

Appendix 1. R code to produce the reclassification files; GRASS code to produce the AOH maps;
R code for the hypergeometric test.

```
#The script produces reclass files to apply to
#a combined map in grass gis to produce maps of area of
#habitat for terrestrial species
#It reads two csv files:
#1. land cover associations, with the following column
#headers: binomial, plus one column per land cover class,
#with numeric column names for land cover (e.g. 10, 20, 210)
#2. elevation range, with the following column headers:
#binomial, min_alt, max_alt
#If elevation range for a species is unknown,
#it must be set to 0-9000 in the elevation csv
#Reclass files are produced for all species listed in the
#land cover csv
rm(list = ls())

lc <- function(x){
  as.numeric(substr(x, 2, nchar(x)))*1000
}

#Disable scientific notation

options(scipen=99999)
#Change the path of the working directory and
#the names of the 2 csv files as necessary
setwd("/media/nas/userdata")
h<-read.csv("/media/spec_hab.csv",stringsAsFactors = FALSE) e<-
read.csv("/media/Altitude.csv",stringsAsFactors = FALSE)

# Select the columns of the elevation data

e[,2]<-round(e[,2]/10,0) # min
e[,3]<-round(e[,3]/10,0) #max

for(i in 1:dim(h)[1]){
  for(j in 2:dim(h)[2]){
    if(h[i,j]==1){
      if(e[i,2]==0 & e[i,3]==900){
        write.table(paste(lc(names(h)[j]),
                          " thru ",
                          lc(names(h)[j])+900,
                          " = 1",sep=""),
                    file=paste(h[i,1],sep=""), append=T,
                    quote=F,row.names=F,col.names=F)
      }
      if(e[i,2]==0 & e[i,3]<900){
        write.table(paste(lc(names(h)[j]),
                          " thru ",
                          lc(names(h)[j])+e[i,3],
                          " = 1",sep=""),
                    file=paste(h[i,1],sep=""), append=T,
                    quote=F,row.names=F,col.names=F)
      }
      if(e[i,2]>0 & e[i,3]==900){
        write.table(paste(lc(names(h)[j])+e[i,2],
                          " thru ",
                          lc(names(h)[j])+900,
```

```

        " = 1", sep=""),
        file=paste(h[i,1], sep=""), append=T,
        quote=F, row.names=F, col.names=F)
    }
    if(e[i,2]>0 & e[i,3]<900){
        write.table(paste(lc(names(h)[j])+e[i,2],
            " thru ",
            lc(names(h)[j])+e[i,3],
            " = 1", sep=""),
            file=paste(h[i,1], sep=""), append=T,
            quote=F, row.names=F, col.names=F)
    }
}
}
write.table("* = 0", file=paste(h[i,1],
sep=""), append=T, quote=F, row.names=F, col.names=F)
write.table("end", file=paste(h[i,1],
sep=""), append=T, quote=F, row.names=F, col.names=F)
}

#####

### GRASS CODE TO GENERATE AOH MAPS ###

# Creat list of files

cd /media/reclass
ls > hlist.txt

#import range
for i in `cat /media/hlist.txt`
do
v.in.ogr input=/media/$i.shp output=$(echo $i | sed 's/\.shp *//')
snap=1e-09 --overwrite
done

#Rasterize

for i in `cat /media/nas/userdata/hlist.txt`
do
g.region -a vector=$i res=0:00:03.571
v.to.rast input=$i type=area use=val output=ras_$i --overwrite
r.mapcalc "$i = $i" --overwrite
done

# produce AOH
for i in `cat /media/nas/userdata/hlist.txt`
do
g.region -a raster=ras_$i
r.mask raster=ras_$i --overwrite
r.reclass in=bm_CGLS out=$i rules=/media/reclas/$i --overwrite
r.colors map=$i rules=-<<EOF
0 160:160:160
1 5:110:7
EOF
r.mapcalc "$i = $i" --overwrite

```

```
r.mask -r
done
```

```
#####
## R code to perform the hypergeometric distributions
```

```
library(raster)
library(sp)
library(rgdal)
library(sf)
library(GISTools)
```

```
setwd("/home/user")
```

```
# Import map of Italy
italy_map<- readOGR(dsn = "/home/", layer = "ITA_adm0")
species_list<-read.table("/home/hlist.txt", header=F, sep="")

for (row in 1:nrow(species_list)){
  current_sp<-as.character(species_list[row,1])

  # raster map to test
  myras<-raster(paste("/home/amphibians/",current_sp, ".tif", sep =
  ""))

  val_count<-freq(myras)
  zeros<-as.numeric(val_count[1,2])
  ones<-as.numeric(val_count[2,2])
  tot_pix = as.numeric(zeros+ones)

  # import shapefile points
  species_pts<-readOGR(dsn = "/home/species_pts", layer =
  paste(current_sp, "_pts", sep = ""))
  n_pts<-as.numeric(poly.counts(species_pts, italy_map)) # tot n°
of points

  # calculate point prevalence
  listy<-extract(myras, species_pts, buffer=150) # SET BUFFER
WIDTH
  pt_in<-0
  pt_out<-0
```

```

for (i in 1:length(listy)){

  if (1 %in% listy[[i]]) {
    pt_in<-pt_in+ 1
  } else { pt_out<-pt_out+ 1}
}

# 1. Define the confidence interval

conlev<-0.95
conlev1 <- (1 - conlev) / 2 # Calculate conlev1.
m=ones
n=zeros
k=n_pts

infs <- qhyper(conlev1,m,n,k) # lower limit
sups <- qhyper(conlev1,m,n,k,lower.tail = F) # upper limit
null.mod<-"hypergeom"

upper_percent=sups/n_pts*100
pt_prevalence=(pt_in/n_pts)*100
model_prevalence=(ones/tot_pix)*100

write(paste(current_sp,
            "\nconfidence interval", conlev,
            "\nn° of points", n_pts,
            "\nupper and lower limit", sups, infs,
            "\nn° of points inside the model", pt_in,
            "\nupper limit %", upper_percent, "%",
            "\npoint prevalence", pt_prevalence, "%",
            "\nmodel prevalence", model_prevalence, "%",
            "\n\n-----"),
file="150_perf_Amph_IUCN.txt", append = T)

}

```