

## Determining priority areas for an Endangered cold-adapted snake on warming mountaintops

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SUPPLEMENTARY MATERIAL 1 The R script for calculating the conservation value layers. The ASCII files produced are also provided.

```
#####  
# Supplementary material  
#-----of-----  
# Determining priority areas for an Endangered cold-adapted snake on warming mountaintops  
#-----by-----  
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#####  
  
#----- R libraries -----  
library(raster)  
library(maptools)  
library(biomod2)  
library(KernSmooth)  
library(dismo)  
library(rgeos)  
library(sp)  
library(gstat)  
library(spatstat)  
library(ggplot2)  
library(boot)  
  
#----- Input data not included -----  
  
#proj_current_VG.grd - raster projection of habitat suitability model  
#area.shp - shape file of poligonized habitat suitability model, area data already  
calculated in the attribute table  
#present.shp - shape file of poligonized habitat suitability model, occupancy is given in  
the attribute table based on occupancy point data not shown here  
#NDVI2003summer.tif, NDVI2013summer.tif, NDVI2003autumn.tif, NDVI2013autumn.tif -  
processed Landsat NDVI rasters  
#presence.csv - Vipera graeca presence dataset  
#present_na.asc, A2020.asc, A2040.asc, A2060.asc, A2080.asc, B2020.asc, B2040.asc,  
B2060.asc, B2080.asc - current and future projections of habitat suitability model
```

```

#srtm.asc - SRTM elevation data masked by the raster projection of habitat suitability
model
#land_use.csv - coordinates of man made objects across the study area

#----- Variables for estimating conservation value -----

#----- 1. Climate suitability -----
climq <- raster("proj_current_VG.grd")

climq <- calc(climq,fun = function(x) {x/1000})

re <- raster(nrow=3000,ncol=4000) # resampling to ~ ha
xmin(re) <- 19
xmax(re) <- 23
ymin(re) <- 38
ymax(re) <- 41
climq <- resample(climq,re)

climq[is.na(climq)] <- 0
NAvalue(climq) <- 0

writeRaster(climq,"climq.asc", format="ascii",overwrite=TRUE)

#----- 2. Habitat size -----
areashp <- readShapePoly("area.shp")
crs(areashp) <- "+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

re <- raster(nrow=3000,ncol=4000) # resampling to ~ ha
xmin(re) <- 19
xmax(re) <- 23
ymin(re) <- 38
ymax(re) <- 41

area <- rasterize(areashp,re,'area')
area <- calc(area,fun = function (x) {x/0.03909722})
area[is.na(area)] <- 0
NAvalue(area) <- 0

writeRaster(area,"area.asc", format="ascii",overwrite=TRUE)

#----- 3. Habitat occupancy -----

```

```

occupied<-readShapePoly("present.shp")
crs(occupied) <- "+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

re <- raster(nrow=3000,ncol=4000) # resampling to ~ ha
xmin(re) <- 19
xmax(re) <- 23
ymin(re) <- 38
ymax(re) <- 41

occupancy <- rasterize(occupied,re)

occupancy[occupancy > 0] <- 1

occupancy[is.na(occupancy)] <- 0
NAvalue(occupancy) <- 0

writeRaster(occupancy,"occupancy.asc", format="ascii",overwrite=TRUE)

#----- 4. Vegetation suitability -----
ndvi2003 <- raster("NDVI2003summer.tif")
ndvi2013 <- raster("NDVI2013summer.tif")

re <- raster(nrow=3000,ncol=4000) # resampling to ~ ha
xmin(re) <- 19
xmax(re) <- 23
ymin(re) <- 38
ymax(re) <- 41

ndvi2003 <- resample(ndvi2003,re)
ndvi2013 <- resample(ndvi2013,re)

ndvistack <-stack(ndvi2003,ndvi2013)
ndvi <-calc(ndvistack, sum)
ndvi <-calc(ndvi,fun = function (x) {x/2})

writeRaster(ndvi,"ndvi.asc", format="ascii",overwrite=T)

# modelling
myExpl <- stack("ndvi.asc")
mySpeciesOcc <- read.csv("presence.csv",header=T,sep=",")

sp.names <- c("VG")
cat('\1',"VG",'modeling...')

```

```

myResp <- as.numeric(mySpeciesOcc[, "VG"])
na.id <- which(is.na(myResp))
myResp <- myResp[-na.id]
myRespCoord = mySpeciesOcc[-na.id, c('x', 'y')]
myRespName = "VG"

myBiomodData <- BIOMOD_FormattingData(
  resp.var = myResp,
  expl.var = myExpl,
  resp.xy = myRespCoord,
  resp.name = myRespName,
  PA.nb.rep = 10,
  PA.nb.absences = 1250,
  PA.strategy = 'random',
  PA.dist.min = 25,
  PA.dist.max = NULL,
  na.rm=TRUE)

myBiomodOption <- BIOMOD_ModelingOptions()

myBiomodModelOut <- BIOMOD_Modeling(
  myBiomodData,
  models = c('GLM'),
  models.options = myBiomodOption,
  NbRunEval=1,
  DataSplit=70,
  Yweights=NULL,
  VarImport=5,
  models.eval.meth = c('TSS'),
  do.full.models = FALSE,
  modeling.id = paste(myRespName, "FirstModeling", sep=""))

myBiomodProjection1 <- BIOMOD_Projection(
  modeling.output = myBiomodModelOut,
  new.env = myExpl,
  proj.name = 'NDVI',
  selected.models = 'all',
  binary.meth= 'TSS',
  filtered.meth = 'TSS',
  compress = F,
  build.clamping.mask = F,
  output.format = '.grd')

# raster operations
vegsuitability <- raster("VG/proj_NDVI/proj_NDVI_VG.grd")

```

```
vegsuitability <- calc(vegsuitability, fun = function (x) {x/759})
```

```
re <- raster(nrow=3000,ncol=4000) # resampling to ~ ha  
xmin(re) <- 19  
xmax(re) <- 23  
ymin(re) <- 38  
ymax(re) <- 41
```

```
vegsuitability <- resample(vegsuitability, re)  
vegsuitability[is.na(vegsuitability)] <- 0  
NAvalue(vegsuitability) <- 0
```

```
writeRaster(vegsuitability, "vegsuitability.asc", format="ascii", overwrite=T)
```

```
#----- 5. Future persistence in the face of climate change -----
```

```
re <- raster(nrow=3000,ncol=4000) # resampling to ~ ha  
xmin(re) <- 19  
xmax(re) <- 23  
ymin(re) <- 38  
ymax(re) <- 41
```

```
# A1B SCENARIO
```

```
a2000 <- raster("raw_data/present_na.asc")  
a2080 <- raster("raw_data/A2080.asc")  
a2060 <- raster("raw_data/A2060.asc")  
a2040 <- raster("raw_data/A2040.asc")  
a2020 <- raster("raw_data/A2020.asc")
```

```
a2000 <- resample(a2000, re)  
a2020 <- resample(a2020, re)  
a2040 <- resample(a2040, re)  
a2060 <- resample(a2060, re)  
a2080 <- resample(a2080, re)
```

```
a2000[is.na(a2000)] <- 0  
a2020[is.na(a2020)] <- 0  
a2040[is.na(a2040)] <- 0  
a2060[is.na(a2060)] <- 0  
a2080[is.na(a2080)] <- 0
```

```
NAvalue(a2000) <- 0  
NAvalue(a2020) <- 0  
NAvalue(a2040) <- 0
```

```

NAvalue(a2060) <- 0
NAvalue(a2080) <- 0

a_climchange <- stack(a2000,
                      a2020,
                      a2040,
                      a2060,
                      a2080)

a_persist <- calc(a_climchange, sum)

a_persist <- calc(a_persist, fun = function(x) {x/5})

a_persist[is.na(a_persist)] <- 0
NAvalue(a_persist) <- 0

writeRaster(a_persist, "a_persist.asc", format="ascii", overwrite=TRUE)

# B1 SCENARIO
b2000 <- raster("raw_data/present_na.asc")
b2080 <- raster("raw_data/B2080.asc")
b2060 <- raster("raw_data/B2060.asc")
b2040 <- raster("raw_data/B2040.asc")
b2020 <- raster("raw_data/B2020.asc")

b2000 <- resample(b2000, re)
b2020 <- resample(b2020, re)
b2040 <- resample(b2040, re)
b2060 <- resample(b2060, re)
b2080 <- resample(b2080, re)

b2000[is.na(b2000)] <- 0
b2020[is.na(b2020)] <- 0
b2040[is.na(b2040)] <- 0
b2060[is.na(b2060)] <- 0
b2080[is.na(b2080)] <- 0

NAvalue(b2000) <- 0
NAvalue(b2020) <- 0
NAvalue(b2040) <- 0
NAvalue(b2060) <- 0
NAvalue(b2080) <- 0

b_climchange <- stack(b2000,
                      b2020,

```

```
        b2040,  
        b2060,  
        b2080)
```

```
b_persist <- calc(b_climchange, sum)
```

```
b_persist <- calc(b_persist, fun = function(x) {x/5})
```

```
b_persist[is.na(b_persist)] <- 0
```

```
NAvalue(b_persist) <- 0
```

```
writeRaster(b_persist, "b_persist.asc", format="ascii", overwrite=TRUE)
```

```
#----- 6. Potential for altitudinal range shift -----
```

```
library(raster)
```

```
alt <- raster("srtm.asc")
```

```
re <- raster(nrow=3000, ncol=4000) # resampling to ~ ha
```

```
xmin(re) <- 19
```

```
xmax(re) <- 23
```

```
ymin(re) <- 38
```

```
ymax(re) <- 41
```

```
alt <- resample(alt, re)
```

```
shift <- calc(alt, fun = function(x) {x/2872.6})
```

```
shift[is.na(shift)] <- 0
```

```
NAvalue(shift) <- 0
```

```
writeRaster(shift, "shift.asc", format="ascii", overwrite=TRUE)
```

```
#----- 7. Habitat alteration by humans -----
```

```
u.df <- read.csv("land_use.csv", header=T, sep=",")
```

```
manmade <- subset(u.df, select=c(id, x, y))
```

```
manmade <- unique(manmade)
```

```
coordinates <- manmade[, 2:3]
```

```
loss <- bkde2D(coordinates,
```

```
        bandwidth=c(0.001, 0.001),
```

```
        gridsize=c(3000, 4000),
```

```
        range.x=list(c(19, 23), c(38, 41)))
```

```

loss <- raster(list(x=loss$x1,y=loss$x2,z=loss$fhat))

re <- raster(nrow=3000,ncol=4000) # resampling to ~ ha
xmin(re) <- 19
xmax(re) <- 23
ymin(re) <- 38
ymax(re) <- 41

loss <- resample(loss,re)
loss <- calc(loss,fun = function (x) {x/141.625})
loss[is.na(loss)] <- 0
NAvalue(loss) <- 0

writeRaster(loss,"loss.asc", format="ascii",overwrite=TRUE)

```

```

#----- 8. Habitat degradation by grazing -----

```

```

ndvi2003s <- raster("NDVI2003summer.tif")
ndvi2013s <- raster("NDVI2013summer.tif")
ndvi2003a <- raster("NDVI2003autumn.tif")
ndvi2013a <- raster("NDVI2013autumn.tif")

```

```

re <- raster(nrow=3000,ncol=4000) # resampling to ~ ha
xmin(re) <- 19
xmax(re) <- 23
ymin(re) <- 38
ymax(re) <- 41

```

```

ndvi2003s <- resample(ndvi2003s,re)
ndvi2013s <- resample(ndvi2013s,re)
ndvi2003a <- resample(ndvi2003a,re)
ndvi2013a <- resample(ndvi2013a,re)

```

```

ndvi2003s[is.na(ndvi2003s)] <- 0
ndvi2013s[is.na(ndvi2013s)] <- 0
ndvi2003a[is.na(ndvi2003a)] <- 0
ndvi2013a[is.na(ndvi2013a)] <- 0

```

```

NAvalue(ndvi2003s) <- 0
NAvalue(ndvi2013s) <- 0
NAvalue(ndvi2003a) <- 0
NAvalue(ndvi2013a) <- 0

```



```

ndvich2003 <- (ndvi2003s-ndvi2003a)
ndvich2013 <- (ndvi2013s-ndvi2013a)

ndvich2003 <- (ndvich2003+2)
ndvich2013 <- (ndvich2013+2)

ndvichstack <- stack(ndvich2003,ndvich2013)
ndvich <- calc(ndvichstack, sum)
degradation <- calc(ndvich,fun = function (x) {x/2})

degradation <- calc(degradation,fun = function (x) {x/3.640344})

degradation[is.na(degradation)] <- 0
NAvalue(degradation) <- 0

writeRaster(degradation,"degradation.asc", format="ascii",overwrite=TRUE)

#----- 9. Disturbance by traditional grazing -----
diminution <- raster("degradation.asc")
diminution <- calc(diminution,fun = function (x) {1-x})
diminution[is.na(diminution)] <- 0
NAvalue(diminution) <- 0

sheepfold <- read.csv("land_use.csv",header=T,sep=",")

sheepfold <- subset(sheepfold,select=c(id,x,y,object,year))
sheepfold <- subset(sheepfold, object=="sheepfold")
sheepfold <- unique(sheepfold)

coordinates(sheepfold) <- ~ x+y
crs(sheepfold) <- "+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

sheepfoldweight <- data.frame(coordinates(sheepfold),
                             extract(diminution, sheepfold))
names(sheepfoldweight) <- c("x", "y", "value")

coordinates(sheepfoldweight) <- ~ x+y
crs(sheepfoldweight) <- "+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

re <- raster(nrow=3000,ncol=4000) # resampling to ~ ha
xmin(re) <- 19
xmax(re) <- 23
ymin(re) <- 38

```

```
ymax(re) <- 41
crs(re) <- "+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

gs <- gstat(formula=value^2~1, locations=sheepfoldweight)#fit a model
idw <- interpolate(re, gs)

writeRaster(idw,"raw_data/grazing_pressure.asc",format="ascii")

disturb <- calc(test3,fun = function (x) {(x-0.9770416)/(1-0.9770416)})

disturb[is.na(disturb)] <- 0
NAvalue(disturb) <- 0

writeRaster(disturb,"disturb.asc", format="ascii",overwrite=TRUE)
```