

Ecography

ECOG-04687

Gábor, L., Moudrý, V., Lecours, V., Malavasi, M., Barták, Fogl, M., Šímová, P., Rocchini, D. and Václavík, T. 2019. The effect of positional error on fine scale species distribution models increases for specialist species. – Ecography doi: 10.1111/ecog.04687

Supplementary material

APPENDIX 1. Study area.

Fig. A1. The study site encompasses the Biosphere Reserve Krkonose Mountains National Park (KRNAP) located in the Czech Republic, Central Europe (AMSL – above mean sea level).

APPENDIX 2. Variograms

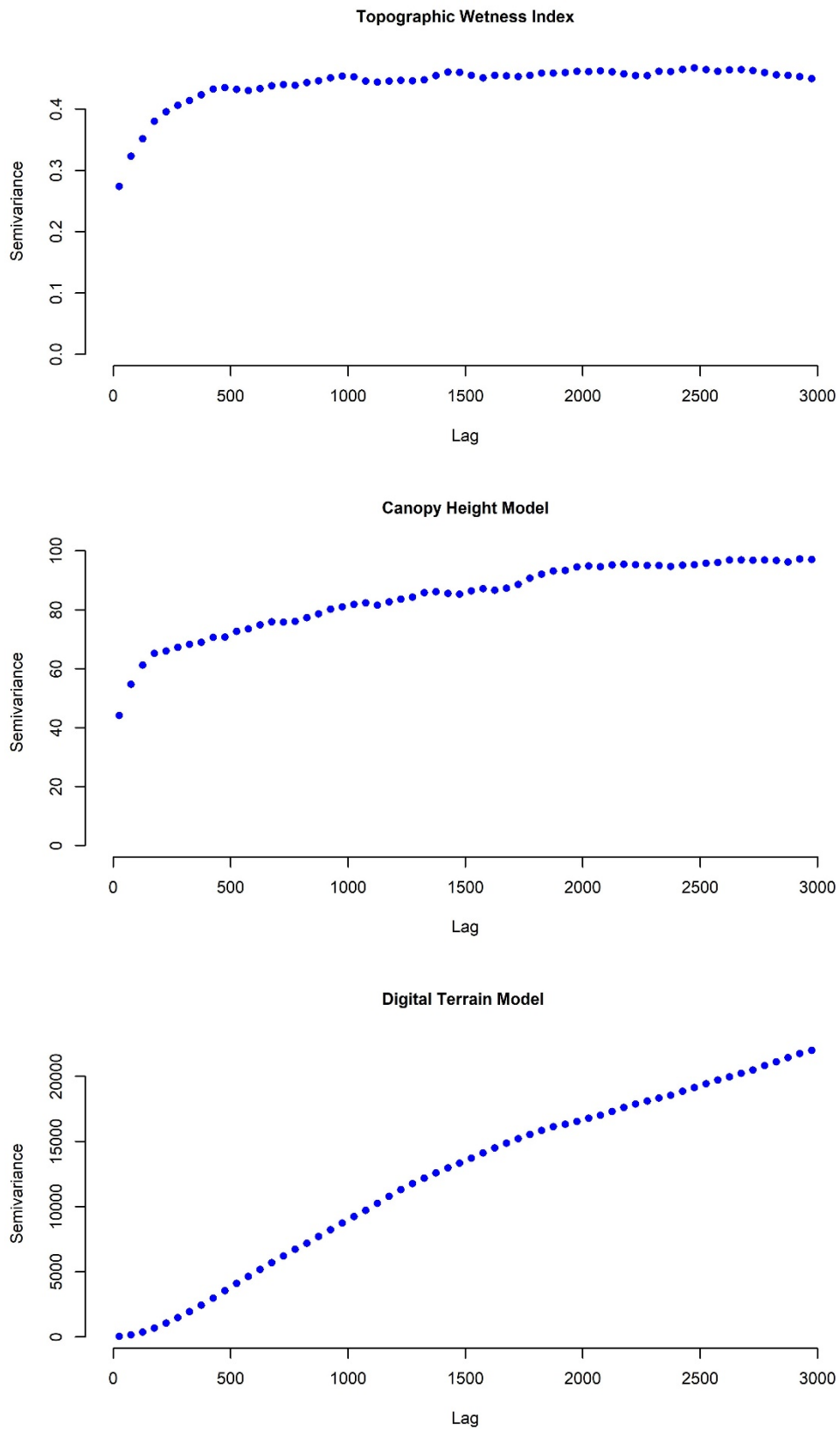


Fig. A2. Variograms of environmental variables used for generating virtual species and modelling species distribution.

APPENDIX 3. Used mean and standard deviation to generate virtual species with different width of species' ecological niche.

Table B1 The mean and standard deviations (sd) of normal distribution curves used to generate virtual species with different relative occurrence areas (ROA)

	Environmental Variables					
	DTM		CHM		TWI	
	<i>mean</i>	<i>sd</i>	<i>mean</i>	<i>sd</i>	<i>mean</i>	<i>sd</i>
rare species (low ROA)	846	±100	9	±4	8	±0.4
intermediate species (medium ROA)	846	±155	9	±6	8	±0.5
common species (high ROA)	846	±205	9	±15	8	±0.8

APPENDIX 4. Range of simulated positional error.

Table C1 Summary of survey designs used to simulate different degrees of positional error in species occurrence data

Survey Design	Range of Shift (m)	Number of Pixels
S1	5 - 10	1 - 2
S2	10 - 15	2 - 3
S3	15 - 20	3 - 4
S4	20 - 50	4 - 10
S5	50 - 100	10 - 20
S6	100 - 500	20 - 100

Appendix 5

Step 1: Loading environmental data

```
library(raster)

Bioall <- stack("chm.tif", "dtm.tif ", "twi.tif ")
names(Bioall) <- c("chm", "dtm", "twi")
```

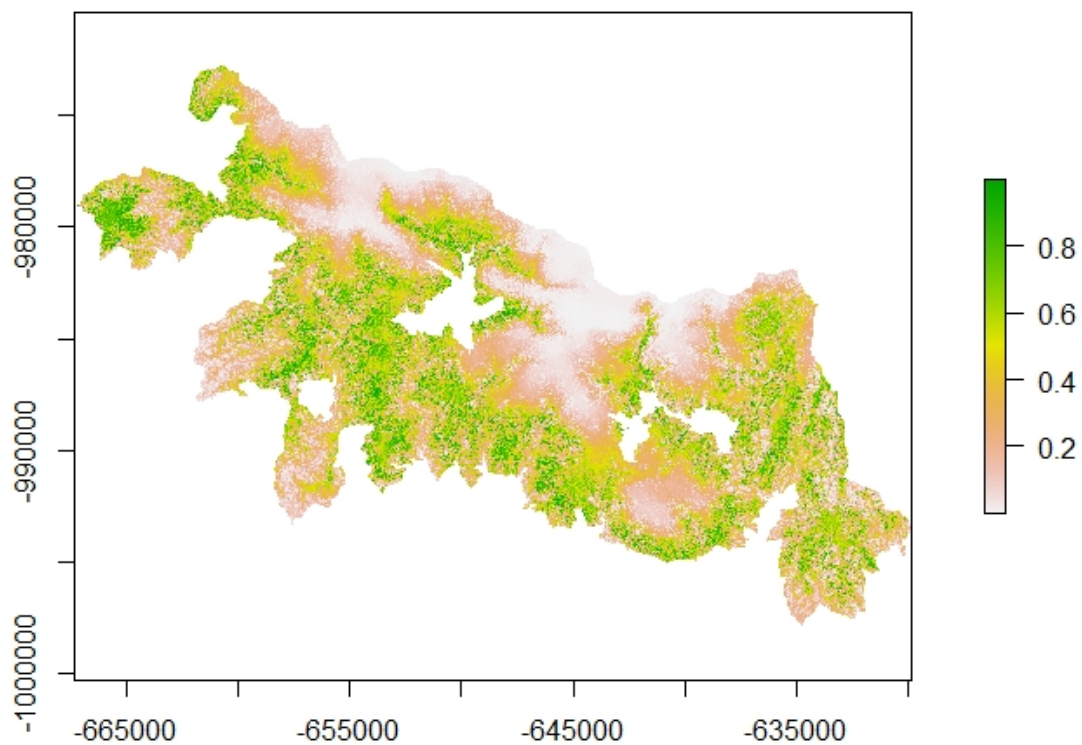
Step 2: Simulation of virtual species with different niche breadths

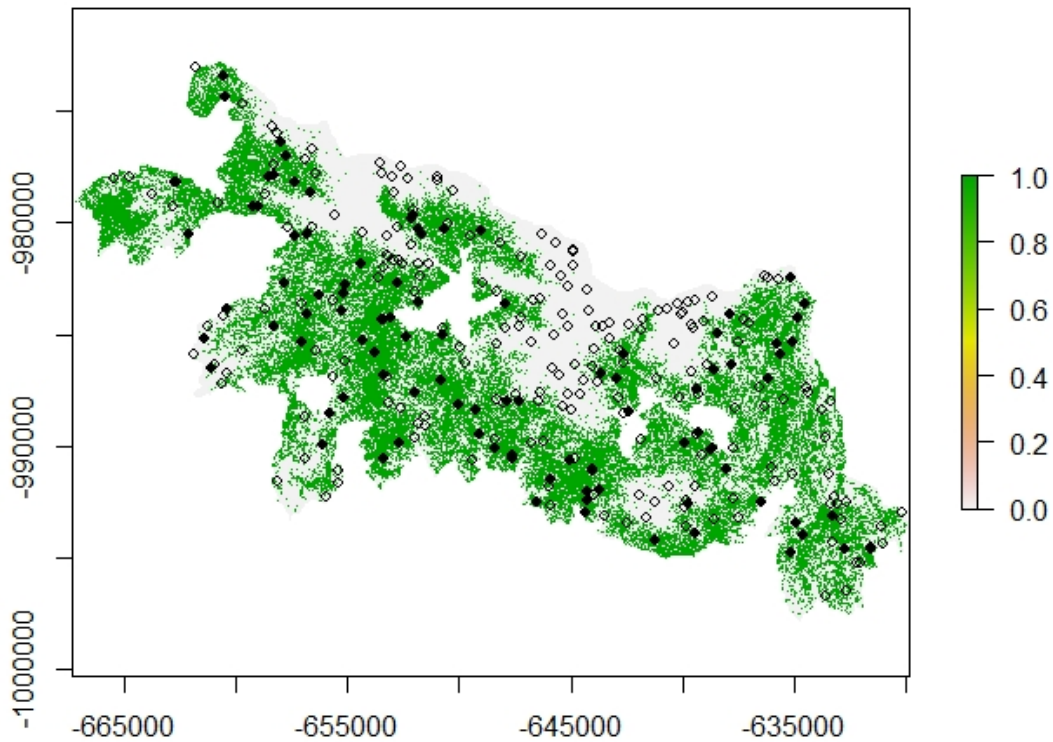
```
library(virtualspecies)

# define environmental suitability function
my.parameters <- formatFunctions(chm = c(fun = 'dnorm', mean = 9, sd = 15),
                                dtm = c(fun = 'dnorm', mean = 846, sd = 205),
                                twi = c(fun = 'dnorm', mean = 8, sd = 0.8))

# generating virtual species environmental suitability
virtual.species <- generateSpFromFun(raster.stack = Bioall,
                                    parameters = my.parameters,
                                    species.type = "multiplicative",
                                    plot = T)
```

Environmental suitability of the virtual species





Step 5: Simulating positional error in species occurrences

```
# loading functions for shifting occurrences

# function limiting the shift only to study area
inside <- function(x, y, mask){
  ins <- ifelse(x < mask@extent@xmin | x > mask@extent@xmax | y < mask@extent@ymin | y >
mask@extent@ymax, FALSE, TRUE)
  if (ins == TRUE) {
    val <- extract(mask, matrix(c(x,y), ncol=2))
    ins <- ifelse(is.na(val), FALSE, TRUE)
  }
  return(ins)
}

# function shifting occurrences in a random direction and specified range
shift <- function(x, y, dist, mask){
  new.x <- x
  new.y <- y
  inside <- FALSE
  while (!inside){
    angle <- runif(1,0,360)*pi/180
    new.x <- x + dist*sin(angle)
    new.y <- y + dist*cos(angle)
    inside <- inside(new.x, new.y, mask)
  }
  return(c(new.x, new.y))
}
```



```

# preparing data frame for shifting species occurrences

DATA.Prepare <- as.data.frame(occ$sample.points)
s <- nrow(DATA.Prepare)
DATA.Prepare$ID <- 1:s

# example of shifting species occurrences from 100 up to 500 metres

DATA.Prepare[,c("S1x", "S1y")] <- t(apply(DATA.Prepare, 1, function(.) shift(.["x"], .["y"],
                                         dist=runif(1, 100, 500), mask=dtm)))

# extracting accurate and shifted occurrences
Presence_Absence_XY <- DATA.Prepare[,1:2]
S1.Presence_Absence_XY <- DATA.Prepare[,7:8]

# Plotting accurate and shifted occurrences
plot(PA.raster$pa.raster)
points(Presence_Absence_XY, col = "blue")
points(S1.Presence_Absence_XY, col = "red")

```

