Vignette ecospat package

Contents

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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)
```

```
## Loading required package: ade4
```

```
## Loading required package: ape

## Loading required package: gbm

## Loading required package: survival

## Loading required package: lattice

## Loading required package: splines

## Loading required package: parallel

## Loaded gbm 2.1.3

## Loading required package: sp
```

```r
citation("ecospat")
```

```
##
## To cite package 'ecospat' in publications use:
##
##   Olivier Broennimann, Valeria Di Cola and Antoine Guisan (2018).
##   ecospat: Spatial Ecology Miscellaneous Methods. R package
##   version 2.2.1.
##   http://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 = {2018},
##     note = {R package version 2.2.1},
##     url = {http://www.unil.ch/ecospat/home/menuguid/ecospat-resources/tools.html},
##   }
```

1.0.1 Test data for the ecospat library

ecospat.testData()

```r
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_anisophyllon"
## [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()

```
fpath <- system.file("extdata", "ecospat.testTree.tre", package="ecospat")
fpath
```

```
## [1] "C:/Users/obroenni/Documents/R/win-library/3.5/ecospat/extdata/ecospat.testTree.tre"
```

```
tree<-read.tree(fpath)
tree$tip.label
```

```
##  [1] "Rumex_acetosa"           "Polygonum_bistorta"
##  [3] "Polygonum_viviparum"     "Rumex_crispus"
##  [5] "Cerastium_latifolium"    "Silene_acaulis"
##  [7] "Gypsophila_repens"       "Vaccinium_gaultherioides"
##  [9] "Soldanella_alpina"       "Cruciata_laevipes"
## [11] "Galium_album"            "Galium_anisophyllon"
## [13] "Galium_megalospermum"    "Gentiana_verna"
## [15] "Gentiana_bavarica"       "Gentiana_purpurea"
## [17] "Gentiana_lutea"          "Bartsia_alpina"
## [19] "Rhinanthus_alectorolophus" "Prunella_grandiflora"
## [21] "Acinos_alpinus"          "Plantago_alpina"
## [23] "Plantago_lanceolata"     "Veronica_officinalis"
## [25] "Veronica_aphylla"        "Veronica_alpina"
## [27] "Veronica_chamaedrys"     "Veronica_persica"
## [29] "Globularia_cordifolia"   "Globularia_nudicaulis"
## [31] "Myosotis_alpestris"      "Myosotis_arvensis"
## [33] "Aposeris_foetida"        "Centaurea_montana"
## [35] "Hieracium_lactucella"    "Leontodon_helveticus"
## [37] "Leontodon_autumnalis"    "Hypochaeris_radicata"
## [39] "Achillea_atrata"         "Achillea_millefolium"
## [41] "Homogyne_alpina"         "Senecio_doronicum"
## [43] "Adenostyles_glabra"      "Arnica_montana"
## [45] "Aster_bellidiastrum"     "Bellis_perennis"
## [47] "Doronicum_grandiflorum"  "Phyteuma_orbiculare"
## [49] "Phyteuma_spicatum"       "Campanula_rotundifolia"
```
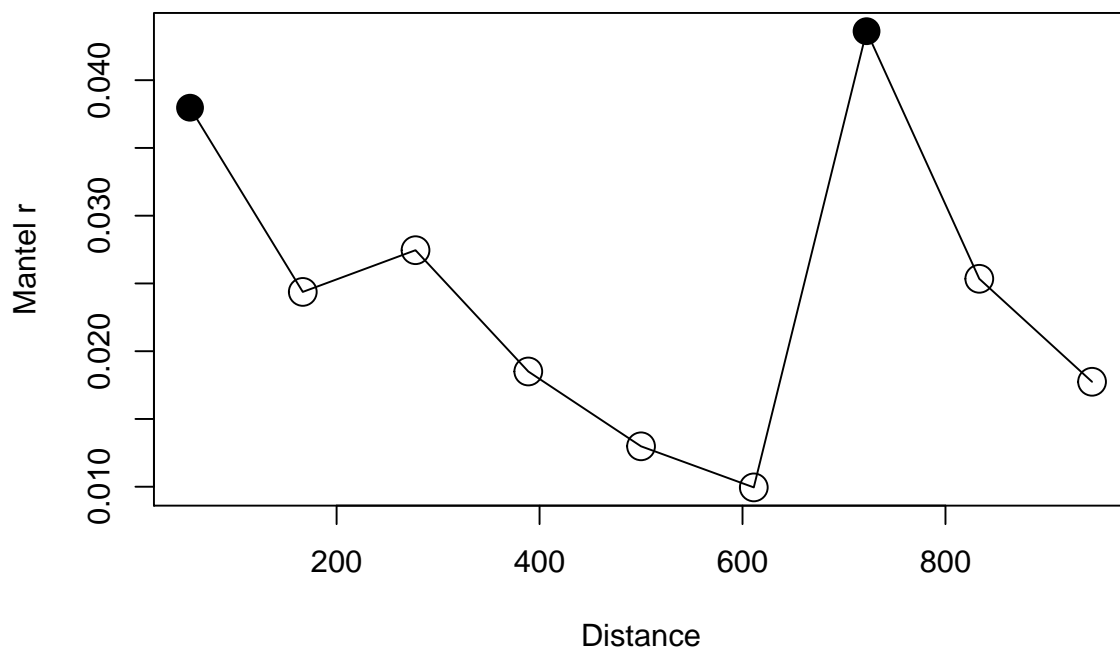
Plot tree

```
plot(tree, cex=0.6)
```
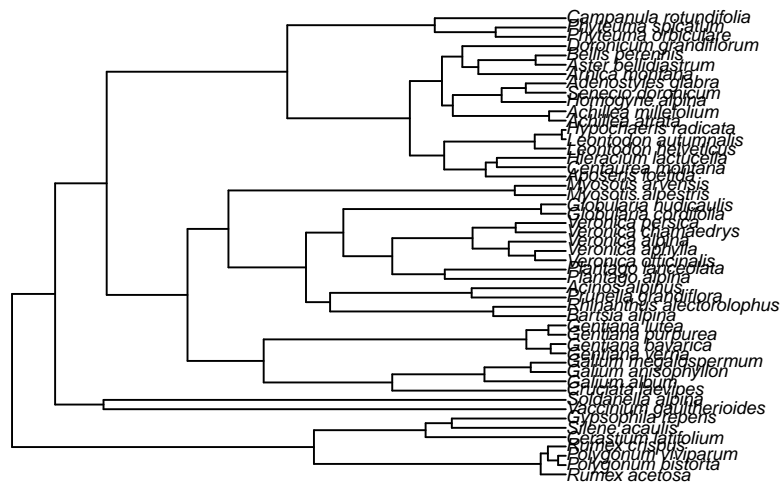
2 Pre-Modelling Analysis

2.1 Spatial Auto-correlation

2.1.1 Mantel Correlogram with *ecospat.mantel.correlogram()*

```
ecospat.mantel.correlogram(dfvar=ecospat.testData[c(2:16)],colxy=1:2, n=100,
                           colvar=3:7, max=1000, nclass=10, nperm=100)
```

The graph indicates that spatial autocorrelation (SA) is minimal at a distance of 180 meters. Note however that SA is not significantly different than zero for several distances (open circles).

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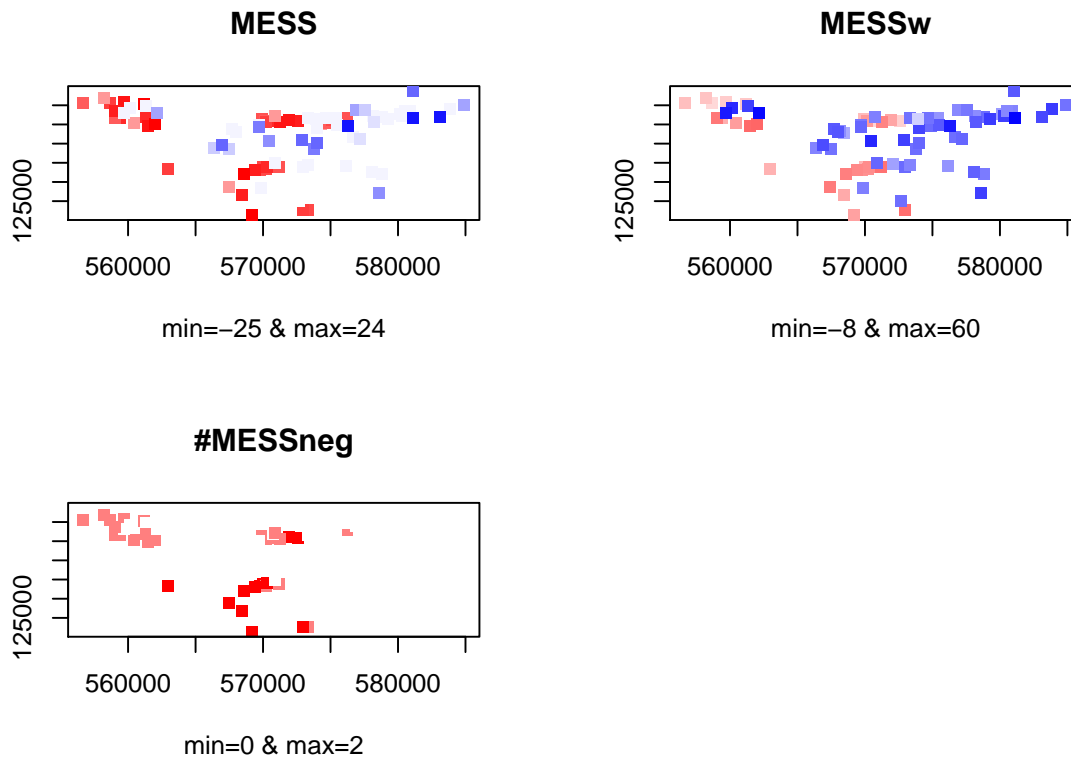
2.3.2   Extrapolation detection, creating a MESS object with *ecospat.mess()*

```
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")
```

2.3.2.1   Plot MESS with *ecospat.plot.mess()*

```
ecospat.plot.mess (mess.object, cex=1, pch=15)
```

MESS

min=−25 & max=24

MESSw

min=−8 & max=60

#MESSneg

min=0 & max=2

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

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

2.4.1 Calculate Phylogenetic Diversity Measures *ecospat.calculate.pd*

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

```
## Progress (. = 100 pixels calculated):
## ... [300]
## All 300 pixels done.
```

```
pd
```

```
##    [1]    6.9782188    6.7981743    4.9964700    4.9964700    4.9964700
##    [6]   29.8820547   58.7451752    6.5223035   30.6152478    1.5258335
##   [11]    0.0000000   44.3661803   38.4155607    6.5223035   24.0929443
##   [16]   78.1607950   38.4155607   29.0894143   29.0894143   89.9839758
##   [21]   27.4135569   40.2827035    1.5258335   56.7686202   18.9535475
##   [26]   34.8871800    0.0000000    1.5258335   39.9291325   48.5997861
```

```
##   [31]  82.8763723  29.0894143  24.0929443  24.0929443  35.0949481
##   [36]  85.1406422  54.7974724  41.2817284  32.4100269  30.0984781
##   [41]  46.8247511  42.8358475  35.6223697  91.5539224  72.7022527
##   [46]   0.0000000  21.1862293  29.7320308  10.1187868  30.6152478
##   [51]  27.4135569  59.0015345  78.1536692  42.6423378  24.0929443
##   [56]  46.8050070  49.3924266  29.0894143  38.5290848  43.3611373
##   [61]  63.6397674  49.6097169  34.6522309  37.1871282 109.8813371
##   [66] 106.6971561  52.2512132  80.6221671  68.3867818  49.1362998
##   [71]  56.6138690  41.9283257  29.0894143  33.2026673  16.1897593
##   [76]  79.1938213  42.8115427  25.6187778  34.6805724  96.9902366
##   [81]  75.2672695   7.5313673  31.4078882  50.5865673  13.9570775
##   [86] 104.4121025  43.0464918  36.6693230  52.8590823  24.8855847
##   [91] 107.2302322  33.9358604  54.0048319  30.6152478 102.0983385
##   [96]   8.3170826  52.3071062   8.3170826  61.8562896  58.1179346
##  [101]  59.7939424   8.3170826  81.6495398  51.1054635  75.8701970
##  [106]  77.6947419  56.7929250  70.3693202  81.3965205  29.9118877
##  [111] 111.0790432  75.7518798 112.5482496  32.9763735  42.5644761
##  [116]  40.4507005  83.8955419  36.6693230   2.3184739  57.5978451
##  [121]  91.3453370  33.3983912  50.1351419   7.7084002  63.9227817
##  [126]   0.7926404  67.2813325  91.2965996  90.9578739 105.9024741
##  [131]  74.6128871  46.1321553  15.2479619  24.0929443  70.4802708
##  [136]  68.8949899 118.6657550 101.3545260 119.8539056  23.6602184
##  [141] 105.8968281  15.9336325 138.4059855  39.6674173  51.7391372
##  [146]  58.4119283  81.1388699  96.6048825  72.2156025  56.3601992
##  [151] 112.9489963  63.3258805  50.1594468  23.0021994  87.1886965
##  [156]  12.7714946  33.7421666  23.2537702  14.3226164   6.9752071
##  [161]   0.7926404  13.5641350  36.2007616  63.9227817  40.3310946
##  [166]  52.8264129  67.9956878  29.5843437   0.0000000 191.7818606
##  [171] 133.6077875  83.3977825 118.6711630  51.1512871  69.3838811
##  [176]  87.7066616  35.8005270  93.7797077  85.8984840  23.4933413
##  [181] 149.7094684  52.4451847 112.1873673  53.4479612  51.4341108
##  [186] 106.6959500  14.4361405  41.6547546  89.4018733  59.1068292
##  [191]   3.0516670  60.7852739  28.1850877  52.1002690 114.3651475
##  [196]  86.2640717  83.7092232  39.8499777  55.3514065 116.1795597
##  [201]  21.2346203  75.4593878 197.8157358 140.3806968  93.2192350
##  [206]  36.5337815 146.3370747 214.5450205  64.2439145  83.3740177
##  [211]  57.0440643 149.5697614 196.9415036  31.0984631  57.4769230
##  [216]  28.4014469  42.3978747 194.5384819  60.5204195  73.0060715
##  [221]  52.1628582  30.2801165  63.1752097  29.1789484  82.7662787
##  [226] 196.8309769   3.4666557   0.0000000  31.5688084  60.5650008
##  [231]  43.3334929  62.5952411  13.9570775  18.9495667  35.2646601
##  [236]  32.6155790   0.0000000  14.6693623  24.2745827  73.9480832
##  [241]  19.2825866   0.0000000  40.6115985  68.9862341   6.9782188
##  [246]  11.5030881  27.9105497  72.4020225  39.6781995  35.4596364
##  [251]  33.9160835  27.5735165  15.9619740  27.9105497  17.8628493
##  [256]  36.0936777  87.0440848  27.9105497  66.6907987  21.6475811
##  [261]  67.5969904   0.0000000   0.0000000   0.0000000  58.0542370
##  [266]   0.0000000   0.0000000  27.9105497   0.0000000   0.0000000
##  [271]  27.9105497  34.8887684  56.5556633  27.9105497  30.3097595
##  [276]  88.4296666  37.8150727  54.2397810  31.6243116   7.5799087
##  [281]  73.0136833  31.8638035  41.7172212 120.5228857  32.2001243
##  [286] 151.4545228  10.1544492  70.8133537  59.3255687  25.7211220
##  [291]  24.1115267  43.1500941 150.0299191  72.2758570  85.9498096
##  [296] 159.7242106  66.8328159  24.0929443   0.0000000  27.9105497
```

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

```r
plot(pd)
```
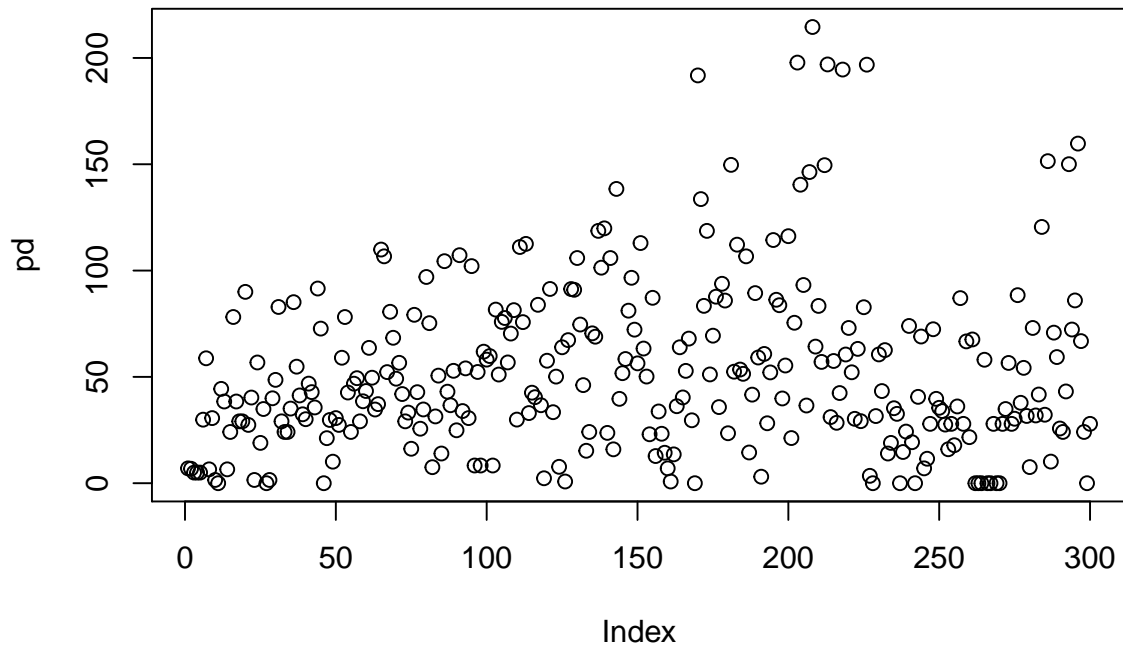

2.5 Niche Quantification and Comparison with Ordination techniques

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

```r
inv <- ecospat.testNiche.inv
```

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

```r
nat <- ecospat.testNiche.nat
```

2.5.1 PCA-ENVIRONMENT

#### 2.5.1.1 The PCA is calibrated on all the sites of the study area

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

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

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

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

correlation circle
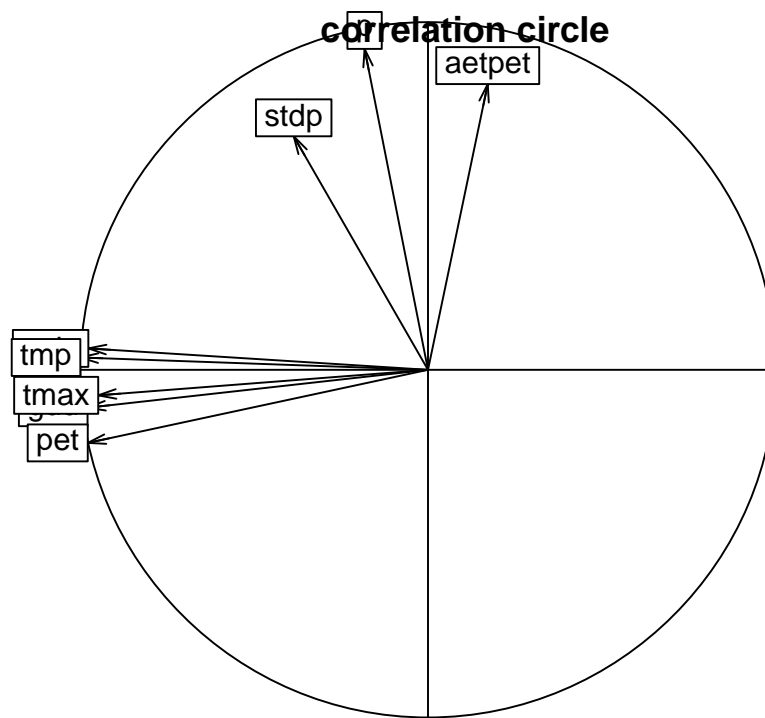
axis1 = 61.14 % axis2 = 25.09 %

The correlation circle indicate the contribution of original predictors to the PCA axes.

2.5.1.3 Predict the scores on the axes

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

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

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

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

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

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

For a species in the native range (North America)

```r
# 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)
```

For a species in the invaded range (Australia)

```r
# 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)
```

2.5.3 Calculate Niche Overlap with *ecospat.niche.overlap()*

```r
# Compute Schoener's D, index of niche overlap
D.overlap <- ecospat.niche.overlap (grid.clim.nat, grid.clim.inv, cor=T)$D
D.overlap
```

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

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

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

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

```r
eq.test <- ecospat.niche.equivalency.test(grid.clim.nat, grid.clim.inv,
                                          rep=10, alternative = "greater")
```

Niche equivalency test H1: Is the overlap between the native and invaded niche higher than two random niches?

2.5.5 Perform the Niche Similarity Test with *ecospat.niche.similarity.test()*

Shifting randomly the invasive niche in the invaded study area It is recomended to use at least 1000 replications for the similarity test. As an example we used rep = 10, to reduce the computational time.

```r
sim.test <- ecospat.niche.similarity.test(grid.clim.nat, grid.clim.inv,
                                          rep=10, alternative = "greater",
                                          rand.type=2)
```

Niche similarity test H1: Is the overlap between the native and invaded higher than when the invasive niche is randomly introduced in the invaded study area?

2.5.5.1 Plot Equivalency test

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

Equivalency

D

p.value = 0.63636
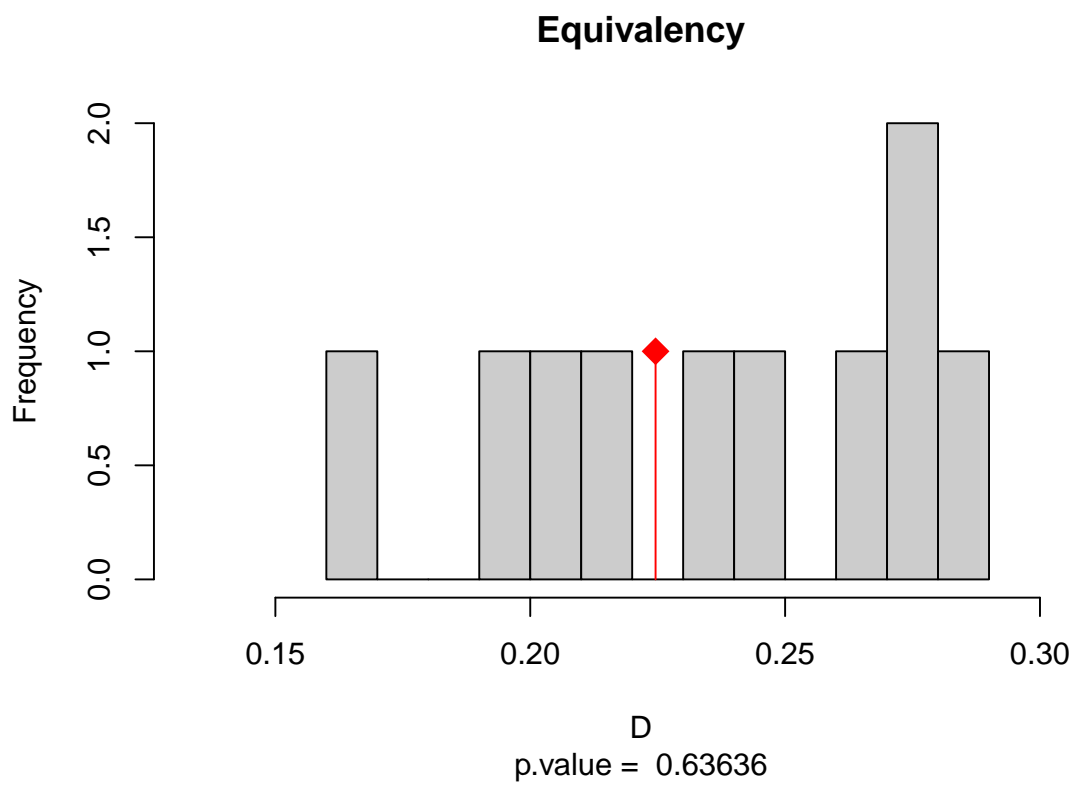
2.5.5.2 Plot Similarity test

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

Similarity

D

p.value = 0.18182

We see that the niche overlap D is 22% and this value is compared to the random distribution of the
niche equivalency and niche similarity tests.

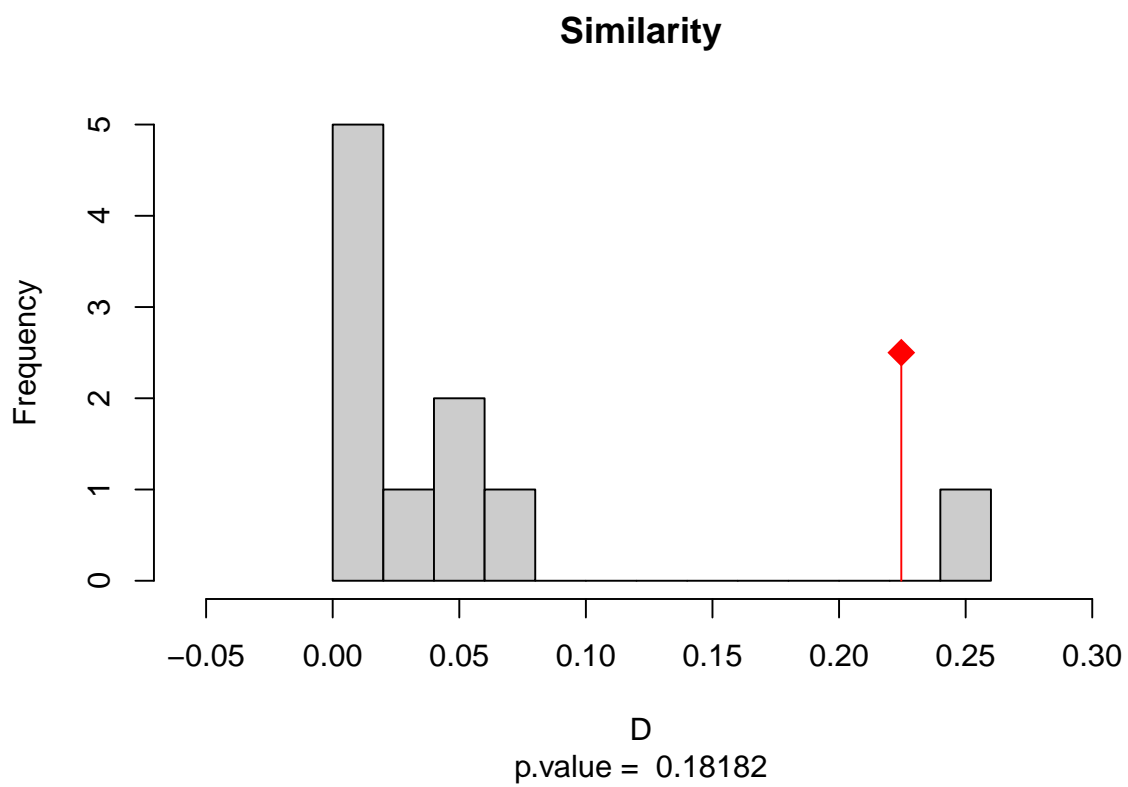### 2.5.6 Delimiting niche categories and quantifying niche dynamics in analogue climates with *ecospat.niche.dyn.index()*

```
niche.dyn <- ecospat.niche.dyn.index (grid.clim.nat, grid.clim.inv, intersection = 0.1)
```

2.5.6.1 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)
```

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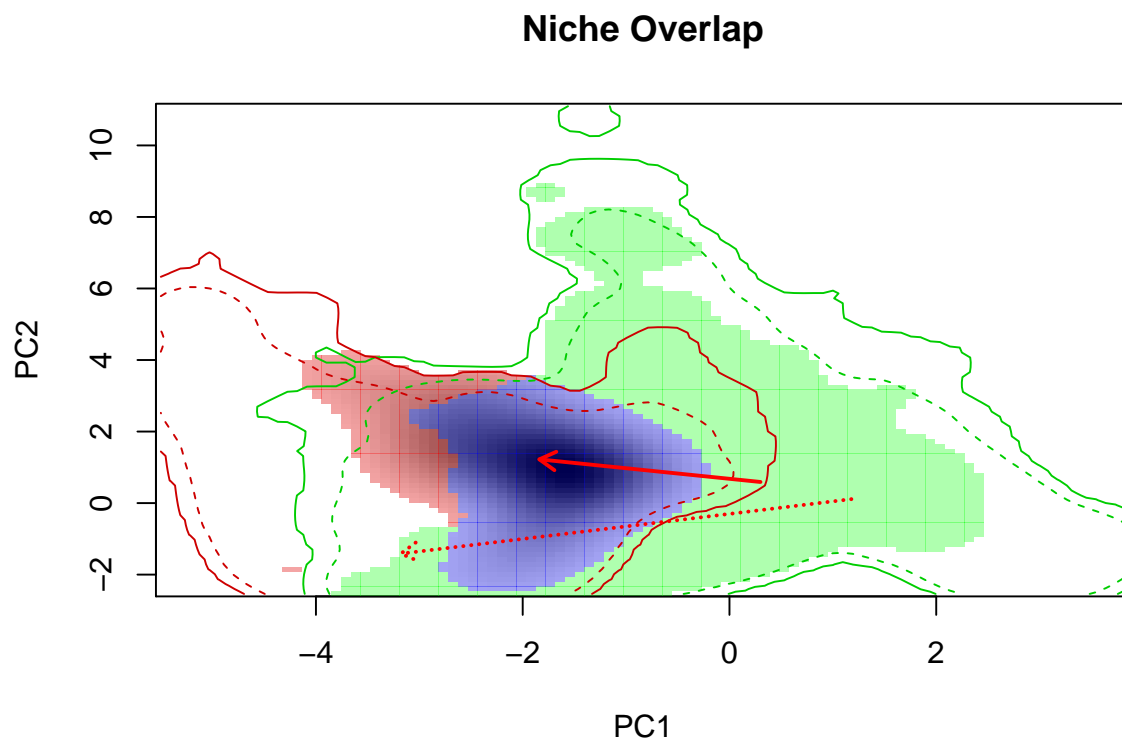
2.5.6.2 Plot the niche dynamics along one gradient (here temperature) with *ecospat.plot.niche.dyn()*

```
# 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,
                    interest=2, title= "Niche Overlap",
                    name.axis1="Average temperature")
```
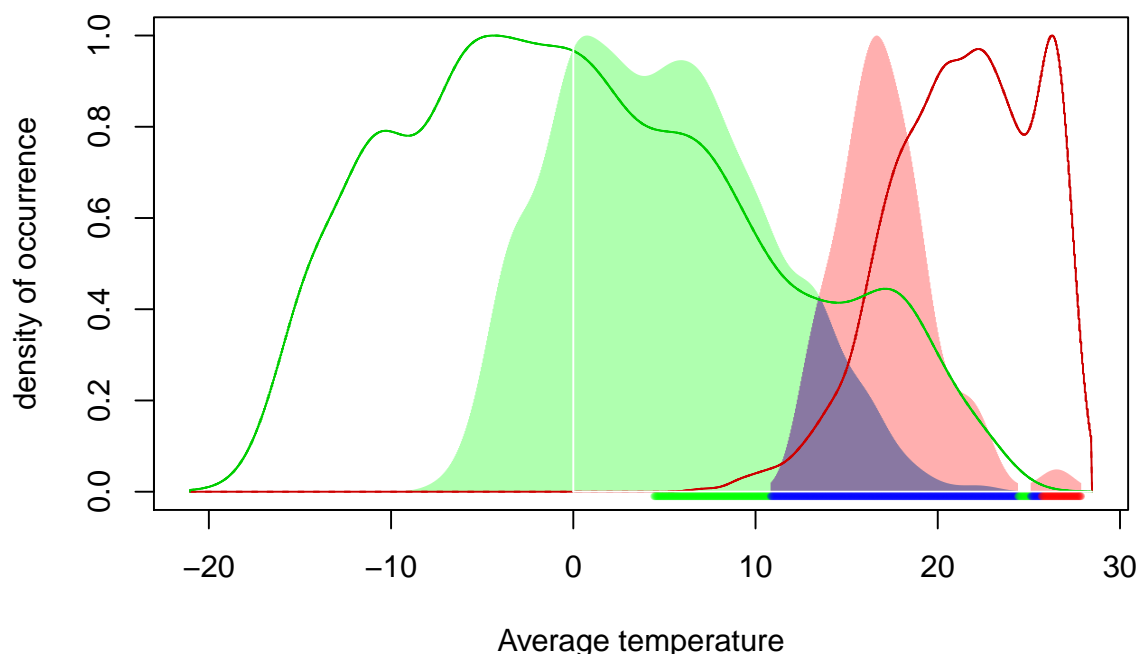

2.6   Biotic Interactions

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 intersects S2) is the number of times species S1 and S2 co-occur, while 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)
```
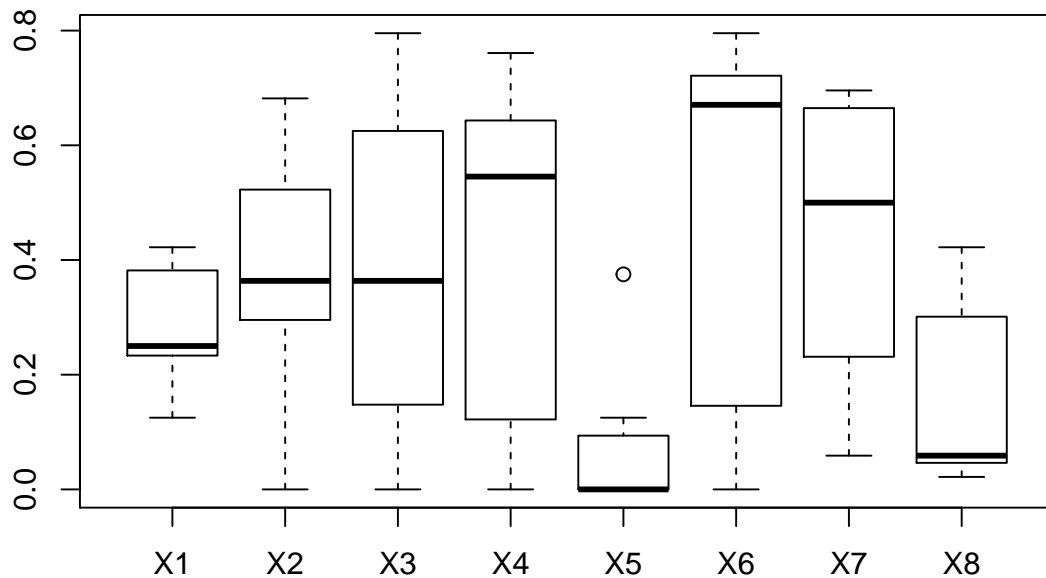
```
##                      Aposeris_foetida Arnica_montana Aster_bellidiastrum
## Aposeris_foetida            1.0000000      0.3636364          0.25000000
## Arnica_montana              0.3636364      1.0000000          0.36363636
## Aster_bellidiastrum         0.2500000      0.3636364          1.00000000
## Bartsia_alpina              0.2222222      0.5454545          0.59090909
## Bromus_erectus_sstr         0.1250000      0.0000000          0.00000000
## Campanula_scheuchzeri       0.2444444      0.6818182          0.79545455
## Carex_sempervirens          0.4000000      0.5000000          0.65909091
## Cynosurus_cristatus         0.4222222      0.2272727          0.04545455
##                      Bartsia_alpina Bromus_erectus_sstr
## Aposeris_foetida         0.22222222              0.1250
## Arnica_montana           0.54545455              0.0000
## Aster_bellidiastrum      0.59090909              0.0000
## Bartsia_alpina           1.00000000              0.0000
## Bromus_erectus_sstr      0.00000000              1.0000
## Campanula_scheuchzeri    0.76086957              0.0000
## Carex_sempervirens       0.69565217              0.0625
## Cynosurus_cristatus      0.02173913              0.3750
##                      Campanula_scheuchzeri Carex_sempervirens
## Aposeris_foetida                0.24444444         0.40000000
## Arnica_montana                  0.68181818         0.50000000
## Aster_bellidiastrum             0.79545455         0.65909091
## Bartsia_alpina                  0.76086957         0.69565217
## Bromus_erectus_sstr             0.00000000         0.06250000
## Campanula_scheuchzeri           1.00000000         0.67058824
## Carex_sempervirens              0.67058824         1.00000000
## Cynosurus_cristatus             0.04705882         0.05882353
##                      Cynosurus_cristatus
## Aposeris_foetida              0.42222222
## Arnica_montana                0.22727273
## Aster_bellidiastrum           0.04545455
```

```
## Bartsia_alpina               0.02173913
## Bromus_erectus_sstr          0.37500000
## Campanula_scheuchzeri        0.04705882
## Carex_sempervirens           0.05882353
## Cynosurus_cristatus          1.00000000
```

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 recomended to use at least 10000 permutatiobns 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)
```

```
## Computing observed co-occurence matrix
## .............
## .............
## .............
## Computing permutations
## .............
## 100  permutations to go
## .............
## 50  permutations to go
## .............
## Computing P-values
## .............
## Exporting dataset
## .............
## .............
## .............
```

Histogram of standardized effect size
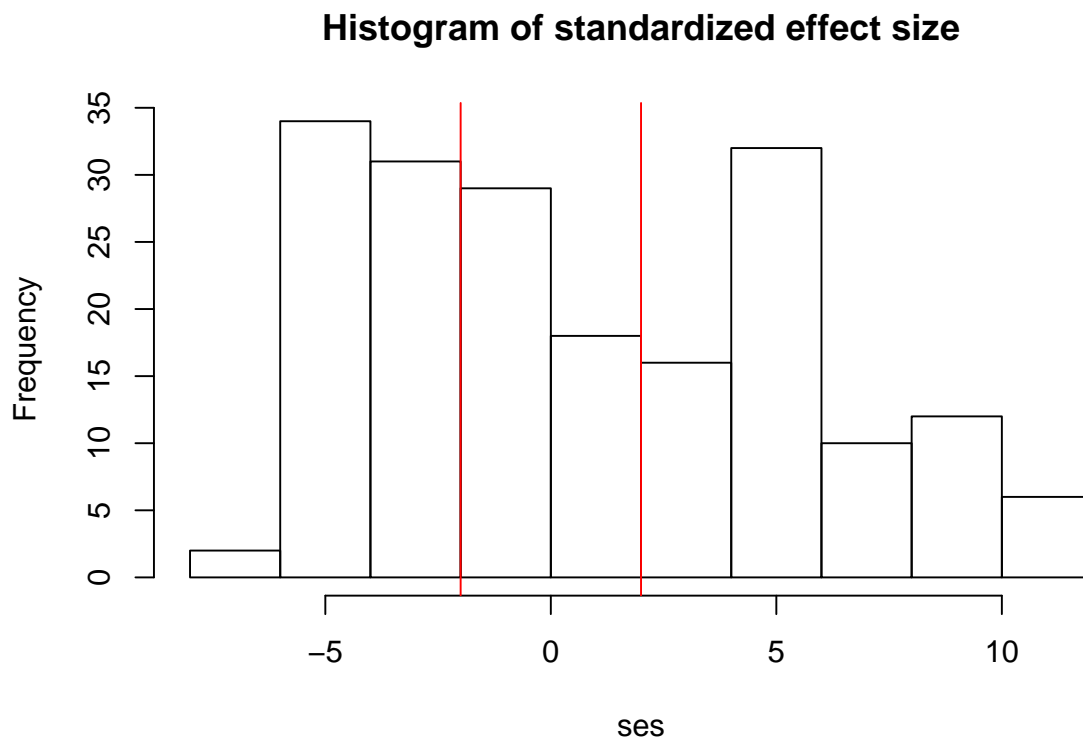

```
## $ObsCscoreTot
## [1] 2675.468
##
## $SimCscoreTot
## [1] 2467.251
##
## $PVal.less
## [1] 1
##
## $PVal.greater
## [1] 0.00990099
##
## $SES.Tot
## [1] 61.75911
```

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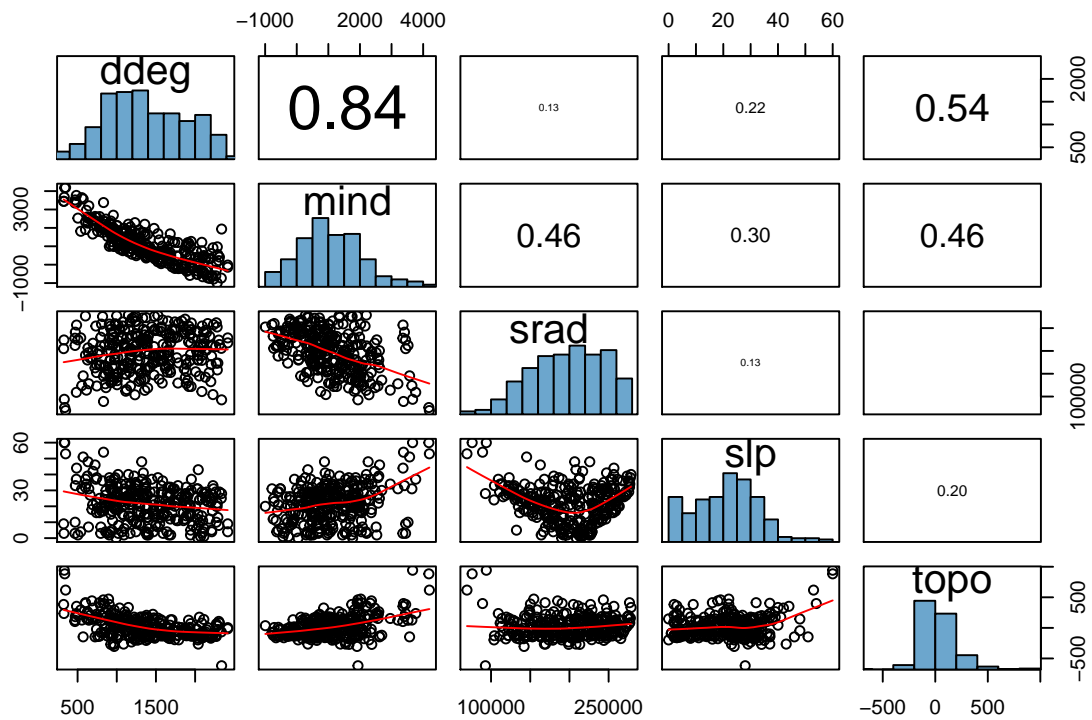
A scatter plot of matrices, with bivariate scatter plots below the diagonal, histograms on the diagonal, and the Pearson correlation above the diagonal. Useful for descriptive statistics of small data sets (better with less than 10 variables).

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)
#caleval
```

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)$Spearman.cor
```
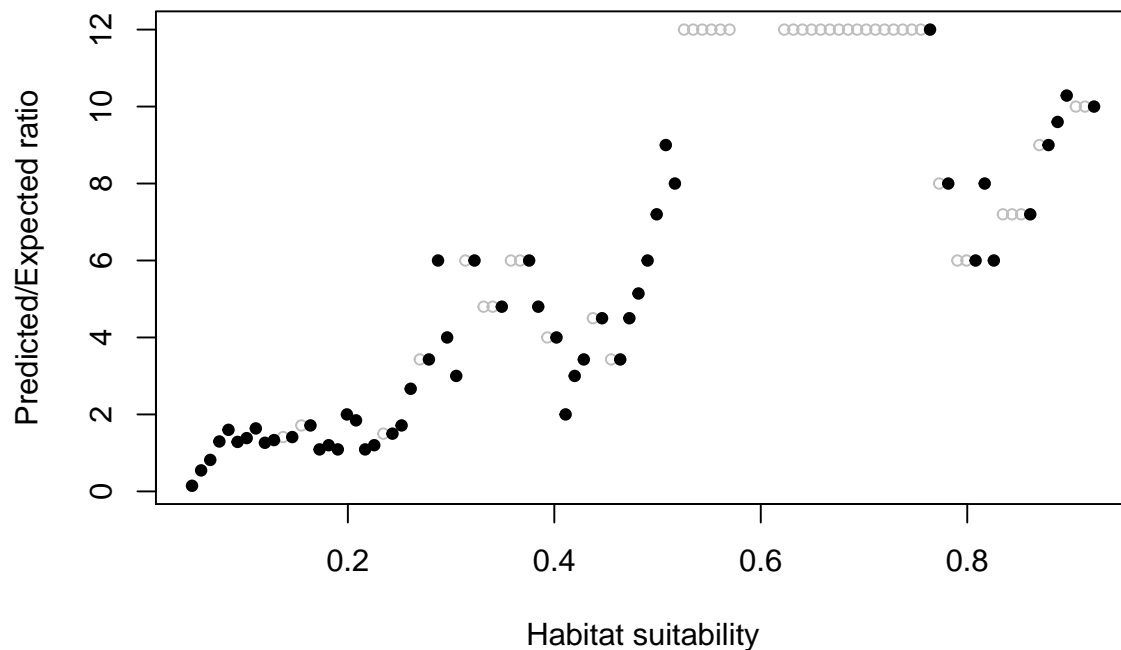


```
## [1] 0.91
```

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)]
```

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

```
## 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

```r
library(biomod2)
```

```
## Loading required package: raster

##
## Attaching package: 'raster'

## The following objects are masked from 'package:ape':
##
##     rotate, zoom

## Loading required package: reshape

## Loading required package: ggplot2

## biomod2 3.3-7 loaded.
##
## Type browseVignettes(package='biomod2') to access directly biomod2 vignettes.
```

```r
path.wd<-getwd()
```

```r
# 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
```

```r
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
setwd(path.wd)
t1 <- Sys.time()
sp<-1
```

Formating the data with the BIOMOD_FormatingData() function form the package biomod2

```
myBiomodData <- BIOMOD_FormatingData( 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 pseudo absences selection !
##        ! No data has been set aside for modeling evaluation
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
```

```
myBiomodOption <- Print_Default_ModelingOptions()
```

```
##
##   Defaut modeling options. copy, change what you want paste it as arg to BIOMOD_ModelingOptions
##
##
## -=-=-=-=-=-=-=-=-=-=-=  'BIOMOD.Model.Options'  -=-=-=-=-=-=-=-=-=-=-=
##
##
## GLM = list( type = 'quadratic',
##             interaction.level = 0,
##             myFormula = NULL,
##             test = 'AIC',
##             family = binomial(link = 'logit'),
##             mustart = 0.5,
##             control = glm.control(epsilon = 1e-08, maxit = 50
## , trace = FALSE) ),
##
##
## GBM = list( distribution = 'bernoulli',
##             n.trees = 2500,
##             interaction.depth = 7,
##             n.minobsinnode = 5,
##             shrinkage = 0.001,
##             bag.fraction = 0.5,
##             train.fraction = 1,
##             cv.folds = 3,
##             keep.data = FALSE,
##             verbose = FALSE,
##             perf.method = 'cv'),
##
## GAM = list( algo = 'GAM_mgcv',
##             type = 's_smoother',
##             k = -1,
##             interaction.level = 0,
##             myFormula = NULL,
```

```
##                 family = binomial(link = 'logit'),
##                 method = 'GCV.Cp',
##                 optimizer = c('outer','newton'),
##                 select = FALSE,
##                 knots = NULL,
##                 paraPen = NULL,
##                 control = list(nthreads = 1, irls.reg = 0, epsilon = 1e-07
## , maxit = 200, trace = FALSE, mgcv.tol = 1e-07, mgcv.half = 15
## , rank.tol = 1.49011611938477e-08
## , nlm = list(ndigit=7, gradtol=1e-06, stepmax=2, steptol=1e-04, iterlim=200, check.analyticals=0)
## , optim = list(factr=1e+07)
## , newton = list(conv.tol=1e-06, maxNstep=5, maxSstep=2, maxHalf=30, use.svd=0)
## , outerPIsteps = 0, idLinksBases = TRUE, scalePenalty = TRUE
## , keepData = FALSE, scale.est = fletcher, edge.correct = FALSE) ),
##
##
## CTA = list( method = 'class',
##              parms = 'default',
##              cost = NULL,
##              control = list(xval = 5, minbucket = 5, minsplit = 5
## , cp = 0.001, maxdepth = 25) ),
##
##
## ANN = list( NbCV = 5,
##              size = NULL,
##              decay = NULL,
##              rang = 0.1,
##              maxit = 200),
##
## SRE = list( quant = 0.025),
##
## FDA = list( method = 'mars',
##              add_args = NULL),
##
## MARS = list( type = 'simple',
##               interaction.level = 0,
##               myFormula = NULL,
##               nk = NULL,
##               penalty = 2,
##               thresh = 0.001,
##               nprune = NULL,
##               pmethod = 'backward'),
##
## RF = list( do.classif = TRUE,
##             ntree = 500,
##             mtry = 'default',
##             nodesize = 5,
##             maxnodes = NULL),
##
## MAXENT.Phillips = list( path_to_maxent.jar = 'W:/40_tools/Ecospat R Package/obroenni/ecospat/ecos
##                  memory_allocated = 512,
##                  background_data_dir = 'default',
##                  maximumbackground = 'default',
##                  maximumiterations = 200,
##                  visible = FALSE,
##                  linear = TRUE,
##                  quadratic = TRUE,
##                  product = TRUE,
```

```
##                 threshold = TRUE,
##                 hinge = TRUE,
##                 lq2lqptthreshold = 80,
##                 l2lqthreshold = 10,
##                 hingethreshold = 15,
##                 beta_threshold = -1,
##                 beta_categorical = -1,
##                 beta_lqp = -1,
##                 beta_hinge = -1,
##                 betamultiplier = 1,
##                 defaultprevalence = 0.5),
##
## MAXENT.Tsuruoka = list( l1_regularizer = 0,
##                         l2_regularizer = 0,
##                         use_sgd = FALSE,
##                         set_heldout = 0,
##                         verbose = FALSE)
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
```

```
myBiomodOption@GLM$test = 'none'
myBiomodOption@GBM$interaction.depth = 2
```

```
### Calibration of simple bivariate models
my.ESM <- ecospat.ESM.Modeling( data=myBiomodData,
                                models=c('GLM','RF'),
                                models.options=myBiomodOption,
                                NbRunEval=1,
                                DataSplit=70,
                                weighting.score=c("AUC"),
                                parallel=F)
```

```
## Warning in dir.create(paste("./ESM.BIOMOD.output", data@sp.name, sep =
## "_")): '.\ESM.BIOMOD.output_species.occ' existe déjà
```

```
##
##  > Automatic weights creation to rise a 0.5 prevalence
##
## Loading required library...
##
## Checking Models arguments...
##
## ! User defined data-split table was given -> NbRunEval, DataSplit and do.full.models argument wil
## Creating suitable Workdir...
##
##  > Automatic weights creation to rise a 0.5 prevalence
##
##
## -=-=-=-=-=-=-=-=-=-= ESM.BIOMOD.1 Modeling Summary -=-=-=-=-=-=-=-=-=-=
##
##  2   environmental variables ( aetpet gdd )
## Number of evaluation repetitions : 2
## Models selected : GLM RF
##
## Total number of model runs : 4
##
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
```

```
##
## -=-=-=- Run :  ESM.BIOMOD.1_AllData
##
##
## -=-=-=----=-=- ESM.BIOMOD.1_AllData_RUN1
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.1 ~ 1 + aetpet + I(aetpet^2) + gdd + I(gdd^2)
## <environment: 0x000000001b54e950>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...
##  Evaluating Model stuff...
##
## -=-=-=----=-=- ESM.BIOMOD.1_AllData_RUN2
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.1 ~ 1 + aetpet + I(aetpet^2) + gdd + I(gdd^2)
## <environment: 0x00000000212623c0>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...


## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred


##
##  Evaluating Model stuff...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=- Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-
##
##
## Loading required library...
##
## Checking Models arguments...
##
## ! User defined data-split table was given -> NbRunEval, DataSplit and do.full.models argument wil
## Creating suitable Workdir...
##
##  > Automatic weights creation to rise a 0.5 prevalence
##
##
## -=-=-=-=-=-=-=-=-= ESM.BIOMOD.2 Modeling Summary -=-=-=-=-=-=-=-=-=
##
##  2  environmental variables ( aetpet p )
## Number of evaluation repetitions : 2
## Models selected : GLM RF
##
## Total number of model runs : 4
##
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
##
```

```
## 
## -=-=-=- Run :  ESM.BIOMOD.2_AllData
## 
## 
## -=-=-=---=-=- ESM.BIOMOD.2_AllData_RUN1
## 
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.2 ~ 1 + aetpet + I(aetpet^2) + p + I(p^2)
## <environment: 0x0000000021d89058>
## 
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...
##  Evaluating Model stuff...
## 
## -=-=-=---=-=- ESM.BIOMOD.2_AllData_RUN2
## 
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.2 ~ 1 + aetpet + I(aetpet^2) + p + I(p^2)
## <environment: 0x0000000021642388>
## 
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...


## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred


## 
##  Evaluating Model stuff...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
## 
## 
## Loading required library...
## 
## Checking Models arguments...
## 
## ! User defined data-split table was given -> NbRunEval, DataSplit and do.full.models argument wil
## Creating suitable Workdir...
## 
##  > Automatic weights creation to rise a 0.5 prevalence
## 
## 
## -=-=-=-=-=-=-=-=-=- ESM.BIOMOD.3 Modeling Summary -=-=-=-=-=-=-=-=-=-=
## 
##  2  environmental variables ( aetpet pet )
## Number of evaluation repetitions : 2
## Models selected : GLM RF
## 
## Total number of model runs : 4
## 
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
## 
```

```
##
## -=-=-=- Run :  ESM.BIOMOD.3_AllData
##
##
## -=-=-=-=-=-=- ESM.BIOMOD.3_AllData_RUN1
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.3 ~ 1 + aetpet + I(aetpet^2) + pet + I(pet^2)
## <environment: 0x000000001e85b180>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...
##  Evaluating Model stuff...
##
## -=-=-=-=-=-=- ESM.BIOMOD.3_AllData_RUN2
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.3 ~ 1 + aetpet + I(aetpet^2) + pet + I(pet^2)
## <environment: 0x0000000021630a50>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...


## Warning: glm.fit: algorithm did not converge


## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred


##
##  Evaluating Model stuff...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## Loading required library...
##
## Checking Models arguments...
##
## ! User defined data-split table was given -> NbRunEval, DataSplit and do.full.models argument wil
## Creating suitable Workdir...
##
##  > Automatic weights creation to rise a 0.5 prevalence
##
##
## -=-=-=-=-=-=-=-=-=-=-= ESM.BIOMOD.4 Modeling Summary -=-=-=-=-=-=-=-=-=-=-=
##
##  2  environmental variables ( aetpet stdp )
## Number of evaluation repetitions : 2
## Models selected : GLM RF
##
## Total number of model runs : 4
##
```

```
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## -=-=-=- Run :  ESM.BIOMOD.4_AllData
##
##
## -=-=-=-=-=-=- ESM.BIOMOD.4_AllData_RUN1
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.4 ~ 1 + aetpet + I(aetpet^2) + stdp + I(stdp^2)
## <environment: 0x000000001cf34938>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...
##  Evaluating Model stuff...
##
## -=-=-=-=-=-=- ESM.BIOMOD.4_AllData_RUN2
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.4 ~ 1 + aetpet + I(aetpet^2) + stdp + I(stdp^2)
## <environment: 0x0000000021aa3e48>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...


## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred


##
##  Evaluating Model stuff...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## Loading required library...
##
## Checking Models arguments...
##
## ! User defined data-split table was given -> NbRunEval, DataSplit and do.full.models argument wil
## Creating suitable Workdir...
##
##  > Automatic weights creation to rise a 0.5 prevalence
##
##
## -=-=-=-=-=-=-=-=-=-=-=- ESM.BIOMOD.5 Modeling Summary -=-=-=-=-=-=-=-=-=-=-=-
##
##  2  environmental variables ( gdd p )
## Number of evaluation repetitions : 2
## Models selected : GLM RF
##
## Total number of model runs : 4
##
```

```
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## -=-=-=- Run :  ESM.BIOMOD.5_AllData
##
##
## -=-=-=-=-=-=- ESM.BIOMOD.5_AllData_RUN1
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.5 ~ 1 + gdd + I(gdd^2) + p + I(p^2)
## <environment: 0x000000001faf0a50>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...
##  Evaluating Model stuff...
##
## -=-=-=-=-=-=- ESM.BIOMOD.5_AllData_RUN2
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.5 ~ 1 + gdd + I(gdd^2) + p + I(p^2)
## <environment: 0x000000002161b8c0>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...


## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred


##
##  Evaluating Model stuff...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## Loading required library...
##
## Checking Models arguments...
##
## ! User defined data-split table was given -> NbRunEval, DataSplit and do.full.models argument wil
## Creating suitable Workdir...
##
##  > Automatic weights creation to rise a 0.5 prevalence
##
##
## -=-=-=-=-=-=-=-=-=-=-=-= ESM.BIOMOD.6 Modeling Summary -=-=-=-=-=-=-=-=-=-=-=-=
##
##  2  environmental variables ( gdd pet )
## Number of evaluation repetitions : 2
## Models selected : GLM RF
##
## Total number of model runs : 4
##
```

29

```
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## -=-=-=- Run :  ESM.BIOMOD.6_AllData
##
##
## -=-=-=-=-=-=- ESM.BIOMOD.6_AllData_RUN1
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.6 ~ 1 + gdd + I(gdd^2) + pet + I(pet^2)
## <environment: 0x000000001cb956d0>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...
##  Evaluating Model stuff...
##
## -=-=-=-=-=-=- ESM.BIOMOD.6_AllData_RUN2
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.6 ~ 1 + gdd + I(gdd^2) + pet + I(pet^2)
## <environment: 0x000000001cf1c6e8>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...

## Warning: glm.fit: algorithm did not converge

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

##
##  Evaluating Model stuff...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## Loading required library...
##
## Checking Models arguments...
##
## ! User defined data-split table was given -> NbRunEval, DataSplit and do.full.models argument wil
## Creating suitable Workdir...
##
##  > Automatic weights creation to rise a 0.5 prevalence
##
##
## -=-=-=-=-=-=-=-=-=-=-= ESM.BIOMOD.7 Modeling Summary -=-=-=-=-=-=-=-=-=-=-=
##
##  2  environmental variables ( gdd stdp )
## Number of evaluation repetitions : 2
## Models selected : GLM RF
##
```

```
## Total number of model runs : 4
##
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## -=-=-=- Run :  ESM.BIOMOD.7_AllData
##
##
## -=-=-=-=-=-=- ESM.BIOMOD.7_AllData_RUN1
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.7 ~ 1 + gdd + I(gdd^2) + stdp + I(stdp^2)
## <environment: 0x000000002156b1d8>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...
##  Evaluating Model stuff...
##
## -=-=-=-=-=-=- ESM.BIOMOD.7_AllData_RUN2
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.7 ~ 1 + gdd + I(gdd^2) + stdp + I(stdp^2)
## <environment: 0x000000002161b2a0>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...


## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred


##
##  Evaluating Model stuff...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## Loading required library...
##
## Checking Models arguments...
##
## ! User defined data-split table was given -> NbRunEval, DataSplit and do.full.models argument wil
## Creating suitable Workdir...
##
##  > Automatic weights creation to rise a 0.5 prevalence
##
##
## -=-=-=-=-=-=-=-=-=-=-=-= ESM.BIOMOD.8 Modeling Summary -=-=-=-=-=-=-=-=-=-=-=-=
##
##  2  environmental variables ( p pet )
## Number of evaluation repetitions : 2
## Models selected : GLM RF
##
```

```
## Total number of model runs : 4
##
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## -=-=-=- Run :  ESM.BIOMOD.8_AllData
##
##
## -=-=-=-=-=-=- ESM.BIOMOD.8_AllData_RUN1
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.8 ~ 1 + p + I(p^2) + pet + I(pet^2)
## <environment: 0x000000001faae810>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...
##  Evaluating Model stuff...
##
## -=-=-=-=-=-=- ESM.BIOMOD.8_AllData_RUN2
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.8 ~ 1 + p + I(p^2) + pet + I(pet^2)
## <environment: 0x0000000021631508>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...


## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred


##
##  Evaluating Model stuff...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## Loading required library...
##
## Checking Models arguments...
##
## ! User defined data-split table was given -> NbRunEval, DataSplit and do.full.models argument wil
## Creating suitable Workdir...
##
##  > Automatic weights creation to rise a 0.5 prevalence
##
##
## -=-=-=-=-=-=-=-=-=-=-=-= ESM.BIOMOD.9 Modeling Summary -=-=-=-=-=-=-=-=-=-=-=-=
##
##  2  environmental variables ( p stdp )
## Number of evaluation repetitions : 2
## Models selected : GLM RF
##
```

```
## Total number of model runs : 4
##
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## -=-=-=- Run :  ESM.BIOMOD.9_AllData
##
##
## -=-=-=-=-=-=- ESM.BIOMOD.9_AllData_RUN1
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.9 ~ 1 + p + I(p^2) + stdp + I(stdp^2)
## <environment: 0x0000000021239fd0>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...


## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred


##
##  Evaluating Model stuff...
##
## -=-=-=-=-=-=- ESM.BIOMOD.9_AllData_RUN2
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.9 ~ 1 + p + I(p^2) + stdp + I(stdp^2)
## <environment: 0x0000000024946608>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...


## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred


##
##  Evaluating Model stuff...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## Loading required library...
##
## Checking Models arguments...
##
## ! User defined data-split table was given -> NbRunEval, DataSplit and do.full.models argument wil
## Creating suitable Workdir...
##
##  > Automatic weights creation to rise a 0.5 prevalence
##
##
## -=-=-=-=-=-=-=-=-=-= ESM.BIOMOD.10 Modeling Summary -=-=-=-=-=-=-=-=-=-=
```

```
##
##  2  environmental variables ( pet stdp )
## Number of evaluation repetitions : 2
## Models selected : GLM RF
##
## Total number of model runs : 4
##
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
##
## -=-=-=- Run :  ESM.BIOMOD.10_AllData
##
##
## -=-=-=-=-=-=- ESM.BIOMOD.10_AllData_RUN1
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.10 ~ 1 + pet + I(pet^2) + stdp + I(stdp^2)
## <environment: 0x000000001fab1e98>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...
##  Evaluating Model stuff...
##
## -=-=-=-=-=-=- ESM.BIOMOD.10_AllData_RUN2
##
## Model=GLM ( quadratic with no interaction )
##  No stepwise procedure
##  ! You might be confronted to models convergence issues !
##  selected formula : ESM.BIOMOD.10 ~ 1 + pet + I(pet^2) + stdp + I(stdp^2)
## <environment: 0x0000000021653ef0>
##
##  Model scaling...
##  Evaluating Model stuff...
## Model=Breiman and Cutler's random forests for classification and regression
##  Model scaling...


## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred


##
##  Evaluating Model stuff...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=

### 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)


##
## -=-=-=-=-=-=-=-=-=-=-=-= Do Models Projections -=-=-=-=-=-=-=-=-=-=-=-=
##
##      ! 'do.stack' arg is always set as TRUE for data.frame/matrix dataset
```

```
## > Projecting ESM.BIOMOD.1_AllData_RUN2_GLM ...
## > Projecting ESM.BIOMOD.1_AllData_RUN2_RF ...
## -=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Models Projections -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##       ! 'do.stack' arg is always set as TRUE for data.frame/matrix dataset
## > Projecting ESM.BIOMOD.2_AllData_RUN2_GLM ...
## > Projecting ESM.BIOMOD.2_AllData_RUN2_RF ...
## -=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Models Projections -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##       ! 'do.stack' arg is always set as TRUE for data.frame/matrix dataset
## > Projecting ESM.BIOMOD.3_AllData_RUN2_GLM ...
## > Projecting ESM.BIOMOD.3_AllData_RUN2_RF ...
## -=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Models Projections -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##       ! 'do.stack' arg is always set as TRUE for data.frame/matrix dataset
## > Projecting ESM.BIOMOD.4_AllData_RUN2_GLM ...
## > Projecting ESM.BIOMOD.4_AllData_RUN2_RF ...
## -=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Models Projections -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##       ! 'do.stack' arg is always set as TRUE for data.frame/matrix dataset
## > Projecting ESM.BIOMOD.5_AllData_RUN2_GLM ...
## > Projecting ESM.BIOMOD.5_AllData_RUN2_RF ...
## -=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Models Projections -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##       ! 'do.stack' arg is always set as TRUE for data.frame/matrix dataset
## > Projecting ESM.BIOMOD.6_AllData_RUN2_GLM ...
## > Projecting ESM.BIOMOD.6_AllData_RUN2_RF ...
## -=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Models Projections -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##       ! 'do.stack' arg is always set as TRUE for data.frame/matrix dataset
## > Projecting ESM.BIOMOD.7_AllData_RUN2_GLM ...
## > Projecting ESM.BIOMOD.7_AllData_RUN2_RF ...
## -=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Models Projections -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##       ! 'do.stack' arg is always set as TRUE for data.frame/matrix dataset
## > Projecting ESM.BIOMOD.8_AllData_RUN2_GLM ...
## > Projecting ESM.BIOMOD.8_AllData_RUN2_RF ...
## -=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Models Projections -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##       ! 'do.stack' arg is always set as TRUE for data.frame/matrix dataset
## > Projecting ESM.BIOMOD.9_AllData_RUN2_GLM ...
## > Projecting ESM.BIOMOD.9_AllData_RUN2_RF ...
```

```
## -=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-= Do Models Projections -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##      ! 'do.stack' arg is always set as TRUE for data.frame/matrix dataset
## > Projecting ESM.BIOMOD.10_AllData_RUN2_GLM ...
## > Projecting ESM.BIOMOD.10_AllData_RUN2_RF ...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=
```

```
### 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()*

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

4   Post-Modelling

4.1   Spatial Predictions of species assamblages

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 recomended to use at least 10000 permutatiobns for the test. As an example we used nperm = 100, to reduce the computational time.

```
nbpermut <- 100
```

Define the outpath

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

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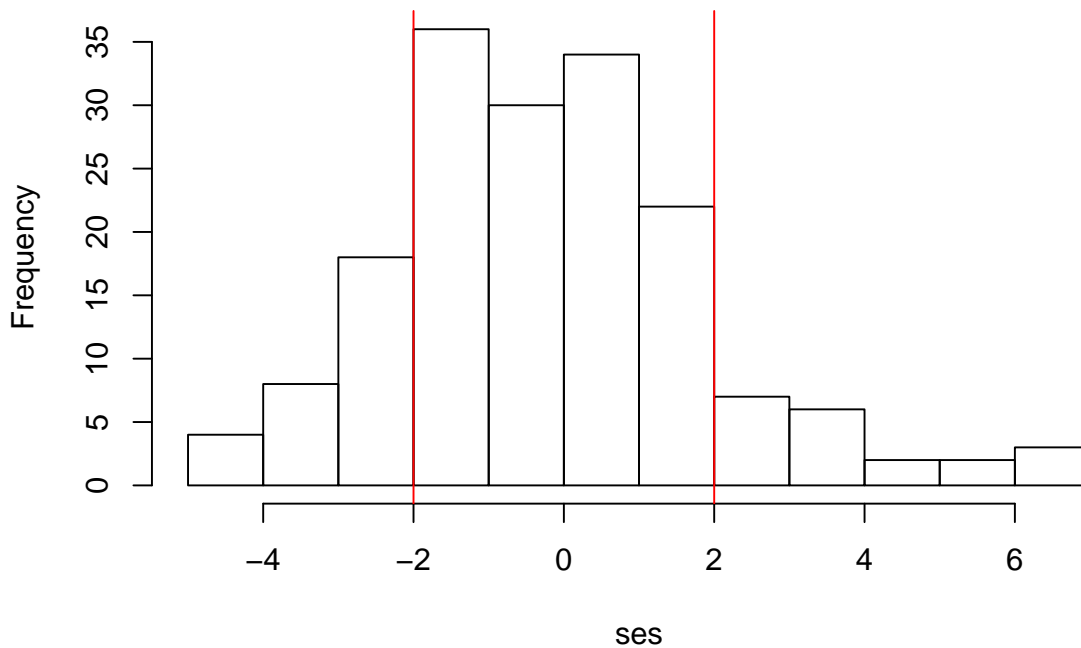
```
ecospat.cons_Cscore(presence, pred, nbpermut, outpath)
```

```
## Computing observed co-occurence matrix
## .............
## .............
## .............
## Computing permutations
## .............
## .............
## .............
```
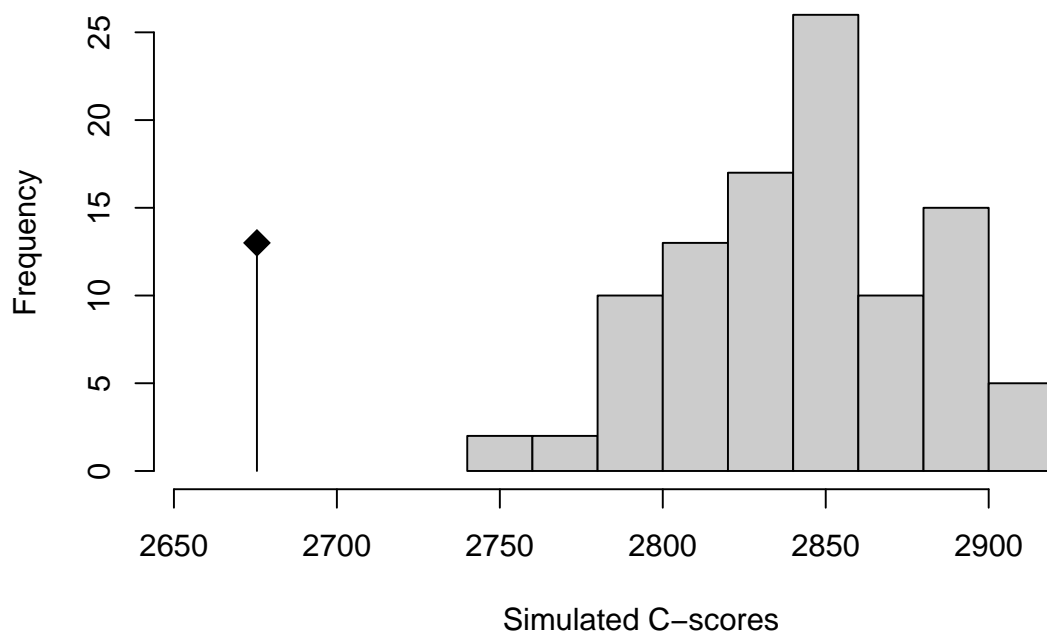


```
## Permutations finished Wed Jun 13 15:41:01 2018
## .............
## .............
## Exporting dataset
## .............
## .............
## .............
```

Histogram of standardized effect size


```
## $ObsCscoreTot
## [1] 2675.468
##
## $SimCscoreTot
## [1] 2842.198
##
## $PVal.less
## [1] 0.00990099
##
## $PVal.greater
## [1] 1
##
## $SES.Tot
## [1] -4.609203
```

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 dominate 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).