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)
citation("ecospat")
```

```
##
## To cite package 'ecospat' in publications use:
##
##   Broennimann O, Di Cola V, Guisan A (2022). _ecospat: Spatial Ecology
##   Miscellaneous Methods_. R package version 3.4,
##   <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 = {2022},
##     note = {R package version 3.4},
##     url = {http://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_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
```

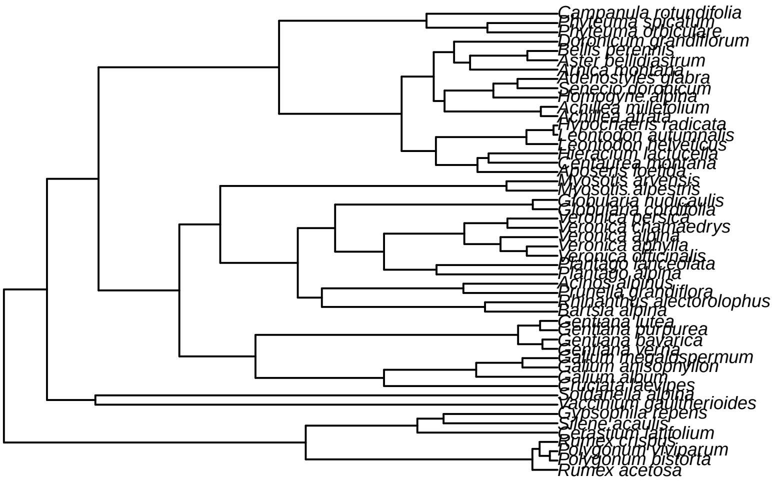
```
## [1] "C:/Users/obroenni/AppData/Local/Temp/Rtmp67ksPL/Rinst418c70f5553d/ecospat/extdata/ecospat.te
```

```
library(ape)
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

```r
plot(tree, cex=0.6)
```

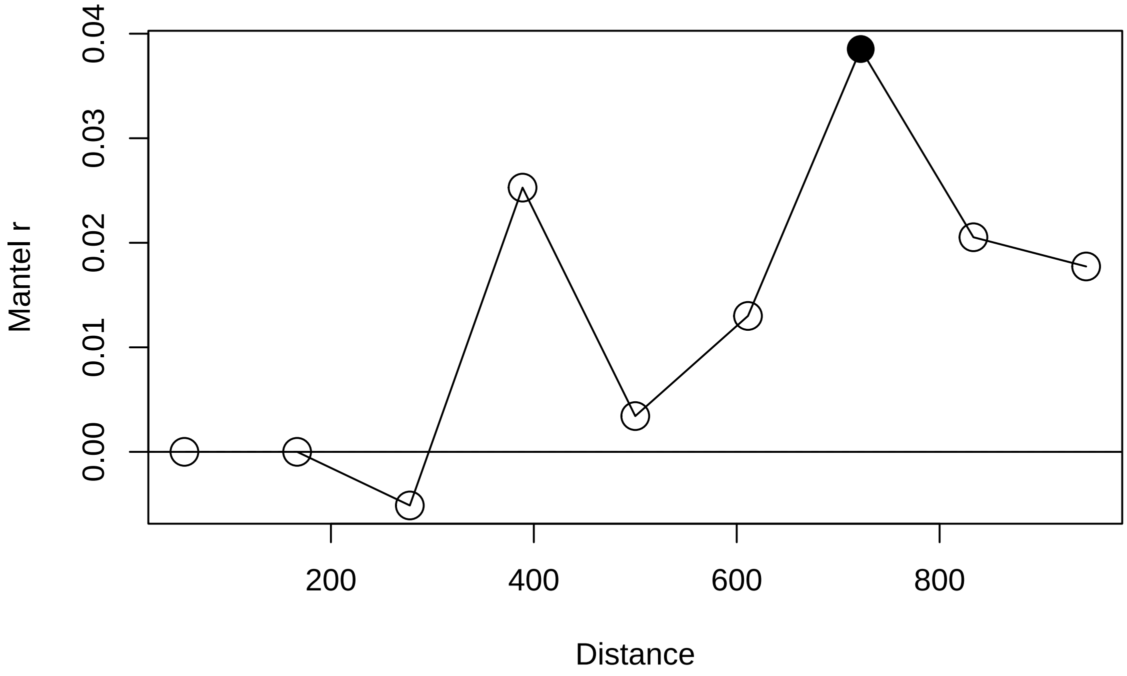


2 Pre-Modelling Analysis

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
```

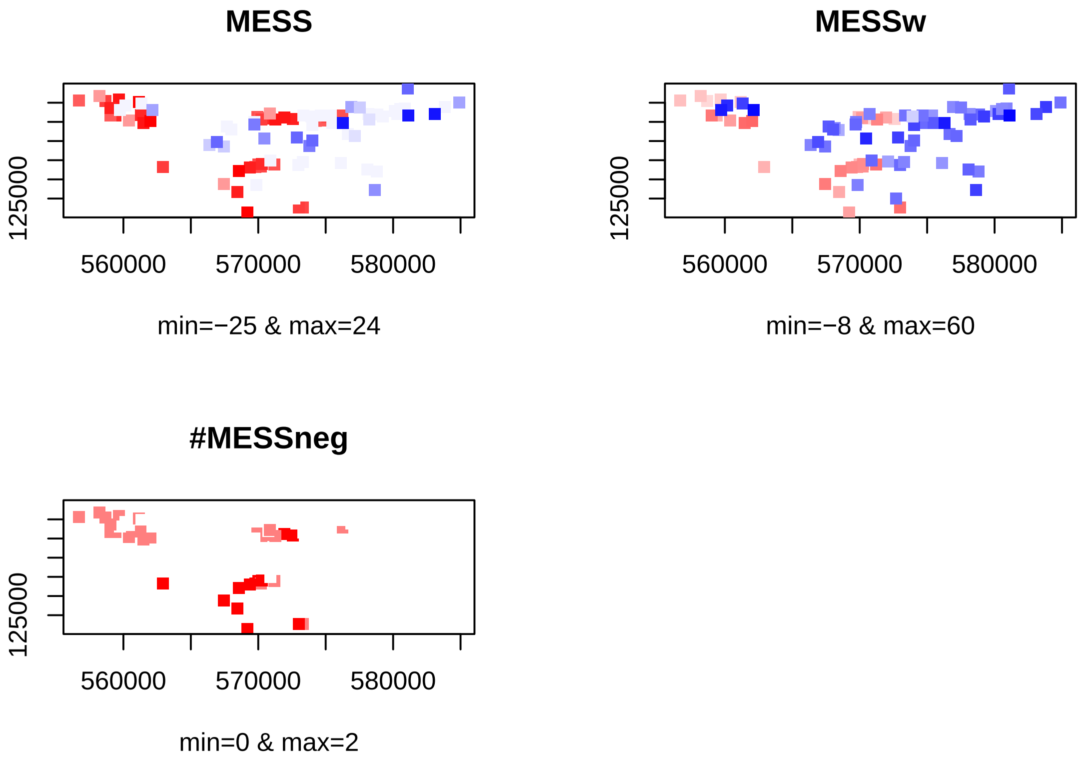
2.3.2 Extrapolation detection, creating a MESS object with *ecospat.mess()*

```
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")
```

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

```
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

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

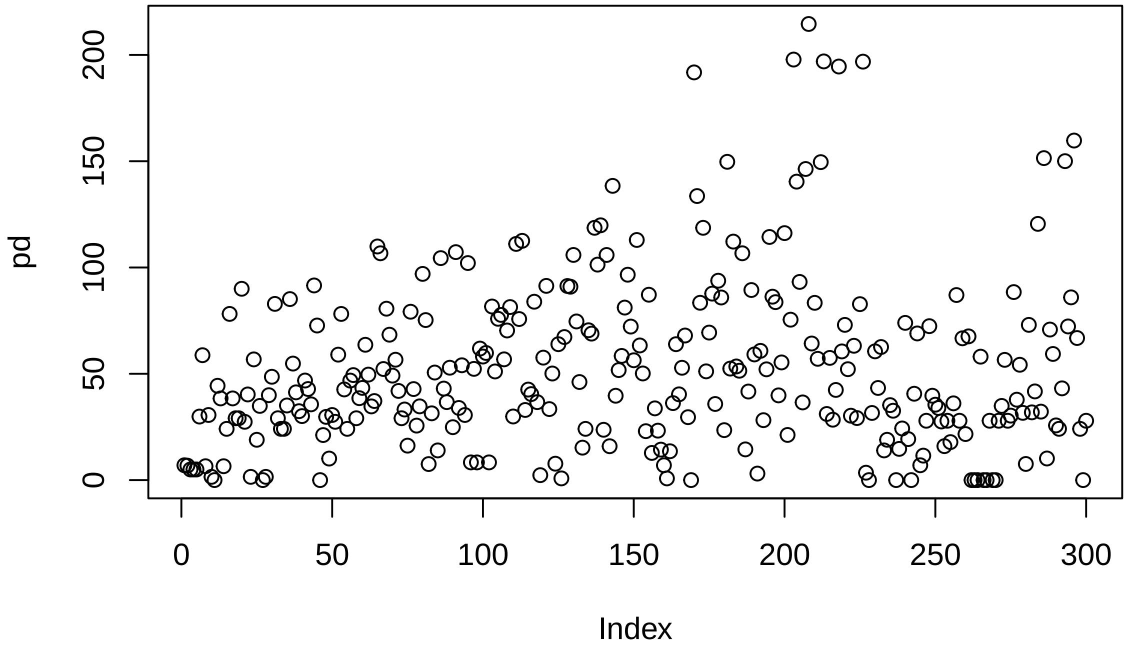
```
pd
```

```
##   [1]  6.9782188  6.7981743  4.9964700  4.9964700  4.9964700 29.8820547
##   [7] 58.7451752  6.5223035 30.6152478  1.5258335  0.0000000 44.3661803
##  [13] 38.4155607  6.5223035 24.0929443 78.1607950 38.4155607 29.0894143
##  [19] 29.0894143 89.9839758 27.4135569 40.2827035  1.5258335 56.7686202
```

```
##  [25]  18.9535475  34.8871800   0.0000000   1.5258335  39.9291325  48.5997861
##  [31]  82.8763723  29.0894143  24.0929443  24.0929443  35.0949481  85.1406422
##  [37]  54.7974724  41.2817284  32.4100269  30.0984781  46.8247511  42.8358475
##  [43]  35.6223697  91.5539224  72.7022527   0.0000000  21.1862293  29.7320308
##  [49]  10.1187868  30.6152478  27.4135569  59.0015345  78.1536692  42.6423378
##  [55]  24.0929443  46.8050070  49.3924266  29.0894143  38.5290848  43.3611373
##  [61]  63.6397674  49.6097169  34.6522309  37.1871282 109.8813371 106.6971561
##  [67]  52.2512132  80.6221671  68.3867818  49.1362998  56.6138690  41.9283257
##  [73]  29.0894143  33.2026673  16.1897593  79.1938213  42.8115427  25.6187778
##  [79]  34.6805724  96.9902366  75.2672695   7.5313673  31.4078882  50.5865673
##  [85]  13.9570775 104.4121025  43.0464918  36.6693230  52.8590823  24.8855847
##  [91] 107.2302322  33.9358604  54.0048319  30.6152478 102.0983385   8.3170826
##  [97]  52.3071062   8.3170826  61.8562896  58.1179346  59.7939424   8.3170826
## [103]  81.6495398  51.1054635  75.8701970  77.6947419  56.7929250  70.3693202
## [109]  81.3965205  29.9118877 111.0790432  75.7518798 112.5482496  32.9763735
## [115]  42.5644761  40.4507005  83.8955419  36.6693230   2.3184739  57.5978451
## [121]  91.3453370  33.3983912  50.1351419   7.7084002  63.9227817   0.7926404
## [127]  67.2813325  91.2965996  90.9578739 105.9024741  74.6128871  46.1321553
## [133]  15.2479619  24.0929443  70.4802708  68.8949899 118.6657550 101.3545260
## [139] 119.8539056  23.6602184 105.8968281  15.9336325 138.4059855  39.6674173
## [145]  51.7391372  58.4119283  81.1388699  96.6048825  72.2156025  56.3601992
## [151] 112.9489963  63.3258805  50.1594468  23.0021994  87.1886965  12.7714946
## [157]  33.7421666  23.2537702  14.3226164   6.9752071   0.7926404  13.5641350
## [163]  36.2007616  63.9227817  40.3310946  52.8264129  67.9956878  29.5843437
## [169]   0.0000000 191.7818606 133.6077875  83.3977825 118.6711630  51.1512871
## [175]  69.3838811  87.7066616  35.8005270  93.7797077  85.8984840  23.4933413
## [181] 149.7094684  52.4451847 112.1873673  53.4479612  51.4341108 106.6959500
## [187]  14.4361405  41.6547546  89.4018733  59.1068292   3.0516670  60.7852739
## [193]  28.1850877  52.1002690 114.3651475  86.2640717  83.7092232  39.8499777
## [199]  55.3514065 116.1795597  21.2346203  75.4593878 197.8157358 140.3806968
## [205]  93.2192350  36.5337815 146.3370747 214.5450205  64.2439145  83.3740177
## [211]  57.0440643 149.5697614 196.9415036  31.0984631  57.4769230  28.4014469
## [217]  42.3978747 194.5384819  60.5204195  73.0060715  52.1628582  30.2801165
## [223]  63.1752097  29.1789484  82.7662787 196.8309769   3.4666557   0.0000000
## [229]  31.5688084  60.5650008  43.3334929  62.5952411  13.9570775  18.9495667
## [235]  35.2646601  32.6155790   0.0000000  14.6693623  24.2745827  73.9480832
## [241]  19.2825866   0.0000000  40.6115985  68.9862341   6.9782188  11.5030881
## [247]  27.9105497  72.4020225  39.6781995  35.4596364  33.9160835  27.5735165
## [253]  15.9619740  27.9105497  17.8628493  36.0936777  87.0440848  27.9105497
## [259]  66.6907987  21.6475811  67.5969904   0.0000000   0.0000000   0.0000000
## [265]  58.0542370   0.0000000   0.0000000  27.9105497   0.0000000   0.0000000
## [271]  27.9105497  34.8887684  56.5556633  27.9105497  30.3097595  88.4296666
## [277]  37.8150727  54.2397810  31.6243116   7.5799087  73.0136833  31.8638035
## [283]  41.7172212 120.5228857  32.2001243 151.4545228  10.1544492  70.8133537
## [289]  59.3255687  25.7211220  24.1115267  43.1500941 150.0299191  72.2758570
## [295]  85.9498096 159.7242106  66.8328159  24.0929443   0.0000000  27.9105497
```

```
plot(pd)
```

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



2.5 Niche Quantification and Comparison with Ordination techniques

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

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

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

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

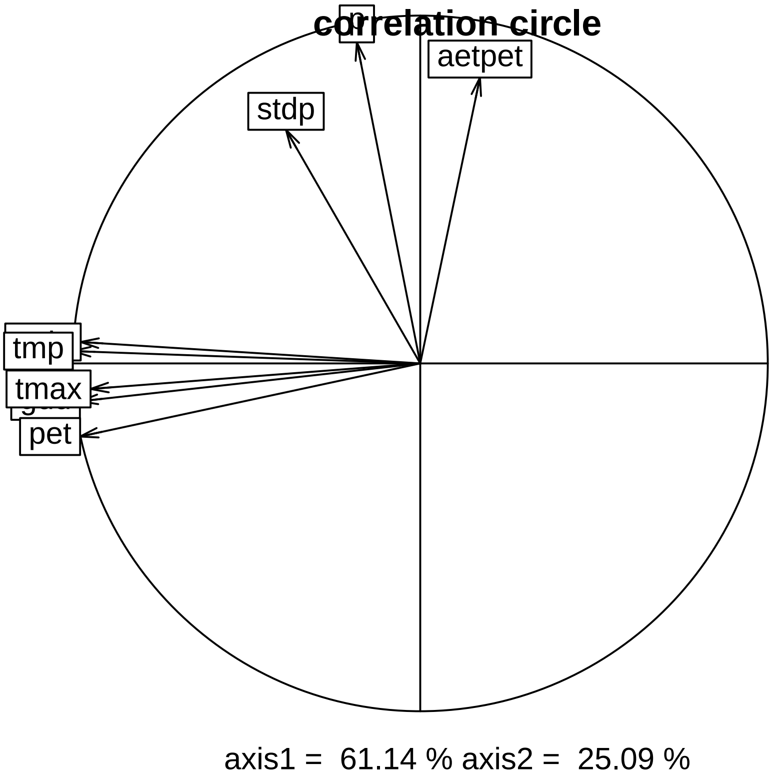
2.5.1 PCA-ENVIRONMENT

The 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)

```
library(ade4)
pca.env <- dudi.pca(rbind(nat,inv)[,3:10],scannf=F,nf=2)
```

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

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



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

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 <- 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)

```
# 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)
```

2.5.3 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%.

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

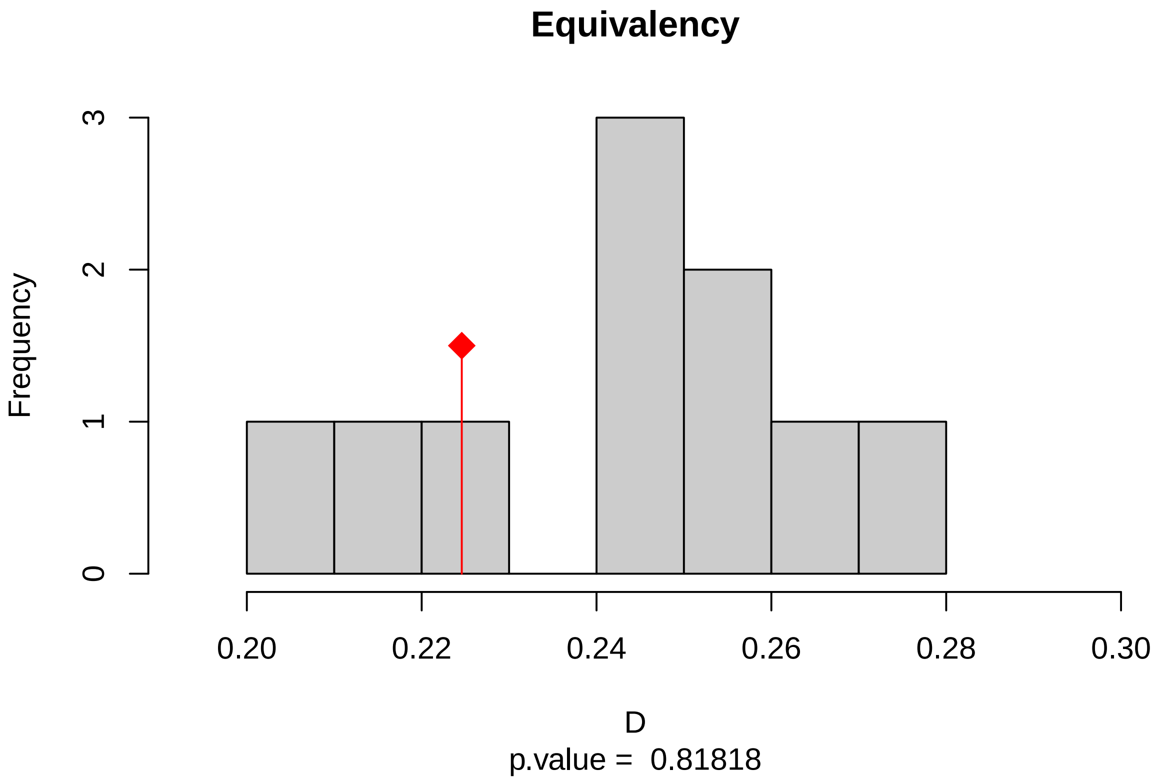
It is reccomended to use at least 1000 replications for the equivalency test. As an example we used rep = 10, to reduce the computational time.

```
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")
```



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

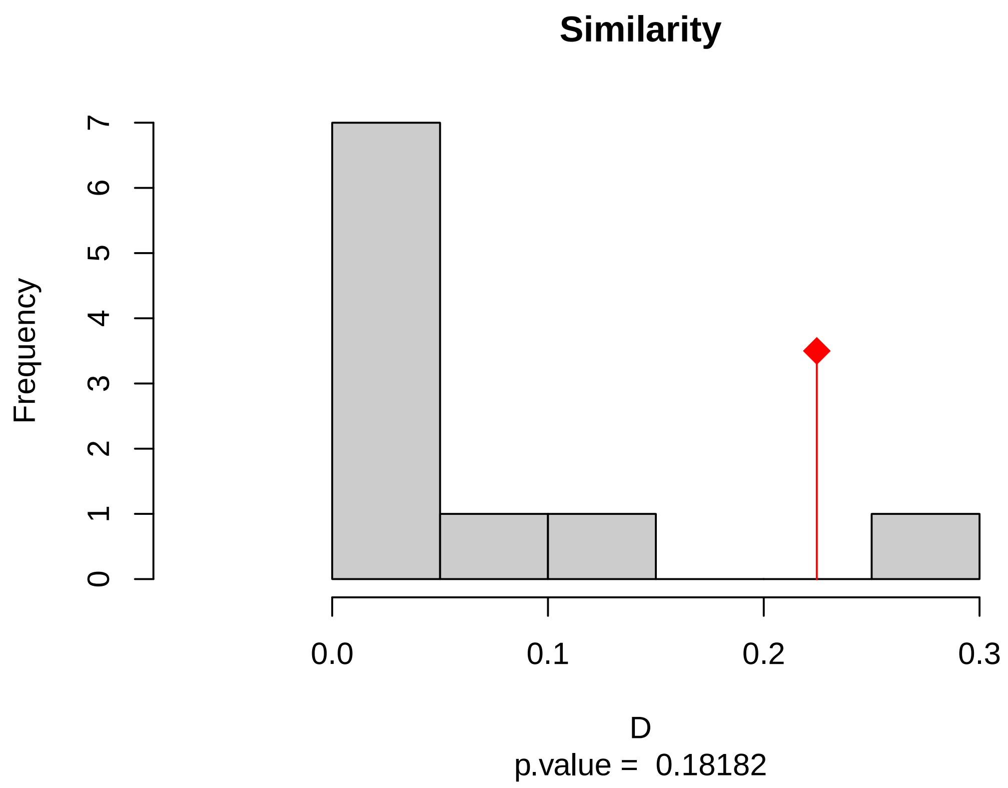
Shifts randomly on niche (here the invasive niche) in the study area It is recomended to use at least 1000 replications for the similarity test. As an example we used rep = 10, to reduce the computational time.

```
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=2)
```

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")
```



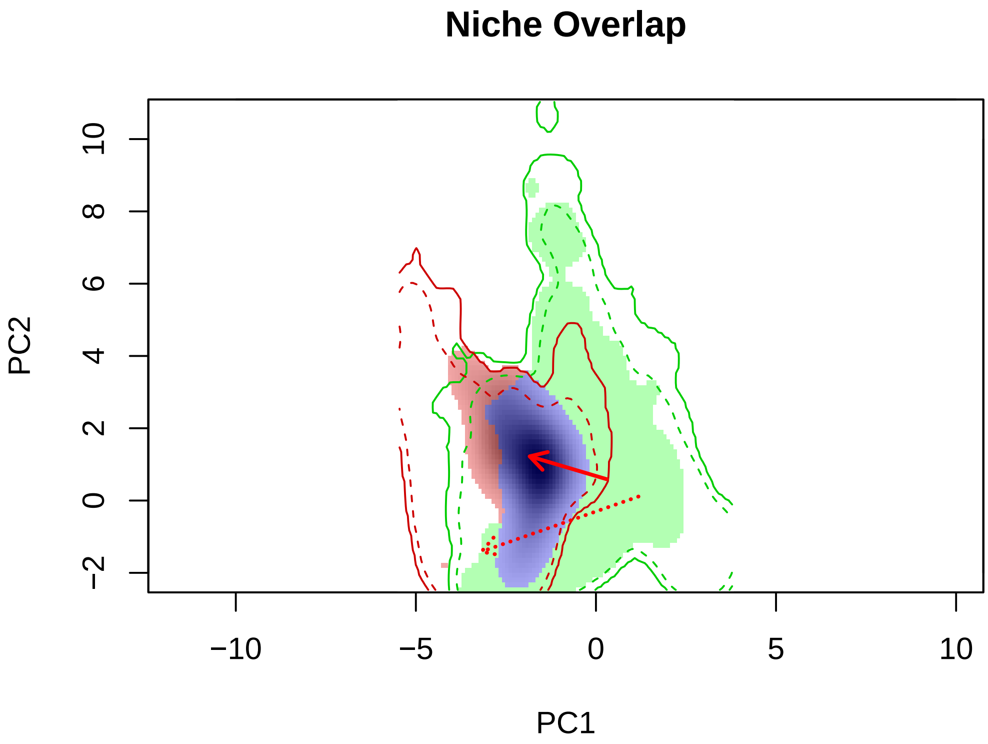
2.5.6 Delimiting niche categories and quantifying niche dynamics in analogue climates with *ecospat.niche.dyn.index()*

```
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()*

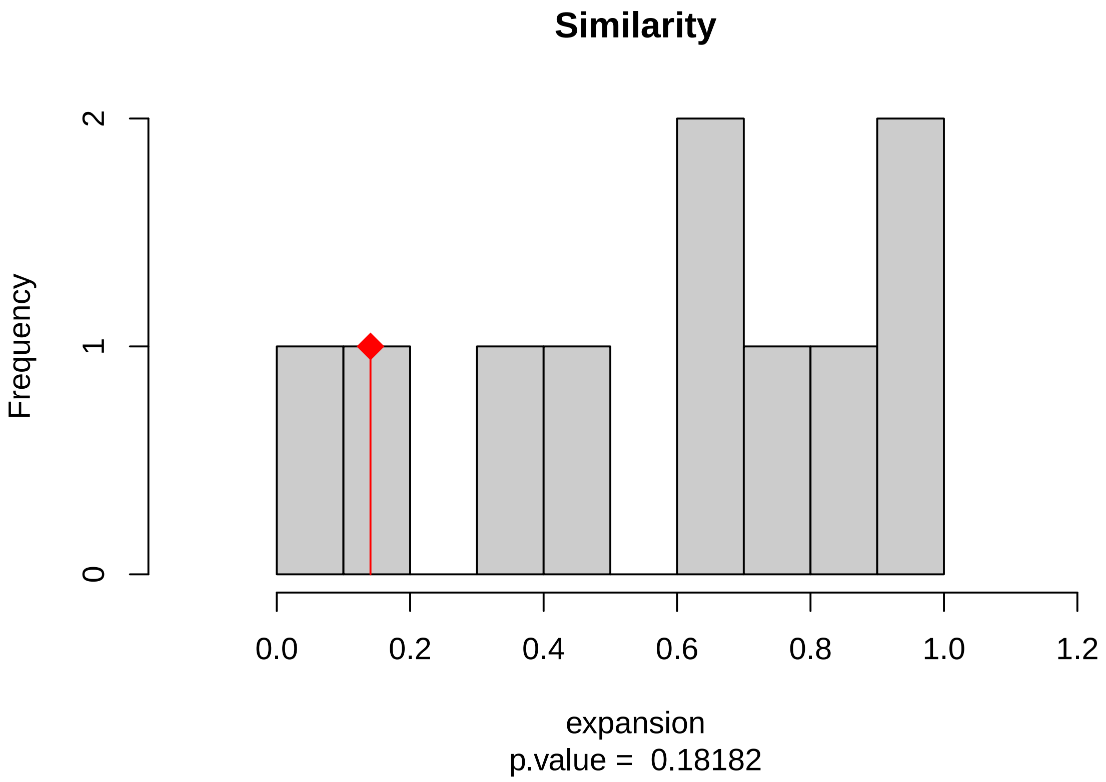
Plot niche overlap

```
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)
```

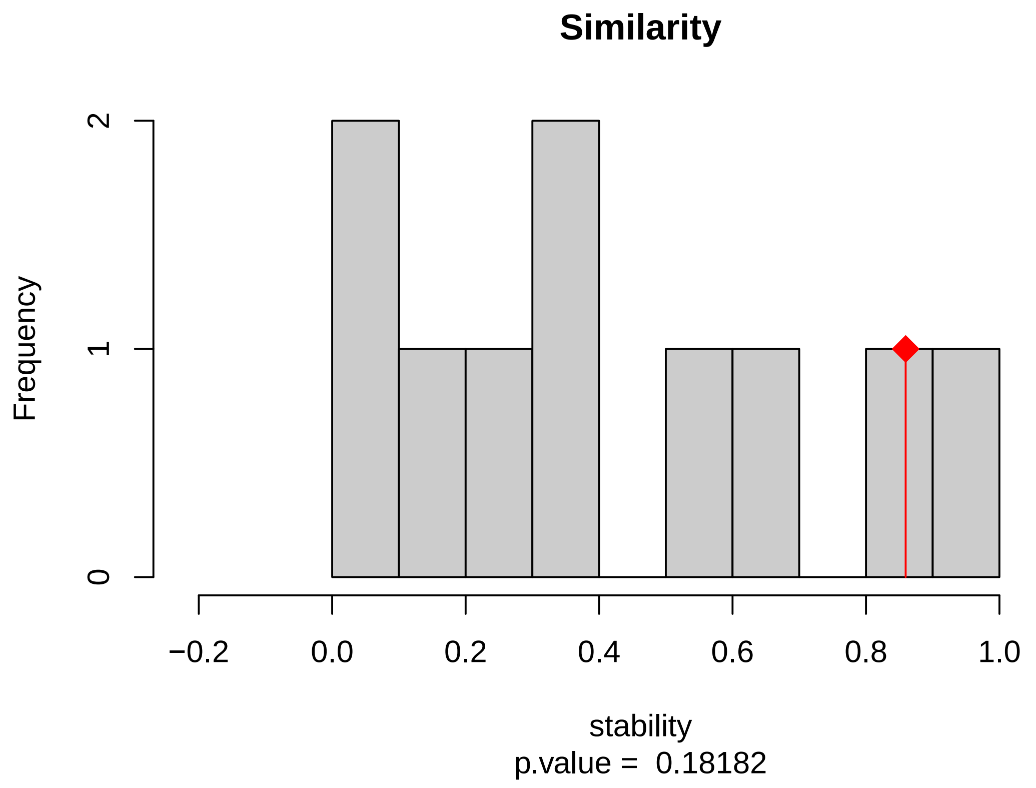


Plot Similarity test for niche expansion, stability and unfilling

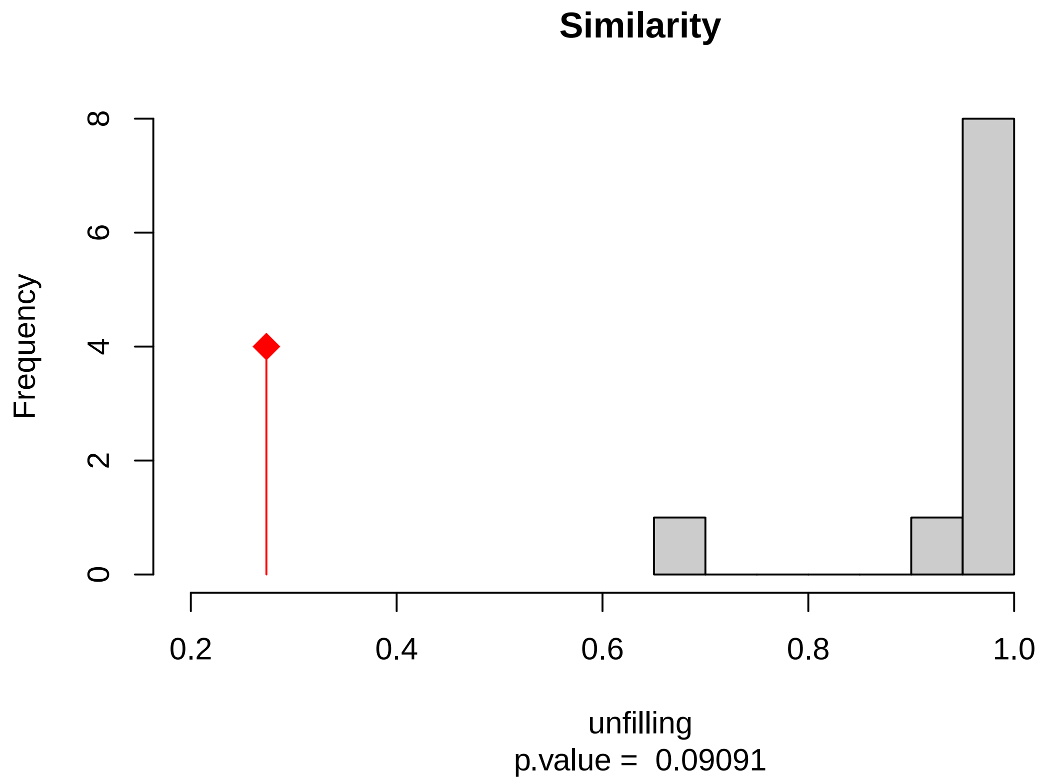
```
ecospat.plot.overlap.test(sim.test, "expansion", "Similarity")
```



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

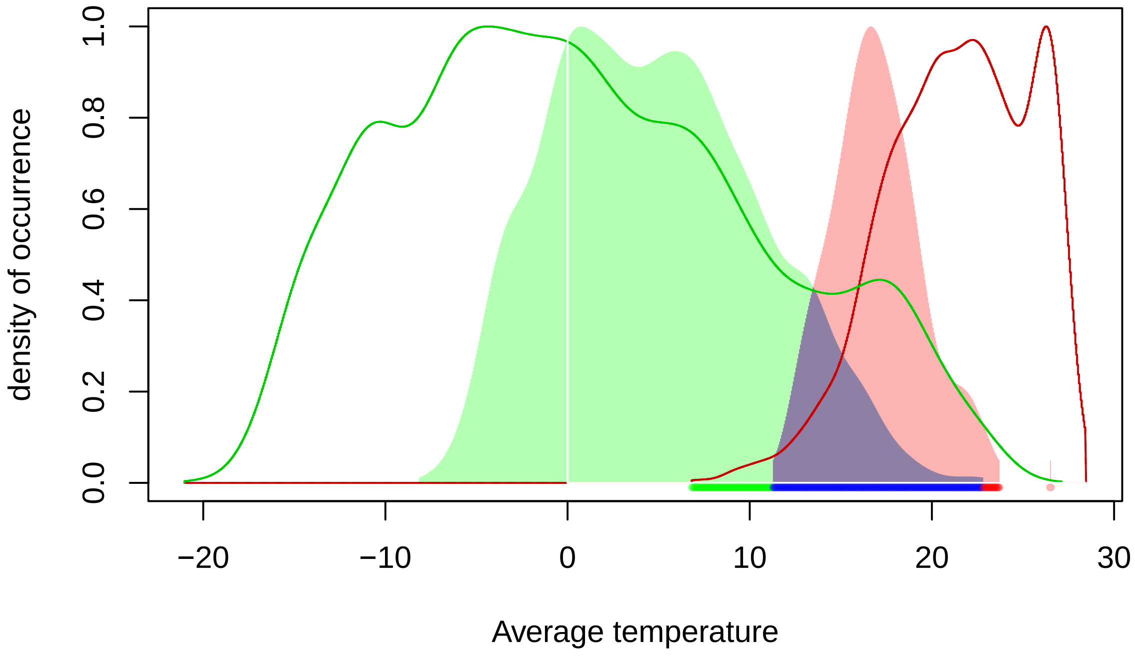


```
ecospat.plot.overlap.test(sim.test, "unfilling", "Similarity")
```



```
# 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")
```

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



2.6 Biotic Interactions

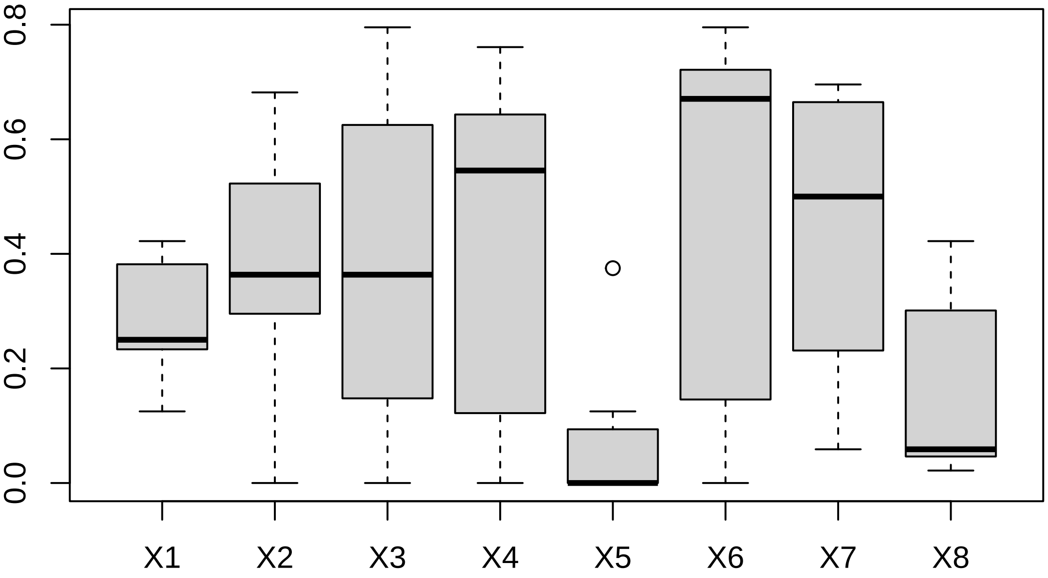
2.6.1 Species Co-occurrences Analysis with a Presence-absence matrix using the function *ecospat.co_occurrences()*

```
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 Campanula_scheuchzeri
## Aposeris_foetida            0.22222222              0.1250            0.24444444
## Arnica_montana              0.54545455              0.0000            0.68181818
## Aster_bellidiastrum         0.59090909              0.0000            0.79545455
## Bartsia_alpina              1.00000000              0.0000            0.76086957
## Bromus_erectus_sstr         0.00000000              1.0000            0.00000000
## Campanula_scheuchzeri       0.76086957              0.0000            1.00000000
## Carex_sempervirens          0.69565217              0.0625            0.67058824
## Cynosurus_cristatus         0.02173913              0.3750            0.04705882
##                         Carex_sempervirens Cynosurus_cristatus
## Aposeris_foetida                0.40000000          0.42222222
## Arnica_montana                  0.50000000          0.22727273
## Aster_bellidiastrum             0.65909091          0.04545455
## Bartsia_alpina                  0.69565217          0.02173913
## Bromus_erectus_sstr             0.06250000          0.37500000
```

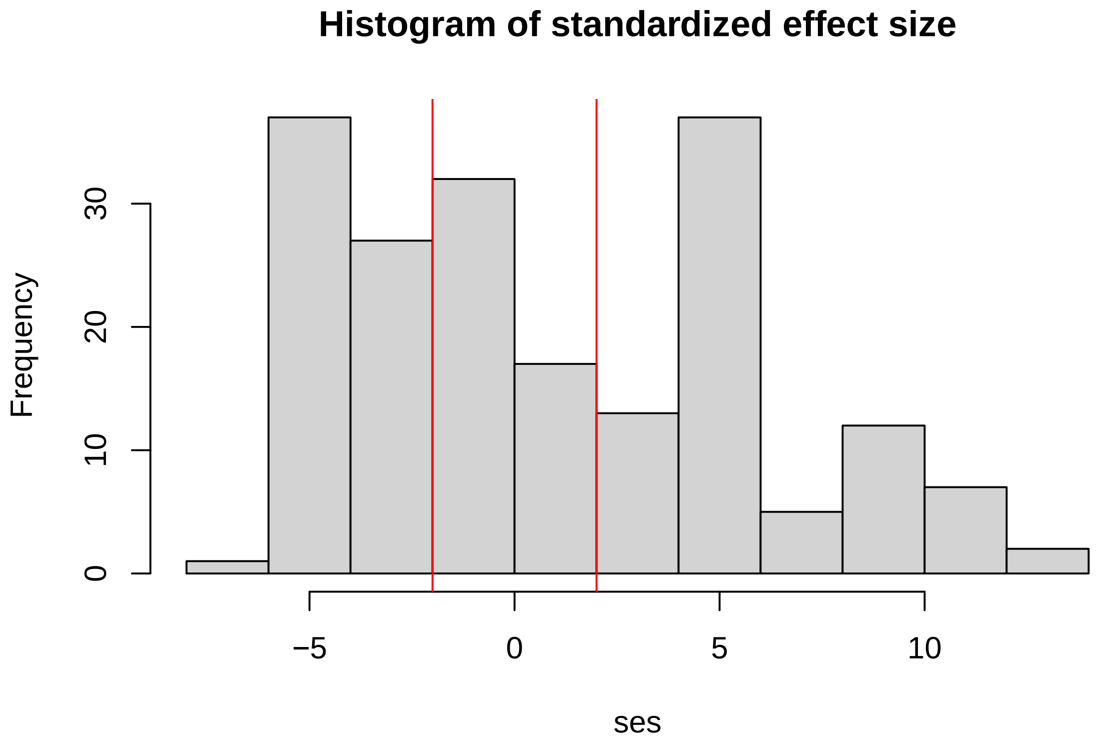
```
## Campanula_scheuchzeri         0.67058824          0.04705882
## Carex_sempervirens            1.00000000          0.05882353
## Cynosurus_cristatus           0.05882353          1.00000000
```

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)
```



```
## $ObsCscoreTot
## [1] 2675.468
##
## $SimCscoreTot
## [1] 2466.673
##
## $PVal.less
## [1] 1
##
## $PVal.greater
## [1] 0.00990099
```

```
##
## $SES.Tot
## [1] 47.6841
```

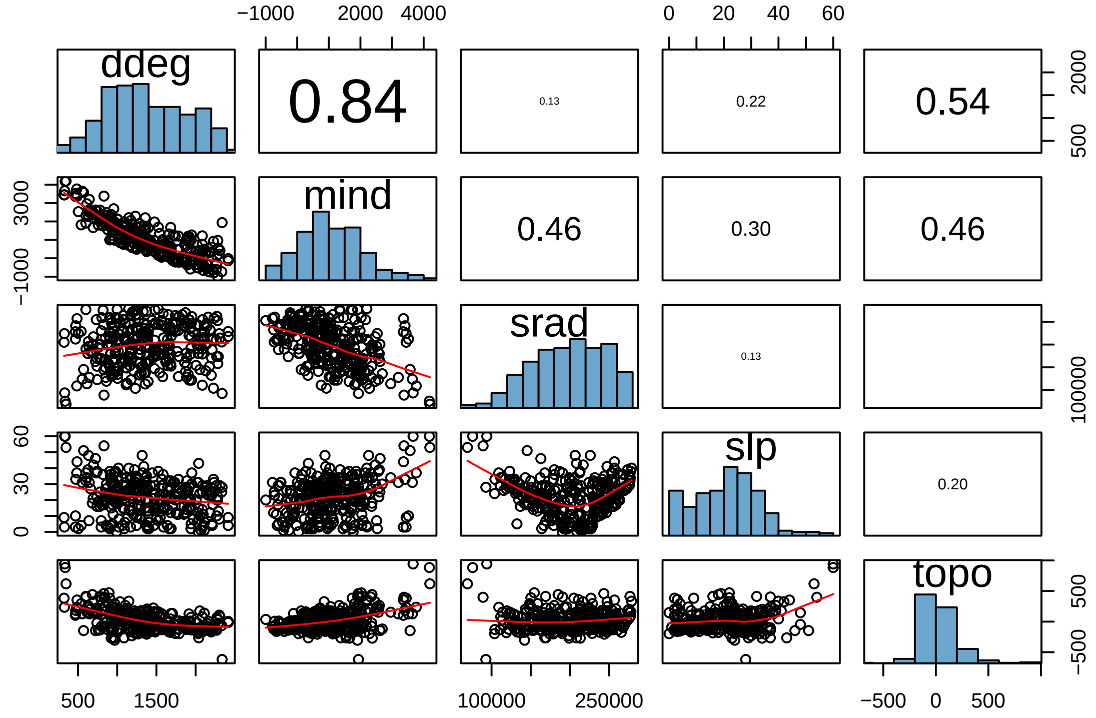
The function returns the C-score index for the observed community (ObsCscoreTot), p.value (PValTot) and standardized effect size (SES.Tot). It saves also a table in the working directory where the same metrics are calculated for each species pair (only the table with species pairs with significant p-values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

```
## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter

## Warning in par(usr): argument 1 does not name a graphical parameter
```



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     NA    NA
## 2     NA    NA
## 3     81    NA
## 4    294   264
## 5    188   269
## 6    114    16
## 7    203   193
## 8    154    57
## 9    200   180
## 10    30   168
## 11   286    45
## 12   100    15
## 13   212   115
## 14   293   262
## 15    14   288
```

```
## 16   169   266
## 17   281   192
## 18   295   273
## 19    24   279
## 20   263    79
## 21   224   182
## 22   246    17
## 23   204    56
## 24    75    24
## 25   234    23
## 26   205   234
## 27   184   237
## 28    94   147
## 29    55    36
## 30   166   267
## 31   123   177
## 32   113   263
## 33   268    94
##
## $cal
##     ycal ycal
## 1     41   NA
## 2     63  129
## 3     25   NA
## 4     NA   NA
## 5     NA   NA
## 6     NA   NA
## 7     10   28
## 8    265  189
## 9    238   49
## 10   156  186
## 11   276    3
## 12   261   27
## 13   231   95
## 14   155  210
## 15   251   34
## 16   244  157
## 17   258  248
## 18   235  249
## 19     8  261
## 20    37  292
## 21   267  152
## 22    33  247
## 23   116  133
## 24   233  296
## 25    20  252
## 26   291  232
## 27   140  272
## 28    11  253
## 29    31  145
## 30   211  110
## 31   229  100
## 32    44  220
## 33   186  206
## 34   222  154
## 35   230  300
## 36   248   43
## 37   171  283
```

```
## 38  236   37
## 39  237  239
## 40    2  214
## 41   53  246
## 42  181  116
## 43   56  228
## 44  157  120
## 45  196  185
## 46  178   71
## 47  242    8
## 48  225  275
## 49  147  276
## 50  300    4
## 51  254  223
## 52   67  255
## 53  259  259
## 54   49  245
## 55   21  289
## 56   18  106
## 57  121   22
## 58  256  254
## 59  299  221
## 60    5  297
## 61   36   30
## 62  110  270
## 63  274   51
## 64  275   18
## 65  177   85
## 66  217   84
## 67  245  250
## 68  290  240
## 69  228  256
## 70  199  278
## 71   34  219
## 72  260  201
## 73   23  243
## 74  241  139
## 75  150  134
## 76  198  271
## 77  201  295
```

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

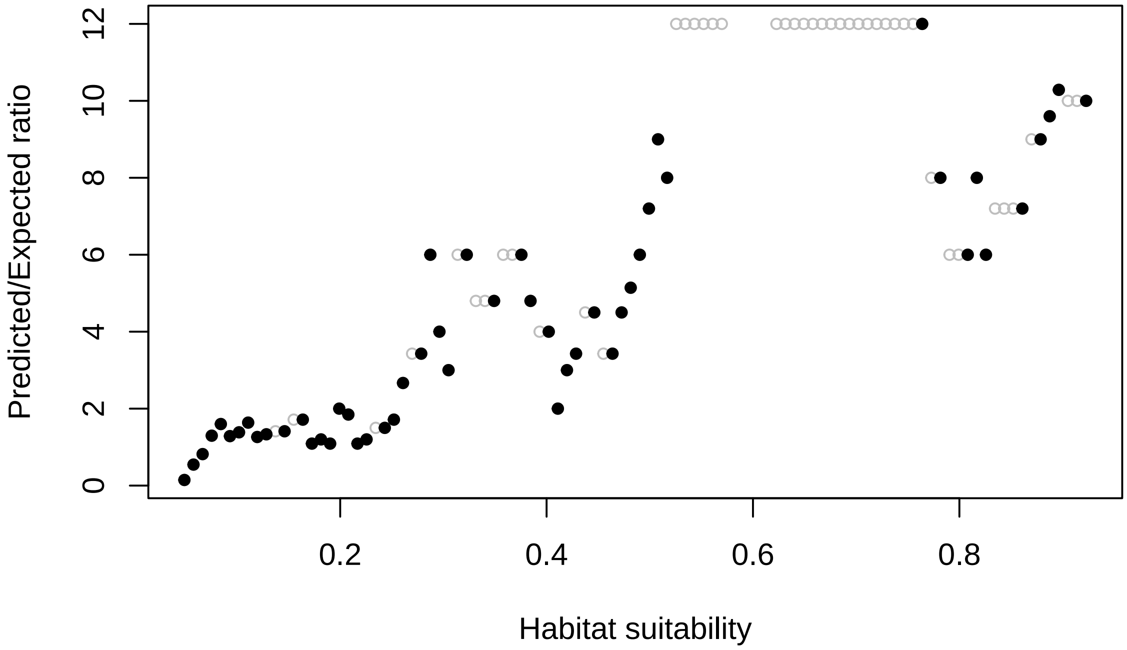
```
fit <- ecospat.testData$glm_Saxifraga_oppositifolia
```

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 4.1-2 loaded.
##  /!\ Package fresh start... meaning some changes in function names and parameters. We apologize f
```

```
# 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
```

```
### 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 -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
```

```r
myBiomodOption <- bm_DefaultModelingOptions()
```

```
##
##  Defaut modeling options. Copy, change what you want, and paste it as arg to BIOMOD_ModelingOptio
##
##
## -=-=-=-=-=-=-=-=-=-=-=-=-=-= BIOMOD.models.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',
##             n.cores = 1),
##
## 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, ncv.threads = 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, efs.lspmax = 15
## , efs.tol = 0.1, 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',
##            sampsize = NULL,
##            nodesize = 5,
##            maxnodes = NULL),
##
## MAXENT.Phillips = list( path_to_maxent.jar = 'C:/Users/obroenni/AppData/Local/Temp/Rtmp67ksPL/Rbu
##                 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.Phillips.2 = list( myFormula = NULL,
##      regmult = 1,
##      regfun = <function> )
## )
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
```

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

```
### Calibration of simple bivariate models

# remove insivible(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'),
                                 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' already exists

## 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)
```

```
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Single Models Projection -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##  > Projecting ESM.BIOMOD.1_AllData_RUN2_GLM ...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Single Models Projection -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##  > Projecting ESM.BIOMOD.2_AllData_RUN2_GLM ...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Single Models Projection -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##  > Projecting ESM.BIOMOD.3_AllData_RUN2_GLM ...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Single Models Projection -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##  > Projecting ESM.BIOMOD.4_AllData_RUN2_GLM ...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Single Models Projection -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##  > Projecting ESM.BIOMOD.5_AllData_RUN2_GLM ...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Single Models Projection -=-=-=-=-=-=-=-=-=-=-=-=-=
```

```
##
##  > Projecting ESM.BIOMOD.6_AllData_RUN2_GLM ...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Single Models Projection -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##  > Projecting ESM.BIOMOD.7_AllData_RUN2_GLM ...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Single Models Projection -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##  > Projecting ESM.BIOMOD.8_AllData_RUN2_GLM ...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Single Models Projection -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##  > Projecting ESM.BIOMOD.9_AllData_RUN2_GLM ...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
##
## -=-=-=-=-=-=-=-=-=-=-=-=-= Do Single Models Projection -=-=-=-=-=-=-=-=-=-=-=-=-=
##
##  > Projecting ESM.BIOMOD.10_AllData_RUN2_GLM ...
## -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= 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()*

```
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 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
```

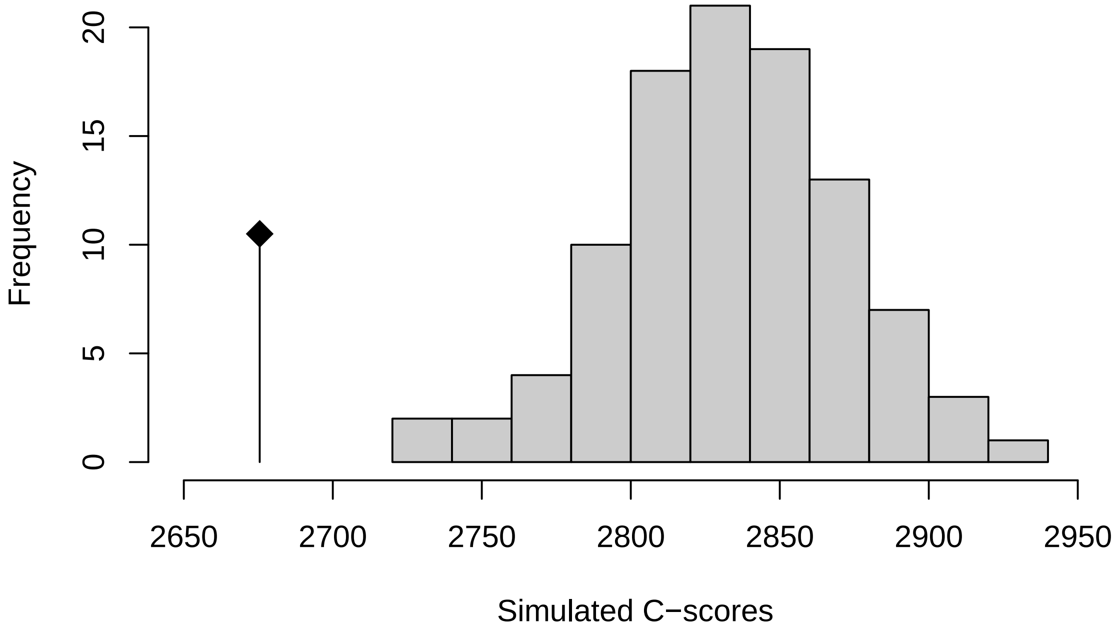
Define the outpath

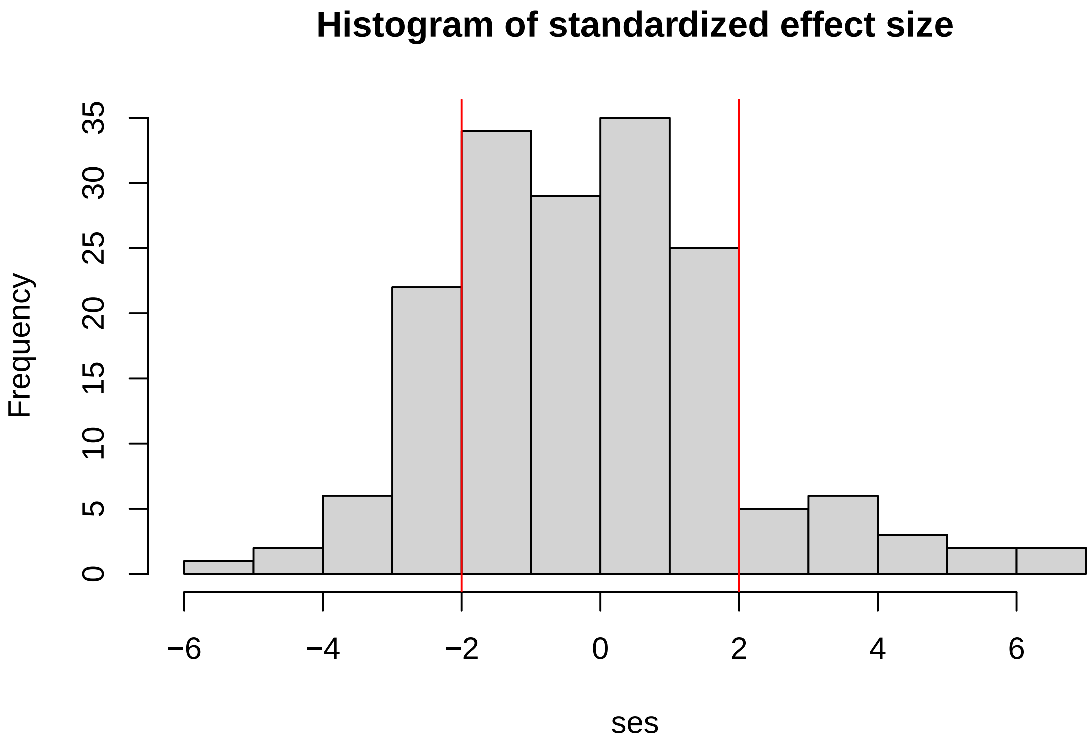
```
outpath <- getwd()
```

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)
```





```
## $ObsCscoreTot
## [1] 2675.468
##
## $SimCscoreTot
## [1] 2831.151
```

```
##
## $PVal.less
## [1] 0.00990099
##
## $PVal.greater
## [1] 1
##
## $SES.Tot
## [1] -4.04848
```

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).