

# Vignette ecospat package

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**Valeria Di Cola, Olivier Broennimann, Blaise Petitpierre, Manuela D’Amen, Frank Breiner & Antoine Guisan #####** 08 November, 2017

Miscellaneous methods and utilities for spatial ecology analysis, written by current and former members and collaborators of the *ecospat* group of Antoine Guisan, Department of Ecology and Evolution (DEE) & Institute of Earth Surface Dynamics (IDYST), University of Lausanne, Switzerland.

*ecospat* offers the possibility to perform Pre-modelling Analysis, such as Spatial autocorrelation analysis, MESS (Multivariate Environmental Similarity Surfaces) analyses, Phylogenetic diversity Measures, Biotic Interactions. It also provides functions to complement *biomod2* in preparing the data, calibrating and evaluating (e.g. boyce index) and projecting the models. Complementary analysis based on model predictions (e.g. co-occurrences analyses) are also provided.

In addition, the *ecospat* package includes Niche Quantification and Overlap functions that were used in Broennimann et al. 2012 and Petitpierre et al. 2012 to quantify climatic niche shifts between the native and invaded ranges of invasive species.

## 1 Load data

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

```
## To cite package 'ecospat' in publications use:
##
##   Broennimann O, Di Cola V, Guisan A (2024). _ecospat: Spatial Ecology
##   Miscellaneous Methods_. R package version 4.1.1,
##   <https://www.unil.ch/ecospat/home/menuguid/ecospat-resources/tools.html>.
##
## A BibTeX entry for LaTeX users is
##
##   @Manual{,
##     title = {ecospat: Spatial Ecology Miscellaneous Methods},
##     author = {Olivier Broennimann and Valeria {Di Cola} and Antoine Guisan},
##     year = {2024},
##     note = {R package version 4.1.1},
##     url = {https://www.unil.ch/ecospat/home/menuguid/ecospat-resources/tools.html},
##   }
```

### 1.0.1 Test data for the ecospat library

*ecospat.testData()*

```
data(ecospat.testData)
names(ecospat.testData)
```

```
## [1] "numplots"           "long"
## [3] "lat"                "ddeg"
## [5] "mind"               "srad"
## [7] "slp"                "topo"
## [9] "Achillea_atrata"    "Achillea_millefolium"
## [11] "Acinos_alpinus"     "Adenostyles_glabra"
## [13] "Aposeris_foetida"   "Arnica_montana"
## [15] "Aster_bellidiastrum" "Bartsia_alpina"
## [17] "Bellis_perennis"    "Campanula_rotundifolia"
## [19] "Centaurea_montana"  "Cerastium_latifolium"
## [21] "Cruciata_laevipes"  "Doronicum_grandiflorum"
## [23] "Galium_album"       "Galium_anisophyllum"
## [25] "Galium_megalospermum" "Gentiana_bavarica"
## [27] "Gentiana_lutea"     "Gentiana_purpurea"
## [29] "Gentiana_verna"     "Globularia_cordifolia"
## [31] "Globularia_nudicaulis" "Gypsophila_repens"
## [33] "Hieracium_lactucella" "Homogyne_alpina"
## [35] "Hypochaeris_radicata" "Leontodon_autumnalis"
## [37] "Leontodon_helveticus" "Myosotis_alpestris"
## [39] "Myosotis_arvensis"  "Phyteuma_orbiculare"
## [41] "Phyteuma_spicatum"  "Plantago_alpina"
## [43] "Plantago_lanceolata" "Polygonum_bistorta"
## [45] "Polygonum_viviparum" "Prunella_grandiflora"
## [47] "Rhinanthus_alectorolophus" "Rumex_acetosa"
## [49] "Rumex_crispus"      "Vaccinium_gaultherioides"
## [51] "Veronica_alpina"    "Veronica_aphylla"
## [53] "Agrostis_capillaris" "Bromus_erectus_sstr"
## [55] "Campanula_scheuchzeri" "Carex_sempervirens"
## [57] "Cynosurus_cristatus" "Dactylis_glomerata"
```

```
## [59] "Daucus_carota" "Festuca_pratensis_sl"
## [61] "Geranium_sylvaticum" "Leontodon_hispidus_sl"
## [63] "Potentilla_erecta" "Pritzelago_alpina_sstr"
## [65] "Prunella_vulgaris" "Ranunculus_acris_sl"
## [67] "Saxifraga_oppositifolia" "Soldanella_alpina"
## [69] "Taraxacum_officinale_aggr" "Trifolium_repens_sstr"
## [71] "Veronica_chamaedrys" "Parnassia_palustris"
## [73] "glm_Agrostis_capillaris" "glm_Leontodon_hispidus_sl"
## [75] "glm_Dactylis_glomerata" "glm_Trifolium_repens_sstr"
## [77] "glm_Geranium_sylvaticum" "glm_Ranunculus_acris_sl"
## [79] "glm_Prunella_vulgaris" "glm_Veronica_chamaedrys"
## [81] "glm_Taraxacum_officinale_aggr" "glm_Plantago_lanceolata"
## [83] "glm_Potentilla_erecta" "glm_Carex_sempervirens"
## [85] "glm_Soldanella_alpina" "glm_Cynosurus_cristatus"
## [87] "glm_Campanula_scheuchzeri" "glm_Festuca_pratensis_sl"
## [89] "glm_Bromus_erectus_sstr" "glm_Saxifraga_oppositifolia"
## [91] "glm_Daucus_carota" "glm_Pritzelago_alpina_sstr"
## [93] "gbm_Bromus_erectus_sstr" "gbm_Saxifraga_oppositifolia"
## [95] "gbm_Daucus_carota" "gbm_Pritzelago_alpina_sstr"
```

### 1.0.2 Test data for the Niche Overlap Analysis

*ecospat.testNiche.inv()*

```
data(ecospat.testNiche.inv)
names(ecospat.testNiche.inv)
```

```
## [1] "x" "y" "aetpet" "gdd" "p"
## [6] "pet" "stdp" "tmax" "tmin" "tmp"
## [11] "species_occ" "predictions"
```

*ecospat.testNiche.nat()*

```
data(ecospat.testNiche.nat)
names(ecospat.testNiche.nat)
```

```
## [1] "x" "y" "aetpet" "gdd" "p"
## [6] "pet" "stdp" "tmax" "tmin" "tmp"
## [11] "species_occ" "predictions"
```

### 1.0.3 Test tree for Phylogenetic Diversity Analysis

*ecospat.testTree()*

```
if(requireNamespace("ape")){
  fpath <- system.file("extdata", "ecospat.testTree.tre", package="ecospat")
  tree<-ape::read.tree(fpath)
  tree$tip.label
  plot(tree, cex=0.6)
}
```

```
## Loading required namespace: ape
```



## 2.2 Predictor Variable Selection

### 2.2.1 Number of Predictors with Pearson Correlation *ecospat.npred()*

```
colvar <- ecospat.testData[c(4:8)]  
x <- cor(colvar, method="pearson")  
ecospat.npred(x, th=0.75)
```

```
## [1] 4
```

### 2.2.2 Number of Predictors with Spearman Correlation *ecospat.npred()*

```
x <- cor(colvar, method="spearman")  
ecospat.npred(x, th=0.75)
```

```
## [1] 4
```

## 2.3 Climate Analogy Tools

### 2.3.1 Climate Analogy with *ecospat.climan()*

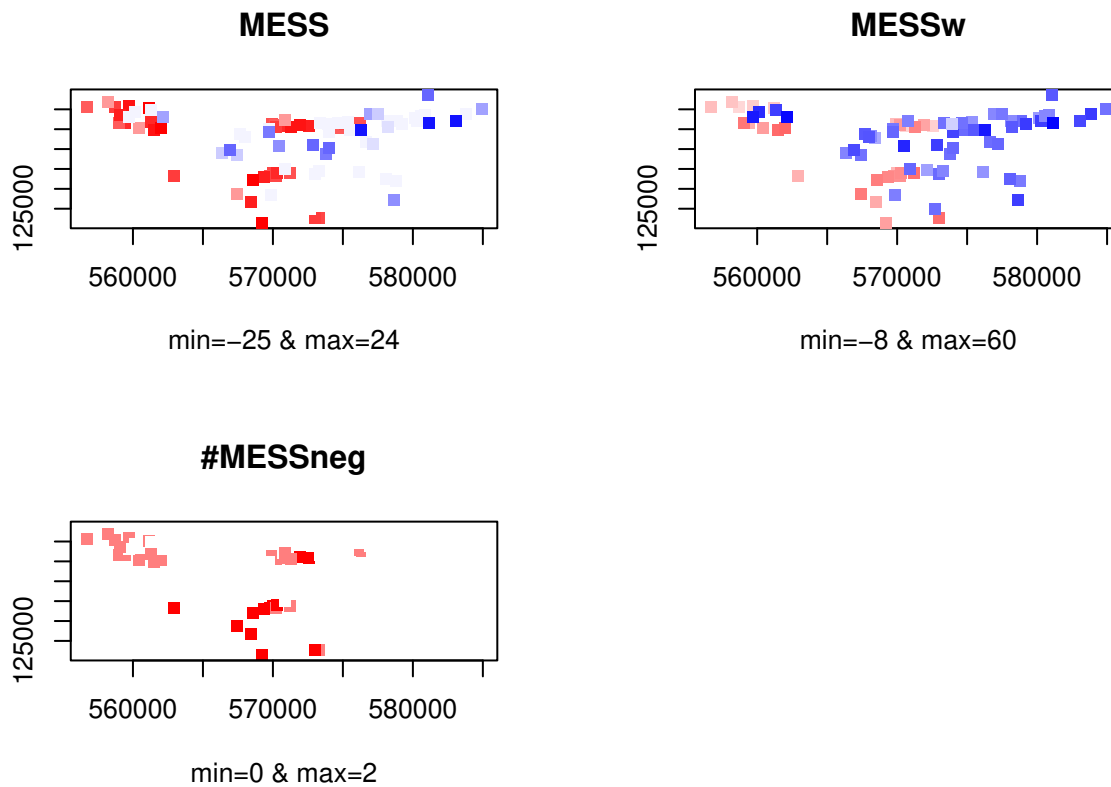
```
x <- ecospat.testData[c(4:8)]  
p<- x[1:90,] #A projection dataset.  
ref<- x[91:300,] # A reference dataset
```

```
ecospat.climan(ref,p)
```

```
## [1] 0.185415746 -0.028290993 -0.032909931 -0.009237875 -0.034642032  
## [6] -0.209006928 -0.084295612 -0.103622863 0.355220600 -0.136258661  
## [11] -0.087182448 -0.209006928 -0.143187067 -0.124711316 -0.114844720  
## [16] -0.230596451 0.276046242 0.249093277 -0.125288684 -0.101226337  
## [21] -0.113883908 -0.204653076 -0.001154734 -0.132217090 -0.100461894  
## [26] 0.464738681 -0.416578541 -0.044457275 -0.018475751 -0.122225532  
## [31] -0.137611720 -0.050808314 0.254605027 -0.062012319 0.238294633  
## [36] -0.159141330 -0.147806005 0.277670365 -0.071593533 -0.019053118  
## [41] 0.390781314 0.175132571 0.401892929 0.843703731 0.286155800  
## [46] 0.321142114 0.668511130 0.252253209 0.440050672 0.177247206  
## [51] 0.831525456 0.303710525 0.197182304 0.219273698 0.196637663  
## [56] 0.195300816 0.142395786 0.176988160 -0.051991905 0.265163111  
## [61] -0.020785219 -0.017898383 0.553965995 0.409635110 0.323633285  
## [66] 0.468693064 0.124983005 -0.032909931 0.165642783 0.147046687  
## [71] 0.202895471 0.341992334 0.225508458 0.133254065 0.485295264  
## [76] -0.047344111 -0.012282931 0.165429659 0.134199992 0.216655251  
## [81] 0.139419127 0.121254775 0.098782992 0.591393741 0.110866239  
## [86] 0.146010655 0.095562156 0.093353356 0.081712342 0.160531262
```

### 2.3.2 Extrapolation detection, creating a MESS object with *ecospat.mess()*

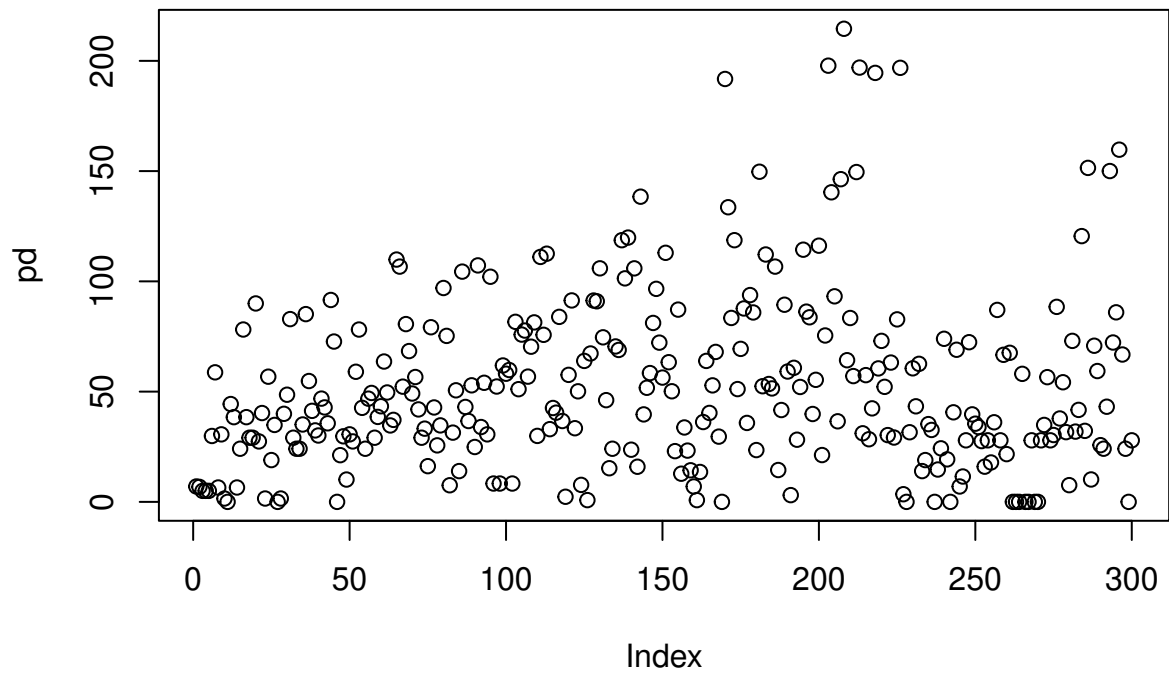
```
x <- ecospat.testData[c(2,3,4:8)]
proj<- x[1:90,] #A projection dataset.
cal<- x[91:300,] #A calibration dataset
mess.object<-ecospat.mess (proj, cal, w="default")
ecospat.plot.mess (mess.object, cex=1, pch=15)
```



In the MESS plot pixels in red indicate sites where at least one environmental predictor has values outside of the range of that predictor in the calibration dataset. In the MESSw plot, same as previous plot but with weighted by the number of predictors. Finally, the MESSneg plot shows at each site how many predictors have values outside of their calibration range.

## 2.4 Phylogenetic Diversity Measures

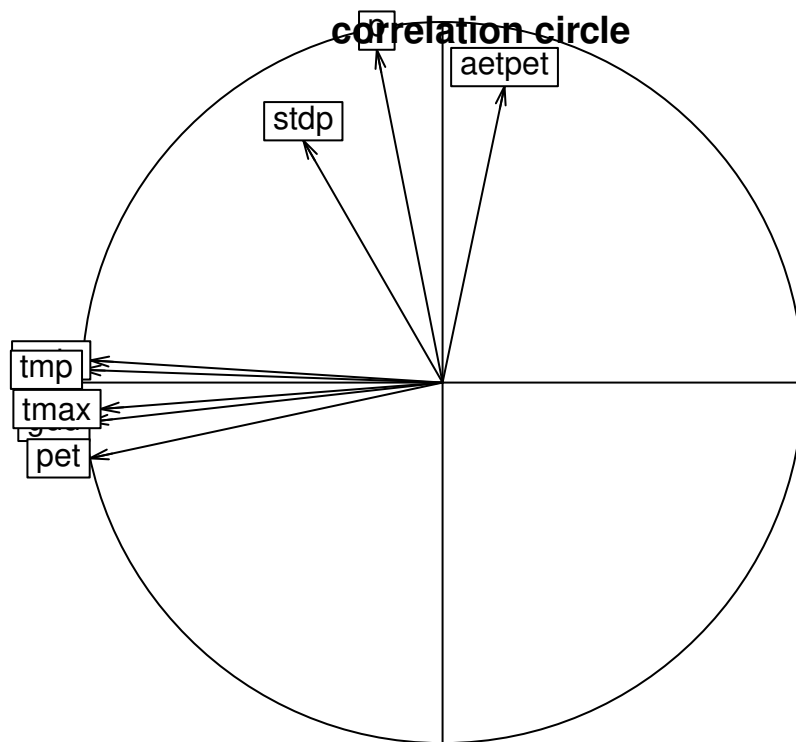
```
if(requireNamespace("ape")){
  fpath <- system.file("extdata", "ecospat.testTree.tre", package="ecospat")
  tree <- ape::read.tree(fpath)
  data <- ecospat.testData[9:52]
  pd<- ecospat.calculate.pd(tree, data, method = "spanning", type = "species", root = TRUE, average
  plot(pd)
}
```



## 2.5 Niche Quantification and Comparison with Ordination techniques

First we load the test data for the niche dynamics analysis in invaded and native range. A PCA is calibrated on all the sites of the study area, including both native and invaded ranges (same as PCAenv in Broenniman et al. 2012). Finally, we plot the variables Contributions

```
library(ade4)
inv <- ecospat.testNiche.inv
nat <- ecospat.testNiche.nat
pca.env <- ade4::dudi.pca(rbind(nat,inv)[,3:10],scannf=F,nf=2)
ecospat.plot.contrib(contrib=pca.env$co, eigen=pca.env$eig)
```



axis1 = 61.14 % axis2 = 25.09 %

The correlation circle indicate the

contribution of original predictors to the PCA axes.

Now we can predict the scores on the axes

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

# PCA scores for the species native distribution
scores.sp.nat <- ade4::suprow(pca.env, nat[which(nat[,11]==1),3:10])$li

# PCA scores for the species invasive distribution
scores.sp.inv <- ade4::suprow(pca.env, inv[which(inv[,11]==1),3:10])$li

# PCA scores for the whole native study area
scores.clim.nat <- ade4::suprow(pca.env, nat[,3:10])$li

# PCA scores for the whole invaded study area
scores.clim.inv <- ade4::suprow(pca.env, inv[,3:10])$li
```

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

For a species in the native range (North America)

```
# gridding the native niche
grid.clim.nat <- ecospat.grid.clim.dyn(glob=scores.globclim,
                                       glob1=scores.clim.nat,
                                       sp=scores.sp.nat, R=100,
                                       th.sp=0)
```

```
## Registered S3 methods overwritten by 'adehabitatMA':
##   method                from
##   print.SpatialPixelsDataFrame sp
##   print.SpatialPixels    sp
```



For a species in the invaded range (Australia)

```
# gridding the invasive niche
grid.clim.inv <- ecospat.grid.clim.dyn(glob=scores.globclim,
                                      glob1=scores.clim.inv,
                                      sp=scores.sp.inv, R=100,
                                      th.sp=0)
```

### 2.5.2 Calculate Niche Overlap with *ecospat.niche.overlap()*

```
# Compute Schoener's D, index of niche overlap
D.overlap <- ecospat.niche.overlap (grid.clim.nat, grid.clim.inv, cor = TRUE)$D
D.overlap
```

```
## [1] 0.224586
```

The niche overlap between the native and the invaded range is 22%.

### 2.5.3 Perform the Niche Equivalency Test with *ecospat.niche.equivalency.test()* according to Warren et al. (2008)

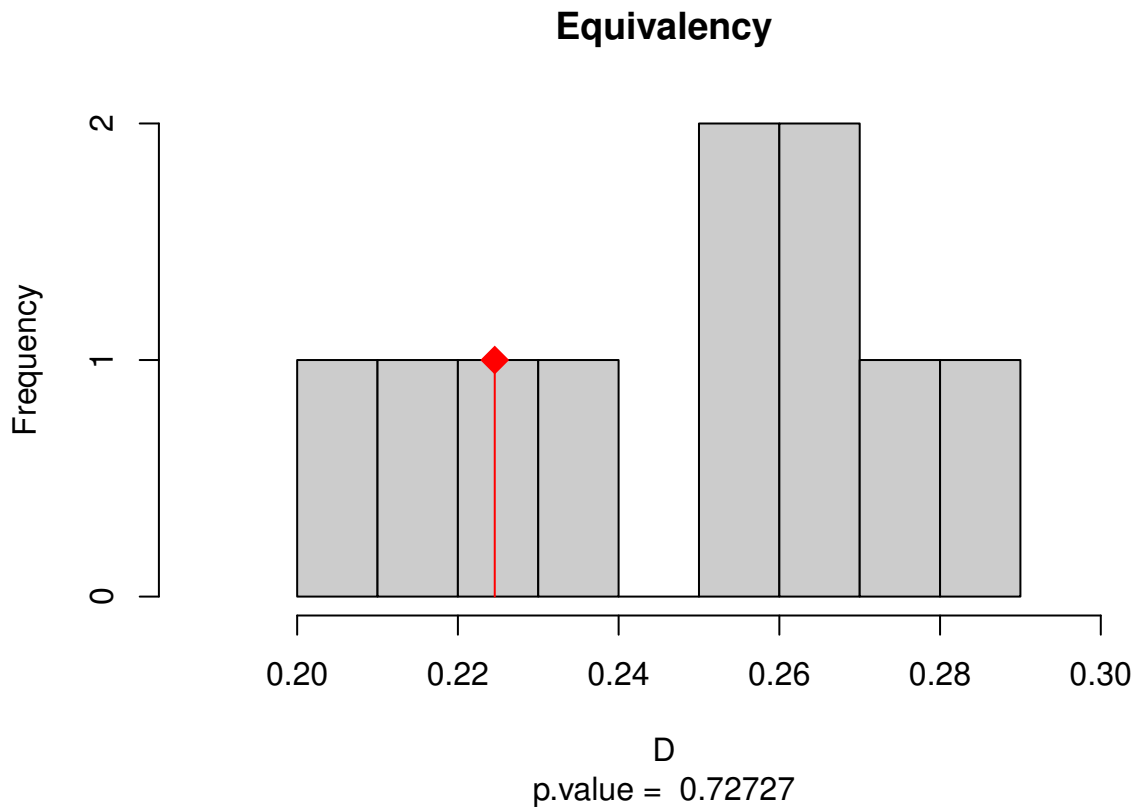
It is recommended to use at least 1000 replications for the equivalency test. As an example we used `rep = 10`, to reduce the computational time.

```
eq.test <- ecospat.niche.equivalency.test(grid.clim.nat, grid.clim.inv,rep=10,
                                         intersection = 0.1,
                                         overlap.alternative = "higher",
                                         expansion.alternative = "lower",
                                         stability.alternative = "higher",
                                         unfilling.alternative = "lower")
```

Niche equivalency test H1: the observed overlap between the native and invaded niche is higher than if the two niches are randomized, the niche expansion of the invaded niche is lower, the niche stability is higher and the niche unfilling is lower than if the two niches are randomized.

Plot Equivalency test

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



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

Shifts randomly on niche (here the invasive niche) in the study area. It is recommended to use at least 1000 replications for the similarity test. As an example we used `rep = 10`, to reduce the computational time.

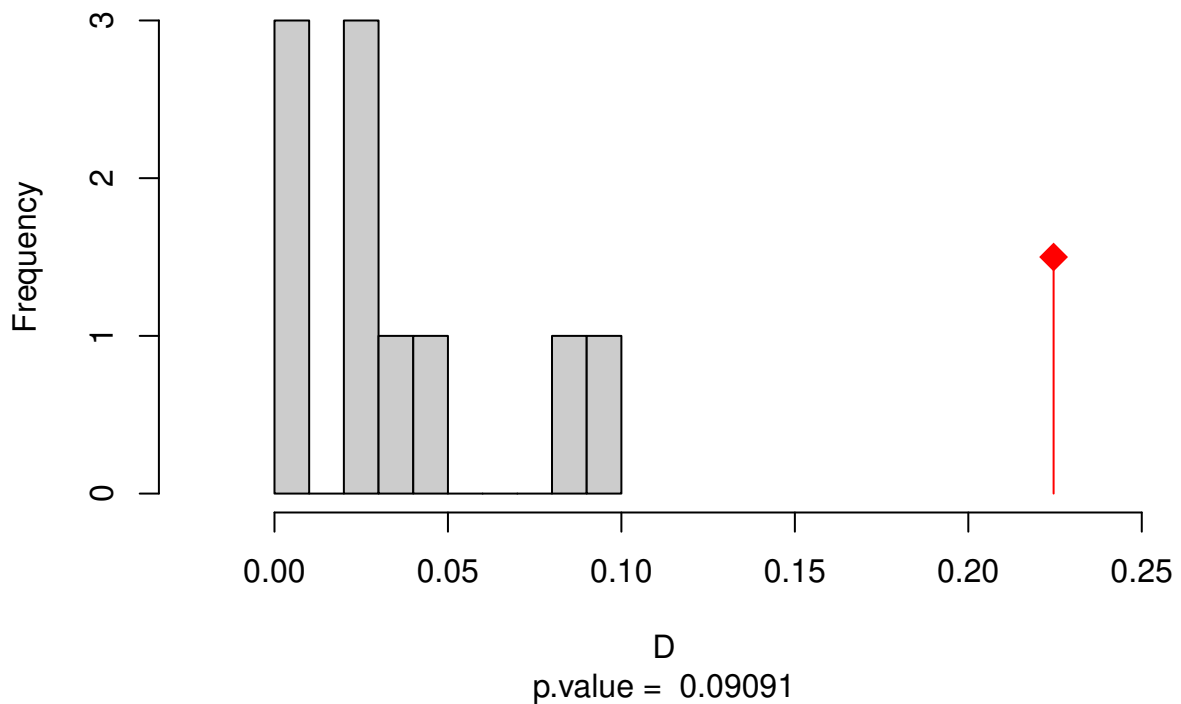
```
sim.test <- ecospat.niche.similarity.test(grid.clim.nat, grid.clim.inv, rep=10,
                                         overlap.alternative = "higher",
                                         expansion.alternative = "lower",
                                         stability.alternative = "higher",
                                         unfilling.alternative = "lower",
                                         intersection = 0.1,
                                         rand.type=1)
```

Niche similarity test H1: the observed overlap between the native and invaded is higher than randomly shifted invasive niches in the invaded study area, the niche expansion of the invaded niche is lower, the niche stability is higher and the niche unfilling is lower than if the two niches are randomized.

Plot Similarity test

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

## Similarity



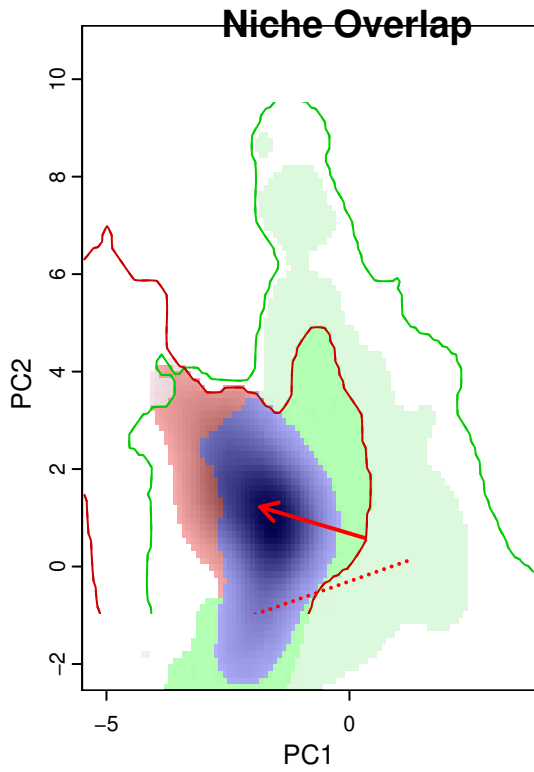
### 2.5.5 Delimiting niche categories and quantifying niche dynamics in analogue climates with *ecospat.niche.dyn.index()*

```
niche.dyn <- ecospat.niche.dyn.index (grid.clim.nat, grid.clim.inv)
```

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

```
ecospat.plot.niche.dyn(grid.clim.nat, grid.clim.inv, quant=0.25, interest=2,  
  title= "Niche Overlap", name.axis1="PC1",  
  name.axis2="PC2")
```

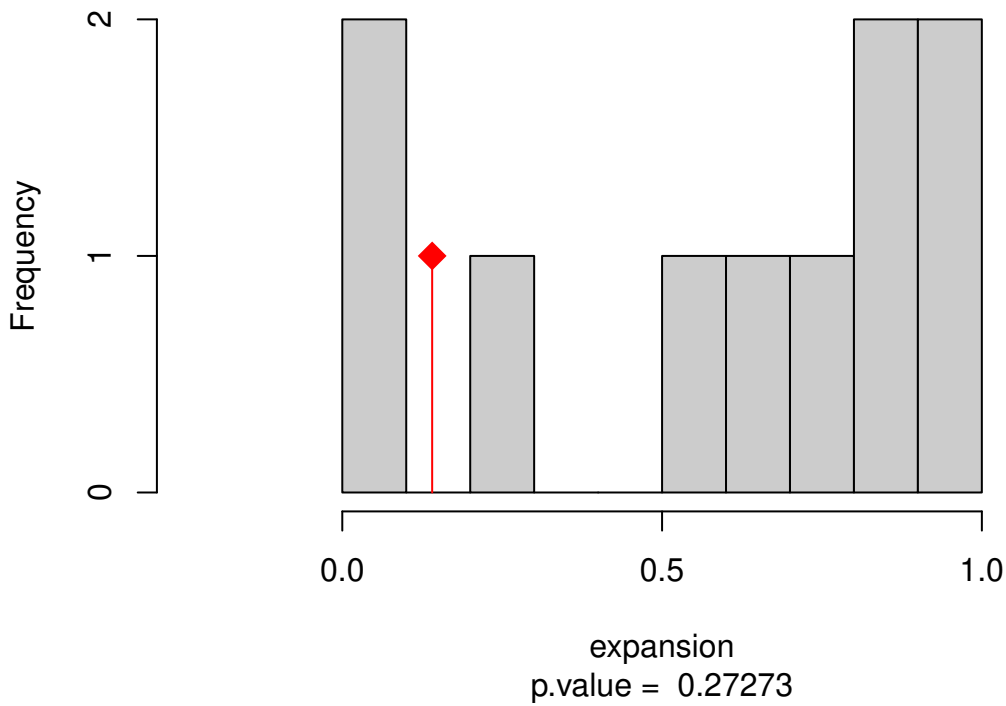
```
ecospat.shift.centroids(scores.sp.nat, scores.sp.inv, scores.clim.nat, scores.clim.inv)
```



Plot Similarity test for niche expansion, stability and unfilling

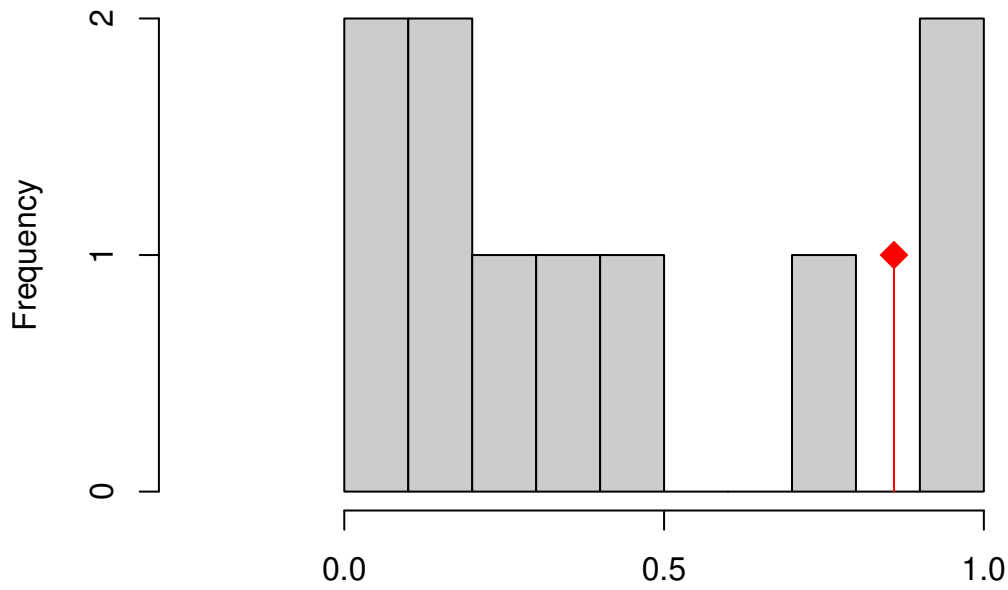
```
ecospat.plot.overlap.test(sim.test, "expansion", "Similarity")
```

### Similarity



```
ecospat.plot.overlap.test(sim.test, "stability", "Similarity")
```

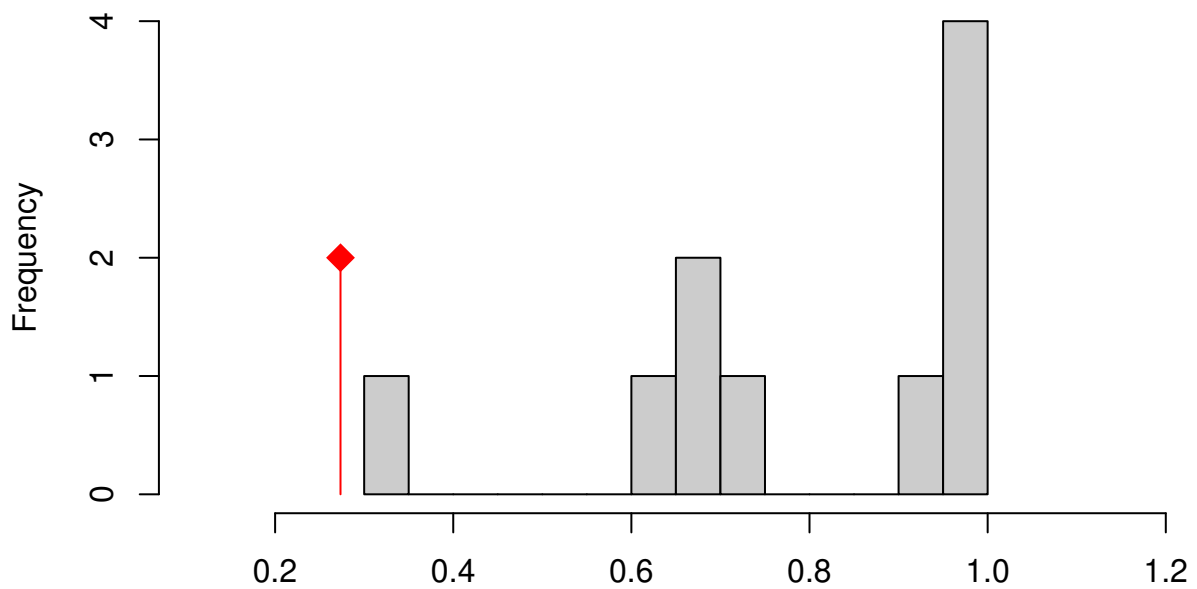
## Similarity



stability  
p.value = 0.27273

```
ecospat.plot.overlap.test(sim.test, "unfilling", "Similarity")
```

## Similarity



unfilling  
p.value = 0.09091

```
# gridding the native niche
```

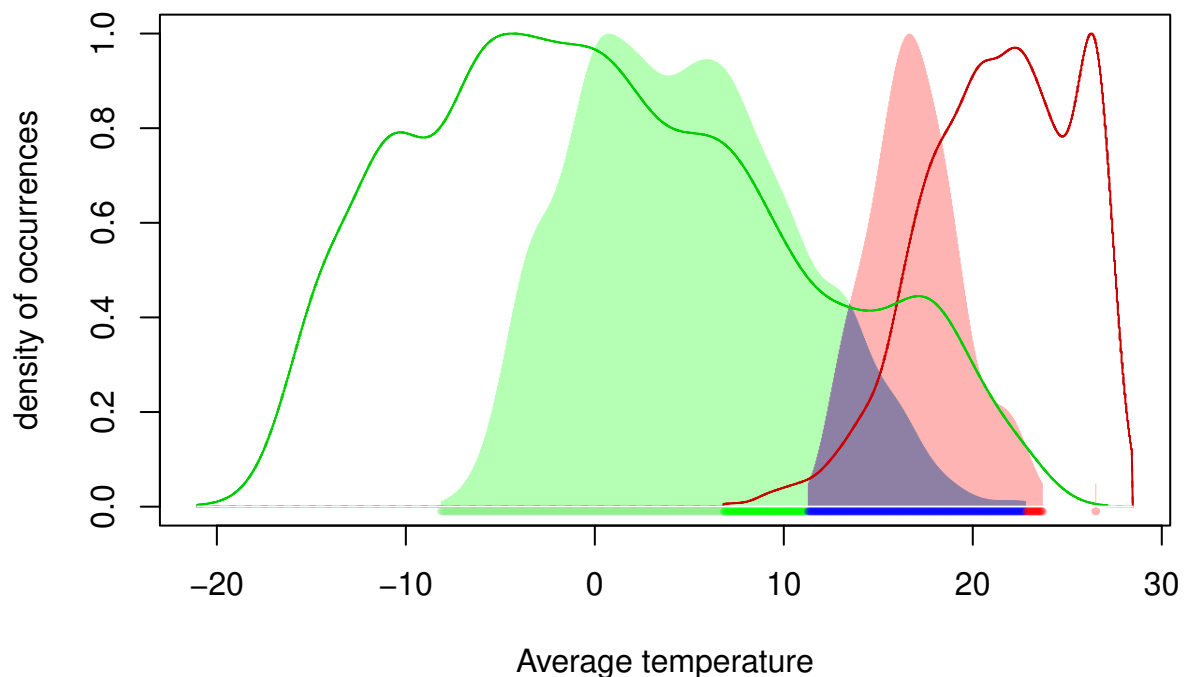
```

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)
ecospat.plot.niche.dyn(grid.clim.t.nat, grid.clim.t.inv, quant=0,
                      interest=2, title= "Niche Overlap",
                      name.axis1="Average temperature")

```

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

### Niche Overlap



## 2.6 Biotic Interactions

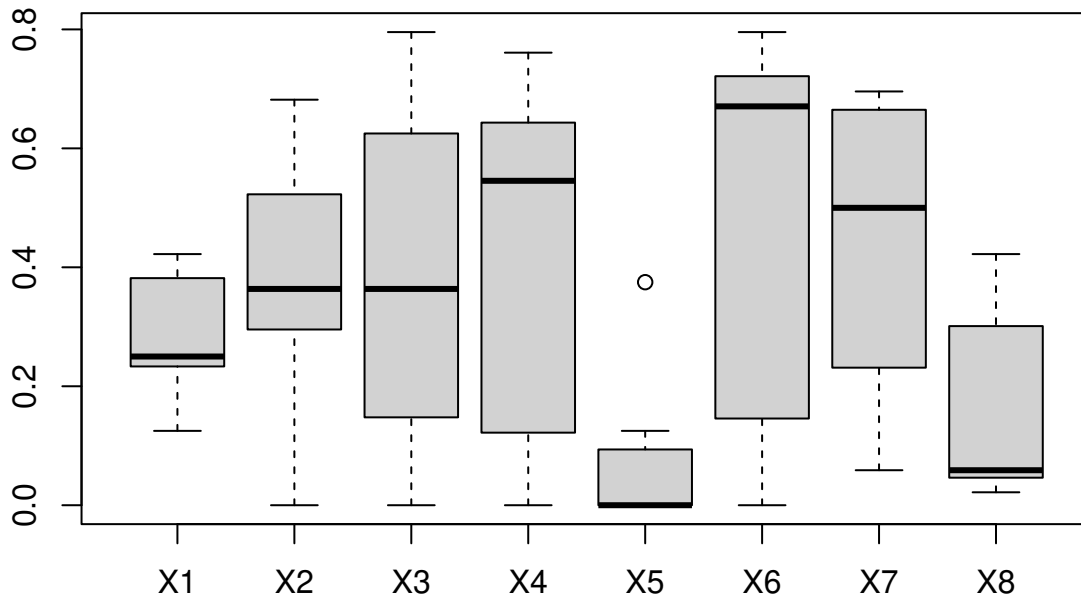
2.6.1 Species Co-occurrences Analysis with a Presence-absence matrix using the function *ecospat.co\_occurrences()*

```
data <- ecospat.testData[c(9:16,54:57)]
```

For each pair of species (sp1, sp2), the number (N) of plots where both species were present is divided by the number of plots where the rarest of the two species is present. This index ranges from 0 (no co-occurrence) to 1 (always in co-occurrence) as given in eq. 1.

where  $N(S1 \text{ intersects } S2)$  is the number of times species S1 and S2 co-occur, while  $\text{Min}(NS1, NS2)$  is the number of times species S1 and S2 co-occur, while is the occurrence frequency of the rarest of the two species.

ecospat.co\_occurrences (data)



```
##
## Aposeris_foetida Arnica_montana Aster_bellidiastrum
## Aposeris_foetida 1.0000000 0.3636364 0.2500000
## Arnica_montana 0.3636364 1.0000000 0.3636364
## Aster_bellidiastrum 0.2500000 0.3636364 1.0000000
## Bartsia_alpina 0.2222222 0.5454545 0.5909091
## Bromus_erectus_sstr 0.1250000 0.0000000 0.0000000
## Campanula_scheuchzeri 0.2444444 0.6818182 0.7954545
## Carex sempervirens 0.4000000 0.5000000 0.6590909
## Cynosurus_cristatus 0.4222222 0.2272727 0.0454545
##
## Bartsia_alpina Bromus_erectus_sstr Campanula_scheuchzeri
## Aposeris_foetida 0.2222222 0.1250 0.2444444
## Arnica_montana 0.5454545 0.0000 0.6818182
## Aster_bellidiastrum 0.5909091 0.0000 0.7954545
## Bartsia_alpina 1.0000000 0.0000 0.7608696
## Bromus_erectus_sstr 0.0000000 1.0000 0.0000000
## Campanula_scheuchzeri 0.7608696 0.0000 1.0000000
## Carex sempervirens 0.6956522 0.0625 0.6705882
## Cynosurus_cristatus 0.0217391 0.3750 0.0470588
##
## Carex sempervirens Cynosurus_cristatus
## Aposeris_foetida 0.4000000 0.4222222
## Arnica_montana 0.5000000 0.2272727
## Aster_bellidiastrum 0.6590909 0.0454545
## Bartsia_alpina 0.6956522 0.0217391
## Bromus_erectus_sstr 0.0625000 0.3750000
## Campanula_scheuchzeri 0.6705882 0.0470588
## Carex sempervirens 1.0000000 0.0588235
## Cynosurus_cristatus 0.0588235 1.0000000
```

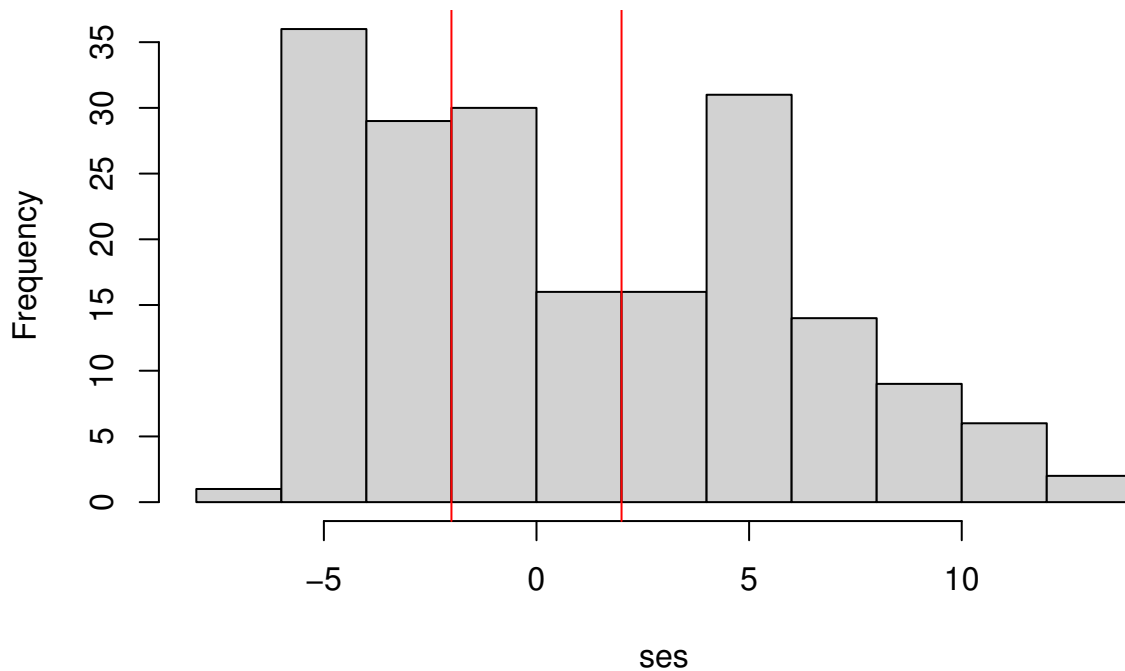
### 2.6.2 Pairwise co-occurrence Analysis with calculation of the C-score index using the function *ecospat.Cscore()*

This function allows to apply a pairwise null model analysis to a presence-absence community matrix to determine which species associations are significant across the study area. The strength of associations is quantified by the C-score index and a ‘fixed-equiprobable’ null model algorithm is applied.

It is recommended to use at least 10000 permutations for the test. As an example we used  $nperm = 100$ , to reduce the computational time.

```
data<- ecospat.testData[c(53,62,58,70,61,66,65,71,69,43,63,56,68,57,55,60,54,67,59,64)]
nperm <- 100
outpath <- getwd()
ecospat.Cscore(data, nperm, outpath)
```

### Histogram of standardized effect size



```
## $ObsCscoreTot
## [1] 2675.468
##
## $SimCscoreTot
## [1] 2466.428
##
## $PVal.less
## [1] 1
##
## $PVal.greater
## [1] 0.00990099
##
## $SES.Tot
## [1] 63.80968
```

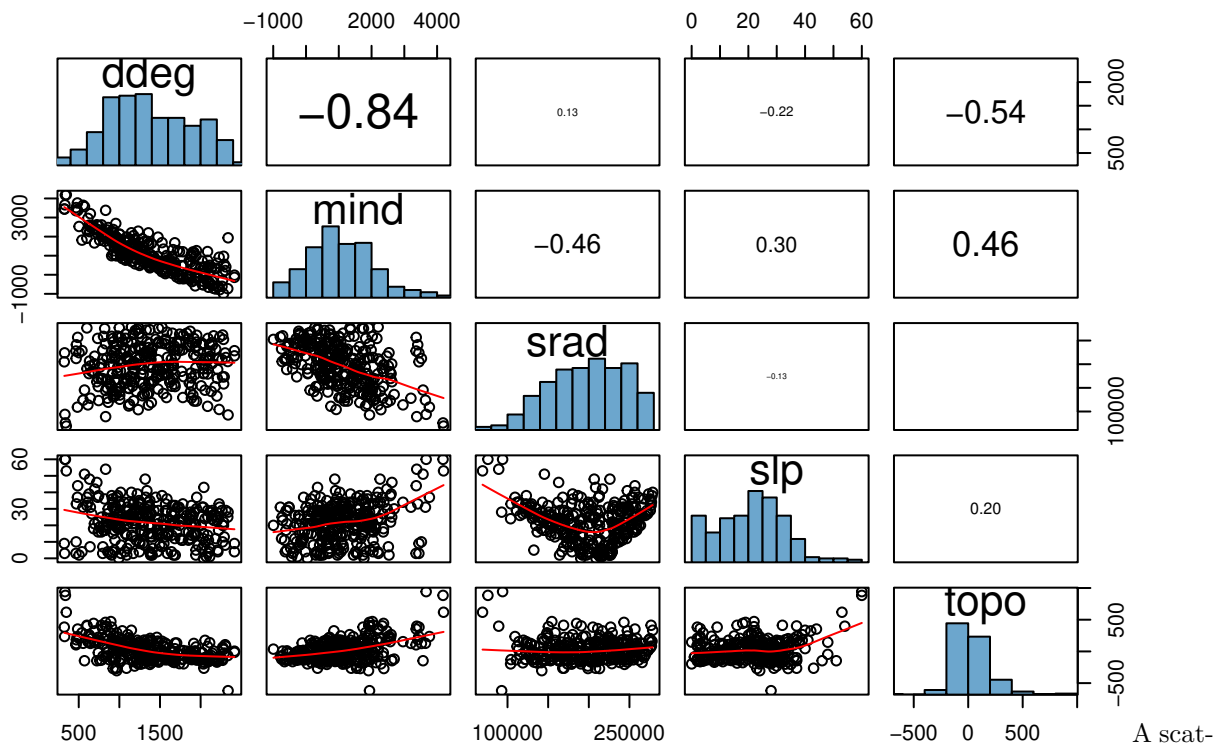
The function returns the C-score index for the observed community (ObsCscoreTot), p.value (PValTot) and standardized effect size (SES.Tot). It saves also a table in the working directory where the same metrics are calculated for each species pair (only the table with species pairs with significant p-values is saved in this version)



## 2.7 Data Preparation

### 2.7.1 Correlation Plot of Variables with `ecospat.cor.plot()`

```
data <- ecospat.testData[,4:8]
ecospat.cor.plot(data)
```



A scatter plot of matrices, with bivariate scatter plots below the diagonal, histograms on the diagonal, and the Pearson correlation above the diagonal. Useful for descriptive statistics of small data sets (better with less than 10 variables).

### 2.7.2 Calibration And Evaluation Dataset

```
data <- ecospat.testData
caleval <- ecospat.caleval (data = ecospat.testData[53], xy = data[2:3],
                           row.num = 1:nrow(data), nrep = 2, ratio = 0.7,
                           disaggregate = 0.2, pseudoabs = 100, npres = 10,
                           replace = FALSE)
head(caleval)
```

```
## $eval
##   yeval yeval
## 1   151   NA
## 2    NA  202
## 3    NA   NA
## 4   157   34
## 5    23  184
## 6   295   14
## 7   171   71
## 8   156  221
## 9   133  237
## 10  150  266
```

```

## 11 272 21
## 12 116 214
## 13 244 31
## 14 20 245
## 15 3 228
## 16 269 8
## 17 182 4
## 18 297 249
## 19 115 292
## 20 250 256
## 21 152 243
## 22 268 247
## 23 120 271
## 24 181 154
## 25 233 55
## 26 2 289
## 27 241 232
## 28 121 186
## 29 110 269
## 30 203 110
## 31 51 293
## 32 252 295
## 33 169 251
##
## $cal
##   ycal ycal
## 1   NA  NA
## 2   87  NA
## 3   64  NA
## 4   46 167
## 5  137  86
## 6  131  NA
## 7   NA 287
## 8  254  37
## 9  293 274
## 10 276 121
## 11 186  23
## 12 232 263
## 13  53 200
## 14 201 296
## 15 222 192
## 16  37 230
## 17 290 248
## 18 281 178
## 19 212 291
## 20 246 211
## 21 147 114
## 22 206 220
## 23 225 264
## 24 262 204
## 25 145  11
## 26 258 258
## 27  33  95
## 28  5 236
## 29 255 238
## 30 224 225
## 31 289  84
## 32 168 299

```

```

## 33 200 157
## 34 253 217
## 35 271 189
## 36 259 242
## 37 134 43
## 38 140 3
## 39 223 18
## 40 278 15
## 41 231 33
## 42 210 152
## 43 240 265
## 44 199 67
## 45 204 22
## 46 242 139
## 47 286 36
## 48 106 300
## 49 155 188
## 50 234 224
## 51 75 185
## 52 235 261
## 53 267 283
## 54 67 279
## 55 154 155
## 56 192 270
## 57 166 49
## 58 55 79
## 59 251 44
## 60 30 294
## 61 44 235
## 62 205 273
## 63 247 193
## 64 113 260
## 65 180 196
## 66 177 198
## 67 288 272
## 68 239 53
## 69 17 100
## 70 22 5
## 71 16 219
## 72 27 244
## 73 94 229
## 74 85 56
## 75 275 45
## 76 123 24
## 77 279 57

```

We obtained an evaluation and calibration dataset with a desired ratio of disaggregation.

## 3 Core Niche Modelling

### 3.1 Model Evaluation

#### 3.1.1 Presence-only Evaluation Indices- Boyce Index

The argument fit is a vector containing the predicted suitability values

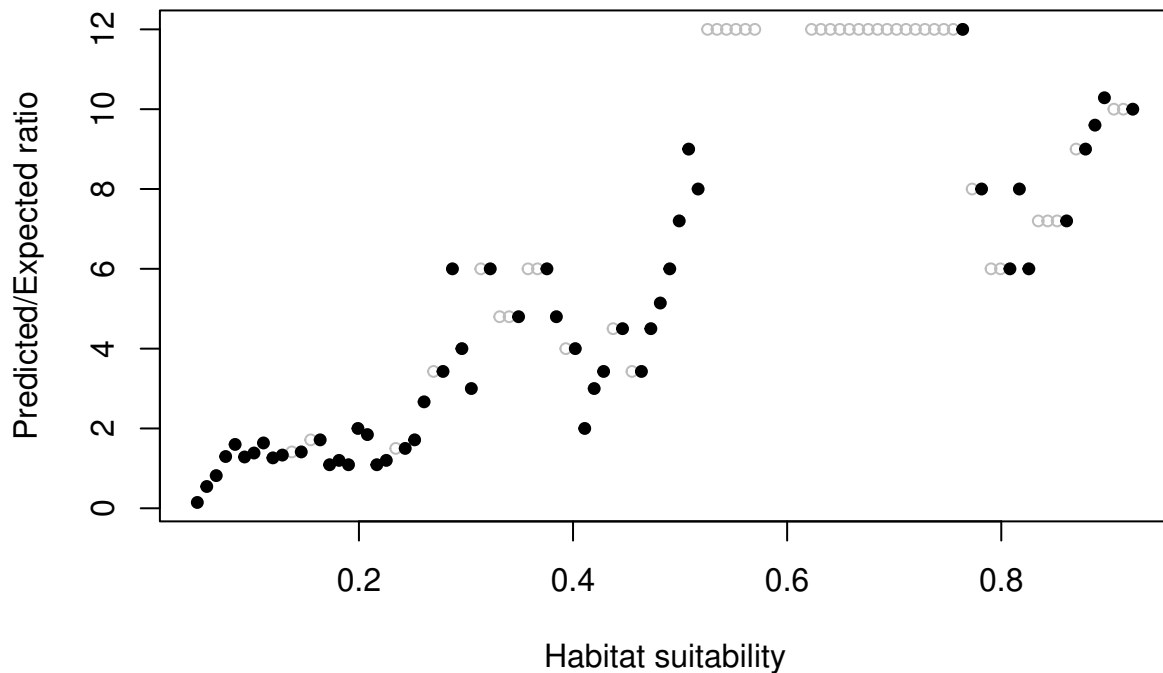
```
fit <- ecospat.testData$glm_Saxifraga_oppositifolia
```

The argument `obs` is a vector containing the predicted suitability values of the validation points (presence records)

```
obs<-ecospat.testData$glm_Saxifraga_oppositifolia[which(ecospat.testData$Saxifraga_oppositifolia==1)
```

Calculate and plot Boyce Index with `ecospat.boyce`

```
ecospat.boyce (fit, obs, nclass = 0, window.w = "default", res = 100,
              PEplot = TRUE)$cor
```



```
## [1] 0.91
```

Here the boyce index is 0.91. If the rank of predicted expected ratio would be completely ordered along habitat suitability axis then boyce index would be 1.

### 3.1.2 Accuracy of Community Prediction

Indices of accuracy of community predictions `ecospat.CommunityEval()`

```
eval<-ecospat.testData[c(53,62,58,70,61,66,65,71,69,43,63,56,68,57,55,60,54,67,59,64)]
pred<-ecospat.testData[c(73:92)]
```

```
CommunityEval<-ecospat.CommunityEval (eval, pred, proba = TRUE, ntir=5,verbose = T)
```

```
## trial 1 on 5
## trial 2 on 5
## trial 3 on 5
## trial 4 on 5
## trial 5 on 5
```

## 3.2 Spatial Predictions and Projections

### 3.2.1 ESM Ensemble of Small Models

```
library(biomod2)
```

```
## biomod2 4.2-5 loaded.
```

```
## /!\ New set up for modeling options. We apologize for the trouble ^[*.*]^
```

```
## Loading required package: nnet
```

```
## Loading required package: rpart
```

```
## Loading required package: mda
```

```
## Warning in library(package, lib.loc = lib.loc, character.only = TRUE,
```

```
## logical.return = TRUE, : there is no package called 'mda'
```

```
## Loading required package: gam
```

```
## Warning in library(package, lib.loc = lib.loc, character.only = TRUE,
```

```
## logical.return = TRUE, : there is no package called 'gam'
```

```
## Loading required package: mgcv
```

```
## Loading required package: nlme
```

```
## This is mgcv 1.9-1. For overview type 'help("mgcv-package")'.
```

```
##
```

```
## Attaching package: 'mgcv'
```

```
## The following object is masked from 'package:nnet':
```

```
##
```

```
##     multinom
```

```
## Loading required package: gbm
```

```
## Loaded gbm 2.1.9
```

```
## This version of gbm is no longer under development. Consider transitioning to gbm3, https://github.com
```

```
## Loading required package: earth
```

```
## Loading required package: Formula
```

```
## Loading required package: plotmo
```

```
## Loading required package: plotrix
```

```
## Loading required package: maxnet
```

```

## Loading required package: randomForest

## randomForest 4.7-1.1

## Type rfNews() to see new features/changes/bug fixes.

## Loading required package: xgboost

## Warning in library(package, lib.loc = lib.loc, character.only = TRUE,
## logical.return = TRUE, : there is no package called 'xgboost'

# species
# occurrences
xy <- inv[,1:2]
head(xy)

##           x           y
## 1 142.25 -10.25
## 2 142.25 -10.75
## 3 131.25 -11.25
## 4 132.25 -11.25
## 5 142.25 -11.25
## 6 142.75 -11.25

sp_occ <- inv[11]

# env
current <- inv[3:7]
head(current)

##      aetpet      gdd      p      pet      stdp
## 1 0.3180346 7965.1 1595.7 1950.320 137.8134
## 2 0.2807616 7888.9 1693.7 1991.475 156.3950
## 3 0.2638533 8165.3 1595.0 2179.968 127.0621
## 4 0.2790938 8195.6 1346.0 1919.897 114.7686
## 5 0.3030646 7858.1 1711.1 1795.255 158.3286
## 6 0.3217786 7888.5 1711.1 1788.220 151.8030

## BIOMOD
t1 <- Sys.time()
sp<-1

### Formatting the data with the BIOMOD_FormattingData() function form the package biomod2

myBiomodData <- biomod2::BIOMOD_FormattingData( resp.var = as.numeric(sp_occ[,sp]),
                                              expl.var = current,
                                              resp.xy = xy,
                                              resp.name = colnames(sp_occ)[sp])

##
## ===== species_occ Data Formating =====
##
##      ! Response variable name was converted into species_occ
##      ! No data has been set aside for modeling evaluation
##      ! No data has been set aside for modeling evaluation
## ===== Done =====

```

```
### Calibration of simple bivariate models
```

```
# remove invisible(capture.output)) to print output in the console  
# this is just to keep the vignette short
```

```
invisible(capture.output(my.ESM <- ecospat.ESM.Modeling( data=myBiomodData,  
  models=c('GLM'),  
  NbRunEval=2,  
  DataSplit=70,  
  weighting.score=c("AUC"),  
  parallel=F)  
)  
)
```

```
## Warning: executing %dopar% sequentially: no parallel backend registered
```

```
### Evaluation and average 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
```

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

```
### Projection of calibrated ESMS into new space
```

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

### 3.3 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))
```

### 3.4 SESAM framework with *ecospat.SESAM.prr()*

```
prr<-ecospat.SESAM.prr(proba, sr)  
head(prr)[,1:4]
```

```
##   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  
##   glm_Trifolium_repens_sstr  
## 1                        0  
## 2                        1
```

```
## 3          1
## 4          1
## 5          1
## 6          1
```

## 4 Post-Modelling

### 4.1 Spatial Predictions of species assemblages

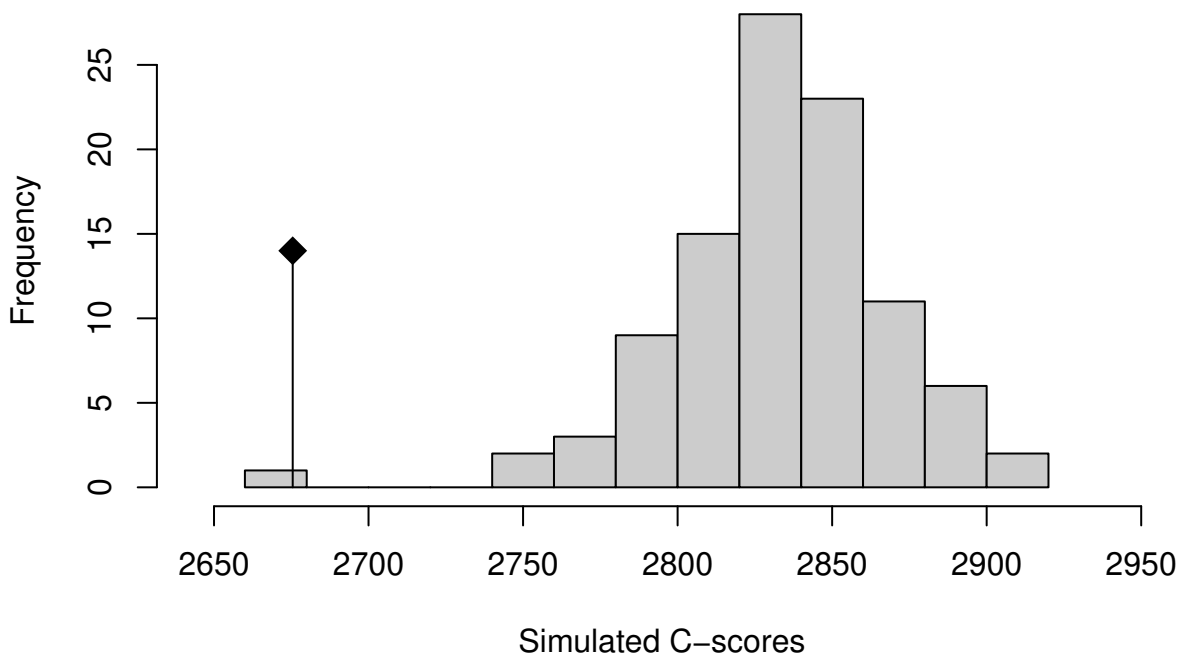
#### 4.1.1 Co-occurrence analysis & Environmentally Constrained Null Models

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(53,62,58,70,61,66,65,71,69,43,63,56,68,57,55,60,54,67,59,64)]
pred<-ecospat.testData[c(73:92)]
```

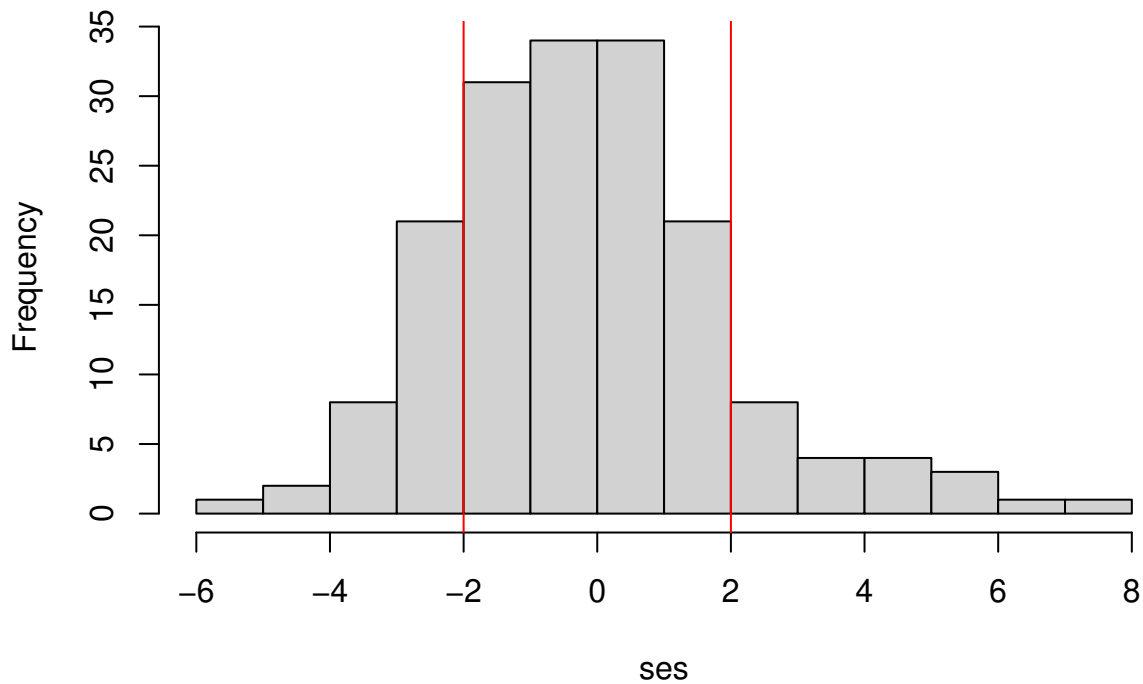
Define the number of permutations. It is recommended to use at least 10000 permutations for the test. As an example we used `nperm = 100`, to reduce the computational time. Then Define the `outpath`. Then we can run Run the function `ecospat.cons_Cscore`. The function tests for non-random patterns of species co-occurrence in a presence-absence matrix. It calculates the C-score index for the whole community and for each species pair. An environmental constraint is applied during the generation of the null communities.

```
nbpermut <- 100
outpath <- getwd()
ecospat.cons_Cscore(presence, pred, nbpermut, outpath)
```





## Histogram of standardized effect size



```
## $ObsCscoreTot
## [1] 2675.468
##
## $SimCscoreTot
## [1] 2833.376
##
## $PVal.less
## [1] 0.01980198
##
## $PVal.greater
## [1] 0.990099
##
## $SES.Tot
## [1] -4.449136
```

The function returns - the C-score index for the observed community (ObsCscoreTot), - the mean of C-score for the simulated communities (SimCscoreTot), - the p.values (PVal.less and PVal.greater) to evaluate the significance of the difference between the former two indices. - the standardized effect size for the whole community (SES.Tot). A SES that is greater than 2 or less than -2 is statistically significant with a tail probability of less than 0.05 (Gotelli & McCabe 2002 - Ecology). If a community is structured by competition, we would expect the C-score to be large relative to a randomly assembled community (positive SES). In this case the observed C-score is significantly lower than expected by chance, this meaning that the community is dominated by positive interactions (aggregated pattern).

A table is saved in the path specified where the same metrics are calculated for each species pair (only the table with species pairs with significant p.values is saved).