Chapter 5

Overlap Indices

Contents

Overlap indices can be useful for determining the spatial interactions between animals using relocations of animals occupying similar areas. There are various overlap indices available and a good reference is Fieberg and Kochanny (2005). The overlap methods presented have code and more detailed descriptions in the adehabitatHR package for R (Calenge 2011). Methods of home range overlap simply require coordinate data after estimating home range. Note that example below is not the same dataset supplied for this exercise.

```
#First we can load some data and create some generic utilization distributions
#before estimating overlap:
library(adehabitatHR)

#Creates a Spatial Points Data Frame for 2 animals by ID
twocats <-read.csv("AllHRlocs.csv", header=T)
data.xy = twocats[c("x","y")]

#Creates class Spatial Points for all locations
xysp <- SpatialPoints(data.xy)
proj4string(xysp) <- CRS("+proj=utm +zone=17N +ellps=WGS84")

#Creates a Spatial Data Frame from all locations
sppt<-data.frame(xysp)

#Creates a spatial data frame of ID
idsp<-data.frame(twocats[1])

#Merges ID data frame with GPS locations data frame
#Data frame is called "idsp" comparable to the "relocs" from puechabon dataset
coordinates(idsp)<-sppt

#First we need to create utilization distributions for each panther
ud <- kernelUD(idsp[,1])
```

```
OR

kernelUD(idsp[,1], h = "href", grid = 200, same4all = TRUE, hlim = c(0.1, 1.5),
     kern = c("bivnorm"), extent = 0.5)

#output of UDs for each panther
image(ud)

NOTE: kerneloverlap will just estimate overlap indices for only the locations
```

5.1 Percent overlap

HR – Proportion of animal i's home range that is overlapped by animal j's home range (Kernohan et al. 2001).

```
kerneloverlaphr(idsp[,1], grid=200, method="HR", percent=95, conditional=TRUE)

      FP048     FP094     FP110      FP113     FP121     FP128     FP130
FP048 1.0000000 0.2539683 0.3611111 0.67857143 0.2738095 0.2738095 0.56746032
FP094 0.1743869 1.0000000 0.3106267 0.23705722 0.3487738 0.3160763 0.12261580
FP110 0.1834677 0.2298387 1.0000000 0.26612903 0.2862903 0.7379032 0.07661290
FP113 0.5135135 0.2612613 0.3963964 1.00000000 0.2672673 0.3273273 0.51051051
FP121 0.1490281 0.2764579 0.3066955 0.19222462 1.0000000 0.2915767 0.11663067
FP128 0.1326923 0.2230769 0.7038462 0.20961538 0.2596154 1.0000000 0.05769231
FP130 0.7150000 0.2250000 0.1900000 0.85000000 0.2700000 0.1500000 1.00000000
```

5.2 Probability overlap

PHR – Probability of animal j being located in animal i's home range and vice versa (i.e., volume measure; Ostfeld 1986).

```
kerneloverlaphr(ud, meth="PHR", conditional=TRUE)

      FP048     FP094      FP110     FP113     FP121     FP128       FP130
FP048 0.9494305 0.1805179 0.42561390 3.1250391 1.1182583 0.3443277   0.0583
FP094 0.2669219 0.8731045 0.73504044 1.2518993 2.1795156 1.6187565   0.0262
FP110 0.4174817 0.3190549 2.67619435 1.6975608 2.8534787 4.5286474   0.0076
FP113 0.7618825 0.2652719 0.52653119 4.8046721 0.9172712 1.7769509   0.0895
FP121 0.2661436 0.3581339 0.93388969 1.2381488 7.5593950 1.7633521   0.0244
FP128 0.1645584 0.2966145 2.33213801 0.8889413 2.5113787 5.3728081   0.0062
FP130 0.6965648 0.1028496 0.07726699 3.4283998 0.4992657 0.1184470   0.0941
```

5.3 Bhattacharyya's affinity

BA – a statistical measure of affinity between 2 populations that assumes they use space independently of one another (Bhattacharyya 1943). Values range from zero (no overlap) to 1 (identical UDs).

```
kerneloverlaphr(ud, meth="BA", conditional=TRUE)

      FP048      FP094      FP110     FP113      FP121      FP128
FP048 0.9494305 0.19300494 0.32460745 1.3935548 0.44029134 0.19713762
FP094 0.1930049 0.87310451 0.42688290 0.4840179 0.76378458 0.60678828
FP110 0.3246075 0.42688290 2.67619435 0.7715258 1.39007501 2.96104840
FP113 1.3935548 0.48401785 0.77152577 4.8046721 0.93867516 1.02377927
FP121 0.4402913 0.76378458 1.39007501 0.9386752 7.55939503 1.53768461
FP128 0.1971376 0.60678828 2.96104840 1.0237793 1.53768461 5.37280812
FP130 0.1649118 0.04089019 0.02278675 0.5029844 0.09429946 0.02478678
```

5.4 Utilization distribution overlap index

UDOI – an UD overlap index similar to Hurlbert index of niche overlap that assumes they use space independently of one another (Hurlbert 1978). Values range from zero (no overlap) to 1 (uniformly distributed and have 100% overlap) but can be >1 if both UDs are nonuniformly distributed and have a high degree of overlap.

```
kerneloverlaphr(ud, meth="UDOI", conditional=TRUE)

       FP048       FP094        FP110       FP113        FP121
FP048 1.88354584 0.058535090 1.200312e-01  2.80355009   0.26373006
FP094 0.05853509 1.215285513 2.373785e-01  0.27909161   0.83782880
FP110 0.12003124 0.237378462 1.218177e+01  0.67534032   2.72820629
FP113 2.80355009 0.279091613 6.753403e-01 34.89888157   1.04793012
FP121 0.26373006 0.837828797 2.728206e+00  1.04793012 128.78219185
FP128 0.04282855 0.596978847 1.608828e+01  1.26045478   3.04242496
FP130 0.03891154 0.002097975 5.547623e-04  0.34714991   0.01114027
```

5.5 Hellinger's distance

HD – a measure of distance between 2 populations (Matusita 1973).

```
kerneloverlaphr(ud, meth="HD", conditional=TRUE)

      FP048     FP094    FP110    FP113    FP121    FP128     FP130
FP048 0.0000000 1.2858818 1.864468 1.722496 2.762445 2.606872 0.8448535
FP094 1.2858818 0.0000000 1.641808 2.605304 2.627723 2.243287 0.9504207
FP110 1.8644681 1.6418079 0.000000 3.212855 2.730465 1.458391 1.6753830
FP113 1.7224962 2.6053041 3.212855 0.000000 3.301337 3.593655 1.9730367
FP121 2.7624454 2.6277234 2.730465 3.301337 0.000000 3.207293 2.7322091
FP128 2.6068720 2.2432869 1.458391 3.593655 3.207293 0.000000 2.3475101
FP130 0.8448535 0.9504207 1.675383 1.973037 2.732209 2.347510 0.0000000
```

5.6 Volume of intersection index

Volume of intersection under the full UDs of 2 animals (Seidel 1992, Millspaugh et al. 2000). Values range from zero (no overlap) to 1 (identical UDs).

```
      kerneloverlaphr(ud, meth="VI", conditional=TRUE)

             FP048       FP094       FP110       FP113       FP121
      FP048 0.94973489 0.015706682 0.081581400 0.356221669 0.015685067
      FP094 0.01570668 0.873256975 0.064468281 0.049201257 0.036421940
      FP110 0.08158140 0.064468281 2.542692800 0.106706398 0.082470262
      FP113 0.35622167 0.049201257 0.106706398 4.804125850 0.126326346
      FP121 0.01568507 0.036421940 0.082470262 0.126326346 7.560716837
      FP128 0.01827549 0.075271608 0.665701571 0.090174304 0.052936190
      FP130 0.01682551 0.001788199 0.002577415 0.039754312 0.000000000
```

```
#Plot out to visualize overlap
plot(idsp, col="yellow")
uds <- getverticeshr(ud)
plot(uds, add=TRUE)

plot(idsp, col="yellow")
ud1 <- getverticeshr(ud[[1]])
plot(ud1, add=TRUE)
ud2 <- getverticeshr(ud[[2]])
plot(ud2, lwd=2, add=TRUE)
ud3 <- getverticeshr(ud[[3]])
plot(ud3, lwd=3, add=TRUE)
ud4 <- getverticeshr(ud[[4]])
plot(ud4, lwd=4, add=TRUE)

#An alternative way with only the locations
kerneloverlap(idsp[,1], grid=200, method="HR", percent=95, conditional=TRUE)
kerneloverlap(idsp[,1], grid=200, method="PHR", percent=95, conditional=TRUE)
kerneloverlap(idsp[,1], grid=200, method="BA", percent=95, conditional=TRUE)
kerneloverlap(idsp[,1], grid=200, method="UDOI", percent=95, conditional=TRUE)
kerneloverlap(idsp[,1], grid=200, method="HD", percent=95, conditional=TRUE)
kerneloverlap(idsp[,1], grid=200, method="VI", percent=95, conditional=TRUE)
```