence')
```

 gbif

Data from GBIF

Description

This function downloads species occurrence records from the Global Biodiversity Information Facility ([GBIF](#)) data portal. You can download either a single species (if you append a '*' to the species name) or a subspecies of comparable level. You can download the data for an entire genus by using `species='*'`. Before using this function, please first check the [GBIF data use agreement](#).

Usage

```
gbif(genus, species="", concept=FALSE, ext=NULL, args=NULL, geo=TRUE, sp=FALSE,
     removeZeros=FALSE, download=TRUE, getAlt=TRUE, returnConcept=FALSE,
     ntries=5, nrecs=1000, start=1, end=NULL, feedback=3)
```

Arguments

genus	character. genus name
species	character. species name. Use '*' to download the entire genus. Append '*' to the species name to get all naming variants (e.g. with and without species author name) and sub-taxa

concept	logical or integer. If TRUE records for species that are synonyms (according to the GBIF species concept key) are also downloaded. If concept is an integer (or character representation thereof, it is interpreted as a GBIF taxonomic concept number, and the query will use that concept (and arguments genus and species are ignored)
ext	Extent object to limit the geographic extent of the records. An extent can be created using functions like drawExtent and extent
args	character. Additional arguments to refine the query. See examples for the format, and the (web service documentation) (under 3. SEARCH FOR RECORDS) for more details. This is intended for use with arguments like 'originisocountrycode' or 'startdate' that narrow down the search. Other arguments such as 'format' may cause the function to fail
geo	logical. If TRUE, only records that have a georeference (longitude and latitude values) will be downloaded
sp	logical. If TRUE, geo will be set to TRUE and a SpatialPointsDataFrame will be returned
removeZeros	logical. If TRUE, all records that have a latitude OR longitude of zero will be removed if geo==TRUE, or set to NA if geo==FALSE. If FALSE, only records that have a latitude AND longitude that are zero will be removed or set to NA.
download	logical. If TRUE, records will be downloaded, else only the number of records will be shown
getAlt	logical. If TRUE, elevation data (4 character variables) will be processed into a single new numerical variable
returnConcept	logical. If TRUE, only the GBIF taxonomic concept number is returned
ntries	integer. How many times should the function attempt to download the data, if an invalid response is returned (perhaps because the GBIF server is very busy)
nrecs	integer. How many records to download in a single request (max is 1000)?
start	integer. Record number from which to start requesting data
end	integer. Last record to request
feedback	integer. Lower values give less feedback (0-no messages; 3-all messages)

Value

data frame

Author(s)

Robert J. Hijmans

References

<http://data.gbif.org/occurrences/>

Examples

```

## Not run:
# note the differences:

gbif('solanum', download=F)
gbif('solanum', '*', download=F)
gbif('solanum', 'acaule', download=F)
gbif('solanum', 'acaule f. acaule', download=F)
gbif('solanum', 'acaule*', download=F)

gbif('Batrachoseps', '*' , geo=F, down=F)
gbif('Batrachoseps', '*' , geo=T, down=F)
gbif('Batrachoseps', 'luciae', geo=T, down=F)
g <- gbif('Batrachoseps', 'luciae', geo=T)
plot(g$lon, g$lat)

gs <- gbif('Batrachoseps', 'luciae', sp=T)
plot(gs)

# using additional 'args'
gbif('solanum', 'nigrum', download=F)
gbif('solanum', 'nigrum', download=F, args='originisocountrycode=NL')
gbif('solanum', 'nigrum', download=F, args=c('originisocountrycode=NL', 'originisocountrycode=BE'))

# taxonomic concepts
g0 <- gbif('solanum', 'brevicaule')
unique(g0$species)

g1 <- gbif('solanum', 'brevicaule*')
unique(g1$species)

g2 <- gbif('solanum', 'brevicaule', concept=TRUE)
unique(g2$species)

gcon <- gbif('solanum', 'brevicaule', returnConcept=TRUE)
g3 <- gbif(concept=gcon)

## End(Not run)

```

gbm.fixed

gbm.fixed

Description

Calculates a gradient boosting (gbm) object with a fixed number of trees. The optimal number of trees can be identified using `gbm.step` or some other procedure. Mostly used as a utility function, e.g., when being called by `gbm.simplify`. It takes as input a dataset and arguments selecting x and y variables, learning rate and tree complexity.

Usage

```
gbm.fixed(data, gbm.x, gbm.y, tree.complexity = 1, site.weights = rep(1, nrow(data)),
  verbose = TRUE, learning.rate = 0.001, n.trees = 2000, bag.fraction = 0.5,
  family = "bernoulli", keep.data = FALSE, var.monotone = rep(0, length(gbm.x)))
```

Arguments

data	data.frame
gbm.x	indices of the predictors in the input dataframe
gbm.y	index of the response in the input dataframe
tree.complexity	the tree depth - sometimes referred to as interaction depth
site.weights	by default set equal
verbose	to control reporting
learning.rate	controls speed of the gradient descent
n.trees	default number of trees
bag.fraction	varies random sample size for each new tree
family	can be any of "bernoulli", "poisson", "gaussian", or "laplace"
keep.data	Logical. If TRUE, original data is kept
var.monotone	constrain to positive (1) or negative monotone (-1)

Value

object of class gbm

Author(s)

John R. Leathwick and Jane Elith

References

Elith, J., J.R. Leathwick and T. Hastie, 2009. A working guide to boosted regression trees. *Journal of Animal Ecology* 77: 802-81

gbm.holdout

gbm holdout

Description

Calculates a gradient boosting (gbm) object in which model complexity is determined using a training set with predictions made to a withheld set. An initial set of trees is fitted, and then trees are progressively added testing performance along the way, using `gbm.perf` until the optimal number of trees is identified.

As any structured ordering of the data should be avoided, a copy of the data set is BY DEFAULT randomly reordered each time the function is run.

Usage

```
gbm.holdout(data, gbm.x, gbm.y, learning.rate = 0.001, tree.complexity = 1,
  family = "bernoulli", n.trees = 200, add.trees = n.trees, max.trees = 20000,
  verbose = TRUE, train.fraction = 0.8, permute = TRUE, prev.stratify = TRUE,
  var.monotone = rep(0, length(gbm.x)), site.weights = rep(1, nrow(data)),
  refit = TRUE, keep.data = TRUE)
```

Arguments

data	data.frame
gbm.x	indices of the predictors in the input dataframe
gbm.y	index of the response in the input dataframe
learning.rate	typically varied between 0.1 and 0.001
tree.complexity	sometimes called interaction depth
family	"bernoulli", "poisson", etc. as for gbm
n.trees	initial number of trees
add.trees	number of trees to add at each increment
max.trees	maximum number of trees to fit
verbose	controls degree of screen reporting
train.fraction	proportion of data to use for training
permute	reorder data to start with
prev.stratify	stratify selection for presence/absence data
var.monotone	allows constraining of response to monotone
site.weights	set equal to 1 by default
refit	refit the model with the full data but id'd no of trees
keep.data	keep copy of the data

Value

A gbm object

Author(s)

John R. Leathwick and Jane Elith

References

Elith, J., J.R. Leathwick and T. Hastie, 2009. A working guide to boosted regression trees. *Journal of Animal Ecology* 77: 802-81

gbm.interactions	<i>gbm interactions</i>
------------------	-------------------------

Description

Tests whether interactions have been detected and modelled, and reports the relative strength of these. Results can be visualised with `gbm.perspec`

The function assesses the magnitude of 2nd order interaction effects in `gbm` models fitted with interaction depths greater than 1. This is achieved by:

1. forming predictions on the linear scale for each predictor pair;
2. fitting a linear model that relates these predictions to the predictor pair, with the the predictors fitted as factors;
3. calculating the mean value of the residuals, the magnitude of which increases with the strength of any interaction effect;
4. results are stored in an array;
5. finally, the `n` most important interactions are identified, where `n` is 25

Usage

```
gbm.interactions(gbm.object, use.weights=FALSE, mask.object)
```

Arguments

<code>gbm.object</code>	A <code>gbm</code> object
<code>use.weights</code>	Logical. If TRUE, weights are used for samples
<code>mask.object</code>	a <code>gbm</code> object describing sample intensity

Value

object of class `gbm`

<code>gbm.perspec</code>	<i>gbm perspective plot</i>
--------------------------	-----------------------------

Description

Takes a `gbm` boosted regression tree object produced by `gbm.step` and plots a perspective plot showing predicted values for two predictors as specified by number using `x` and `y`. Values for all other variables are set at their mean by default but values can be specified by giving a list consisting of the variable name and its desired value, e.g., `c(name1 = 12.2, name2 = 57.6)`

Usage

```
gbm.perspec(gbm.object, x = 1, y = 2, pred.means = NULL, x.label = NULL, x.range = NULL,
  y.label = NULL, z.label = "fitted value", y.range = NULL, z.range = NULL,
  leg.coords = NULL, ticktype = "detailed", theta = 55, phi = 40, smooth = "none",
  mask = FALSE, perspective = TRUE, ...)
```

Arguments

<code>gbm.object</code>	object of class <code>gbm</code>
<code>x</code>	the first variable to be plotted
<code>y</code>	the second variable to be plotted
<code>pred.means</code>	allows specification of values for other variables
<code>x.label</code>	allows manual specification of the x label
<code>x.range</code>	manual range specification for the x variable
<code>y.label</code>	and y label
<code>z.label</code>	default z label
<code>y.range</code>	and the y
<code>z.range</code>	allows control of the vertical axis
<code>leg.coords</code>	can specify coords (x, y) for legend
<code>ticktype</code>	specify detailed types - otherwise "simple"
<code>theta</code>	rotation
<code>phi</code>	and elevation
<code>smooth</code>	controls smoothing of the predicted surface
<code>mask</code>	controls masking using a sample intensity model
<code>perspective</code>	controls whether a contour or perspective plot is drawn
<code>...</code>	allows the passing of additional arguments to plotting routine useful options include <code>shade</code> , <code>ltheta</code> , <code>lphi</code> for controlling illumination and <code>cex</code> for controlling text size - <code>cex.axis</code> and <code>cex.lab</code> have no effect

Author(s)

John R. Leathwick and Jane Elith

References

Elith, J., J.R. Leathwick and T. Hastie, 2009. A working guide to boosted regression trees. *Journal of Animal Ecology* 77: 802-81

 gbm.plot

gbm plot

Description

Function to plot gbm response variables, with the option of adding a smooth representation of the response if requested additional options in this version allow for plotting on a common scale. Note that fitted functions are centered by subtracting their mean.

Usage

```
gbm.plot(gbm.object, variable.no=0, smooth=FALSE, rug=TRUE, n.plots=length(pred.names),
  common.scale=TRUE, write.title=TRUE, y.label="fitted function", x.label=NULL,
  show.contrib=TRUE, plot.layout=c(3, 4), ...)
```

Arguments

gbm.object	a gbm object - could be one from gbm.step
variable.no	the var to plot - if zero then plots all
smooth	Logical. If TRUE, a smoothed version of the fitted function is added
rug	Logical. If TRUE, a rug of deciles is plotted
n.plots	plot the first n most important preds
common.scale	Logical. If TRUE, a common scale is used on the y axis
write.title	Logical. If TRUE, the plot gets a title
y.label	the default y-axis label
x.label	the default x-axis label
show.contrib	Logical. If TRUE, the contribution is shown on the x axis
plot.layout	define the default layout for graphs on the page
...	other arguments to pass to the plotting useful options include cex.axis, cex.lab, etc.

Author(s)

John R. Leathwick and Jane Elith

References

Elith, J., J.R. Leathwick and T. Hastie, 2009. A working guide to boosted regression trees. *Journal of Animal Ecology* 77: 802-81

gbm.plot.fits	<i>gbm plot fitted values</i>
---------------	-------------------------------

Description

Plots the fitted values from a gbm object returned by any of the model fitting options. This can give a more reliable guide to the shape of the fitted surface than can be obtained from the individual functions, particularly when predictor variables are correlated and/or samples are unevenly distributed in environmental space. Allows masking out of absences to enable focus on sites with high predicted values.

Usage

```
gbm.plot.fits(gbm.object, v=0, mask.presence=FALSE, use.factor=FALSE )
```

Arguments

gbm.object	a gbm object
v	variable numbers to be plotted (if 0 then all are plotted)
mask.presence	Logical. If TRUE, the function only plots fitted values for presences
use.factor	Logical. If TRUE, forces to use quicker printing box and whisker plot

Author(s)

John R. Leathwick and Jane Elith

References

Elith, J., J.R. Leathwick and T. Hastie, 2009. A working guide to boosted regression trees. *Journal of Animal Ecology* 77: 802-81

gbm.simplify	<i>gbm simplify</i>
--------------	---------------------

Description

The function takes an initial cross-validated model as produced by gbm.step and then assesses the potential to remove predictors using k-fold cross validation. This done for each fold, removing the lowest contributing predictor, and repeating this process for a set number of steps. After the removal of each predictor, the change in predictive deviance is computed relative to that obtained when using all predictors. The function returns a list containing the mean change in deviance and its standard error as a function of the number of variables removed. Having completed the cross validation, it then identifies the sequence of variable to remove when using the full data set, testing this up to the number of steps used in the cross-validation phase of the analysis with results reported to the screen.

The function returns a table containing the order in which variables are to be removed and some vectors, each of which specifies the predictor column numbers in the original dataframe - the latter can be used as an argument to `gbm.step` e.g., `gbm.step(data = data, gbm.x = simplify.object$pred.list[[4]]...` would implement a new analysis with the original predictor set, minus its four lowest contributing predictors.

Usage

```
gbm.simplify(gbm.object, n.folds = 10, n.drops = "auto", alpha = 1, prev.stratify = TRUE,
  eval.data = NULL, plot = TRUE)
```

Arguments

<code>gbm.object</code>	a gbm object describing sample intensity
<code>n.folds</code>	number of times to repeat the analysis
<code>n.drops</code>	can be automatic or an integer specifying the number of drops to check
<code>alpha</code>	controls stopping when <code>n.drops = "auto"</code>
<code>prev.stratify</code>	use prevalence stratification in selecting evaluation data
<code>eval.data</code>	an independent evaluation data set - leave here for now
<code>plot</code>	plot results

Value

A list with these elements: `deviance.summary`, `deviance.matrix`, `drop.count`, `final.drops`, `pred.list`, and `gbm.call = gbm.call()`

Author(s)

John R. Leathwick and Jane Elith

References

Elith, J., J.R. Leathwick and T. Hastie, 2009. A working guide to boosted regression trees. *Journal of Animal Ecology* 77: 802-81

Description

Function to assess the optimal number of boosting trees using k-fold cross validation. Implements the cross-validation procedure described on page 215 of Hastie T., R. Tibshirani, and J.H. Friedman (2001) *The Elements of Statistical Learning: Data Mining, Inference, and Prediction* Springer-Verlag, New York.

The data is divided into 10 subsets, with stratification by prevalence if required for presence/absence data. The function then fits a gbm model of increasing complexity along the sequence from `n.trees` to `n.trees + (n.steps * step.size)`, calculating the residual deviance at each step along the way. After each fold processed, the function calculates the average holdout residual deviance and its standard error and then identifies the optimal number of trees as that at which the holdout deviance is minimised. It fits a model with this number of trees, returning it as a gbm model along with additional information from the cross-validation selection process

Usage

```
gbm.step(data, gbm.x, gbm.y, offset = NULL, fold.vector = NULL, tree.complexity = 1,
  learning.rate = 0.01, bag.fraction = 0.75, site.weights = rep(1, nrow(data)),
  var.monotone = rep(0, length(gbm.x)), n.folds = 10, prev.stratify = TRUE,
  family = "bernoulli", n.trees = 50, step.size = n.trees, max.trees = 10000,
  tolerance.method = "auto", tolerance = 0.001, keep.data = FALSE, plot.main = TRUE,
  plot.folds = FALSE, verbose = TRUE, silent = FALSE, keep.fold.models = FALSE,
  keep.fold.vector = FALSE, keep.fold.fit = FALSE, ...)
```

Arguments

<code>data</code>	input data.frame
<code>gbm.x</code>	predictor variables
<code>gbm.y</code>	response variable
<code>offset</code>	offset
<code>fold.vector</code>	a fold vector to be read in for cross validation with offsets
<code>tree.complexity</code>	sets the complexity of individual trees
<code>learning.rate</code>	sets the weight applied to individual trees
<code>bag.fraction</code>	sets the proportion of observations used in selecting variables
<code>site.weights</code>	allows varying weighting for sites
<code>var.monotone</code>	restricts responses to individual predictors to monotone
<code>n.folds</code>	number of folds
<code>prev.stratify</code>	prevalence stratify the folds - only for presence/absence data
<code>family</code>	family - bernoulli (=binomial), poisson, laplace or gaussian
<code>n.trees</code>	number of initial trees to fit
<code>step.size</code>	numbers of trees to add at each cycle
<code>max.trees</code>	max number of trees to fit before stopping
<code>tolerance.method</code>	method to use in deciding to stop - "fixed" or "auto"

tolerance	tolerance value to use - if method == fixed is absolute, if auto is multiplier * total mean deviance
keep.data	Logical. keep raw data in final model
plot.main	Logical. plot hold-out deviance curve
plot.folds	Logical. plot the individual folds as well
verbose	Logical. control amount of screen reporting
silent	Logical. to allow running with no output for simplifying model)
keep.fold.models	Logical. keep the fold models from cross valiation
keep.fold.vector	Logical. allows the vector defining fold membership to be kept
keep.fold.fit	Logical. allows the predicted values for observations from cross-validation to be kept
...	Logical. allows for any additional plotting parameters

Value

object of S3 class gbm

Note

This and other boosted regression trees (BRT) functions in the dismo package do not work if you use only one predictor. There is an easy work around: make a dummy variable with a constant value and then fit a model with two predictors, the one of interest and the dummy variable, which will be ignored by the model fitting as it has no useful information.

Author(s)

John R. Leathwick and Jane Elith

References

Elith, J., J.R. Leathwick and T. Hastie, 2009. A working guide to boosted regression trees. *Journal of Animal Ecology* 77: 802-81

Examples

```
data(Anguilla_train)
# reduce data set to speed things up a bit
Anguilla_train = Anguilla_train[1:200,]
angaus.tc5.lr01 <- gbm.step(data=Anguilla_train, gbm.x = 3:14, gbm.y = 2, family = "bernoulli",
  tree.complexity = 5, learning.rate = 0.01, bag.fraction = 0.5)
```

 geocode

Georeferencing with Google

Description

A wrapper around the Google geocoding web-service. It returns 0 to n matches. It is important to be as precise as possible, e.g. always include the country in the locality description.

The purpose of using this function should be to display the locations on a map in a browser. You should check the Google terms of use <http://code.google.com/apis/maps/terms.html> to see if your usage of this function (and the underlying Google API) is permitted.

Usage

```
geocode(x, oneRecord=FALSE, extent=NULL, progress='', ...)
```

Arguments

x	A vector of locality descriptions
oneRecord	Logical. If TRUE a single record for each item in x is returned. If the API returned multiple records, the values of this record are computed by averaging the coordinates and taking the union of all bounding boxes
extent	An Extent object, or an object that can be coerced to one, to bias the search towards that region
progress	Character. Valid values are "" (no progress indicator), "text" or "window"
...	additional arguments (currently none implemented)

Value

data.frame with the following fields:

originalPlace	the locality description as provided (in argument x)
interpretedPlace	the locality as interpreted by the Google API
lon	longitude
lat	latitude
lonmin	minimum longitude of the bounding box
lonmax	maximum longitude of the bounding box
latmin	minimum latitude of the bounding box
latmax	maximum latitude of the bounding box
uncertainty	distance from c(lon, lat) to the farthest corner of the bounding box

Note

It is important to compare fields originalPlace and interpretedPlace as the Google interpretation of a (perhaps vague) locality description can be very speculative

Author(s)

Robert J. Hijmans

Examples

```
## Not run:
geocode(c('1600 Pennsylvania Ave NW, Washington DC', 'Luca, Italy', 'Kampala'))
geocode(c('San Jose', 'San Jose, Mexico'))
geocode(c('San Jose', 'San Jose, Mexico'), oneRecord=TRUE)

## End(Not run)
```

Geographic Distance *Geographic distance model*

Description

The geographic distance model predicts that the likelihood of presence is highest near places where a species has been observed. It can be used as a null-model to calibrate cross-validation scores with.

The predicted values are the inverse distance to the nearest known presence point. Distances smaller than or equal to zero are set to 1 (highest score).

Usage

```
geoDist(p, ...)
```

Arguments

<code>p</code>	point locations (presence). Two column matrix, data.frame or SpatialPoints* object
<code>...</code>	Additional arguments. You must supply a lonlat= argument (logical), unless p is a SpatialPoints* object and has a valid CRS (coordinate reference system). You can also supply an additional argument 'a' for absence points (currently ignored). Argument 'a' should be of the same class as argument 'p'

Value

An object of class 'GeographicDistance' (inherits from [DistModel-class](#))

Author(s)

Robert J. Hijmans

See Also

[predict](#), [convHull](#), [maxent](#), [domain](#), [mahal](#), [voronoiHull](#), [geoIDW](#)

Examples

```
r <- raster(system.file("external/rlogo.grd", package="raster"))
#presence data
pts <- matrix(c(17, 42, 85, 70, 19, 53, 26, 84, 84, 46, 48, 85, 4, 95, 48, 54, 66, 74, 50, 48,
              28, 73, 38, 56, 43, 29, 63, 22, 46, 45, 7, 60, 46, 34, 14, 51, 70, 31, 39, 26), ncol=2)
colnames(pts) <- c('x', 'y')

train <- pts[1:12, ]
test <- pts[13:20, ]

gd <- geoDist(train, lonlat=FALSE)
p <- predict(gd, r)

## Not run:
plot(p)
points(test, col='black', pch=20, cex=2)
points(train, col='red', pch=20, cex=2)

## End(Not run)
```

gmap

Get a Google map

Description

Retrieve a 'Google Map' that can be used as a background for plotting points and other spatial data.

You should check the terms of service before you use these maps: <http://code.google.com/apis/maps/terms.html>

The projection of the returned Raster object is "Mercator" (unless you use `lonlat=TRUE`), and other spatial data may need to be transformed before it can be plotted on top of the Google map. You can use the `Mercator` function to transform points from longitude/latitude to Mercator. For `SpatialLines` and `SpatialPolygons` objects, use `spTransform` in the `rgdal` package.

This function uses the Google static maps web-service, and is based on functions by Markus Loecher for the `RgoogleMaps` package.

The purpose of using this function should be to display the map in a browser. You should check the Google terms of use <http://code.google.com/apis/maps/terms.html> to see if your usage of this function (and the underlying Google API) is permitted.

Usage

```
gmap(x, exp=1, type='terrain', filename='', style=NULL, scale=1, zoom=NULL,
     size=c(640, 640), rgb=FALSE, lonlat=FALSE, ...)
```

```
Mercator(p, inverse = FALSE)
```

Arguments

x	a textual locality description, or an Extent object or an object that can be coerced to one (e.g. a Raster* or Spatial* object)
exp	numeric. An expansion factor to enlarge (by multiplication) the extent specified by x
type	character. Choose from 'roadmap', 'satellite', 'hybrid', 'terrain'
filename	character. Filename (optional). You can open the resulting file in a GIS program
style	character. Additional style arguments. See http://code.google.com/apis/maps/documentation/staticmaps/#StyledMapFeatures . Note that certain style features do not work in combination with (the default) type='terrain'
scale	1 or 2. Using 2 doubles the number of pixels returned (and thus gives you better image quality if you need a large image)
zoom	integer between 0 (the whole world) to 21 (very small area), centered on the center of the extent
size	vector of two integers indicating the number of columns and rows that is requested (what is returned depends on other factors as well). Maximum values are c(640, 640), so you can only select a smaller area than the default. Note that the number of pixels returned can be doubled by using scale=2
rgb	logical. If TRUE, a RasterBrick is returned with three layers (red, green, blue). This can be plotted with <code>plotRGB</code>
lonlat	logical. If TRUE the Raster object returned has a longitude/latitude CRS instead of Mercator
...	additional parameters
p	Points. A two-column matrix, or a SpatialPoints object
inverse	Should the inverse projection be done (from Mercator to longitude/latitude?)

Details

If argument x is a textual locality description, the `geocode` function is used to retrieve the extent that should be mapped.

Change the type to 'roadmap' if the map returned says "sorry we have no imagery here"; or use a larger extent.

The returned RasterLayer has a Mercator projection. To plot points (or lines or polygons) on top of it, these need to be transformed first.

A matrix of longitude/latitude data can be transformed with the Mercator function used in the example below. 'Spatial*' objects can be transformed with `spTransform p <- spTransform(x, "+proj=merc +a=6378137 +b=6378137 +lat_ts=0.0 +lon_0=0.0 +x_0=0.0 +y_0=0 +k=1.0 +units=m +nadgrids=@null +no_defs")`

Value

RasterLayer

Author(s)

Robert Hijmans and Sebastien Rochette, based on code by Markus Loecher, Sense Networks <markus at sensenetworks.com> in the RgoogleMaps package

Examples

```
## Not run:
library(rgdal)

# get a map using names
g = gmap('Australia')
plot(g, inter=TRUE)
gs = gmap('Sydney, New South Wales, Australia', type='satellite')
plot(gs, inter=TRUE)
gs = gmap('Sydney, Australia', type='satellite', exp=3)
plot(gs, inter=TRUE)
gs = gmap('Sydney, Australia', type='hybrid', zoom=10, scale=2)
plot(gs, inter=TRUE)

# from a matrix with lon/lat points
x = runif(30)*10 + 40
y = runif(30)*10 - 20
xy = cbind(x, y)
g = gmap(xy, type='hybrid')
plot(g, inter=TRUE)
points(Mercator(xy) , col='red', pch=20)

# or from an Extent object
e = extent( -121.9531 , -120.3897 , 35.36 , 36.61956 )
# you can also get an Extent object by clicking on the map twice after using:
# drawExtent()
r = gmap(e)
plot(r, interpolate=TRUE)

# transform points to Mercator for plotting on top of map:
pt <- matrix(c(-121, 36), ncol=2)
ptm <- Mercator(pt)
points(ptm, cex=3, pch=20, col='blue')
Mercator(ptm, inverse=TRUE)

# transform Spatial objects to Mercator for plotting on top of map
# here for points, but particularly relevant for lines and polygons
pt <- data.frame(pt)
coordinates(pt) <- ~X1 + X2
proj4string(pt) <- "+proj=longlat +datum=WGS84 +ellps=WGS84"
ptm2 <- spTransform(pt, CRS("+proj=merc +a=6378137 +b=6378137 +lat_ts=0.0
+lon_0=0.0 +x_0=0.0 +y_0=0 +k=1.0 +units=m +nadgrids=@null +no_defs"))
points(ptm, col='red', pch='x', cex=3)

# styles:
gmap("Brooklyn", style="feature:road.local|element:geometry|hue:0x00ff00|saturation:100
&style=feature:landscape|element:geometry|lightness:-100", type='roadmap')
```

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

```
gridSample          Stratified regular sample on a grid
```

Description

Sample points from `xy`, using a grid (raster) as stratification. Up to `n` points are sampled from each stratum (cell). For "chessboard" sampling (i.e. sampling from half the cells), use the argument `chess='black'`, or `chess='white'`.

Usage

```
gridSample(xy, r, n=1, chess='')
```

Arguments

<code>xy</code>	A two column matrix or data.frame with x and y coordinates (or longitude and latitude), or a <code>SpatialPoints*</code> object
<code>r</code>	<code>Raster*</code> object
<code>n</code>	Maximum number of samples per cell
<code>chess</code>	Character. <code>"</code> , <code>'black'</code> , or <code>'white'</code> . If <code>'black'</code> or <code>'white'</code> , "chess-board" sampling is used. I.e. only the <code>'white'</code> fields, or only the <code>'black'</code> fields are sampled. Cell number 1 (the upper left corner of <code>r</code>) is white.

Value

A two column matrix with x and y coordinates (or longitude and latitude)

Author(s)

Robert J. Hijmans

See Also

[pwdSample](#)

Examples

```
x <- rnorm(1000, 10, 5)
y <- rnorm(1000, 50, 5)
xy <- cbind(x,y)
res <- 5
r <- raster(extent(range(xy[,1]), range(xy[,2])) + res)
res(r) <- res

samp <- gridSample(xy, r, n=1)
plot(xy, cex=0.1)
points(samp, pch='x', col='red')
```

InvDistW *Inverse-distance weighted model*

Description

Inverse-distance weighted predictions for presence/absence data. Computed with the `gstat` function from the `gstat` package.

Usage

```
geoIDW(p, a, ...)
```

Arguments

<code>p</code>	Presence points. Two column matrix, data.frame, or a <code>SpatialPoints*</code> object
<code>a</code>	Absence points. Must be of the same class as <code>p</code>
<code>...</code>	Additional arguments. None implemented

Value

An object of class `InvDistWeightModel` (inherits from `DistModel-class`)

Author(s)

Robert J. Hijmans

Examples

```
r <- raster(system.file("external/rlogo.grd", package="raster"))
# presence points
p <- matrix(c(17, 42, 85, 70, 19, 53, 26, 84, 84, 46, 48, 85, 4, 95, 48, 54, 66, 74, 50, 48,
             28, 73, 38, 56, 43, 29, 63, 22, 46, 45, 7, 60, 46, 34, 14, 51, 70, 31, 39, 26), ncol=2)

# absence points
a <- matrix(c(30, 23, 5, 5, 31, 33, 91, 63, 60, 88, 93, 97, 65, 68, 85, 97, 35, 32, 29, 55,
             3, 8, 19, 71, 49, 36, 69, 41, 20, 28, 18, 9, 5, 9, 25, 71, 8, 32, 46, 60), ncol=2)

idw <- geoIDW(p, a)
prd <- predict(r, idw)

## Not run:
plot(prd)
points(p)
points(a, pch='x')

## End(Not run)
```

kfold	<i>k-fold partitioning</i>
-------	----------------------------

Description

k-fold partitioning of a data set for model testing purposes. Each record in a matrix (or similar data structure) is randomly assigned to a group. Group numbers are between 1 and k.

Usage

```
kfold(x, k=5, by)
```

Arguments

x	a vector, matrix, data.frame, or Spatial object
k	number of groups
by	Optional argument. A vector or factor with sub-groups (e.g. species). Its length should be the same as the number of records in x

Value

a vector with group assignments

Author(s)

Robert J. Hijmans

Examples

```
#library(disdat)
#data(NSWtrain)
## a single species
#srsp1 <- subset(NSWtrain, spid=='srsp1')
#kfold(srsp1, k = 5)

## all species
#k = kfold(NSWtrain, k=5, by=NSWtrain$spid)

#k[NSWtrain$spid=='srsp1']
## each group has the same number of records
##(except for adjustments if the number of records divided by k is not an integer)
#table(k[NSWtrain$spid=='srsp1'])
#k[NSWtrain$spid=='ousp5']
```

lookup	<i>lookup</i>
--------	---------------

Description

Look up the elevation or the names of countries of administrative subdivisions for point locations (longitude/latitude)

Usage

```
country(lonlat, radius=0)
adm(lonlat, radius=0, maxrows=1)
alt(lonlat)
```

Arguments

lonlat	matrix with longitude and latitude values
radius	radius around each point to consider
maxrows	maximum number of rows (records) to be returned

Value

Character or numeric

Author(s)

Robert J. Hijmans

mahal	<i>Mahalanobis model</i>
-------	--------------------------

Description

Distribution model based on the Mahalanobis distance. The predictions are (1-distance). I.e. the highest possible value is 1, and there will likely be large negative numbers.

Usage

```
mahal(x, p, ...)
```

Arguments

x	Raster* object or matrix
p	two column matrix or SpatialPoints* object
...	Additional arguments. Currently not used

Value

An object of class Mahalanobis (inherits from [DistModel-class](#))

Author(s)

Robert J. Hijmans

See Also

[predict](#), [maxent](#), [bioclim](#), [domain](#)

Examples

```
logo <- stack(system.file("external/rlogo.grd", package="raster"))

#presence data
pts <- matrix(c(48.243420, 48.243420, 47.985820, 52.880230, 49.531423, 46.182616,
  54.168232, 69.624263, 83.792291, 85.337894, 74.261072, 83.792291, 95.126713,
  84.565092, 66.275456, 41.803408, 25.832176, 3.936132, 18.876962, 17.331359,
  7.048974, 13.648543, 26.093446, 28.544714, 39.104026, 44.572240, 51.171810,
  56.262906, 46.269272, 38.161230, 30.618865, 21.945145, 34.390047, 59.656971,
  69.839163, 73.233228, 63.239594, 45.892154, 43.252326, 28.356155), ncol=2)

# fit model
m <- mahal(logo, pts)

# make a prediction
predict(m, logo[1])

x <- predict(m, logo)

# or x <- predict(logo, m) via raster::predict

# plot(x > 0)
```

maxent

Maxent

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 [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. On
- args** Additional argument that can be passed to MaxEnt. See the MaxEnt help for more information. The
- 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 l

Value

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

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
Java was started on the first thread. Make sure StartOnFirstThread is not specified in your applicatio
```

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/>

Author(s)

Steven Phillips and Robert J. Hijmans

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>

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='')

# 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=''),
                    pattern='grd', full.names=TRUE )
predictors <- stack(fnames)
#plot(predictors)

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

# withholding 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"
# 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')
}
```

mess *Multivariate environmental similarity surfaces (MESS)*

Description

Compute multivariate environmental similarity surfaces (MESS), as described by Elith et al., 2010

Usage

```
mess(x, v, full=FALSE, filename='', ...)
```

Arguments

x	Raster* object
v	matrix or data.frame containing the reference values. Each column should correspond to one layer of the Raster* object
full	logical. If FALSE a RasterLayer with the MESS values is returned. If TRUE, a RasterBrick is returned with n layers corresponding to the layers of the input Raster object and an additional layer with the MESS values
filename	character. Output filename (optional)
...	additional arguments as for writeRaster

Details

v can be obtained for a set of points using [extract](#) .

Value

A RasterBrick with layers corresponding to the input layers and an additional layer with the mess values (if full=TRUE and nlayers(x) > 1) or a RasterLayer with the MESS values (if full=FALSE).

Author(s)

Jean-Pierre Rossi <jean-pierre.rossi@supagro.inra.fr>, Robert Hijmans, Paulo van Breugel

References

Elith J., M. Kearney M., and S. Phillips, 2010. The art of modelling range-shifting species. *Methods in Ecology and Evolution* 1:330-342.

Examples

```

set.seed(9)
r <- raster(ncol=10, nrow=10)
r1 <- setValues(r, (1:ncell(r))/10 + rnorm(ncell(r)))
r2 <- setValues(r, (1:ncell(r))/10 + rnorm(ncell(r)))
r3 <- setValues(r, (1:ncell(r))/10 + rnorm(ncell(r)))
s <- stack(r1,r2,r3)
names(s) <- c('a', 'b', 'c')
xy <- cbind(rep(c(10,30,50), 3), rep(c(10,30,50), each=3))
refpt <- extract(s, xy)

ms <- mess(s, refpt, full=TRUE)
plot(ms)

## Not run:
filename <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
bradypus <- read.table(filename, header=TRUE, sep=',')
bradypus <- bradypus[,2:3]
files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
  pattern='grd', full.names=TRUE )
predictors <- stack(files)
predictors <- dropLayer(x=predictors,i=9)
reference_points <- extract(predictors, bradypus)
mss <- mess(x=predictors, v=reference_points, full=TRUE)
plot(mss)

## End(Not run)

```

ModelEvaluation

Class "ModelEvaluation"

Description

Class to store results of model cross-validation with presence/absence (0/1) data

Slots

presence: presence data used
absence: absence data used
np: number of presence points
na: number of absence points
auc: Area under the receiver operator (ROC) curve
pauc: p-value for the AUC (for the Wilcoxon test W statistic
cor: Correlation coefficient

pcor: p-value for correlation coefficient
t: vector of thresholds used to compute confusion matrices
confusion: confusion matrices
prevalence: Prevalence
ODP: Overall diagnostic power
CCR: Correct classification rate
TPR: True positive rate
TNR: True negative rate
FPR: False positive rate
FNR: False negative rate
PPP: Positive predictive power
NPP: Negative predictive power
MCR: Misclassification rate
OR: Odds-ratio
kappa: Cohen's kappa

Author(s)

Robert J. Hijmans

References

Fielding, A. H. & J.F. Bell, 1997. A review of methods for the assessment of prediction errors in conservation presence/absence models. *Environmental Conservation* 24: 38-49

Liu, C., M. White & G. Newell, 2011. Measuring and comparing the accuracy of species distribution models with presence-absence data. *Ecography* 34: 232-243.

See Also

[evaluate](#)

nicheEquivalency *Niche equivalency*

Description

Compute niche equivalency for two species following Warren et al. (2009). The statistic ranges from 0 to 1.

Usage

```
nicheEquivalency(sp1, sp2, predictors, n=99, model=maxent, verbose=TRUE, ...)
```

Arguments

sp1	coordinates for species 1 (matrix with (x, y) or (lon, lat), or SpatialPoints)
sp2	coordinates for species 2 (matrix with (x, y) or (lon, lat), or SpatialPoints)
predictors	Raster object with environmental variables
n	integer. Number of randomizations
model	function. modeling algorithm to me used
verbose	logical. If TRUE some progress indicators are printed
...	additional arguments (none)

Value

numeric

Author(s)

Brian Anacker. Based on a similar function in by Christoph Heibl in the phyloclim package

References

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

nicheOverlap

Niche overlap

Description

Compute niche overlap from predictions of species distributions with the 'I' or 'D' similarity statistic of Warren et al. (2009). The statistic ranges from 0 (no overlap) to 1 (the distributions are identical).

Usage

```
nicheOverlap(x, y, stat='I', mask=TRUE, checkNegatives=TRUE)
```

Arguments

x	RasterLayer with non-negative values (predictions of the probability that a site is suitable for a species)
y	RasterLayer with non-negative values, as above
stat	character either 'I' or 'D' to get the statistic with that name
mask	logical. If TRUE the function removes cells from x that are NA in y and vice-versa. If you are sure that such cases do not occur you can set this to FALSE to speed up computations
checkNegatives	logical. If TRUE the function checks if any of the values in x and y are negative. If you are sure that such cases do not occur you can set this to FALSE to speed up computations

Value

numeric

Author(s)

Based on SDMTools::Istat by Jeremy VanDerWal

References

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

Examples

```
r1 <- raster(nr=18, nc=36)
r2 <- raster(nr=18, nc=36)
set.seed(0)
r1[] <- runif(ncell(r1))
r2[] <- runif(ncell(r1))
nicheOverlap(r1, r2)
```

pairs

Pair plots

Description

Pair plots of presence and absence (background) data.

Methods

```
pairs(x, v=NULL, pa='pa', hist=TRUE, cor=TRUE)
```

x Object of class `DistModel` or derived from that class (such as `'MaxEnt'`, `'Bioclim'`)
v numeric, to select a subset of pairs, e.g. `v=1:3` to plot only the first three variables
pa Character. Either `'pa'`, `'p'`, or `'a'` to show presence and absence, presence, or absence data respectively
hist logical. If `TRUE` a histogram of the values is shown on the diagonal
cor logical. If `TRUE` the correlation coefficient is shown in the upper panels

Author(s)

Robert J. Hijmans

See Also

[density](#), [plot](#)

plot	<i>Plot predictor values</i>
------	------------------------------

Description

Plot predictor values for occurrence (presence and absence) data in a `DistModel` (or derived) object.

Methods

usage: `plot(x, y, ...)`

x	Object of class <code>DistModel</code> or from a class that inherits from it
y	missing
...	Additional arguments that can be passed to plot

Author(s)

Robert J. Hijmans

See Also

[density](#), [pairs](#), [plot](#)

pointValues	<i>point values</i>
-------------	---------------------

Description

Extract values from a `Raster*` object for point locations. This function adds a few options that can be useful in the context of species distribution modeling to [extract](#) function in the raster package.

Usage

`pointValues(x, p, a, uniquecells = TRUE, na.rm = TRUE)`

Arguments

x	A <code>Raster*</code> object
p	Points. Two-column matrix or <code>data.frame</code> ; or a <code>SpatialPoints*</code> object
a	Additional points (absences). Two-column matrix or <code>data.frame</code> ; or a <code>SpatialPoints*</code> object
uniquecells	Logical. If TRUE, each cell can be included only once (i.e. 'duplicate' points are removed)
na.rm	Logical. If TRUE, cell values of NA are not returned

Value

matrix

Author(s)

Robert J. Hijmans

See Also[extract](#)

predict	<i>Distribution model predictions</i>
---------	---------------------------------------

Description

Make a RasterLayer with a prediction based on a model object of class the inherits from 'Dist-Model', including: Bioclim, Domain, MaxEnt, Mahalanobis, and GeographicDistance. Predictions with model objects that do not inherit from DistModel can be made using the similar [predict](#) function in the 'raster' package.

Provide a Raster* object with the independent variables. The names of the layers in the Raster* object should include those expected by the model.

Value

A RasterLayer or, (if x is a matrix), a vector.

Methods

```
predict(object, x, ext=NULL, filename='', progress='text', ...)
```

object	A fitted model of class Bioclim, Domain, MaxEnt, ConvexHull, or Mahalanobis (classes that inherit from Dist-Model)
x	A Raster* object or a data.frame
ext	An extent object to limit the prediction to a sub-region of 'x'. Or an object that can be coerced to an Extent object
filename	Output filename for a new raster; if NA the result is not written to a file but returned with the RasterLayer object
progress	Character. Valid values are "" (no progress bar), "text" and "windows" (on that platform only)
...	Additional model specific arguments. And additional arguments for file writing as for writeRaster

For [maxent](#) models, there is an additional argument 'args' used to pass arguments (options) to the maxent software. See the help page for [maxent](#) for more information.

For [bioclim](#) models, there is an additional argument 'tails' which you can use to ignore the left or right tail of the percentile distribution for a variable. If supplied, tails should be a character vector with a length equal to the number of variables used in the model. Valid values are "both" (the default), "low" and "high". For example, if you have a variable x with an observed distribution between 10 and 20 and you are predicting the bioclim value for a value 25, the default result would be zero (outside of all observed values); but if you use

tail='low', the high (right) tail is ignored and the value returned will be 1.

For [geoDist](#) models, there is an additional argument `fun` that allows you to use your own (inverse) distance function, and argument `scale=1` that allows you to scale the values (distances smaller than this value become one, and the others are divided by this value before computing the inverse distance).

Author(s)

Robert J. Hijmans

See Also

For spatial predictions with GLM, GAM, BRT, randomForest, etc., see [predict](#) in the Raster package.

To fit a model that can be used with this predict method, see [maxent](#), [bioclim](#), [mahal](#), [domain](#), [geoDist](#), [convHull](#)

Extent object: [extent](#)

Examples

```
logo <- stack(system.file("external/rlogo.grd", package="raster"))
pts <- matrix(c(48, 48, 48, 53, 50, 46, 54, 70, 84, 85, 74, 84, 95, 85, 66,
  42, 26, 4, 19, 17, 7, 14, 26, 29, 39, 45, 51, 56, 46, 38, 31, 22, 34, 60,
  70, 73, 63, 46, 43, 28), ncol=2)
b <- bioclim(logo, pts)
# prediction for a sub-region
e <- extent(30,90,20,60)
p <- predict(b, logo, progress='text', ext=e)
plot(p)
```

prepareData

Prepare data for model fitting

Description

Simple helper function to prepare data for model fitting

Usage

```
prepareData(x, p, b, factors, xy=FALSE)
```

Arguments

<code>x</code>	Raster* object
<code>p</code>	presence points
<code>b</code>	background (or absence) points
<code>factors</code>	vectors indicating which variables are factors (using layer names or numbers)
<code>xy</code>	logical. If TRUE, the first two columns of the returned data.frame will be the coordinates of p and b (labeled 'x' and 'y')

Value

data.frame with $nlayers(x)+1$ columns and $nrow(p) + nrow(b)$ rows. The first column, 'pb' indicates whether a record represents presence '1' or background '0' values. The other columns have the values from the Raster* object.

Author(s)

Robert J. Hijmans

pwwSample

Pair-wise distance sampling

Description

Select pairs of points from two sets (without replacement) that have a similar distance to their nearest point in another set of points.

For each point in "fixed", a point is selected from "sample" that has a similar distance (as defined by threshold) to its nearest point in "reference" (note that these are likely to be different points in reference). The select point is either the nearest point nearest=TRUE, or a randomly select point nearest=FALSE that is within the threshold distance. If no point within the threshold distance is found in sample, the point in fixed is dropped.

Hijmans (2012) proposed this sampling approach to remove 'spatial sorting bias' (ssb) from evaluation data used in cross-validation of presence-only species distribution models. In that context, fixed are the testing-presence points, sample the testing-absence (or testing-background) points, and reference the training-presence points.

Usage

```
pwwSample(fixed, sample, reference, tr=0.33, nearest=TRUE, n=1, lonlat=TRUE, warn=TRUE)
```

Arguments

fixed	two column matrix (x, y) or (longitude/latitude) or SpatialPoints object, for point locations for which a pair should be found in sample
sample	as above for point locations from which to sample to make a pair with a point from fixed
reference	as above for reference point locations to which distances are computed
n	How many pairs do you want for each point in fixed
tr	Numeric, normally below 1. The threshold distance for a pair of points (one of fixed and one of sample) to their respective nearest points in reference to be considered a valid pair. The absolute difference in distance between the candidate point pairs in fixed and reference (dfr) and the distance between candidate point pairs in sample and reference (dsr) must be smaller than $tr * dfr$. I.e. if the $dfr = 100$ km, and $tr = 0.1$, dsr must be between >90 and <110 km to be considered a valid pair.

nearest	Logical. If TRUE, the pair with the smallest difference in distance to their nearest reference point is selected. If FALSE, a random point from the valid pairs (with a difference in distance below the threshold defined by <code>tr</code>) is selected (generally leading to higher <code>ssb</code>)
lonlat	Logical. Use TRUE if the coordinates are spherical (in degrees), and use FALSE if they are planar
warn	Logical. If TRUE a warning is given if <code>nrow(fixed) < nrow(sample)</code>

Value

A matrix of `nrow(fixed)` and `ncol(n)`, that indicates, for each point (row) in `fixed` which point(s) in `sample` it is paired to; or NA if no suitable pair was available.

Author(s)

Robert J. Hijmans

References

Hijmans, R.J., 2012. Cross-validation of species distribution models: removing spatial sorting bias and calibration with a null-model. *Ecology* 93: 679-688

See Also

[gridSample](#)

Examples

```
ref <- matrix(c(-54.5,-38.5, 2.5, -9.5, -45.5, 1.5, 9.5, 4.5, -10.5, -10.5), ncol=2)
fix <- matrix(c(-56.5, -30.5, -6.5, 14.5, -25.5, -48.5, 14.5, -2.5, 14.5,
               -11.5, -17.5, -11.5), ncol=2)
r <- raster()
extent(r) <- c(-110, 110, -45, 45)
r[] <- 1
set.seed(0)
sam <- randomPoints(r, n=50)

par(mfrow=c(1,2))
plot(sam, pch='x')
points(ref, col='red', pch=18, cex=2)
points(fix, col='blue', pch=20, cex=2)

i <- pwdSample(fix, sam, ref, lonlat=TRUE)
i
sfix <- fix[!is.na(i), ]
ssam <- sam[i[!is.na(i)], ]
ssam

plot(sam, pch='x', cex=0)
points(ssam, pch='x')
points(ref, col='red', pch=18, cex=2)
```

```
points(sfix, col='blue', pch=20, cex=2)

# try to get 3 pairs for each point in 'fixed'
pwdSample(fix, sam, ref, lonlat=TRUE, n=3)
```

Random null model *Random null model*

Description

Null model based on randomization of locations as suggested by Raes and ter Steege (2007).

Usage

```
nullRandom(x, model, n=25, rep=25, pa=FALSE)
```

Arguments

x	data.frame with environmental predictor values for collecting localities
model	Model function that creates a model of class 'DistModel'
n	Sample size
rep	Number of repetitions
pa	Boolean. Presence-only or presence/background model (e.g. Maxent)

Value

List with n object of class [ModelEvaluation-class](#)

Author(s)

Robert J. Hijmans

References

Raes, N. & H. ter Steege, 2007. A null-model for significance testing of presence-only species distribution models. *Ecography* 30:727-736.

See Also

[geoDist](#)

Examples

```

predictors <- stack(list.files(path=paste(system.file(package="dismo"), '/ex', sep=''),
                                pattern='grd', full.names=TRUE ))
occurrence <- paste(system.file(package="dismo"), '/ex/bradypus.csv', sep='')
occ <- read.table(occurrence, header=TRUE, sep=',')[,-1]

x <- extract(predictors, occ)
nr <- nullRandom(x, bioclim, n=25, rep=25, pa=FALSE)
mean(sapply(nr, function(x)x@auc))

```

randomPoints

*Random points***Description**

Generate random points that can be used to extract background values ("random-absence"). The points are sampled (without replacement) from the cells that are not 'NA' in raster 'mask'.

If the coordinate reference system (of mask) is longitude/latitude, sampling is weighted by the size of the cells. That is, because cells close to the equator are larger than cells closer to the poles, equatorial cells have a higher probability of being selected.

Usage

```

randomPoints(mask, n, p, ext=NULL, extf=1.1, excludep=TRUE, prob=FALSE,
             cellnumbers=FALSE, tryf=5, warn=2)

```

Arguments

mask	Raster* object. If the object has cell values, cells with NA are excluded (or the first layer of the object if there are multiple layers), unless weights=TRUE
n	integer. Number of points
p	Presence points (if provided, random points won't be in the same cells (as defined by mask))
ext	Extent object. Can be used to restrict sampling to a spatial extent
extf	numeric. Multiplier to adjust the size of extent 'ext'. The default increases of 1.1 increases the extent a little (5% at each side of the extent)
excludep	logical. If TRUE, presence points are excluded from background
prob	logical. If TRUE the values in mask are interpreted as probability weights (and the values should be positive numbers (or NA)). NOTE: this currently only works for rasters of a relatively modest size (that can be loaded into RAM)
cellnumbers	logical. If TRUE, cell numbers for jcodemask are returned rather than coordinates
tryf	numeric > 1. Multiplier used for initial sample size from which the requested sample size is extracted after removing NA points (outside of mask)
warn	integer. 2 or higher gives most warnings. 0 or lower gives no warnings if sample size n is not reached

Value

matrix with coordinates, or, if `cellnumbers=TRUE`, a vector with cell numbers.

Author(s)

Robert J. Hijmans

response	<i>response plots</i>
----------	-----------------------

Description

Generate 'response plots', i.e. single variable response curves for a model

Usage

```
response(x, ...)
```

Arguments

x	Model object that inherits from 'DistModel', e.g. 'MaxEnt'. Also works for some other models (e.g. GLM)
...	Additional arguments. See Details

Details

var	Variable to be plotted (if NULL, all variables will be plotted)
at	Function to indicate at what level the other variables should be. E.g. median (the default), mean, min, max. Note
range	'pa' (default) or 'p'. Show responses for the range of the presence data (p) or presence and absence (background)
expand	percentage to expand the range of values with. Default is 10
rug	Logical. If TRUE (the default) a 'rug' of deciles is plotted on the horizontal axes
data	data.frame with data to use, normally this is the data used to fit the model and does not need to be supplied as th
fun	predict function. The default is "predict"; but you may change this to e.g., function(x, y, ...) predict(x, y, type='re
...	Additional graphical parameters

Value

Used for the side-effect of a plot

Author(s)

Robert J. Hijmans

See Also

[density](#), [plot](#), [pairs](#)

ssb *Spatial sorting bias*

Description

Determine "spatial sorting bias", or the difference between two point data sets in the average distance to the nearest point in a reference dataset.

Usage

```
ssb(p, a, reference, lonlat=TRUE, avg=TRUE)
```

Arguments

p	two column matrix (x, y) or (longitude/latitude) or SpatialPoints object, for point locations
a	two column matrix (x, y) or (longitude/latitude) or SpatialPoints object, for point locations
reference	as above for reference point locations to which distances are computed
lonlat	Logical. Use TRUE if the coordinates are spherical (in degrees), and use FALSE if they are planar
avg	Logical. If TRUE the distances are averaged

Value

matrix with two values. 'dp': the average distance from a point in p to the nearest point in reference and 'da': the average distance from a point in a to the nearest point in reference. Distance is in meters if lonlat=TRUE, and in mapunits (typically also meters) if lonlat=FALSE

Author(s)

Robert J. Hijmans

References

Hijmans, R.J., 2012. Cross-validation of species distribution models: removing spatial sorting bias and calibration with a null-model. *Ecology* 93: 679-688.

See Also

[pwdSample](#)

Examples

```

ref <- matrix(c(-54.5,-38.5, 2.5, -9.5, -45.5, 1.5, 9.5, 4.5, -10.5, -10.5), ncol=2)
p <- matrix(c(-56.5, -30.5, -6.5, 14.5, -25.5, -48.5, 14.5, -2.5, 14.5,
             -11.5, -17.5, -11.5), ncol=2)
r <- raster()
extent(r) <- c(-110, 110, -45, 45)
r[] <- 1
set.seed(0)
a <- randomPoints(r, n=50)
b <- ssb(p, a, ref)

# distances in km
b / 1000

# an index of spatial sorting bias (1 is no bias, near 0 is extreme bias)
b[1] / b[2]

```

threshold

Find a threshold

Description

Find a threshold (cut-off) to transform model predictions (probabilities, distances, or similar values) to a binary score (presence or absence).

Usage

```

## S4 method for signature 'ModelEvaluation'
threshold(x, stat='', sensitivity=0.9, ...)

```

Arguments

x	A ModelEvaluation object (see evaluate)
stat	character. To select a particular threshold (see section 'value' for possible values)
sensitivity	numeric between 0 and 1. For the fixed sensitivity threshold
...	Additional arguments. None implemented

Value

data.frame with the following columns:

kappa: the threshold at which kappa is highest ("max kappa")

spec_sens: the threshold at which the sum of the sensitivity (true positive rate) and specificity (true negative rate) is highest

no_omission: the highest threshold at which there is no omission

prevalence: modeled prevalence is closest to observed prevalence

equal_sens_spec: equal sensitivity and specificity
sensitivty: fixed (specified) sensitivity

Author(s)

Robert J. Hijmans and Diego Nieto-Lugilde

See Also

[evaluate](#)

Examples

```
## See ?maxent for an example with real data.  
# this is a contrived example:  
# p has the predicted values for 50 known cases (locations)  
# with presence of the phenomenon (species)  
p <- rnorm(50, mean=0.7, sd=0.3)  
# b has the predicted values for 50 background locations (or absence)  
a <- rnorm(50, mean=0.4, sd=0.4)  
e <- evaluate(p=p, a=a)  
  
threshold(e)
```

voronoi

Voronoi polygons

Description

Voronoi polygons

Usage

```
voronoi(xy)
```

Arguments

xy SpatialPoints* or two column matrix

Value

SpatialPolygonsDataFrame

Author(s)

Adapted from code by Carson Farmer: <http://www.carsonfarmer.com/?p=455>

Examples

```
# points
p <- matrix(c(17, 42, 85, 70, 19, 53, 26, 84, 84, 46, 48, 85, 4, 95, 48, 54, 66, 74, 50, 48,
             28, 73, 38, 56, 43, 29, 63, 22, 46, 45, 7, 60, 46, 34, 14, 51, 70, 31, 39, 26), ncol=2)

v <- voronoi(p)
v
```

Voronoi Hull

Voronoi hull model

Description

Voronoi polygons for presence/absence data

Usage

```
voronoiHull(p, a, ...)
```

Arguments

p	Presence points. Two column matrix, data.frame, or a SpatialPoints* object
a	Absence points. Must be of the same class as p
...	Additional arguments

Value

A VoronoiHull object (inherits from [DistModel-class](#))

Note

This function is only correct when using a planar coordinate reference system (not longitude/latitude).

Author(s)

Robert J. Hijmans. Adapted from code by Carson Farmer: <http://www.carsonfarmer.com/?p=455>

See Also

[convexHull](#)

Examples

```
r <- raster(system.file("external/rlogo.grd", package="raster"))
# presence points
p <- matrix(c(17, 42, 85, 70, 19, 53, 26, 84, 84, 46, 48, 85, 4, 95, 48, 54, 66, 74, 50, 48,
             28, 73, 38, 56, 43, 29, 63, 22, 46, 45, 7, 60, 46, 34, 14, 51, 70, 31, 39, 26), ncol=2)

# absence points
a <- matrix(c(30, 23, 5, 5, 31, 33, 91, 63, 60, 88, 93, 97, 65, 68, 85, 97, 35, 32, 29, 55,
             3, 8, 19, 71, 49, 36, 69, 41, 20, 28, 18, 9, 5, 9, 25, 71, 8, 32, 46, 60), ncol=2)

v <- voronoiHull(p, a)

x <- predict(r, v)

## Not run:
plot(x)
points(p, col='black', pch=20, cex=2)
points(a, col='red', pch=20, cex=2)

## End(Not run)
```

Index

- *Topic **classes**
 - DistModel, 13
 - ModelEvaluation, 46
- *Topic **datasets**
 - acaule, 3
 - Anguilla data, 3
- *Topic **methods**
 - predict, 51
- *Topic **package**
 - dismo-package, 3
- *Topic **spatial**
 - bioclim, 4
 - biovars, 6
 - boxplot, 8
 - calc.deviance, 8
 - Circles, 9
 - Convex Hull, 10
 - dcEvaluate, 11
 - density, 12
 - dismo-package, 3
 - domain, 13
 - ecocrop, 14
 - ecolim, 15
 - evaluate, 17
 - evaluateROCR, 19
 - Evaluation plots, 19
 - gbif, 20
 - gbm.fixed, 22
 - gbm.holdout, 23
 - gbm.interactions, 25
 - gbm.perspec, 25
 - gbm.plot, 27
 - gbm.plot.fits, 28
 - gbm.simplify, 28
 - gbm.step, 29
 - geocode, 32
 - Geographic Distance, 33
 - gmap, 34
 - gridSample, 37
 - InvDistW, 38
 - kfold, 39
 - lookup, 40
 - mahal, 40
 - maxent, 41
 - pairs, 49
 - plot, 50
 - pointValues, 50
 - predict, 51
 - prepareData, 52
 - pwdSample, 53
 - Random null model, 55
 - randomPoints, 56
 - response, 57
 - ssb, 58
 - threshold, 59
 - voronoi, 60
 - Voronoi Hull, 61
- acaule, 3
- adm (lookup), 40
- alt (lookup), 40
- Anguilla data, 3
- Anguilla_grids (Anguilla data), 3
- Anguilla_test (Anguilla data), 3
- Anguilla_train (Anguilla data), 3

- bioclim, 4, 13, 14, 41, 51, 52
- bioclim, data.frame, missing-method (bioclim), 4
- bioclim, matrix, missing-method (bioclim), 4
- bioclim, Raster, data.frame-method (bioclim), 4
- bioclim, Raster, matrix-method (bioclim), 4
- bioclim, Raster, SpatialPoints-method (bioclim), 4
- bioclim, SpatialGridDataFrame, matrix-method (bioclim), 4

- bioclim, SpatialGridDataFrame, SpatialPoints-method (bioclim), 4
- Bioclim-class (bioclim), 4
- biovars, 6
- biovars, matrix, matrix, matrix-method (biovars), 6
- biovars, Raster, Raster, Raster-method (biovars), 6
- biovars, vector, vector, vector-method (biovars), 6
- boxplot, 8, 8
- boxplot, ModelEvaluation-method (boxplot), 8

- calc.deviance, 8
- Circles, 9
- circles (Circles), 9
- circles, data.frame-method (Circles), 9
- circles, matrix-method (Circles), 9
- circles, SpatialPoints-method (Circles), 9
- CirclesRange-class (Circles), 9
- Convex Hull, 10
- convexHull, 9, 61
- ConvexHull-class (Convex Hull), 10
- convHull, 9, 33, 52
- convHull (Convex Hull), 10
- convHull, data.frame-method (Convex Hull), 10
- convHull, matrix-method (Convex Hull), 10
- convHull, SpatialPoints-method (Convex Hull), 10
- country (lookup), 40

- dcEvaluate, 11
- density, 12, 20, 49, 50, 58
- density, DistModel-method (density), 12
- density, ModelEvaluation-method (density), 12
- dismo (dismo-package), 3
- dismo-package, 3
- DistModel, 13
- DistModel-class (DistModel), 13
- domain, 5, 9, 11, 13, 13, 33, 41, 52
- domain, data.frame, missing-method (domain), 13
- domain, matrix, missing-method (domain), 13
- domain, Raster, data.frame-method (domain), 13
- domain, Raster, matrix-method (domain), 13
- domain, Raster, SpatialPoints-method (domain), 13
- Domain-class (domain), 13
- drawExtent, 21

- ecocrop, 14
- ECOCROP-class (ecocrop), 14
- ECOCROPcrop-class (ecocrop), 14
- ECOCrops (ecocrop), 14
- ecolim, 15
- ecolim, matrix, matrix-method (ecolim), 15
- EcoLim-class (ecolim), 15
- evaluate, 8, 12, 17, 47, 59, 60
- evaluateROCR, 19
- Evaluation plots, 19
- Extent, 56
- extent, 21, 52
- extract, 45, 50, 51

- gbif, 3, 20
- gbm.fixed, 22
- gbm.holdout, 23
- gbm.interactions, 25
- gbm.perspec, 25
- gbm.plot, 27
- gbm.plot.fits, 28
- gbm.simplify, 28
- gbm.step, 29
- geocode, 32, 35
- geoDist, 9, 11, 52, 55
- geoDist (Geographic Distance), 33
- geoDist, data.frame-method (Geographic Distance), 33
- geoDist, matrix-method (Geographic Distance), 33
- geoDist, SpatialPoints-method (Geographic Distance), 33
- Geographic Distance, 33
- GeographicDistance-class (Geographic Distance), 33
- geoIDW, 33
- geoIDW (InvDistW), 38
- geoIDW, data.frame, data.frame-method (InvDistW), 38
- geoIDW, matrix, matrix-method (InvDistW), 38

- geoIDW, SpatialPoints, SpatialPoints-method (InvDistW), 38
- getCrop (ecocrop), 14
- gmap, 34
- gridSample, 37, 54
- InvDistW, 38
- InvDistWeightModel-class (InvDistW), 38
- kfold, 39
- lookup, 40
- mahal, 5, 9, 11, 13, 14, 33, 40, 52
- mahal, data.frame, missing-method (mahal), 40
- mahal, matrix, missing-method (mahal), 40
- mahal, Raster, data.frame-method (mahal), 40
- mahal, Raster, matrix-method (mahal), 40
- mahal, Raster, SpatialPoints-method (mahal), 40
- Mahalanobis-class (mahal), 40
- maxent, 5, 9, 11, 13, 14, 33, 41, 41, 51, 52
- maxent, data.frame, vector-method (maxent), 41
- maxent, missing, missing-method (maxent), 41
- maxent, Raster, ANY-method (maxent), 41
- maxent, SpatialGridDataFrame, ANY-method (maxent), 41
- MaxEnt-class (maxent), 41
- MaxEntReplicates-class (maxent), 41
- Mercator (gmap), 34
- mess, 45
- ModelEvaluation, 46
- ModelEvaluation-class (ModelEvaluation), 46
- nicheEquivalency, 47
- nicheOverlap, 48
- nullRandom (Random null model), 55
- pairs, 20, 49, 50, 58
- pairs, DistModel-method (pairs), 49
- plot, 20, 49, 50, 50, 58
- plot, Bioclim, missing-method (plot), 50
- plot, DistModel, numeric-method (plot), 50
- plot, ModelEvaluation, character-method (Evaluation plots), 19
- plotRGB, 35
- points, DistModel-method (plot), 50
- pointValues, 50
- predict, 5, 9, 11, 14, 33, 41, 43, 51, 51, 52
- predict, Bioclim-method (predict), 51
- predict, CirclesRange-method (predict), 51
- predict, ConvexHull-method (predict), 51
- predict, Domain-method (predict), 51
- predict, EcoLim-method (ecolim), 15
- predict, GeographicDistance-method (predict), 51
- predict, InvDistWeightModel-method (predict), 51
- predict, Mahalanobis-method (predict), 51
- predict, MaxEnt-method (predict), 51
- predict, MaxEntReplicates-method (predict), 51
- predict, VoronoiHull-method (predict), 51
- prepareData, 52
- pwdSample, 12, 37, 53, 58
- Random null model, 55
- randomPoints, 56
- response, 57
- response, ANY-method (response), 57
- response, DistModel-method (response), 57
- response, MaxEntReplicates-method (response), 57
- SpatialPointsDataFrame, 21
- ssb, 12, 53, 54, 58
- threshold, 18, 59
- threshold, ModelEvaluation-method (threshold), 59
- voronoi, 60
- Voronoi Hull, 61
- voronoiHull, 33
- voronoiHull (Voronoi Hull), 61
- voronoiHull, data.frame, data.frame-method (Voronoi Hull), 61
- voronoiHull, matrix, matrix-method (Voronoi Hull), 61
- voronoiHull, SpatialPoints, SpatialPoints-method (Voronoi Hull), 61
- VoronoiHull-class (Voronoi Hull), 61
- writeRaster, 45, 51