

Ecography

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Supplementary material

Appendix 1

Supplementary material for the software note:

ecospat: an R package for the support of spatial analyses and modelling of species niches and distributions.

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Dependencies of the *ecospat* package

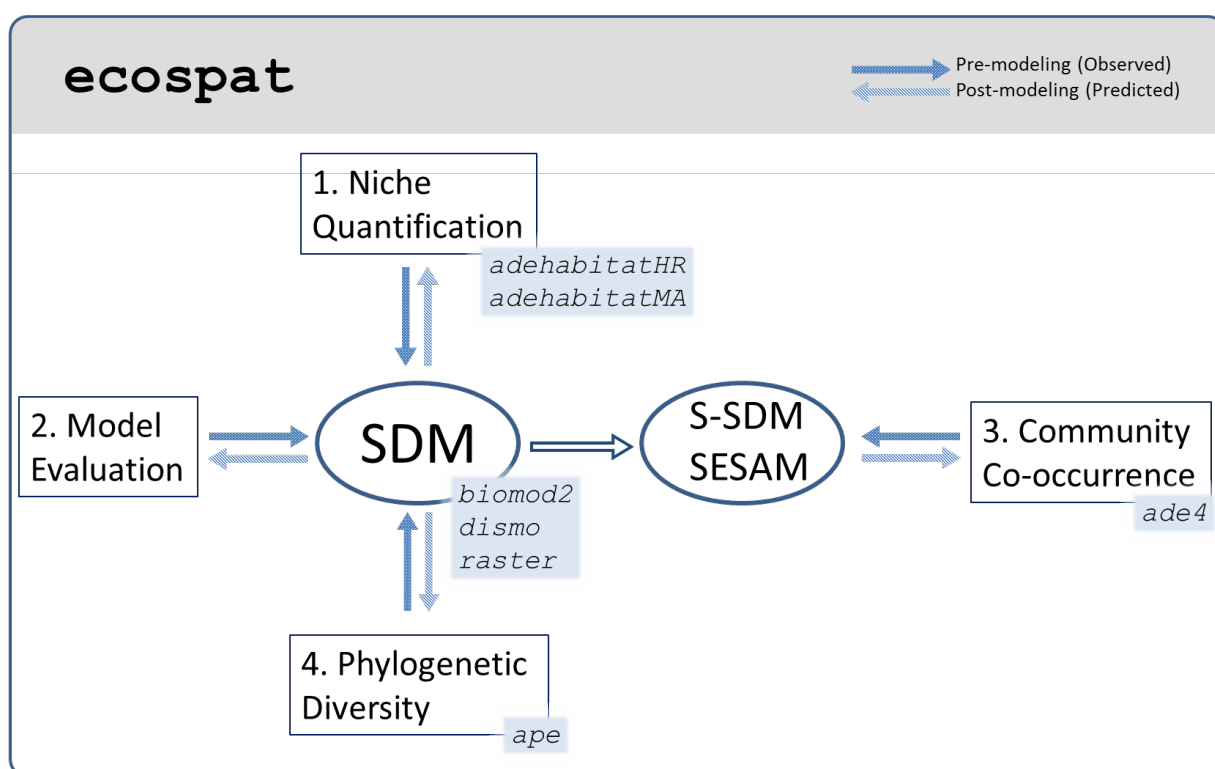


Figure A1. The major functionalities of the *ecospat* R package and its dependencies in relation to SDMs.

Table A1. List of dependent packages (versions) and associated functions, used in the *ecospat* package.

Function	Depends on
<code>ecospat.mantel.correlogram</code>	" <i>ecodist</i> " ($\geq 1.2.9$), <i>mgram</i>
<code>ecospat.calculate.pd</code>	" <i>ape</i> " (≥ 3.2)

ecospat.grid.clim.dyn	"adehabitatMA" (>= 0.3.8), ascgen "adehabitatHR" (>= 0.4.11), kernelUD "raster" (>= 2.5-8), cellStats, crs
ecospat.cv.glm	"dismo" (>= 0.9-3), predict
ecospat.cv.gam	"dismo" (>= 0.9-3), predict "gam" (>= 1.09.1), step.gam, gam
ecospat.cv.gbm	"gbm" (>= 2.1)
ecospat.cv.me	"dismo" (>= 0.9-3), predict, maxent Java software: maxent.jar
ecospat.cv.rf	"dismo" (>= 0.9-3), predict "randomForest" (>= 4.6-7), randomForest
ecospat.ESM.Modeling	"gtools" (>= 3.4.1), mixedsort, combinations
ecospat.ESM.EnsembleModeling	"PresenceAbsence" (>= 1.1.9), presence.absence.accuracy, optimal.thresholds "gtools" (>= 3.4.1), mixedsort "sp" (>= 1.0-15), aggregate
ecospat.ESM.Projection	"gtools" (>= 3.4.1), mixedsort, combinations
ecospat.ESM.EnsembleProjection	"raster" (>= 2.5-8), nlayers, stack
ecospat.migclim	"MigClim" (>= 1.6)
ecospat.cons_Cscore	"ade4" (>= 1.6-2)
ecospat.boyce	"raster" (>= 2.5-8), getValues, extract

Liaw and Wiener (2002), Paradis et al. (2004), (Pebesma and Bivand 2005), Calenge (2006), (Dray and Dufour 2007), Goslee and Urban (2007), Freeman and Moisen (2008), Bivand et al. (2013), (Engler et al. 2013), Hastie (2013), Ridgeway (2013), Warnes et al. (2014), (Hijmans 2015), Hijmans et al. (2016)

Supplementary R scripts for the two examples with outputs

Load the library

```
> library(ecospat)
> citation("ecospat")
```

Script Example 1. Niche quantification and modelling of an invasive species

Loading test data for the niche dynamics analysis in the invaded range

```
> inv <- ecospat.testNiche.inv
```

Loading test data for the niche dynamics analysis in the native range

```
> nat <- ecospat.testNiche.nat
```

Niche quantification and comparaison

PCA-ENVIRONMENT

the pca is calibrated on all the sites of the study area

```
> pca.env<-dudi.pca(rbind(nat,inv)[,3:10],scannf=FALSE,nf=2) #
```

Calibrating the PCA in the whole study area, including both native and invaded ranges (same as PCAenv in Broenniman et al. 2012)

Plot Variables Contribution with *ecospat.plot.contrib()*

```
> ecospat.plot.contrib(contrib=pca.env$co, eigen=pca.env$eig)
```

predict the scores on the axes

```
> scores.globclim<-pca.env$li # PCA scores for the whole study area
```

```
> scores.sp.nat<-suprow(pca.env,nat[which(nat[,11]==1),3:10])$li #
```

PCA scores for the species native distribution

```
> scores.sp.inv<-suprow(pca.env,inv[which(inv[,11]==1),3:10])$li #
```

PCA scores for the species invasive distribution

```
> scores.clim.nat<-suprow(pca.env,nat[,3:10])$li # PCA scores for the whole
```

native study area

```
> scores.clim.inv<-suprow(pca.env,inv[,3:10])$li # PCA scores for the whole
```

invaded study area

```
# Calculate the Occurrence Densities Grid with ecospat.grid.clim.dyn()
```

```
# For a species in the native range (North America)
```

```
> grid.clim.nat<-ecospat.grid.clim.dyn(glob=scores.globclim,
```

```
globl=scores.clim.nat, sp=scores.sp.nat, R=100, th.sp=0)
```

```
# For a species in the invaded range (Australia)
```

```
> grid.clim.inv<-ecospat.grid.clim.dyn(glob=scores.globclim,
```

```
globl=scores.clim.inv, sp=scores.sp.inv, R=100, th.sp=0)
```

```
# Calculate Niche Overlap with ecospat.niche.overlap()
```

```
> ecospat.niche.overlap (grid.clim.nat, grid.clim.inv, cor=TRUE)
```

```
$D
```

```
[1] 0.2243085
```

```
# Perform the Niche Equivalency Test with ecospat.niche.equivalency.test()
```

```
> eq.test<-ecospat.niche.equivalency.test(grid.clim.nat,
```

```
grid.clim.inv, rep=100, alternative = "greater", ncores = 2)
```

```
# Niche Similarity Test with ecospat.niche.similarity.test()
```

```

# shifting randomly the invasive niche in the invaded study area

> sim.test<-ecospat.niche.similarity.test(grid.clim.nat,
grid.clim.inv, rep=100, alternative = "greater", rand.type = 2,
ncores = 2)

# Plot Equivalency test

> ecospat.plot.overlap.test(eq.test, "D", "Equivalency")

# Plot Similarity test

> ecospat.plot.overlap.test(sim.test, "D", "Similarity")

# Delimiting niche categories and quantifying niche dynamics in analogue climates with
ecospat.niche.dyn.index()

> ecospat.niche.dyn.index (grid.clim.nat, grid.clim.inv,
intersection=0.1)

$dynamic.index.w
expansion stability unfilling
0.1521472 0.8478528 0.2763685

#Visualizing niche categories, niche dynamics and climate analogy between ranges with
ecospat.plot.niche.dyn()

> ecospat.plot.niche.dyn(grid.clim.nat, grid.clim.inv, quant=0.1,
interest=2, title= "Niche Overlap", name.axis1="PC1",
name.axis2="PC2")

# Plot Variables Contribution with ecospat.plot.contrib()

> ecospat.plot.contrib(contrib=pca.env$co, eigen=pca.env$eig)

```

```

# Plot the niche dynamics along one gradient (here temperature) with
ecospat.plot.niche.dyn()

# gridding the native niche
> grid.clim.t.nat <- ecospat.grid.clim.dyn
  (glob=as.data.frame(rbind(nat,inv)[,10]),
  glob1=as.data.frame(nat[,10]),
  sp=as.data.frame(nat[which(nat[,11]==1),10]), R=1000, th.sp=0)

# gridding the invaded niche
> grid.clim.t.inv <- ecospat.grid.clim.dyn
  (glob=as.data.frame(rbind(nat,inv)[,10]),
  glob1=as.data.frame(inv[,10]),
  sp=as.data.frame(inv[which(inv[,11]==1),10]), R=1000, th.sp=0)

> t.dyn <- ecospat.niche.dyn.index (grid.clim.t.nat,
  grid.clim.t.inv, intersection=0.1)
> ecospat.plot.niche.dyn(grid.clim.t.nat, grid.clim.t.inv,
  quant=0.1, interest=2, title= "Niche Overlap", name.axis1="Average
  temperature")

# Showing the shift of the niche centroid along the temperature gradient (compared to the shift of
the available climate in the study area) with ecospat.shift.centroid()
> ecospat.shift.centroids(nat[which(nat[,11]==1),10],
  inv[which(inv[,11]==1),10],nat[,10],inv[,10])

## ESM Ensemble of Small Models

```

Calibration of simple bivariate models

```
> my.ESM <- ecospat.ESM.Modeling( data=myBiomodData,
                                models=c('GLM', 'RF'),
                                models.options=myBiomodOption,
                                NbRunEval=2,
                                DataSplit=70,
                                weighting.score=c("AUC"),
                                parallel=FALSE)
```

Evaluation and averaging of simple bivariate models to ESMs

```
my.ESM_EF <-
ecospat.ESM.EnsembleModeling(my.ESM, weighting.score=c("SomersD"),
                             threshold=0)
```

Projection of simple bivariate models into new space or time

```
my.ESM_proj_current <- ecospat.ESM.Projection(ESM.modeling.output=my.ESM,
                                              new.env=current)
```

Projection of calibrated ESMs into new space or time

```
my.ESM_EFproj_current <-
ecospat.ESM.EnsembleProjection(ESM.prediction.output=my.ESM_proj_current,
                               ESM.EnsembleModeling.output=my.ESM_EF)
```

Evaluating SDMs' ability to predict the invasive distribution with the Boyce index, a presence only

evaluator `ecospat.boyce()`

The argument fit is a vector containing the predicted suitability values

```
> fit <- inv[,12]
```

The argument obs is a vector containing the predicted suitability values of the validation points

(presence records)

```
> obs <- inv[which(inv[,11]==1),12]
```

```
> ecospat.boyce(fit, obs, PEplot=TRUE)$Spearman.cor
[1] 0.889
```

Script Example 2: Species assemblage's structure and spatial predictions

Phylogenetic diversity predictions

Load the tree and data set from the ecospat package

```
> fpath <- system.file("extdata", "ecospat.testTree.tre",  
package="ecospat")  
> tree <- read.tree(fpath)  
> data <- ecospat.testData[9:52]
```

Run the function

```
> pd <- ecospat.calculate.pd(tree, data, method = "spanning", type =  
"species", root = FALSE, average = FALSE, verbose = TRUE )
```

Plot the results (correlation of phylogenetic diversity with species richness)

```
> plot(pd)
```

SESAM framework: Spatial prediction of communities

Input data for the first argument (proba) as data frame of rough probabilities from SDMs for all species in columns in the considered sites in rows.

```
> proba<-ecospat.testData[,73:92]
```

Input data for the second argument (sr) as data frame with richness value in the first column and sites.

```
> sr<-as.data.frame(rowSums(proba))
```

#Run the function

```
> ecospat.SESAM.prr(proba, sr)
```

#Output of the function contains a table with the community prediction by the SESAM framework

```
> head(community.prediction.prr)  
glm_Agrostis_capillaris glm_Leontodon_hispidus_sl glm_Dactylis_glomerata  
1 0 1 1  
2 1 0 1  
3 1 0 1  
4 1 0 1  
5 1 0 1  
6 1 0 1
```

Evaluating community predictions

#Define the argument eval, which is the observed presence-absence

```
> eval <-  
ecospat.testData[c(53,62,58,70,61,66,65,71,69,43,63,56,68,57,55,60,54,67,59,  
,64)]
```

#Define the argument pred that are the predictions of the distribution for those species

```
> pred<-ecospat.testData[c(73:92)]
```

```
#Run the function
```

```
> ecospat.CommunityEval (eval, pred, proba=TRUE, ntir=1)
```

```
#Returned objects of the function
```

\$deviation. rich.pred	\$underpredi ction	\$sensitivit y	\$kappa	\$similarity
1 0	1 0.6666667	1 0.3333333	1 0.2156863	1 0.3333333
2 -7	2 0.0000000	2 0.3636364	2 0.3396226	2 0.5333333
3 -6	3 0.0000000	3 0.4545455	3 0.4285714	3 0.6250000
4 -5	4 0.0000000	4 0.5000000	4 0.5000000	4 0.6666667
5 -11	5 0.0000000	5 0.1538462	5 0.1129032	5 0.2666667
6 -1	6 0.2000000	6 0.7272727	6 0.5000000	6 0.7619048

\$overpredic tion	\$prediction .success	\$specificit y	\$TSS	\$Jaccard
1 0.1176471	1 0.80	1 0.8823529	1 0.2156863	1 0.2000000
2 0.4375000	2 0.65	2 1.0000000	2 0.3636364	2 0.3636364
3 0.4000000	3 0.70	3 1.0000000	3 0.4545455	3 0.4545455
4 0.3333333	4 0.75	4 1.0000000	4 0.5000000	4 0.5000000
5 0.6111111	5 0.45	5 1.0000000	5 0.1538462	5 0.1538462
6 0.3000000	6 0.75	6 0.7777778	6 0.5050505	6 0.6153846

```
## Environmentally-constrained species co-occurrence analyses
```

```
# Input data as a matrix of plots (rows) x species (columns). Input matrices should have column  
names (species names) and row names (sampling plots).
```

```
> presence <- ecospat.testData[c(9:24)]  
> pred <- ecospat.testData[65:82]
```

```
# Define the number of permutations
```

```
> nbpermut <- 10000
```

```
# Define the outpath
```

```
> outpath <- getwd()
```

```
# Run the function
```

```
> ecospat.cons_Cscore(presence, pred, nbpermut, outpath)
```

#Returned objects of the function

\$ObsCscoreTot

[1] 3308.25

\$SimCscoreTot

[1] 4876.848

\$PVal.less

[1] 9.999e-05

\$PVal.greater

[1] 1

\$SES.Tot

[1] -40.77995

Supplementary Reference

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