

wsl.biodiv

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Type Package

Title A toolbox to efficiently handle Species Distribution Modelling (SDMs) in collaborative projects

Version 0.1.0

Depends R (>= 3.1.0), snow, mgcv, dismo, MASS, NMOF, gbm, randomForest, ROCR, cluster, spatstat, raster, terra, foreach, doParallel, usdm, glmnet, neuralnet, rgdal, lme4, MuMIn

Description Package aiming at varied and flexible model fitting and tools for SDMs.

Meta information should be stored (author, date, taxon,...) efficiently.

Model evaluation and prediction should flexibly handle various fitted model objects.

Evaluation metrics for pres-only and pres-abs models should be mutually implemented.

Relationships between saved objects should be preserved.

Filtering and testing tools should help the user to find adequate predictors.

Poisson Point Process models (PPPM) implementation should remain user-friendly.

Regularization and variable selection should be implemented in this framework.

License GPL (>=3)

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

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boycei

Boyce index model evaluation sub-function II

Description

Not to be called directly by the user

Usage

```
boycei(interval, obs, fit)
```

Author(s)

'boycei' from the 'ecospat' package

| | |
|-------|--|
| ceval | <i>Do the actual model evaluations</i> |
|-------|--|

Description

Not to be called directly by the user

Usage

```
ceval(f, pa, crit, tre = numeric())
```

Author(s)

Philipp Brun

| | |
|--------------|---|
| copy_PseuAbs | <i>Copy pseudoabsences from wsl.pseudoabsences object for new species</i> |
|--------------|---|

Description

Copy pseudoabsences from existing wsl.pseudoabsences object to wsl.pseudoabsences object for new species

Usage

```
copy_PseuAbs(env.stack, pres = SpatialPoints(), taxon = character(), x)
```

Arguments

| | |
|-----------|---|
| env.stack | RasterStack with environmental layers for sampling and extraction. Need to be the same layers as in the wsl.pseudoabsences object. |
| pres | SpatialPoints object. Location of presence points. Necessary for 'geographic' sampling strategy and the best adding point if the downstream functions will be used. |
| taxon | Character; name of taxon of interest to keep track of meta information. |
| x | A wsl.pseudoabsences object |

Details

if the desired pseudoabsence sampling strategy is not species-specific it may be more efficient to copy on the sampled pseudoabsences from another object.

Value

an object of class 'wsl.pseudoabsences' that can be plotted and passed on to wsl.flex

Author(s)

Philipp Brun

References

Descombes, P., Chauvier, Y., Brun, P., Righetti, D., Wüest, R. O., Karger, D. N., ... & Zimmermann, N. E. (2022). Strategies for sampling pseudo-absences for species distribution models in complex mountainous terrain. *bioRxiv*, 2022-03.

Examples

```
### =====
### Data preparation
### =====

# Predictors
bio=raster::getData('worldclim',var='bio',lon=16, lat=48,res=.5)
bio=bio[[c(1,4,12)]]

# install.packages("rgbif")
library(rgbif)
# extract species
spn1='Boletus aestivalis'
xt=as.vector(extent(bio))
baest <- occ_search(scientificName=spn1,
                    hasCoordinate=TRUE,
                    decimalLongitude=paste0(xt[1],"",xt[3]),
                    decimalLatitude=paste0(xt[2],"",xt[4]))

pbaest=baest$data[,c('decimalLongitude','decimalLatitude')]
baest_spp=SpatialPoints(pbaest,proj4string = crs(bio))

spn2='Boletus edulis'
bedu <- occ_search(scientificName=spn2,
                    hasCoordinate=TRUE,
                    decimalLongitude=paste0(xt[1],"",xt[3]),
                    decimalLatitude=paste0(xt[2],"",xt[4]))

pbedu=bedu$data[,c('decimalLongitude','decimalLatitude')]
bedu_spp=SpatialPoints(pbedu,proj4string = crs(bio))

### =====
### Sample pseudoabsences
### =====

# Geo.start
pseu.abs1=ws1.samplePseuAbs(type="geo.strat",
                             n=5000,
                             env.stack=bio,
                             pres=baest_spp,
                             geores_fact=3,
                             add.strat=0,
                             taxon=spn1)

plot(pseu.abs1)

pseu.abs2=copy_PseuAbs(env.stack=bio,
                        pres=bedu_spp,
                        taxon=spn2,
                        x=pseu.abs1)
```

```
plot(pseu.abs2)
```

| | |
|-----------------|---|
| create_envstrat | <i>Create environmental strata for environmentally stratified pseudoabsence sampling.</i> |
|-----------------|---|

Description

Create environmental strata for environmentally stratified pseudoabsence sampling.

Usage

```
create_envstrat(
  env.stk,
  rAll = TRUE,
  save_it = TRUE,
  strat_dir = NA,
  poolsiz = 5 * 10^6,
  sampsiz = 4e+05,
  type
)
```

Arguments

| | |
|-----------|---|
| env.stk | raster stack with environmental layers of interest |
| rAll | should raster be read entirely into memory? This is faster but may blow the RAMs of your machine. |
| save_it | Should a stratified sample of c. 400000 points be saved |
| strat_dir | Directory to save the stratified sample in, Not to be called directly by the user |

Author(s)

Philipp Brun

| | |
|------------|--|
| df_or_rast | <i>Predict to data.frame or raster</i> |
|------------|--|

Description

Not to be called directly by the user

Usage

```
df_or_rast(mod, nwdat, clust, ...)
```

Author(s)

Philipp Brun

| | |
|----------------|--|
| eco.adj.D2.glm | <i>Function originally written by A. Guisan (UNIL-ECOSPAT,Switzerland) and modified by C. Randin (UNIL-ECOSPAT,Switzerland) S-Plus Function for calculating an adjusted D2 (see Weisberg, 1980) Takes any GLM object as argument</i> |
|----------------|--|

Description

Not to be called directly by the user

Usage

```
eco.adj.D2.glm(glm.obj)
```

Author(s)

'ecospat.adj.D2.glm' from the 'ecospat' package

| | |
|----------|--|
| ecoBoyce | <i>Boyce index model evaluation sub-function I</i> |
|----------|--|

Description

Not to be called directly by the user

Usage

```
ecoBoyce(fit, obs, nclass = 0, window.w = "default", res = 100, PEplot = TRUE)
```

Author(s)

'ecospat.boyce' from the 'ecospat' package

| | |
|--------|------------------------------------|
| fitdoc | <i>Fit presence-absence models</i> |
|--------|------------------------------------|

Description

Flexibly fit various types of functions but let framework take care of resampling, meta-info storage, and file saving. wsl.flex basically allows supplying any possible model, however, there may be problems with prediction/evaluation for exotic functions. Available model algorithms for fitting are: Generalized Linear Models (GLM), Generalized additive models (GAM), Maximum Entropy (MaxEnt), Artificial Neural Networks (ANN), Generalized Boosted regression Models/Boosted Regression Trees (GBM) and Random Forest (RF)

Usage

```
wsl.glm(  
  x = numeric(),  
  pa = numeric(),  
  env_vars = data.frame(),  
  taxon = character(),  
  replicatetype = character(),  
  reps,  
  strata = NA,  
  save = FALSE,  
  project = NA,  
  path = NA,  
  step = FALSE,  
  mod_tag = "",  
  xy = NULL,  
  ...  
)  
  
wsl.gam(  
  x = numeric(),  
  pa = numeric(),  
  env_vars = data.frame(),  
  taxon = character(),  
  replicatetype = character(),  
  reps,  
  strata = NA,  
  save = FALSE,  
  project = NA,  
  path = NA,  
  step = FALSE,  
  mod_tag = "",  
  xy = NULL,  
  ...  
)  
  
wsl.maxent(  
  x = numeric(),  
  pa = numeric(),  
  env_vars = data.frame(),  
  taxon = character(),  
  replicatetype = character(),  
  reps,  
  strata = NA,  
  save = FALSE,  
  project = NA,  
  path = NA,  
  mod_tag = "",  
  xy = NULL,  
  ...  
)  
  
wsl.gbm(  
  x = numeric(),  
  pa = numeric(),  
  env_vars = data.frame(),  
  taxon = character(),  
  replicatetype = character(),  
  reps,  
  strata = NA,  
  save = FALSE,  
  project = NA,  
  path = NA,  
  mod_tag = "",  
  xy = NULL,  
  ...  
)  
  
wsl.gbm(  
  x = numeric(),  
  pa = numeric(),  
  env_vars = data.frame(),  
  taxon = character(),  
  replicatetype = character(),  
  reps,  
  strata = NA,  
  save = FALSE,  
  project = NA,  
  path = NA,  
  mod_tag = "",  
  xy = NULL,  
  ...  
)
```



```

    x = numeric(),
    pa = numeric(),
    env_vars = data.frame(),
    taxon = character(),
    replicatetype = character(),
    reps,
    strata = NA,
    save = FALSE,
    project = NA,
    path = NA,
    mod_tag = "",
    xy = NULL,
    ...
)

wsl.ann(
  x = numeric(),
  pa = numeric(),
  env_vars = data.frame(),
  taxon = character(),
  replicatetype = character(),
  reps,
  strata = NA,
  save = FALSE,
  project = NA,
  path = NA,
  mod_tag = "",
  xy = NULL,
  ...
)

wsl.flex(
  x = numeric(),
  pa = numeric(),
  env_vars = data.frame(),
  taxon = character(),
  replicatetype = character(),
  reps,
  strata = NA,
  save = FALSE,
  project = NA,
  path = NA,
  mod_args = list(),
  xy = NULL
)

```

Arguments

| | |
|----------|---|
| x | Optional. Object of class 'wsl.pseudoabsences'. If used 'pa', 'env_vars' and 'taxon' will be replaced by new set of values set in the object. |
| pa | Object of class 'vector' with presence/absence values |
| env_vars | Object of class 'data.frame' with environmental predictors |

| | |
|---------------|---|
| taxon | Name of the taxon for which models are fitted |
| replicatetype | (How) should replicates be generated? May be 'none', 'splitsample', 'cv' or 'block-cv' |
| reps | Number of replicates |
| strata | A numeric vector of the same length as observations with integers separating cross validation replicates. Only used when replicatetype='block-cv' |
| save | Should the model be saved in a structured way? (not implemented yet) |
| project | Character indicating the name of the project within which the models are run (later used to define saving directories) |
| path | Where to save? (not implemented yet) |
| step | For glms and gams only. Should the models be updated with the step function? |
| mod_tag | Not in wsl.flex. Descriptive label for current model |
| xy | Optional. XY coordinates of observations. Used for post evaluation with presence-only metric when pres_abs=TRUE in wsl.evaluate.pres(). Must be a data.frame() or matrix(). |
| mod_args | List with elements of class 'multi.input' which specify models to be fitted in wsl.flex |

Value

Object of class wsl.fit including slots for meta info, testing data for evaluation, and model objects

Author(s)

Philipp Brun, Yohann Chauvier

Examples

```
# Take anguilla data set from dismo package
data("Anguilla_train")
vrs=c("SegSumT", "USRainDays", "USSlope")
env=Anguilla_train[,vrs]

### Check out wsl.glm
form.glm=as.formula(paste("Presence~",paste(paste0("poly(",vrs,",2)"),collapse="+")))

modi1=wsl.glm(pa=Anguilla_train$Angaus,
              env_vars = env,
              taxon="Angaus",
              replicatetype="cv",
              reps=5,
              project="prototest",
              mod_tag="test-glm",
              formula=form.glm,
              family="binomial",
              step=TRUE)

# Try out custom summary function
summary(modi1)

# Access glm object of first replicate
```

```
summary(modi1@fits$replicate_01$`test-glm`)

# Evaluate the model
eval1=wsl.evaluate.pa(modi1)

# Get evaluation summary
summary(eval1)

### Check out wsl.gam
form.gam=as.formula(paste("Presence~",paste(paste0("s(",vrs,")"),collapse="+")))

# Try out wsl.glm funcion
modi2=wsl.gam(pa=Anguilla_train$Angaus,
              env_vars = env,
              taxon="Angaus",
              replicatetype="splitsample",
              reps=3,
              project="prototest",
              mod_tag="test-gam",
              formula=form.gam,
              family="binomial",
              step=FALSE)

# Try out custom summary function
summary(modi2)

# Access glm object of first replicate
summary(modi2@fits$replicate_01$`test-gam`)

# Evaluate the model
eval2=wsl.evaluate.pa(modi2,crit="maxTSS")

# Get evaluation summary
summary(eval2)

### Check out wsl.gbm
form.gbm=as.formula(Presence ~ .)

# Try out wsl.glm funcion
modi3=wsl.gbm(pa=Anguilla_train$Angaus,
              env_vars = env,
              taxon="Angaus",
              replicatetype="none",
              reps=1,
              project="prototest",
              mod_tag="test-brt",
              formula= form.gbm,
              distribution = "bernoulli",
              interaction.depth = 1,
              shrinkage=.01,
              n.trees = 3500)

# Try out custom summary function
summary(modi3)

# Access glm object of first replicate
summary(modi3@fits$replicate_01$`test-brt`)
```

```

# Prepare external testing data
tste=data.frame(Presence=Anguilla_train$Angaus,CV=1,env)

# Evaluate the model
eval3=wsl.evaluate.pa(modi3,crit="maxTSS",tester=tste)

# Get evaluation summary
summary(eval3)

### Check out wsl.maxent
feat=c("linear=true","quadratic=true","hinge=true","product=true","threshold=false")

# Try out wsl.glm funcion
modi4=wsl.maxent(pa=Anguilla_train$Angaus,
                env_vars = env,
                taxon="Angaus",
                replicatetype="block-cv",
                reps=3,
                strata=sample(1:3,nrow(env),replace=TRUE),
                project="prototest",
                mod_tag="test-mxe",
                args=feat)

# Try out custom summary function
summary(modi4)

# Access glm object of first replicate
summary(modi4@fits$replicate_01$`test-mxe`)

# Define external threshold
thmxe=c(`test-mxe`=0.5)

# Evaluate the model
eval4=wsl.evaluate.pa(modi4,crit="external",thres=thmxe)

# Get evaluation summary
summary(eval4)

# Get thresholds
thr.4=get_thres(eval4,mean=FALSE)

### Check out wsl.flex
form.glm.2=as.formula(paste("Presence~",paste(vrs,collapse="+")))

modinp=list(multi("glm",list(formula=form.glm,family="binomial"),"glm-simple",step=TRUE,weight=TRUE),
            multi("gbm",list(formula=form.gbm,
                             distribution = "bernoulli",
                             interaction.depth = 1,
                             shrinkage=.01,
                             n.trees = 3500),"gbm-simple"),
            multi("gam",list(formula=form.gam,family="binomial"),"gam-simple",step=FALSE,weight=TRUE),
            multi("maxent",list(args=feat),"mxe-simple"),
            multi("randomForest",list(formula=form.gbm,ntree=500,maxnodes=NULL),"waud1"),
            multi("glm",list(formula=form.glm.2,family="binomial"),"glm-lin",step=TRUE,weight=TRUE))

# Try out wsl.glm funcion

```

```

modi5=wsl.flex(pa=Anguilla_train$Angaus,
               env_vars = env,
               taxon="Angaus",
               replicatetype="block-cv",
               reps=3,
               strata=sample(1:3,nrow(env),replace=TRUE),
               project="multitest",
               mod_args=modinp)

# Try out custom summary function
summary(modi5)

# Access glm object of first replicate
summary(modi5@fits$replicate_01$`glm-simple`)

# Evaluate the model
eval5<-wsl.evaluate.pa(modi5,crit="pp=op")

# Get evaluation summary
summary(eval5)

# Get thresholds
thr.5=get_thres(eval5, mean=FALSE)

```

fitppm

Fit Poisson Point Process Models (PPPM)

Description

PPPM (Poisson Point Process Models) is a modelling approach genrally design to use observation-only data aka point occurences. It allows the user to model species observations intensity per unit area (i.e. the density of presence points over a spatial grid) as a log linear function of predictors. Quadrature points (or background points) are necessary in the model, and may be generated with the 'wsl.quadrature' function. Those points apply a spatial scaling proportional to the study area and estimate the maximised model log likelihood (see Renner 2013, Renner et al. 2015). 'wsl.ppmGlasso' applies a point process model, but also by choosing to implement regularisation and variable selection following the package "glmnet".

Usage

```

wsl.ppmGlasso(
  pres = data.frame(),
  env_vars = matrix(),
  quadPoints = wsl.quads(),
  asurface = numeric(),
  taxon = character(),
  replicatetype = character(),
  reps,
  strata = NA,
  save = FALSE,
  project = NA,
  path = NA,

```

```

    mod_tag = "",
    poly = TRUE,
    which_poly = NULL,
    lasso = TRUE,
    penalty.glmnet = NULL,
    ...
)

```

Arguments

| | |
|-----------------------------|---|
| <code>pres</code> | Object of class 'data.frame' or 'matrix'. Coordinates xy of Species observations. |
| <code>env_vars</code> | If 'wsl.ppmGlasso' used, must be an object of class 'matrix' or 'data.frame' with environmental predictor values. Note that categorical predictor values must be of class factor for both 'env_vars' and 'quadPoints@Qenv' |
| <code>quadPoints</code> | If 'wsl.ppmGlasso' used, must a 'wsl.quads' object generated with 'wsl.quadrature' function and 'lasso=TRUE'. |
| <code>asurface</code> | Only when 'wsl.ppmGlasso' used. The surface of the study area in square kilometers |
| <code>taxon</code> | Name of the taxon for which models are fitted |
| <code>replicatetype</code> | (How) should replicates be generated? may be 'none', 'splitsample', 'cv' or 'block-cv' |
| <code>reps</code> | Number of replicates |
| <code>strata</code> | A numeric vector of the same length as observations + quadrature points with integers assigning cross validation replicates. Only used when replicatetype='block-cv'. Note: the vector must first integrate CV information for observation points. |
| <code>save</code> | Should the model be saved in a structured way? (not implemented yet) |
| <code>project</code> | Character indicating the name of the project within which the models are run (later used to define saving directories) |
| <code>path</code> | Where to save? (not implemented yet) |
| <code>mod_tag</code> | Descriptive label for current model |
| <code>poly</code> | If TRUE, PPPM fits a second order polynomial regression |
| <code>which_poly</code> | Which predictors should be using polynomial terms? Use a binary vector that specify which variables/predictors. Length of vector must be equal to the number of input variables. '1' stands for poly=TRUE whereas '0' stands for poly=FALSE. Default is polynomial for all if poly=TRUE. |
| <code>lasso</code> | If FALSE no regularisation is applied |
| <code>penalty.glmnet</code> | If 'lasso=TRUE', a binary vector that specify which variables/predictors used to model should be shrinked. Length of vector must be equal to the number of input variables. '1' stands for shrinkage whereas '0' stands for no shrinkage, i.e. the variable will always be included in the model. |
| <code>...</code> | If 'wsl.ppmGlasso' used with lasso = TRUE, arguments passed on to the cv.glmnet() function (package 'glmnet') use to apply a Lasso, Ridge or Elastic Net regularisation. To notice that the package's argument 'penalty.factor' is not needed here. If used, the parameter 'penalty.glmnet' must instead be filled for each 'env_vars'. If lasso = FALSE, arguments passed on to the glm("poisson") function. |
| <code>formula</code> | Equation of the desired fit |

Value

Object of class `wsl.fit` including slots for meta info, testing data for evaluation, and model objects

Author(s)

Yohann Chauvier, Philipp Brun

Examples

```
### Load

data(AlpineConvention_lonlat)
data(exrst)
rst = rst[[1:6]]
data(xy_ppm)
mypoints = xy.ppm[,c("x", "y")]

### Define mask

maskR = mask(rst[[1]], shp.lonlat)

### Run 'wsl.ppm.window' function

wind = wsl.ppm.window(mask = maskR,
                      val = 1,
                      owin = TRUE)

### Define quadrature points for 'wsl.ppmGlasso'

# Grid regular
quadG1 = wsl.quadrature(mask = maskR,
                       area.win = wind,
                       random = FALSE,
                       lasso = TRUE,
                       env_vars = rst)

### Define your environments

# For 'wsl.ppmGlasso' (observations focus)
envG = raster::extract(rst, mypoints)

### Modelling

# 'wsl.ppmGlasso' (alpha = 0.5 => Elastic net, see package 'glmnet')
# Complex PPM lasso (poly = TRUE & lasso=TRUE)

lasso1 = wsl.ppmGlasso(pres = mypoints,
                      quadPoints = quadG1,
                      asurface = raster::area(shp.lonlat)/1000,
                      env_vars = envG,
                      taxon = "species_eg1",
                      replicatetype = "cv",
                      reps = 5,
                      strata = NA,
                      save=FALSE,
```

```

project = "lasso_eg1",
path = NA,
poly = TRUE,
lasso = TRUE,
alpha = 0.5,
type.measure = "mse",
standardize = TRUE,
nfolds = 5,
nlambda = 100)

# Simple PPM non lasso (poly = FALSE & lasso=FALSE)

lasso2 = wsl.ppmGlasso(pres = mypoints,
                      quadPoints = quadG1,
                      asurface = raster::area(shp.lonlat)/1000,
                      env_vars = envG,
                      taxon = "species_eg2",
                      replicatetype = "cv",
                      reps = 5,
                      strata = NA,
                      save = FALSE,
                      project = "lasso_eg2",
                      path = NA,
                      poly = FALSE,
                      lasso = FALSE)

```

get_thres

*Get threshold***Description**

Extracts thresholds from wsl.evaluation objects and names them so they can be fed to the wsl.predict function. At the moment only averages over replicates can be obtained.

Usage

```
get_thres(x, mean)
```

Arguments

| | |
|------|---|
| x | An object of class wsl.evaluation |
| mean | Logical. If TRUE, a mean is applied to all thresholds |

Value

numeric() or 'vector' with thresholds

Author(s)

Philipp Brun, Yohann Chauvier

Examples

```
# Take anguilla data set from dismo package
data("Anguilla_train")
vrs=c("SegSumT", "USRainDays", "USSlope")
env=Anguilla_train[,vrs]

### Check out wsl.glm
form.glm=as.formula(paste("Presence~",paste(paste0("poly(",vrs,",2)"),collapse="+")))

modi1=wsl.glm(pa=Anguilla_train$Angaus,
              env_vars = env,
              taxon="Angaus",
              replicatetype="cv",
              reps=5,
              project="prototest",
              mod_tag="test-glm",
              formula=form.glm,
              family="binomial",
              step=TRUE)

# Evaluate the model
eval1=wsl.evaluate.pa(modi1)

# Get thresholds
get_thres(eval1, mean = FALSE)
get_thres(eval1, mean = TRUE)
```

hde

Hide annoying prints

Description

Not to be called directly by the user

Usage

`hde(x)`

Author(s)

Philipp Brun

make_blocks

*Block-wise split data into training and testing***Description**

Creates a stratum vector based on a data.frame with n columns. If the data.frame has one column strata are created based on clusters separated by quantiles. If the data.frame has two or more columns, strata are created based on k-medoid clusters (function 'pam' from package cluster). Instead of a data.frame also the argument 'npoints' can be provided, then groups are created by random sampling. An optimization algorithm (function 'gridSearch' from package NMOF) optimizes for equal stratum sizes.

Usage

```
make_blocks(
  nstrat = 4,
  df = data.frame(),
  nclusters = nstrat * 5,
  npoints = NA,
  pres = numeric()
)
```

Arguments

| | |
|-----------|---|
| nstrat | Number of approximately equal-sized classes to separate groups in block-cross validation |
| df | Object of class 'data.frame' with n columns containing criteria for cluster building. Not necessary if argument npoints is supplied |
| nclusters | Number of clusters based on which strata should be built. Minimum is the same number as 'nstrat'. Maximum is nrow(df)/10. |
| npoints | Optional argument if 'df' is not supplied. For how many points should random sampling be made? |
| pres | Optional argument if 'df' is not supplied. For how many points should random sampling be made? |

Value

Object of class 'vector' of length nrow(df) or 'npoints', with integers defining different strata

Author(s)

Philipp Brun

Examples

```
### Test out block generation function

data("Anguilla_train")
vrs=c("SegSumT", "USRainDays", "USSlope")
env=Anguilla_train[,vrs]
```

```

# No layers supplied
strt.1=make_blocks(npoints=1000)
table(strt.1)

# Stratified by 1d layer a
strt.2=make_blocks(df=env[,1,drop=F],nstrat=5,nclusters=5)
table(strt.2)

# Stratified by 1d layer b
strt.3=make_blocks(df=env[,1,drop=F],nstrat=5,nclusters=15)
table(strt.3)

# Stratified by 2d layer a
strt.4=make_blocks(df=env[,c(1,3)],nstrat=3,nclusters=3)
table(strt.4)

# Stratified by 2d layer b
strt.5=make_blocks(df=env[,c(1,3)],nstrat=5,nclusters=50)
table(strt.5)

# Stratified by 3d layer
strt.6=make_blocks(df=env[,1:3],nstrat=5,nclusters=50)
table(strt.6)

par(mfrow=c(3,2))
plot(env[,c(1,3)],col=strt.1)
plot(env[,c(1,3)],col=strt.2)
plot(env[,c(1,3)],col=strt.3)
plot(env[,c(1,3)],col=strt.4)
plot(env[,c(1,3)],col=strt.5)
plot(env[,c(1,3)],col=strt.6)

```

make_tiles

Create a specific number of tiles based on a raster extent

Description

Based on a specific extent, one or several tiles are generated. Tiles can be smaller raster extents or geometry arguments POLYGON(). The original extent is therefore either converted into a POLYGON() argument, or divided into Ntiles of regular fragments which are converted into POLYGON() arguments and smaller SpatExtent.

Usage

```
make_tiles(geo, Ntiles, sext = TRUE)
```

Arguments

| | |
|--------|--|
| geo | Object of class 'Extent', 'SpatExtent', 'SpatialPolygon', 'SpatialPolygonDataframe', or 'SpaVector' (WGS84 or planar) to define the study's area extent. Default is NULL i.e. the whole globe. |
| Ntiles | Numeric. In how many tiles/fragments should geo be divided approximately? |
| sext | Logical. Should a list of SpatExtent also be returned for each generated POLYGON()? |

Value

A list of geometry arguments POLYGON() of length Ntiles (and of SpatExtent if sext=TRUE)

References

Chauvier, Y., Thuiller, W., Brun, P., Lavergne, S., Descombes, P., Karger, D. N., ... & Zimmermann, N. E. (2021). Influence of climate, soil, and land cover on plant species distribution in the European Alps. *Ecological monographs*, 91(2), e01433. 10.1002/ecm.1433

Examples

```
# Load the European Alps Extent
data(geo_dat)

# Apply the function to divide the extent in ~20 fragments
mt = make_tiles(geo=shp.lonlat,Ntiles=20,sext=TRUE); mt
```

multi

Define settings for function that should be supplied to wsl.flex

Description

Create a multi.input object that efficiently stores model specifications

Usage

```
multi(mod, args, tag = "", step = FALSE, weight = FALSE)
```

Arguments

| | |
|------|---|
| mod | A character with the name of the function to be called. E.g. "gam" |
| args | A list with arguments to be passed to the function specified in 'mod' |
| tag | Character with name for model set-up |
| step | Should step function be applied to update model |

Value

Object of class 'multi'

Author(s)

Philipp Brun

Examples

```
### Preliminary

data("Anguilla_train")
vrs=c("SegSumT", "USRainDays", "USSlope")

form.glm=as.formula(paste("Presence~",paste(paste0("poly(",vrs,",2)"),collapse="+"))))
form.gbm=as.formula(Presence ~ .)
form.glm.2=as.formula(paste("Presence~",paste(vrs,collapse="+"))))
feat=c("linear=true","quadratic=true","hinge=true","product=true","threshold=false")
form.gam=as.formula(paste("Presence~",paste(paste0("s(",vrs,")"),collapse="+"))))

### Multi examples

multi("glm",list(formula=form.glm,family="binomial"),"glm-simple",step=TRUE)
multi("gbm",list(formula=form.gbm,
                 distribution = "bernoulli",
                 interaction.depth = 1,
                 shrinkage=.01,
                 n.trees = 3500),"gbm-simple")
multi("gam",list(formula=form.gam,family="binomial"),"gam-simple",step=FALSE)
multi("maxent",list(args=feat),"mxe-simple")
multi("randomForest",list(formula=form.gbm,ntree=500,maxnodes=NULL),"wald1")
multi("glm",list(formula=form.glm.2,family="binomial"),"glm-lin",step=TRUE)
```

| | |
|-------------------|---|
| multi.input-class | <i>An S4 class to store evaluation data</i> |
|-------------------|---|

Description

An S4 class to store evaluation data

Slots

mod Name of model algorithm to be called (character) e.g., 'glm'

args A list of arguments to be supplied to the model fitting algorithm

tag The name of the model setup (character)

step A logical indicating whether step function should be ran (for glm and gam)

weight Should observations be weighted based on their prevalence?

Author(s)

Philipp Brun

| | |
|-------|---|
| optme | <i>Optimization function to create equal-sized strata in the 'make_blocks' function</i> |
|-------|---|

Description

Not to be called directly by the user

Usage

```
optme(x, nms, grps, tot)
```

Author(s)

Philipp Brun

| | |
|--------|---|
| prd.pa | <i>Correctly feed the predict functions depending on model type (glm, gbm, maxent...)</i> |
|--------|---|

Description

Not to be called directly by the user

Usage

```
prd.pa(mod, tst, clust = FALSE)
```

Author(s)

Philipp Brun

| | |
|----------|--|
| prd.pres | <i>Correctly feed the predict functions depending on model type (ppm, glm, gbm, maxent...)</i> |
|----------|--|

Description

Not to be called directly by the user

Usage

```

prd.pres(
  mod,
  env_vars,
  window,
  polly,
  meta,
  coefs,
  id.fact = NULL,
  valid.pres = NULL,
  env_samp = NULL
)

```

Author(s)

Yohann Chauvier

| | |
|-------|---|
| preps | <i>Check input data, collect meta information, take care of data subsetting. Called by model fitting functions.</i> |
|-------|---|

Description

Not to be called directly by the user

Usage

```
preps(env = parent.frame(), call)
```

Author(s)

Philipp Brun, Yohann Chauvier

| | |
|------------|--|
| preva.meta | <i>Generate meta information for prediction and evaluation</i> |
|------------|--|

Description

Not to be called directly by the user

Usage

```
preva.meta(env = parent.frame(), type = character())
```

Author(s)

Philipp

| | |
|---------------|---|
| prop.sampling | <i>Sample pseudo-absences proportional to target group distribution</i> |
|---------------|---|

Description

Uses the 'density' function from the package spatstat to create a density surface of the supplied point pattern and samples pseudo-absences from this density-distribution.

Usage

```
prop.sampling(points, nsamples = 1000, res = 1, ...)
```

Arguments

| | |
|----------|--|
| points | matrix or data.frame with column names 'x' and 'y' assumed to be on the same scale and metric distances (m, km,...) |
| nsamples | number of pseudoabsences to be generated |
| res | resolution of the density grid from which pseudo-absences are drawn. default (1) corresponds to 1000 cells on the x-axis |
| ... | arguments passed on to the 'density' function from package spatstat. Note in particular the argument 'adjust' which controls the kernel size in the density interpolation. |

Value

nsamples x 2 matrix with drawn pseudo-absences

Author(s)

Philipp Brun

Examples

```
### Load points
data(mypts)

### Test proportional sampling

pseu.1=prop.sampling(points=my.pts,nsamples=10000,adjust=1,res=1)
pseu.2=prop.sampling(points=my.pts,nsamples=10000,adjust=.5,res=1)
pseu.3=prop.sampling(points=my.pts,nsamples=10000,adjust=.2,res=1)
pseu.4=prop.sampling(points=my.pts,nsamples=10000,adjust=.1,res=1)

par(mfrow=c(2,2))

plot(pseu.1,pch=16,col="red",cex=.5)
points(my.pts)
plot(pseu.2,pch=16,col="red",cex=.5)
points(my.pts)
plot(pseu.3,pch=16,col="red",cex=.5)
```



```

points(my.pts)
plot(pseu.4,pch=16,col="red",cex=.5)
points(my.pts)

```

pseu.targr

Sample pseudo-absences proportional to target group distribution 2.0

Description

This is essentially an improved version of `prop.sampling`. It uses the 'density' function from the package 'spatstat' to create a density surface of the supplied point pattern and samples pseudo-absences from this density-distribution. It additionally requires a raster layer (`env.layer`) as input, typically containing an environmental variable used for modelling to extract information about the extent of the study area and the resolution of the environmental information. Furthermore, a mask of class `Spatial` can be supplied to constrain the area within which pseudoabsences should be sampled. If no mask is supplied, pseudoabsences are sampled in the non-NA cells of the `env.layer`.

Usage

```

pseu.targr(
  points,
  nsamples = 1000,
  p.avoid = NULL,
  env.layer,
  mask = NULL,
  ...
)

```

Arguments

| | |
|------------------------|---|
| <code>points</code> | Matrix or data.frame with column names 'x' and 'y' assumed to be on the same scale and metric distances (m, km,...) |
| <code>nsamples</code> | Number of pseudoabsences to be generated |
| <code>p.avoid</code> | Same type and conditions as "points" argument; avoid sampling pseudo-absences in cells where input coordinates fall |
| <code>env.layer</code> | A raster layer of desired resolution and extent (and area of interest -> non_NA cells) |
| <code>mask</code> | Optional. An object of class <code>Spatial</code> to mask for sampling area of interest |
| <code>...</code> | Additional arugements to the density.ppp function (package 'spatstat') |

Value

nsamples x 2 matrix with drawn psuedo-absences

Author(s)

Philipp Brun, Yohann Chauvier

Examples

```
# Load files

data(AlpineConvention_lonlat)
data(exrst)
data(xy_ppm)
mypoints=xy.ppm[,c("x","y")]
id.avoid=sample(1:nrow(mypoints),500,replace=TRUE)
xy.avoid=mypoints[id.avoid,]
xy.process=mypoints[-id.avoid,]

# Run pseu.targr()

dens1=pseu.targr(points=xy.process,nsamples=5000,p.avoid=xy.avoid,
  env.layer=rst[[1]],mask=shp.lonlat,adjust=0.1)
dens2=pseu.targr(points=xy.process,nsamples=5000,p.avoid=xy.avoid,
  env.layer=rst[[1]],mask=shp.lonlat,adjust=0.5)
dens3=pseu.targr(points=xy.process,nsamples=1000,p.avoid=NULL,
  env.layer=rst[[1]],mask=NULL,adjust=0.1)
dens4=pseu.targr(points=xy.process,nsamples=1000,p.avoid=NULL,
  env.layer=rst[[1]],mask=NULL,adjust=0.5)

# Plot results

par(mfrow=c(2,2))

plot(rst[[1]])
points(dens1,pch=20,cex=0.3)
plot(rst[[1]])
points(dens2,pch=20,cex=0.3)
plot(rst[[1]])
points(dens3,pch=20,cex=0.3)
plot(rst[[1]])
points(dens4,pch=20,cex=0.3)
```

stratify

Subsample based on two stratification criteria

Description

Subsample based on two stratification criteria

Usage

```
stratify(spp, type, sampsiz)
```

Arguments

| | |
|---------|---|
| spp | Spatial data.frame |
| type | either 'env.strat' or 'env.semi.strat' |
| sampsiz | desired size of the subsample Not to be called directly by the user |

Author(s)

Philipp Brun

References

Descombes, P., Chauvier, Y., Brun, P., Righetti, D., Wüest, R. O., Karger, D. N., ... & Zimmermann, N. E. (2022). Strategies for sampling pseudo-absences for species distribution models in complex mountainous terrain. *bioRxiv*, 2022-03.

| | |
|-----------|---|
| thin_them | <i>Thin a spatial points object by number of points or minimum distance</i> |
|-----------|---|

Description

Thin a spatial points object by number of points or minimum distance

Usage

```
thin_them(spdf, lim_dist = NA, lim_n = NA)
```

Arguments

| | |
|----------|--|
| spdf | SpatialPoints or SpatialPointsDataFrame object |
| lim_dist | Minimum tolerated distance between the points |
| lim_n | Number of points to be kept |

Details

iteratively the closest point pairs are compared and the point with the lower overall distinctiveness is removed

Value

thinned SpatialPoints or SpatialPointsDataFrame object

Author(s)

Philipp Brun

References

Descombes, P., Chauvier, Y., Brun, P., Righetti, D., Wüest, R. O., Karger, D. N., ... & Zimmermann, N. E. (2022). Strategies for sampling pseudo-absences for species distribution models in complex mountainous terrain. *bioRxiv*, 2022-03.

| | |
|--------------------|---|
| upsample_strategic | <i>Sample a subsample from a large set of points with a minimum distance constraint</i> |
|--------------------|---|

Description

Thin a spatial points object by number of points or minimum distance

Usage

```
upsample_strategic(spdf, lim_dist, n_tot, warnig = TRUE)
```

Arguments

| | |
|----------|--|
| spdf | SpatialPoints or SpatialPointsDataFrame object |
| lim_dist | Minimum tolerated distance between the points |
| n_tot | Minimum tolerated distance between the points |

Details

iteratively samples points and rejects them if min thist to all existing points i the sample are not respected

Value

SpatialPoints or SpatialPointsDataFrame with at least lim_dist between all points

Author(s)

Philipp brun

References

Descombes, P., Chauvier, Y., Brun, P., Righetti, D., Wüest, R. O., Karger, D. N., ... & Zimmermann, N. E. (2022). Strategies for sampling pseudo-absences for species distribution models in complex mountainous terrain. *bioRxiv*, 2022-03.

| | |
|---------------|---|
| upsample_thin | <i>Sample a subsample from a large set of points with a minimum distance constraint</i> |
|---------------|---|

Description

Thin a spatial points object by number of points or minimum distance

Usage

```
upsample_thin(spdf, lim_dist, n_tot)
```

Arguments

| | |
|----------|--|
| spdf | SpatialPoints or SpatialPointsDataFrame object |
| lim_dist | Minimum tolerated distance between the points |
| n_tot | Minimum tolerated distance between the points |

Details

iteratively samples points and rejects them if min thist to all existing points i the sample are not respected

Value

SpatialPoints or SpatialPointsDataFrame with at least lim_dist between all points

Author(s)

Philipp Brun

References

Descombes, P., Chauvier, Y., Brun, P., Righetti, D., Wüest, R. O., Karger, D. N., ... & Zimmermann, N. E. (2022). Strategies for sampling pseudo-absences for species distribution models in complex mountainous terrain. *bioRxiv*, 2022-03.

| | |
|---------|--|
| wsl.ebc | <i>Correct environmental bias of species observations via environmental clustering</i> |
|---------|--|

Description

Our wsl.ebc function corrects environmental bias from an observational dataset based on environmental stratification / clustering. A map of n clusters is generated based on input raster layers (in the article, climate predictors used in PPMs are employed as inputs). Following random equal-stratified sampling design (EBCE; Hirzel & Guisan, 2002), for each cluster, the number of observations per species (relative to all others) is artificially rescaled to the total number of observations found in the cluster presenting the highest observation density. Proportional-stratified sampling design (EBCp; Hirzel & Guisan, 2002) adds a second step: for each cluster, the number of observations per species may additionally be multiplied by the cluster's area (i.e. proportion of pixels in percentage relative to the study area), or by its logarithm (default; consensus between EBCE and EBCp). Resulting output indicates a new number of observations per cluster and species, that the function automatically sub-samples with replacement over the original observational dataset. This function may be used for presences and absences distinctively.

Usage

```
wsl.ebc(
  obs = NULL,
  ras = NULL,
  pportional = TRUE,
  plog = TRUE,
  nclust = 50,
```

```

    sp.specific = TRUE,
    sp.cor = 0.5,
    keep.bias = TRUE,
    filter = FALSE,
    path = NULL,
    ...
)

```

Arguments

| | |
|-------------|---|
| obs | Object of class matrix or data frame with three columns named sp.id (character), x (numeric) and y (numeric). More than one observation per species must be referenced. |
| ras | Object of class RasterBrick, RasterStack, list of RasterLayer of desired resolution and extent. Used to generate the map of clusters needed to summarize the environmental space of the study area. |
| pportional | Logical. Should environmental stratification of observations be proportional to the clusters' areas? If TRUE, EBCp applies. |
| plog | Logical. Should EBCp apply with a logarithm? If TRUE, a stratification consensus between EBCp and EBCe applies. |
| nclust | Number of chosen clusters. Default is 50. |
| sp.specific | Logical. Should EBC apply only for species whose environmental bias follows the overall one (i.e. the number of original species observations per cluster is correlated with that of the full dataset)? |
| sp.cor | If sp.specific = TRUE, spearman's correlation tests are by default set to 0.5; i.e. species with $r < 0.5$ are excluded from the function outputs. |
| keep.bias | Default is TRUE. Strongly recommended to use when sp.cor = TRUE. Per species, should the number of observations of the cluster in which the species was originally sampled most often, be preserved? Said differently, for each species, should the cluster with the most original species observations be as representative as the cluster with the most corrected observations? If TRUE, after EBC applies, the number of observations per species in their densest original cluster is set to that of the densest corrected cluster. |
| filter | Logical. Should the observations be filtered according to 'ras' resolution? |
| path | Path folder where the new species observation files should be saved. |
| ... | Additional arguments passed on to the 'clara' function (package 'cluster') |

Value

The function returns in 'path', one text file of corrected observations (presences or absences) per species. If the number of new EBC observations per species is too large, sampling those randomly without replacement before model calibrations is advised.

Author(s)

Yohann Chauvier

References

Chauvier, Y., Zimmermann, N. E., Poggiato, G., Bystrova, D., Brun, P., & Thuiller, W. (2021). Novel methods to correct for observer and sampling bias in presence-only species distribution models. *Global Ecology and Biogeography*, 30(11), 2312-2325.

wsl.evaluate.pa

Evaluate presence-absence models

Description

Assess several model skill metrics for all models in a wsl.fit object. Currently AUC, RMSE, TSS, PPV, Accuracy, and Cohen's Kappa are evaluated. Furthermore, the threshold applied is returned.

Usage

```
wsl.evaluate.pa(
  x,
  tester = data.frame(),
  window = NULL,
  thres = numeric(),
  crit = "pp=op",
  prevalence_correction = FALSE,
  pres_only = FALSE,
  log_trans = TRUE,
  bias_cov = NULL
)
```

Arguments

| | |
|-----------------------|--|
| x | A wsl.fit object |
| tester | Optional. A data.frame with testing data. Only mandatory if replicatetype='none' was chosen when models were fitted. Otherwise, used when evaluation against external dataset is needed. Must be a data.frame with as columns in order : "Presence" ('0' and '1'), "CV" (numeric: chosen cv-folds; if replicatetype='none' -> only '1') and associated environmental values (same ones as for fitted models; i.e. same columns order and names). Note that categorical predictor values must be of class factor. NB: Here, model evaluation will only be initiated for the new testing data. |
| window | Only when 'wsl.ppmO' used'. Same object of class 'owin' used for models (in developments) |
| thres | Vector of the same length as the number of reps in model fit object. For wsl.flex model outputs, thresholds have to be labelled with the same names provided to models. |
| crit | Which threshold criterion should be considered? Currently 'pp=op' (predicted prevalence = observed prevalence), 'maxTSS' (threshold yielding maximum TSS), and 'external' (thresholds manually supplied) are possible |
| prevalence_correction | logical. Should imbalanced presence/absence data be upsampled to prevalence 0.5 for model evaluation. |

| | |
|-----------|--|
| pres_only | Logical. If TRUE, evaluation metrics of presence-absence models is applied to a wsl.fit object of presence-only models i.e. generated with wsl.ppmGlasso() |
| log_trans | Logical. Use only if pres_only=TRUE. Should predictions be converted to log-arithm before evaluation? Prevent model evaluation errors. |
| bias_cov | A numerical vector whose length equal the number of environmental layers/columns. Only used when a bias covariate is implemented in the model calibration i.e. to fit species obs. with a potential spatial observer bias. Default is 1 for each variable, whereas designated bias covariate(s) (i.e. 0) will be reset everywhere to zero in order to evaluate corrected predictions |

Value

An object of class 'wsl.evaluation'

Author(s)

Philipp Brun, Yohann Chauvier

Examples

```
# Take anguilla data set from dismo package
data("Anguilla_train")
vrs=c("SegSumT","USRainDays","USSlope")
env=Anguilla_train[,vrs]

### Check out wsl.gam
form.gam=as.formula(paste("Presence~",paste(paste0("s(",vrs,")"),collapse="+")))

# Try out wsl.gam fonction
modi2=wsl.gam(pa=Anguilla_train$Angaus,
  env_vars = env,
  taxon="Angaus",
  replicatetype="split-sample",
  reps=3,
  project="prototest",
  mod_tag="test-gam",
  formula=form.gam,
  family="binomial",
  step=FALSE)

# Try out custom summary function
summary(modi2)

# Access gam object of first replicate
summary(modi2@fits$replicate_01$`test-gam`)

# Evaluate the model
eval2=wsl.evaluate.pa(modi2,crit="maxTSS")

# Get evaluation summary
summary(eval2)
```

wsl.evaluate.pres *Evaluate presence-only models*

Description

Assess model skill metrics for presence-only models in a wsl.fit object. Currently Boyce index is evaluated. Furthermore, the threshold applied is returned.

Usage

```
wsl.evaluate.pres(
  x,
  tester = data.frame(),
  env_vars,
  window = NULL,
  thres = numeric(),
  pres_abs = FALSE,
  log_trans = TRUE,
  speedup = FALSE,
  env_samp = 5000,
  bias_cov = NULL,
  ...
)
```

Arguments

| | |
|-----------|---|
| x | A wsl.ppm fit object |
| tester | Optional. A data.frame with testing data. Only mandatory if replicatetype='none' was chosen when models were fitted. Otherwise, used when evaluation against external dataset is needed. Must be a data.frame with as columns in order: "x", "y", "Presence" ('0' and '1'), "CV" (numeric: chosen cv-folds; if replicatetype='none' -> only '1') and associated environmental values (same ones as for fitted models; i.e. same columns order and names). Note that categorical predictor values must be of class factor. NB: Here, model evaluation will only be initiated for the new testing data. |
| env_vars | Same spatial layers used in the fitted model or an object of class 'data.frame' or 'matrix' defining a sample of the target layers by keeping same order for columns. If spatial layers are used, object of class 'RasterStack' or 'RasterBrick'. |
| thres | Vector of the same length as the number of reps in model fit object |
| pres_abs | Logical. If TRUE, evaluation metrics of presence-only models is applied to a wsl.fit object of presence-absence models |
| log_trans | Logical. Use only if pres_abs=FALSE. Should predictions be converted to logarithm before evaluation? Prevent model evaluation errors. |
| speedup | If env_vars is a 'RasterStack' or 'RasterBrick', should the boyce evaluation be faster? If TRUE, the algorithm uses a sample of the environmental layers |
| env_samp | If speedup=TRUE, how many environmental cells should be sampled with replacement? Default is 50'000 samples. The sample may be smaller than requested because of NAs |

bias_cov A numerical vector whose length equal the number of environmental layers/columns. Only used when a bias covariate is implemented in the PPM calibration i.e. to fit species observations with a potential spatial observer bias. Default is 1 for each variable, whereas designated bias covariate(s) (i.e. 0) will be reset everywhere to zero in order to evaluate corrected predictions

... Additional arguments supplied to ecospat.boyce function (package 'ecospat')

Value

an object of class 'wsl.evaluation'. If in slot "performance" NA as thresholds are found, it indicates a lack of convergence in the model tested, and so, a biased/invalid threshold

Author(s)

Yohann Chauvier, Philipp Brun

Examples

```
#### Load

data(AlpineConvention_lonlat)
data(exrst)
rst = rst[[1:6]]
data(xy_ppm)
mypoints = xy.ppm[,c("x", "y")]

#### Define mask

maskR = mask(rst[[1]], shp.lonlat)

#### Run 'wsl.ppm.window' function

wind = wsl.ppm.window(mask = maskR,
                      val = 1,
                      owin = TRUE)

#### Define quadrature points for 'wsl.ppmGlasso'

# Grid regular
quadG1 = wsl.quadrature(mask = maskR,
                       area.win = wind,
                       random = FALSE,
                       lasso = TRUE,
                       env_vars = rst)

#### Define your environments

# For 'wsl.ppmGlasso' (observations focus)
envG = raster::extract(rst, mypoints)

#### Modelling

# 'wsl.ppmGlasso' (alpha = 0.5 => Elastic net, see package 'glmnet')
# Complex PPPM lasso (poly = TRUE & lasso=TRUE)
```

```

lasso1 = wsl.ppmGlasso(pres = mypoints,
                      quadPoints = quadG1,
                      asurface = raster::area(shp.lonlat)/1000,
                      env_vars = envG,
                      taxon = "species_eg1",
                      replicatetype = "cv",
                      reps = 5,
                      strata = NA,
                      save=FALSE,
                      project = "lasso_eg1",
                      path = NA,
                      type = "binomial",
                      poly = TRUE,
                      lasso = TRUE,
                      alpha = 0.5,
                      type.measure = "mse",
                      standardize = TRUE,
                      nfolds = 5,
                      nlambda = 100)

# Simple PPM non lasso (poly = FALSE & lasso=FALSE)

lasso2 = wsl.ppmGlasso(pres = mypoints,
                      quadPoints = quadG1,
                      asurface = raster::area(shp.lonlat)/1000,
                      env_vars = envG,
                      taxon = "species_eg2",
                      replicatetype = "cv",
                      reps = 5,
                      strata = NA,
                      save = FALSE,
                      project = "lasso_eg2",
                      path = NA,
                      type = "binomial",
                      mask = maskR,
                      poly = FALSE,
                      lasso = FALSE)

### Evaluation

# Example for 'wsl.ppmGlasso'

eval1 = wsl.evaluate.pres(x = lasso1,
                        env_vars = rst)

eval2 = wsl.evaluate.pres(x = lasso2,,
                        env_vars = rst,
                        thres = 0.001)

summary(eval1)
summary(eval2)

```

Description

An S4 class to store evaluation data

Slots

meta A list with meta information

thres A vector with externally supplied thresholds

performance A list with model performance estimates

Author(s)

Philipp Brun

wsl.fit-class

An S4 class to store fitted objects

Description

An S4 class to store fitted objects

Slots

meta A list with meta information

tesdat A list with held out data to be used for testing

performance fitted model objects

call the function call

Author(s)

Philipp Brun, Yohann Chauvier

wsl.obs.filter

Filter set of observations

Description

Filter presences / absences through a chosen resolution grid.

Usage

```
wsl.obs.filter(o.xy, a.xy = NULL, grid)
```

Arguments

| | |
|-------------------|---|
| <code>o.xy</code> | Object of class 'matrix' or 'data frame' with two columns named "x" and "y". Must be used alone to apply grid filtering to one set of observations (presences or absences). |
| <code>a.xy</code> | Object of class 'matrix' or 'data frame' with two columns named "x" and "y". NULL by default. If used, "o.xy" becomes presences and "a.xy" absences. Resolution grid filtering is applied to both observation sets, but coordinates of "a.xy" falling within the same grid cells as "o.xy" are removed. |
| <code>grid</code> | Object of class 'RasterLayer', 'RasterBrick' or 'RasterStack' of desired resolution and extent. |

Value

Object of class 'matrix' or 'data frame' with two columns named "x" and "y" comprising the new set of observations filtered at grid resolution. If "a.xy" is used the output is a list of two data.frame: filtered presences and filtered absences

Author(s)

Yohann Chauvier

Examples

```
### Load my binary observations species data

library(raster)

data(var_select_XYtest)
data(exrst)

### wsl.obs.filter(): example for the first species

# Loading observations: presences and absences

presences = coordinates(mySP[[1]])[myPA[[1]] %in% "1",]
absences = coordinates(mySP[[1]])[myPA[[1]] %in% "0",]

# Loading grid

r.layer = rst[[1]]

# To filter observations by the grid only

pres.filtered = wsl.obs.filter(presences,grid=r.layer)
abs.filtered = wsl.obs.filter(absences,grid=r.layer)

# To filter observations by the grid & remove abs. in cells where we also find pres.

PresAbs.filtered = wsl.obs.filter(presences,absences,r.layer)

# Count presences (same filtering)

nrow(PresAbs.filtered[[1]])
nrow(pres.filtered)
```

```

# Count Absences (filtering plus removal of duplicated absences)

nrow(abs.filtered)
nrow(PresAbs.filtered[[2]])

# Visual

par(mfrow=c(1,2))
plot(presences)
plot(pres.filtered)

par(mfrow=c(1,2))
plot(absences)
plot(abs.filtered)

```

wsl.ppm.env

*Poisson Point Process Models (PPPM) 'env'***Description**

Convert environmental data for 'wsl.ppmO' fitting.

Usage

```
wsl.ppm.env(env_vars, mask)
```

Arguments

| | |
|----------|--|
| env_vars | Object of class 'RasterBrick' or 'RasterStack'. Same extent and resolution as 'mask' |
| mask | Object of class 'RasterLayer' or 'RasterBrick' or 'RasterStack'. Mask is defined according to non NAs values and the resolution of the study |

Value

List of objects of class 'im'

Author(s)

Yohann Chauvier

Examples

```

### Load

data(exrst)
data(xy_ppm)
mypoints = xy.ppm[,c("x", "y")]

### Define mask

```

```

maskR = mask(rst[[1]],shp.lonlat)

### Define your environments

# For 'wsl.ppmGlasso' (observations focus)
envG = raster::extract(rst,mypoints)

# For 'wsl.ppmO' (study area focus)
envO = wsl.ppm.env(rst,maskR)

```

| | |
|-----------------|---|
| wsl.ppm.qscheme | <i>To prepare PPM general quadratic environment with input species points</i> |
|-----------------|---|

Description

Not to be called directly by the user

Usage

```
wsl.ppm.qscheme(data, area.win, quads)
```

Author(s)

Yohann Chauvier

| | |
|----------------|---|
| wsl.ppm.window | <i>Poisson Point Process Models (PPPM) 'window'</i> |
|----------------|---|

Description

Set up a study window of class 'owin' or 'im' necessary to run 'wsl.ppmO' fit function.

Usage

```
wsl.ppm.window(mask, val = 1, owin)
```

Arguments

| | |
|------|---|
| mask | Object of class 'RasterLayer' or 'RasterBrick' or 'RasterStack'. Mask is defined according to non NAs values. Defined study area in pixels. Same as in 'wsl.quadrature' |
| val | Values that are assigned to the 'owin' or 'im' mask |
| owin | TRUE or FALSE |

Value

Object of class 'owin' or 'im'

Author(s)

Yohann Chauvier

Examples

```

### Load

data(AlpineConvention_lonlat)
data(exrst)

### Define mask

maskR = mask(rst[[1]],shp.lonlat)

### Run function

wind = wsl.ppm.window(mask = maskR,
                      val = 1,
                      owin = TRUE)

```

wsl.predict.pa

*Make predictions***Description**

Make predictions with all models from a wsl.fit object. If thresholds are supplied binary predictions are made if convert=TRUE, otherwise continuous predictions and separate description of thresholds are returned

Usage

```

wsl.predict.pa(
  x,
  predat = data.frame(),
  thres = numeric(),
  bias_cov = NULL,
  clust = FALSE
)

```

Arguments

| | |
|----------|---|
| x | An object of class wsl.fit |
| predat | Data.frame or raster for which predictions should be made |
| thres | Optional. Object of the same length as the number of replicates, or model types if a mean is applied accross model types. Obtained with 'get_thres' |
| bias_cov | A numerical vector whose length equal the number of environmental layers/columns. Only used when a bias covariate is implemented in calibrations i.e. to fit species observations with a potential spatial observer bias. Default is 1 for each variable, whereas designated bias covariate(s) (i.e. 0) will be reset everywhere to zero in order to evaluate corrected predictions |
| clust | Logical. If raster predictions are made, should the operation be run in parallel ? |

Value

Object of class wsl.prediction with slots for meta info, and model predictions

Author(s)

Philipp Brun, Yohann Chauvier

Examples

```
# Take anguilla data set from dismo package
data("Anguilla_train")
vrs=c("SegSumT", "USRainDays", "USSlope")
env=Anguilla_train[,vrs]

### Check out wsl.glm
form.glm=as.formula(paste("Presence~", paste(paste0("poly(", vrs, ", 2)"), collapse="+")))

modi1=wsl.glm(pa=Anguilla_train$Angaus,
              env_vars = env,
              taxon="Angaus",
              replicatetype="cv",
              reps=5,
              project="prototest",
              mod_tag="test-glm",
              formula=form.glm,
              family="binomial",
              step=TRUE)

# Try out custom summary function
summary(modi1)

# Access glm object of first replicate
summary(modi1@fits$replicate_01$`test-glm`)

# Evaluate the model
eval1=wsl.evaluate.pa(modi1)

# Get evaluation summary
summary(eval1)

### Check out wsl.gam
form.gam=as.formula(paste("Presence~", paste(paste0("s(", vrs, ")"), collapse="+")))

# Try out wsl.glm funcion
modi2=wsl.gam(pa=Anguilla_train$Angaus,
              env_vars = env,
              taxon="Angaus",
              replicatetype="splitsample",
              reps=3,
              project="prototest",
              mod_tag="test-gam",
              formula=form.gam,
              family="binomial",
              step=FALSE)
```

```

# Try out custom summary function
summary(modi2)

# Access glm object of first replicate
summary(modi2@fits$replicate_01$`test-gam`)

# Evaluate the model
eval2=wsl.evaluate.pa(modi2,crit="maxTSS")

# Get evaluation summary
summary(eval2)

### Check out wsl.gbm
form.gbm=as.formula(Presence ~ .)

# Try out wsl.glm funcion
modi3=wsl.gbm(pa=Anguilla_train$Angaus,
              env_vars = env,
              taxon="Angaus",
              replicatetype="none",
              reps=1,
              project="prototest",
              mod_tag="test-brt",
              formula= form.gbm,
              distribution = "bernoulli",
              interaction.depth = 1,
              shrinkage=.01,
              n.trees = 3500)

# Try out custom summary function
summary(modi3)

# Access glm object of first replicate
summary(modi3@fits$replicate_01$`test-brt`)

# Prepare external testing data
tste=data.frame(Presence=Anguilla_train$Angaus,CV=1,env)

# Evaluate the model
eval3=wsl.evaluate.pa(modi3,crit="maxTSS",tester=tste)

# Get evaluation summary
summary(eval3)

### Check out wsl.maxent
feat=c("linear=true","quadratic=true","hinge=true","product=true","threshold=false")

# Try out wsl.glm funcion
modi4=wsl.maxent(pa=Anguilla_train$Angaus,
                 env_vars = env,
                 taxon="Angaus",
                 replicatetype="block-cv",
                 reps=3,
                 strata=sample(1:3,nrow(env),replace=TRUE),
                 project="prototest",
                 mod_tag="test-mxe",
                 args=feat)

```

```

# Try out custom summary function
summary(modi4)

# Access glm object of first replicate
summary(modi4@fits$replicate_01$`test-mxe`)

# Define external threshold
thmxe=c(`test-mxe`=0.5)

# Evaluate the model
eval4=wsl.evaluate.pa(modi4,crit="external",thres=thmxe)

# Get evaluation summary
summary(eval4)

# Get thresholds
thr.4=get_thres(eval4, mean=FALSE)

### Check out wsl.flex
form.glm.2=as.formula(paste("Presence~",paste(vrs,collapse="+")))

modinp=list(multi("glm",list(formula=form.glm,family="binomial"),"glm-simple",step=TRUE,weight=TRUE),
  multi("gbm",list(formula=form.gbm,
    distribution = "bernoulli",
    interaction.depth = 1,
    shrinkage=.01,
    n.trees = 3500),"gbm-simple"),
  multi("gam",list(formula=form.gam,family="binomial"),"gam-simple",step=FALSE,weight=TRUE),
  multi("maxent",list(args=feat),"mxe-simple"),
  multi("randomForest",list(formula=form.gbm,ntree=500,maxnodes=NULL),"waud1"),
  multi("glm",list(formula=form.glm.2,family="binomial"),"glm-lin",step=TRUE,weight=TRUE))

# Try out wsl.glm funcion
modi5=wsl.flex(pa=Anguilla_train$Angaus,
  env_vars = env,
  taxon="Angaus",
  replicatetype="block-cv",
  reps=3,
  strata=sample(1:3,nrow(env),replace=TRUE),
  project="multitest",
  mod_args=modinp)

# Try out custom summary function
summary(modi5)

# Access glm object of first replicate
summary(modi5@fits$replicate_01$`glm-simple`)

# Evaluate the model
eval5<-wsl.evaluate.pa(modi5,crit="pp=op")

# Get evaluation summary
summary(eval5)

# Get thresholds
thr.5=get_thres(eval5, mean=FALE)

```

```
### Make some predictions
pred4=wsl.predict.pa(modi4,predat=env)
pred5=wsl.predict.pa(modi5,predat=env,thres=thr.5)
```

| | |
|------------------|-------------------------|
| wsl.predict.pres | <i>Make predictions</i> |
|------------------|-------------------------|

Description

Make predictions with all models from a wsl.fit object. If thresholds are supplied binary predictions are made, otherwise continuous predictions are returned.

Usage

```
wsl.predict.pres(
  x,
  thres = numeric(),
  predat = list(),
  window = NULL,
  log_trans = TRUE,
  raster = FALSE,
  bias_cov = NULL
)
```

Arguments

| | |
|-----------|--|
| x | An object of class wsl.fit |
| thres | Optional. Object of the same length as the number of replicates, or model types if a mean is applied accross model types. Obtained with 'get_thres' |
| predat | Same spatial layers used in the fitted model or an object of class 'data.frame' or 'matrix' defining a sample of the target layers by keeping same order for columns. If spatial layers, when wsl.ppmGlasso' used, object of class 'RasterStack' or RasterBrick'. |
| log_trans | Logical. Should the predictions be converted to logarithm before converting to binary ? Should be TRUE if log.trans was TRUE when using wsl.evaluate |
| raster | Logical. Should the output be a list of rasters or matrix ? |
| bias_cov | A numerical vector whose length equal the number of environmental layers/columns. Only used when a bias covariate is implemented in the PPM calibration i.e. to fit species observations with a potential spatial observer bias. Default is 1 for each variable, whereas designated bias covariate(s) (i.e. 0) will be reset everywhere to zero in order to evaluate corrected predictions |

Value

Object of class wsl.prediction with slots for meta info, and model predictions

Author(s)

Yohann Chauvier, Philipp Brun

Examples

```

#### Load

data(AlpineConvention_lonlat)
data(exrst)
rst = rst[[1:6]]
data(xy_ppm)
mypoints = xy.ppm[,c("x","y")]

#### Define mask

maskR = mask(rst[[1]],shp.lonlat)

#### Run 'wsl.ppm.window' function

wind = wsl.ppm.window(mask = maskR,
                      val = 1,
                      owin = TRUE)

#### Define quadrature points for 'wsl.ppmGlasso'

# Grid regular
quadG1 = wsl.quadrature(mask = maskR,
                      area.win = wind,
                      random = FALSE,
                      lasso = TRUE,
                      env_vars = rst)

#### Define your environments

# For 'wsl.ppmGlasso' (observations focus)
envG = raster::extract(rst,mypoints)

#### Modelling

# 'wsl.ppmGlasso' (alpha = 0.5 => Elastic net, see package 'glmnet')
# Complex PPPM lasso (poly = TRUE & lasso=TRUE)

lasso1 = wsl.ppmGlasso(pres = mypoints,
                      quadPoints = quadG1,
                      asurface = raster::area(shp.lonlat)/1000,
                      env_vars = envG,
                      taxon = "species_eg1",
                      replicatetype = "cv",
                      reps = 5,
                      strata = NA,
                      save=FALSE,
                      project = "lasso_eg1",
                      path = NA,
                      type = "binomial",
                      mask = maskR,
                      poly = TRUE,
                      lasso = TRUE,
                      alpha = 0.5,
                      type.measure = "mse",

```

```

        standardize = TRUE,
        nfolds = 5,
        nlambda = 100)

# Simple PPPM non lasso (poly = FALSE & lasso=FALSE)

lasso2 = wsl.ppmGlasso(pres = mypoints,
                      quadPoints = quadG1,
                      asurface = raster::area(shp.lonlat)/1000,
                      env_vars = envG,
                      taxon = "species_eg2",
                      replicatetype = "cv",
                      reps = 5,
                      strata = NA,
                      save = FALSE,
                      project = "lasso_eg2",
                      path = NA,
                      type = "binomial",
                      mask = maskR,
                      poly = FALSE,
                      lasso = FALSE)

### Evaluation

# Example for 'wsl.ppmGlasso'

eval1 = wsl.evaluate.pres(x = lasso1,
                          env_vars = rst)

eval2 = wsl.evaluate.pres(x = lasso2,,
                          env_vars = rst,
                          thres = 0.001)

summary(eval1)
summary(eval2)

### Thresholds

get_thres(eval1, mean = FALSE)
get_thres(eval1, mean = TRUE)

get_thres(eval2, mean = FALSE)
get_thres(eval2, mean = TRUE)

### Predictions

# 'wsl.ppmGlasso'
pred1 = wsl.predict.pres(x = lasso1,
                        predat = rst,
                        mask = maskR,
                        thres = get_thres(eval1,mean=FALSE),
                        raster = TRUE)

par(mfrow=c(2,3))
sapply(1:5,function(x) plot(pred1@predictions[[x]][[1]]))

pred2 = wsl.predict.pres(x = lasso2,

```

```

        predat = rst,
        mask = maskR,
        thres = NULL,
        raster = TRUE)

par(mfrow=c(2,3))
sapply(1:5,function(x) plot(pred2@predictions[[x]][[1]]))

pred3 = wsl.predict.pres(x = lasso1,
        predat = rst,
        mask = maskR,
        thres = get_thres(eval1,mean=TRUE),
        raster = TRUE)

par(mfrow=c(2,3))
sapply(1:5,function(x) plot(pred3@predictions[[x]][[1]]))

pred4 = wsl.predict.pres(x = lasso2,
        predat = rst,
        mask = maskR,
        thres = NULL,
        raster = FALSE)

```

wsl.prediction-class *An S4 class to store prediction data*

Description

An S4 class to store prediction data

Slots

meta A list with meta information
thres A vector with externally supplied thresholds
predictions A list with model predictions

Author(s)

Philipp Brun

wsl.pseudoabsences-class
An S4 class to store pseudoabsence data

Description

An S4 class to store pseudoabsence data

Slots

meta A list with meta information
 type The type of pseudoabsence sampling
 pa a vector with presences and pseudo absences
 env_vars data.frame with environmental predictors
 xy a matrix with coordinates of the points

Author(s)

Philipp Brun

wsl.quadrature

Poisson Point Process Models (PPPM) 'quadrature'

Description

Set up quadrature points (or "background points") necessary to run 'wsl.ppmO' and 'wsl.ppmGlasso' fit functions. Those points apply a spatial scaling proportional to the study area and estimate the maximised model log likelihood (see Renner 2013, Renner et al. 2015)

Usage

```
wsl.quadrature(  
  mask,  
  area.win,  
  random = FALSE,  
  nQ = 1e+05,  
  lasso = TRUE,  
  env_vars = NULL  
)
```

Arguments

| | |
|----------|--|
| mask | Object of class 'RasterLayer' or 'RasterBrick' or 'RasterStack'. Mask is defined according to non NAs values. Defines study area in pixels used to grid sample the quadrature points. Sampling is done over raster centroids so the resolution of the mask defines the desired sampling. |
| area.win | Object of class 'owin'. 'owin' output of 'wsl.ppm.window' |
| random | Logical. Should quadrature points be generated randomly or according to a regular mask ? |
| nQ | To choose the number of random quadrature points in case 'random=TRUE' |
| lasso | Logical. Form of the output. If TRUE, 'wsl.ppmGlasso' is used |
| env_vars | Only when 'lasso=TRUE'. Object of class 'RasterBrick' or 'RasterStack'. Set of predictors the user wants to use to fit the model |

Value

Object of class 'ppp' or 'wsl.quads'. Points associated to NAs env. values are removed

Author(s)

Yohann Chauvier

Examples

```
#### Load

data(AlpineConvention_lonlat)
data(exrst)

### Define mask

maskR = mask(rst[[1]],shp.lonlat)

### Run 'wsl.ppm.window' function

wind = wsl.ppm.window(mask = maskR,
                      val = 1,
                      owin = TRUE)

### Define quadrature points for 'wsl.ppmGlasso'

# Grid regular
quadG1 = wsl.quadrature(mask = maskR,
                      area.win = wind,
                      random = FALSE,
                      lasso = TRUE,
                      env_vars = rst)

# Randomly
quadG2 = wsl.quadrature(mask = maskR,
                      area.win = wind,
                      random = TRUE,
                      nQ = 100000,
                      lasso = TRUE,
                      env_vars = rst)

### Define quadrature points for 'wsl.ppm0'

# Grid regular
quad01 = wsl.quadrature(mask = maskR,
                      area.win = wind,
                      random = FALSE,
                      lasso = FALSE,
                      env_vars = NULL)

# Randomly
quad02 = wsl.quadrature(mask = maskR,
                      area.win = wind,
                      random = TRUE,
                      nQ = 100000,
                      lasso = FALSE,
                      env_vars = NULL)
```

| | |
|-----------------|--|
| wsl.quads-class | <i>An S4 class to store quadrature objects</i> |
|-----------------|--|

Description

An S4 class to store quadrature objects

Slots

coordinates informations on the generated quadratures

predictors values extracted for each quadrature

Author(s)

Yohann Chauvier, Philipp Brun

| | |
|-------------------|---|
| wsl.samplePseuAbs | <i>Sample pseudoabsences using various strategies</i> |
|-------------------|---|

Description

Flexible function to sample pseudoabsences with various strategies and store the results in a 'wsl.pseudoabsences' object that can be passed on in the 'wsl.biodiv' pipeline.

Usage

```
wsl.samplePseuAbs(
  n = 10000,
  env.stack,
  type = "geographic",
  add.strat = 0,
  pres = numeric(),
  taxon = character(),
  geodist_fact = 1,
  geores_fact = 20,
  template_dir = NA,
  geo_nrep = 7,
  target.group_dir = NA,
  env.strat_path = NA,
  rAll = TRUE,
  force_spat_thin = "no",
  limdist = NA,
  set_max_npres_to_nabs = TRUE
)
```

Arguments

| | |
|------------------------------------|--|
| <code>n</code> | number of pseudoabsence points desired. Default is 10000. |
| <code>env.stack</code> | RasterStack with environmental layers for sampling and extraction |
| <code>type</code> | Desired sampling strategy. Options are 'geographic', 'density', 'random', 'target.group', 'geo.strat', 'env.strat' and 'env.semi.strat' (see details). Default is 'geographic' |
| <code>add.strat</code> | Fraction between 0 and 1; should strategy be complemented by a fraction of environmental strata. |
| <code>pres</code> | SpatialPoints object. Location of presence points. Necessary for 'geographic' sampling strategy and the best adding point if the downstream functions will be used. |
| <code>taxon</code> | Character; name of taxon of interest to keep track of meta information. |
| <code>geodist_fact</code> | Factor to adjust spatial autocorrelation lengths: for 'geographic' pseudoabsence point patterns, values below 1 increase autocorrelation length; values above 1 decrease it; for 'density' sampling it is the other way around. |
| <code>geores_fact</code> | Aggregation factor 'geographic' template. Larger values save calculation time, but decrease resolution of sampling points. |
| <code>template_dir</code> | Directory where template raster for 'geographic' sampling should be saved in/loaded from. If NA, nothing will be saved; if provided, template will be saved in/loaded from directory depending on whether a file already exists. |
| <code>geo_nrep</code> | number of replicates of geographic models. More will create a smoother pattern but increase computation time. |
| <code>target.group_dir</code> | Directory where xy files of target group taxa are stored. Must be supplied if sampling strategy is 'target.group', must contain a column names 'x' and 'y' with coordinates in the same projection as other spatial data |
| <code>env.strat_path</code> | Directory where sample of environmental strata for 'env.strat' sampling should be saved in/loaded from. If NA, nothing will be saved; if provided, environmental strata will be saved in/loaded from directory depending on whether a file already exists. |
| <code>rAll</code> | should all data be read into memory for computation of environmental strata? this is faster but you may run into memory issues for large rasters. |
| <code>force_spat_thin</code> | Should minimum distance be enforced between points? Options are 'no', 'presences', 'absences', and 'both'. By default thinning is defined for pseudoabsences from 'geographic', 'density', 'random', and 'geo.strat' methods with minimum distance according to the resolution of the template raster. 'presences' takes the minimum distance criterion from the template raster over to the 'presence' points; 'absences' takes the criterion over to 'env.strat', 'env.semi.strat', and 'target.group'; 'both' does it for both. |
| <code>limdist</code> | The minimum distance accepted for spatial thinning. Units should be km if the spatial data is projected, otherwise the units of the coordinate reference system used. If no value is supplied, the maximum distance between two cells of the template raster will be taken. |
| <code>set_max_npres_to_nabs</code> | logical. Should the maximum number of presences be equal to the number of pseudoabsences defined. |

Details

'geographic' samples pseudoabsences with a sampling probability. inversely proportional to the geographic distance to presence observations. 'density' samples pseudoabsences proportional to the density of presence observations. 'random' samples pseudoabsences randomly with a sampling probability proportional the area of the cells. 'target.group' samples pseudoabsences from the presences of the taxa of the target group, attempting to correct for sampling bias. It depends on a directory with taxa defined by the user as target group. 'geo.strat' samples pseudoabsences geographically stratified either on a plane, or on a sphere depending on the projection of the supplied env.stack. 'env.strat' samples pseudoabsences environmentally stratified. Points are sampled from all realized combinations of environmental conditions occurring in the environmental stack that have a minimal occurrence frequency. By default environmental strata are calculated based on all raster layers supplied. If a directory is supplied as 'env.strat_path', a large sample of stratified points will be saved to speed up computations for follow-up species. If environmental strata based on different predictors than supplied are preferred 'env.strat_path' can be an .RData file from a previous sampling of strata from different environmental predictors. 'env.semi.strat' is similar to 'env.strat' but samples environmental strata proportional to the logarithm of the area they cover.

Value

an object of class 'wsl.pseudoabsences' that can be plotted and passed on to wsl.flex

Author(s)

Philipp Brun

References

Descombes, P., Chauvier, Y., Brun, P., Righetti, D., Wüest, R. O., Karger, D. N., ... & Zimmermann, N. E. (2022). Strategies for sampling pseudo-absences for species distribution models in complex mountainous terrain. *bioRxiv*, 2022-03.

Examples

```
### =====
### Data preparation
### =====

# Predictors
bio=getData('worldclim',var='bio',lon=16, lat=48,res=.5)
bio=bio[[c(1,4,12)]]

# install.packages("rgbif")
library(rgbif)
# extract species
spn='Boletus aestivalis'
xt=as.vector(extent(bio))
baest <- occ_search(scientificName=spn,
                    hasCoordinate=TRUE,
                    decimalLongitude=paste0(xt[1],",",xt[3]),
                    decimalLatitude=paste0(xt[2],",",xt[4]))

pbaest=baest$data[,c('decimalLongitude','decimalLatitude')]
baest_spp=SpatialPoints(pbaest,proj4string = crs(bio))

# extract target group
```

```

targr <- occ_search(familyKey = 8789,
                    hasCoordinate=TRUE,
                    limit = 10000,
                    decimalLongitude=paste0(xt[1],",",xt[3]),
                    decimalLatitude=paste0(xt[2],",",xt[4]))

ptargr=as.matrix(targr$data[,c('decimalLongitude','decimalLatitude')])
colnames(ptargr)=c("x","y")

# create temporary directory for target.group info
tdir=paste0(tempdir(),"trgr")
dir.create(tdir)
write.table(ptargr,file=paste0(tdir,"/targetxy.txt"),row.names = F)

# create temporary directory for template raster and env strata
strdir=paste0(tempdir(),"str")
dir.create(strdir)

# Note that for these should not be temporary files for a real analysis.

### =====
### Sample pseudoabsences
### =====

# Geographic method with 20% env strata
pseu.abs1=wsl.samplePseuAbs(type="geographic",
                            n=5000,
                            env.stack=bio,
                            pres=baest_spp,
                            add.strat=0.2,
                            template_dir=strdir,
                            env.strat_path=strdir,
                            geodist_fact=1,
                            geores_fact=3,
                            geo_nrep=7,
                            taxon=spn)

plot(pseu.abs1)

# Only geographic with longer autocorrelation length
pseu.abs2=wsl.samplePseuAbs(type="geographic",
                            n=5000,
                            env.stack=bio,
                            pres=baest_spp,
                            add.strat=0,
                            template_dir=strdir,
                            env.strat_path=strdir,
                            geodist_fact=.5,
                            geores_fact=3,
                            geo_nrep=7,
                            taxon=spn)

plot(pseu.abs2)

# Random and thin presences
pseu.abs3=wsl.samplePseuAbs(type="random",
                            n=5000,

```

```

env.stack=bio,
template_dir=strdir,
pres=baest_spp,
geores_fact=3,
add.strat=0,
taxon=spn,
force_spat_thin="presences")

plot(pseu.abs3)

# Geo.start
pseu.abs4=wsl.samplePseuAbs(type="geo.strat",
n=5000,
env.stack=bio,
template_dir=strdir,
pres=baest_spp,
geores_fact=3,
add.strat=0,
taxon=spn)

plot(pseu.abs4)

# Target group with 20% env strat
pseu.abs5=wsl.samplePseuAbs(type="target.group",
n=5000,
env.stack=bio,
template_dir=strdir,
target.group_dir=tdir,
env.strat_path=strdir,
geores_fact=3,
pres=baest_spp,
add.strat=0.2,
taxon=spn,
force_spat_thin="both")

plot(pseu.abs5)

# Environmental semi-stratified
pseu_abs6=wsl.samplePseuAbs(n = 5000,
env.stack=bio,
type = "env.semi.strat",
add.strat = 0,
pres = baest_spp,
taxon = spn,
template_dir=strdir,
env.strat_path=strdir)

plot(pseu_abs6)

# Environmental semi-stratified with min dist
pseu_abs7=wsl.samplePseuAbs(n = 5000,
env.stack=bio,
type = "env.semi.strat",
add.strat = 0,
geores_fact=3,
pres = baest_spp,
taxon = spn,

```

```

        template_dir=strdir,
        env.strat_path=strdir)

plot(pseu_abs7)

# Density dependent
pseu_abs8=wsl.samplePseuAbs(n = 5000,
                           env.stack=bio,
                           type = "density",
                           add.strat = 0,
                           pres = baest_spp,
                           taxon = spn,
                           geores_fact=3,
                           template_dir=strdir,
                           env.strat_path=strdir)

plot(pseu_abs8)

### =====
### Fit SDMs
### =====

# Define model settings
vrs=names(bio)
form.glm=as.formula(paste("Presence~",paste(paste0("poly(",vrs,",2)"),collapse="+")))
form.gam=as.formula(paste("Presence~",paste(paste0("s(",vrs,")"),collapse="+")))
form.tree=as.formula(Presence ~ .)

modinp=list(multi("glm",list(formula=form.glm,family="binomial"),"glm-simple",step=FALSE),
            multi("gbm",list(formula=form.tree,
                             distribution = "bernoulli",
                             interaction.depth = 1,
                             shrinkage=.01,
                             n.trees = 3500),"gbm-simple"),
            multi("gam",list(formula=form.gam,family="binomial"),"gam-simple",step=FALSE),
            multi("randomForest",list(formula=form.tree,ntree=500,maxnodes=NULL),"wald1"))

# Fit models using wsl.flex function
library(gam)
library(gbm)
library(randomForest)
modi5=wsl.flex(x=pseu.abs5,
               replicatetype="block-cv",
               reps=3,
               strata=sample(1:3,nrow(pseu.abs5@env_vars),replace=TRUE),
               project="multitest",
               mod_args=modinp)

### =====
### Evaluate
### =====

# Evaluate the models with wsl.evaluate function
eval5<-wsl.evaluate(modi5,crit="maxTSS",prevalence_correction = TRUE)
summary(eval5)

### =====

```

```

### Predict
### =====

modi_pred=wsl.flex(x=pseu.abs5,
                   replicatetype="none",
                   reps=1,
                   project="test_pred",
                   mod_args=modinp[c(1:2)])

# Get thresholds
thr.5=get_thres(eval5)[1:2]

### Make some predictions
pred5=wsl.predict(modi_pred,predat=bio,thres = thr.5)

par(mfrow=c(1,2))
plot(pred5@predictions[[1]]$`glm-simple`,main="GLM")
plot(pred5@predictions[[1]]$`gbm-simple`,main="GBM")

```

| | |
|----------------|---|
| wsl.test.quads | <i>Poisson Point Process Models (PPPM) 'quadrature' for presence-absence evaluation metrics</i> |
|----------------|---|

Description

Sample independent test quadrature points over the study area used for evaluating presence-only models with presence-absence metrics (i.e. AUC, TSS, Kappa, PPV...). Presence-only models can be evaluated with other metrics than Boyce index by using random sampling points as absences. But these absences validation data need to be generated independently over the study area i.e. by avoiding resampling quadrature points already used in the models.

Usage

```
wsl.test.quads(mask, quadrature, env_vars, nQ = 10000, replace = TRUE)
```

Arguments

| | |
|------------|---|
| mask | Object of class 'RasterLayer' or 'RasterBrick' or 'RasterStack' of. Mask is defined according to non NAs values. Defines study area in pixels used to grid sample the quadrature points. Sampling is done over raster centroids so the resolution of the mask defines the desired sampling. Same as in 'wsl.quadrature' |
| quadrature | Object of class 'wsl.quads' or 'ppp'. May be one object or a list of object. Same as in wsl.ppm.fit |
| env_vars | An object of class 'RasterStack' or 'RasterBrick'. Same spatial layers used in the models. Use to extract env values from test quadrature points |
| nQ | Number of random quadrature points to sample |
| replace | Logical. If TRUE, quadrature sampling is done with replacements |

Value

Object of class 'wsl.quads' or 'list'. Points associated to NAs env. values are removed

Author(s)

Yohann Chauvier

Examples

```
#### Load

data(AlpineConvention_lonlat)
data(exrst)

### Define mask

maskR = mask(rst[[1]],shp.lonlat)

### Define quadrature points for 'wsl.ppmGlasso'

quadG2 = wsl.quadrature(mask = maskR,
                        area.win = wind,
                        random = TRUE,
                        nQ = 10000,
                        lasso = TRUE,
                        env_vars = rst)

### Define quadrature points for 'wsl.ppm0'

quad02 = wsl.quadrature(mask = maskR,
                        area.win = wind,
                        random = TRUE,
                        nQ = 10000,
                        lasso = FALSE,
                        env_vars = NULL)

### Define quadrature test points for 'wsl.ppmGlasso'

test.quadG2=wsl.quads.test(mask=maskR,
                           quadrature=quadG2,
                           nQ=1000,
                           replace=TRUE)

### Define quadrature test points for 'wsl.ppm0'

test.quadG2=wsl.quads.test(mask=maskR,
                           quadrature=quad02,
                           nQ=1000,
                           replace=TRUE)
```

Description

Rank spatial predictors "ras" in descending order following their mean predictive power found with `wsl.varPPower()`, and apply descending successive correlations tests to obtain a pre-selection of predictors. Additionally a Variance Inflation Factor Test (VIF) may also be applied to predictors which succeeded the descending tests to identify the ones that show high multicollinearity.

Usage

```
wsl.varKeep(
  PPower.object,
  ras,
  corTEST = 0.7,
  vifTEST = FALSE,
  corVIF = 0.7,
  ...
)
```

Arguments

| | |
|----------------------------|---|
| <code>PPower.object</code> | 'wsl.varPPower' object |
| <code>ras</code> | Object of class 'RasterLayer' or 'list' of 'RasterLayer'. Same as in <code>wsl.varPPower()</code> . Layers must be of same resolution i.e. exactly the same number of cells |
| <code>corTEST</code> | Numeric. Threshold of accepted correlation applied in the descending tests |
| <code>vifTEST</code> | Logical. If TRUE, a VIF test is applied to the set of predictors that succeeded descending correlation tests |
| <code>corVIF</code> | Numeric. Threshold of accepted correlation within VIF if "vifTEST=TRUE" |
| <code>...</code> | Arguments passed on to the <code>cor()</code> function used for "corTEST" |

Value

Object of class list with three elements: 1) ranking of non correlated predictors, 2) ranking of leftovers correlated predictors, 3) vif test results

Author(s)

Yohann Chauvier

Examples

```
### Data Preparation

# Load environmental rasters and assign random raster Class
data(exrst)
rCLASS = c(rep("Pollution",4),rep("Climate",4),rep("LandCover",4))

# Create a list of rasters out of the rasterBRICK
rasterL = unstack(rst)

# Load my binary observations species data
data(var_select_XYtest.RData)

### wsl.varPPower(): example with a data.frame & rasters not in classes
```

```

PPower.DF = wsl.varPPower(points=sp.DF[,c("x","y")],
                           val = sp.DF$myPA,
                           species = sp.DF$spCODES,
                           ras = rasterL,
                           rasCLASS = NULL,
                           mlinear = FALSE,
                           glmMODE = "binomial",
                           weight = sp.DF$myWEIGHT,
                           poly = TRUE,
                           polyBRUT = TRUE,
                           parallel = FALSE,
                           cores = NULL)

```

wsl.varPPower(): example with SpatialPointsDataFrame & rasters in classes

```

PPower.DF = wsl.varPPower(points=sp.DF[,c("x","y")],
                           val = sp.DF$myPA,
                           species = sp.DF$spCODES,
                           ras = rasterL,
                           rasCLASS = NULL,
                           mlinear = FALSE,
                           glmMODE = "binomial",
                           weight = sp.DF$myWEIGHT,
                           poly = TRUE,
                           polyBRUT = TRUE,
                           parallel = FALSE,
                           cores = NULL)

```

wsl.varPPower(): example with SpatialPointsDataFrame & rasters in classes

```

# Checking length of every species input
c(length(mySP),length(myPA),length(spCODES),length(myWEIGHT))

```

```

# Running the function
PPower.SPDPF = wsl.varPPower(points = mySP,
                              val = myPA,
                              species = spCODES,
                              ras = rasterL,
                              rasCLASS = rCLASS,
                              mlinear = FALSE,
                              glmMODE = "binomial",
                              weight = myWEIGHT,
                              poly = TRUE,
                              polyBRUT = TRUE,
                              parallel = FALSE,
                              cores = NULL)

```

wsl.varKeep() with a descending correlation of 0.7 with a VIF test at 0.7

```

# Example with no raster classes
KeepVar = wsl.varKeep(PPower.object = PPower.DF,
                      ras = rasterL,
                      corTEST = 0.7,
                      vifTEST = TRUE,
                      corVIF = 0.7,

```

```

use="complete.obs")

#Example with raster classes
KeepVar = wsl.varKeep(PPower.object = PPower.SPDF,
                      ras = rasterL,
                      corTEST = 0.7,
                      vifTEST = TRUE,
                      corVIF = 0.7,
                      use = "complete.obs")

```

wsl.varPPower

Predictive power assessments of predictors

Description

Evaluate the predictive power of single spatial predictors for fitting spatial observations or continuous values. Predictors may be classify in classes to separate the outputs, and data to explain (Y input) may be binary (e.g. presences/absences), discrete (e.g. diversity count) or continuous. Fix and random effects may be used with generalized linear model (GLM) and simple linear model (LM). Therefore, the function currently implement D2.adj::glm(), R2.adj::lm(), pseudo-R2::glmer() and pseudo-R2::lmer(). D2 is calculated via the ecospat package and pseudo-R2 with the MuMIn package for mixed models. Quadratic terms may also be used for more flexible fits, and a parallel argument is available if processing the data is too time consuming.

Usage

```

wsl.varPPower(
  points,
  val,
  species = NULL,
  ras,
  rasCLASS = NULL,
  mlinear = FALSE,
  mixEffect = FALSE,
  mixCat = NULL,
  glmMODE = "binomial",
  weight = 1,
  poly = FALSE,
  polyBRUT = FALSE,
  parallel = FALSE,
  parINFOS = NULL,
  cores = detectCores()/2,
  ...
)

```

Arguments

| | |
|--------|--|
| points | Numeric. Object of class 'matrix' or 'data frame' with two columns named "x" and "y", or 'SpatialPoints', or 'list' of 'SpatialPoints'. "points" should be of same length as "val", "species" and "weight" |
|--------|--|

| | |
|-----------|--|
| val | Numeric. Object of class 'vector' if "points" is of class 'matrix' or 'data.frame', otherwise object of class 'list'. Binary observations if "glmMODE="binomial", discrete if "glmMODE="poisson", continuous if "mlinear=TRUE". Must be of same length as "points", "species" and "weight" |
| species | Character. Object of class 'vector' specifying the ID of your observations. No mandatory use except when "points" is a 'list' of 'SpatialPoints'. If used, must be of same length as "points", "val" and "weight" |
| ras | Object of class 'RasterLayer' or 'list' of 'RasterLayer'. Layers must be of exact same resolution and extent i.e. exactly the same number of cells |
| rasCLASS | Object of class 'vector' to associate IDs to the raster(s) if "ras" is a 'list' of 'RasterLayer' |
| mlinear | 'TRUE' run lm(), 'FALSE' run glm() |
| mixEffect | Default is FALSE. If 'TRUE' run mLinear with random effect (i.e. mix LM or GLM) |
| mixCat | Character. Object of class 'vector' if "points" is of class 'matrix' or 'data.frame', otherwise object of class 'list'. Use to assign categories to your observations. Those are used for potential random effects. Must be of same length as "points", "val" and "species" |
| glmMODE | glm() link function if "mlinear=FALSE" (default::"binomial" or "poisson") |
| weight | Numeric. Object of class 'vector' if "points" is of class 'matrix' or 'data.frame', otherwise object of class 'list'. Used for weighting your observations when running glm() or lm(). Must be of same length as "points", "val" and "species" |
| poly | If TRUE, glm() or lm() uses a polynomial quadratic transformation on "ras" |
| polyBRUT | If TRUE, force "poly" parameter in cases NAs are found in "ras" |
| parallel | If TRUE, parallelisation is active |
| parINFOS | Path. Create a txt file to write parallelisation infos if "parallel=TRUE". |
| cores | Number of cores if "parallel=TRUE" |
| ... | Arguments passed on to the lm() or glm() function |

Value

'wsl.varPPower' object with n slots corresponding to n "rasCLASS". In each slots: matrix of nrow::c("species" + mean + standard deviation) & ncol::"ras". Where NAs occur, models could not correctly converged.

Author(s)

Yohann Chauvier

Examples

```
### Data Preparation

rm(list = setdiff(ls(), lsf.str()))

# Load environmental rasters and assign random raster Class
data(exrst)
rCLASS = c(rep("Pollution",4),rep("Climate",4),rep("LandCover",4))

# Create a list of rasters out of the rasterBRICK
```

```

rasterL = unstack(rst)

# Load my binary observations species data
data(var_select_XYtest)

# Create a category vector
mixV = sample(LETTERS[1:3], 35743, replace=TRUE)

### wsl.varPPower(): example with a data.frame & rasters not in classes

PPower.DF = wsl.varPPower(points=sp.DF[,c("x","y")],
                          val = sp.DF$myPA,
                          species = sp.DF$spCODES,
                          ras = rasterL,
                          rasCLASS = NULL,
                          mlinear = FALSE,
                          glmMODE = "binomial",
                          weight = sp.DF$myWEIGHT,
                          poly = TRUE,
                          polyBRUT = TRUE,
                          parallel = FALSE,
                          cores = NULL)

### wsl.varPPower(): Same example including random effect
PPower.DF = wsl.varPPower(points = sp.DF[,c("x","y")],
                          val = sp.DF$myPA,
                          species = sp.DF$spCODES,
                          ras = rasterL,
                          rasCLASS = NULL,
                          mlinear = FALSE,
                          mixEffect = TRUE,
                          mixCat = mixV,
                          glmMODE = "binomial",
                          weight = sp.DF$myWEIGHT,
                          poly = TRUE,
                          polyBRUT = FALSE,
                          parallel = FALSE,
                          cores = NULL)

### wsl.varPPower(): example with a data.frame & rasters in classes
PPower.DF = wsl.varPPower(points=sp.DF[,c("x","y")],
                          val = sp.DF$myPA,
                          species = sp.DF$spCODES,
                          ras = rasterL,
                          rasCLASS = rCLASS,
                          mlinear = FALSE,
                          glmMODE = "binomial",
                          weight = sp.DF$myWEIGHT,
                          poly = TRUE,
                          polyBRUT = TRUE,
                          parallel = FALSE,
                          cores = NULL)

### wsl.varPPower(): Same example including random effect
PPower.DF = wsl.varPPower(points=sp.DF[,c("x","y")],
                          val = sp.DF$myPA,
                          species = sp.DF$spCODES,

```

```

        ras = rasterL,
        rasCLASS = rCLASS,
        mlinear = FALSE,
        mixEffect = TRUE,
        mixCat = mixV,
        glmMODE = "binomial",
        weight = sp.DF$myWEIGHT,
        poly = TRUE,
        polyBRUT = TRUE,
        parallel = FALSE,
        cores = NULL)

### wsl.varPPower(): example with SpatialPointsDataFrame & rasters in classes

# Checking length of every species input
c(length(mySP),length(myPA),length(spCODES),length(myWEIGHT))

# Generate new random effect classes
mixL = lapply(sapply(mySP,length),function(x) sample(LETTERS[1:3],x, replace=TRUE))

# Running the function
PPower.SPDF = wsl.varPPower(points = mySP[[1]],
                             val = myPA[[1]],
                             species = NULL,
                             ras = rasterL,
                             rasCLASS = rCLASS,
                             mlinear = FALSE,
                             mixEffect=TRUE,
                             mixCat=mixL[[1]],
                             glmMODE = "binomial",
                             weight = myWEIGHT[[1]],
                             poly = TRUE,
                             polyBRUT = TRUE,
                             parallel = FALSE,
                             cores = NULL)

```

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