

Running ENMs

EBellis

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Description

This document describes running of ENMs for the three species.

```
options(java.parameters = "-Xmx100G")
library(raster)
```

```
## Loading required package: sp
```

```
library(ENMeval)
```

```
## Loading required package: dismo
```

```
e <- extent(20,55,-10,15)
```

```
env1 <- raster('~/scratch/data/env/CHELSEA/CHELSEA_bio10_01.tif', header=T)
env1 <- crop(env1, e)
```

```
env3 <- raster('~/scratch/data/env/CHELSEA/CHELSEA_bio10_03.tif', header=T)
env3 <- crop(env3, e)
```

```
env15 <- raster('~/scratch/data/env/CHELSEA/CHELSEA_bio10_15.tif', header=T)
env15 <- crop(env15, e)
```

```
env17 <- raster('~/scratch/data/env/CHELSEA/CHELSEA_bio10_17.tif', header=T)
env17 <- crop(env17, e)
```

```
env18 <- raster('~/scratch/data/env/CHELSEA/CHELSEA_bio10_18.tif', header=T)
env18 <- crop(env18, e)
```

```
env <- stack(env1, env3, env15, env17, env18)
```

C. kilimanjari

```
randoz <- read.table('Data/Ckilimanjari.bg.txt', header=T)
occ <- unique(read.table('Data/Ckilimanjari.occ.txt', header=T))
ck.mod <- ENMevaluate(occ=cbind(occ$Long, occ$Lat), env=env, method='checkerboard2', parallel=F, bg.coor
```

```
# get best model
ck.mod@results[which(ck.mod@results$delta.AICc==0),]
# settings features rm train.AUC avg.test.AUC var.test.AUC avg.diff.AUC
# 2 LQ_0.5 LQ 0.5 0.7149 0.6752653 0.006274111 0.04792127
# var.diff.AUC avg.test.orMTP var.test.orMTP avg.test.or10pct var.test.or10pct
# 2 0.007240996 0.03125 0.00390625 0.148539 0.01790897
```

```

#      AICc delta.AICc      w.AIC parameters
# 2 1187.571          0 0.6478819          6

# permutation importances
aic.opt <- ck.mod@models[[2]]
aic.opt@results
# CHELSA_bio10_01.permutation.importance      6.1921
# CHELSA_bio10_03.permutation.importance     14.5640
# CHELSA_bio10_15.permutation.importance      0.5208
# CHELSA_bio10_17.permutation.importance      0.1157
# CHELSA_bio10_18.permutation.importance     78.6073

# save model and project to current environment
save(ck.mod, file='ck.RDA')

predict(aic.opt, env, filename = "ck.tif", format="GTiff", outputformat="logistic", overwrite=TRUE, prog

```

C. reflexa

```

randoz <- read.table('Data/Creflexa.bg.txt', header=T)
occ <- unique(read.table('Data/Creflexa.occ.txt', header=T)) #66
cr.mod <- ENMevaluate(occ=cbind(occ$Long, occ$Lat), env=env, method='checkerboard2', parallel=F, bg.coor

# get best model
# cr.mod@results[which(cr.mod@results$delta.AICc==0),]
# settings features rm train.AUC avg.test.AUC var.test.AUC avg.diff.AUC
# 2  LQ_0.5      LQ 0.5      0.9221      0.9016403 0.0001436953      0.01660462
#  var.diff.AUC avg.test.orMTP var.test.orMTP avg.test.or10pct var.test.or10pct
# 2 3.587957e-05      0.015625      0.0009765625      0.1645833      0.01946181
#      AICc delta.AICc w.AIC parameters
# 2 1794.534          0      1          9

# CHELSA_bio10_01.permutation.importance      20.0070
# CHELSA_bio10_03.permutation.importance       2.7319
# CHELSA_bio10_15.permutation.importance       7.4776
# CHELSA_bio10_17.permutation.importance       8.3014
# CHELSA_bio10_18.permutation.importance     61.4821

```

C. campestris

```

# settings features rm train.AUC avg.test.AUC var.test.AUC avg.diff.AUC
# 45  H_4      H 4      0.8227      0.7584497      0.05184338      0.09972872
#  var.diff.AUC avg.test.orMTP var.test.orMTP avg.test.or10pct var.test.or10pct
# 45 0.04318858      0.08522727      0.01390324      0.1931818      0.05836777
#      AICc delta.AICc w.AIC parameters
# 45 1195.505          0 0.8055264          8
#
# CHELSA_bio10_01.permutation.importance     43.3709
# CHELSA_bio10_03.permutation.importance      2.6373
# CHELSA_bio10_15.permutation.importance      0.0000

```

# CHELSA_bio10_17.permutation.importance	49.1009
# CHELSA_bio10_18.permutation.importance	4.8909

Methods Summary

ENMs were based on the Maxent algorithm[cite]. Models were tuned and evaluated with ENMeval[cite] using the checkerboard2 method for data partitioning. The best models had test set AUC of X (C. kilimanjari), X (C. reflexa), or X (C. campestris).

```
citation('ENMeval')
```

```
##
## To cite ENMeval in publications please use:
##
## Muscarella, R., Galante, P.J., Soley-Guardia, M., Boria, R.A., Kass,
## J., Uriarte, M. and R.P. Anderson (2014). ENMeval: An R package for
## conducting spatially independent evaluations and estimating optimal
## model complexity for ecological niche models. Methods in Ecology and
## Evolution.
##
## A BibTeX entry for LaTeX users is
##
## @Article{,
##   title = {ENMeval: An R package for conducting spatially independent evaluations and estimating optimal
##   author = {R. Muscarella and P.J. Galante and M. Soley-Guardia and R.A. Boria and J. Kass and M. Uriarte and R.P. Anderson},
##   journal = {Methods in Ecology and Evolution},
##   year = {2014},
##   volume = {5},
##   number = {11},
##   pages = {1198-1205},
## }
```