

1.10 Creating Buffers

Manual of Applied Spatial Ecology

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For this exercise, we will again be working with the Colorado mule deer locations and rasters from earlier sections (1.3, 1.7). Creating buffers around locations of animals, plots, or some other variable may be necessary to determine what occurs around the locations. Often times, in resource selection studies, we may want to generate buffers that can be considered used habitat within the buffer as opposed to simply counting only the habitat that the location is found. Lets begin with loading the proper packages and mule deer locations from previous exercise. Because we are dealing with the raster layer projected in Albers, we will need to project our mule deer locations as we did above.

1. Exercise 1.10 - Download and extract zip folder into your preferred location
2. Set working directory to the extracted folder in R under Session - Set Working Directory...
3. Now open the script "BufferScript.Rmd" and run code directly from the script
4. First we need to load the packages needed for the exercise

```
library(sp)
library(raster)
library(rgeos)
```

5. Now let's have a separate section of code to include projection information we will use throughout the exercise. In previous versions, these lines of code were within each block of code

```
crs<-"+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"
Albers.crs <-CRS("+proj=aea +lat_1=29.5 +lat_2=45.5 +lat_0=23
+lon_0=-96 +x_0=0 +y_0=0 +ellps=GRS80 +towgs84=0,0,0,0,0,0 +units=m +no_defs")
```

```
## Warning in showSRID(uprojargs, format = "PROJ", multiline = "NO", prefer_proj
## = prefer_proj): Discarded datum Unknown based on GRS80 ellipsoid in Proj4
## definition
```

6. Now open the script "BufferScript.Rmd" and run code directly from the script

```
muleys <-read.csv("muleysexample.csv", header=T)
summary(muleys$id)
```

```
##      Length      Class      Mode
##      1091 character character
```

```
#Let us subset data so there are fewer locations to work with
muley8 <- subset(muleys, id=="D8")
```

```
#Remove outlier locations if needed
summary(muley8$Long)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -111.8  -108.9  -108.9  -108.9  -108.9  -108.8
```

```
#NOTE: Min. of -111.8 is an outlier so remove
summary(muley8$Lat)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 33.38  37.84   37.84   37.83   37.85   37.86
```

```
#NOTE: Min. of 33.38 is an outlier so remove
newmuley8 <-subset(muley8, muley8$Long > -111.7 & muley8$Lat > 37.80)
muley8 <- newmuley8
```

```
#Make a spatial data frame of locations after removing outliers
coords<-data.frame(x = muley8$Long, y = muley8$Lat)
```

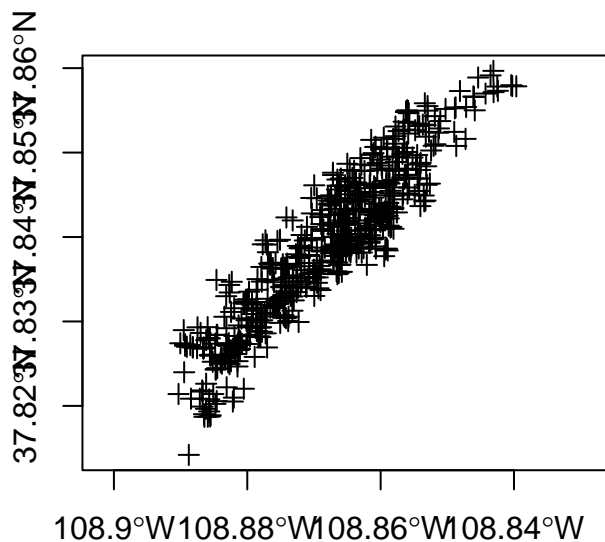
```
deer.spdf <- SpatialPointsDataFrame(coords= coords, data = muley8, proj4string = CRS(crs))
#head(deer.spdf)
class(deer.spdf)
```

```
## [1] "SpatialPointsDataFrame"
## attr("package")
## [1] "sp"
```

```
proj4string(deer.spdf)
```

```
## [1] "+proj=longlat +datum=WGS84 +no_defs"
```

```
plot(deer.spdf, axes=T)
```



```
#Again let's project the deer.spdf to Albers
deer.albers <-spTransform(deer.spdf, CRS=Albers.crs)
class(deer.albers)
```

```
## [1] "SpatialPointsDataFrame"
```

```
## attr(,"package")
## [1] "sp"
```

```
proj4string(deer.albers)
```

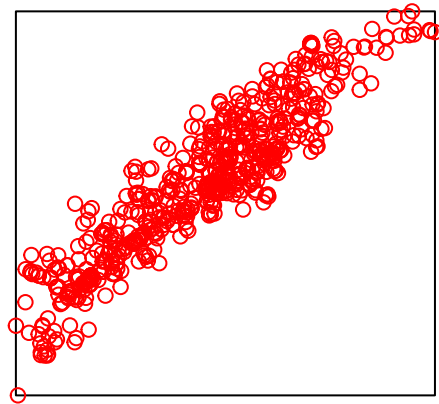
```
## [1] "+proj=aea +lat_0=23 +lon_0=-96 +lat_1=29.5 +lat_2=45.5 +x_0=0 +y_0=0 +ellps=GRS80 +units=m +no_
```

7. Clip the study.zoom so we can zoom in on mule deer 8 locations as we did in previous exercise but with a bounding box of only mule deer 8 locations.

```
bbox(deer.albers)
```

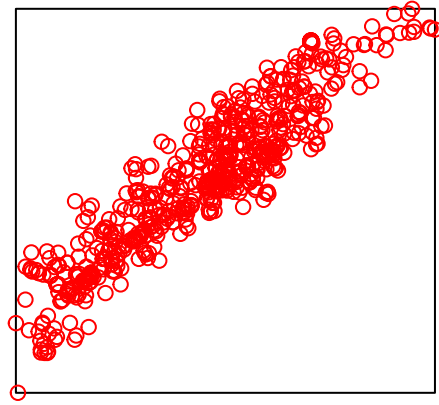
```
##          min          max
## x -1120488 -1115562
## y  1718097  1722611
```

```
bb1 <- cbind(x=c(-1115562,-1115562,-1120488,-1120488, -1115562),
             y=c(1718097,1722611,1722611,1718097,1718097))
AlbersSP <- SpatialPolygons(list(Polygons(list(Polygon(bb1)),"1")),
                             proj4string=CRS(proj4string(deer.albers)))
plot(AlbersSP)
points(deer.albers, col="red")
```



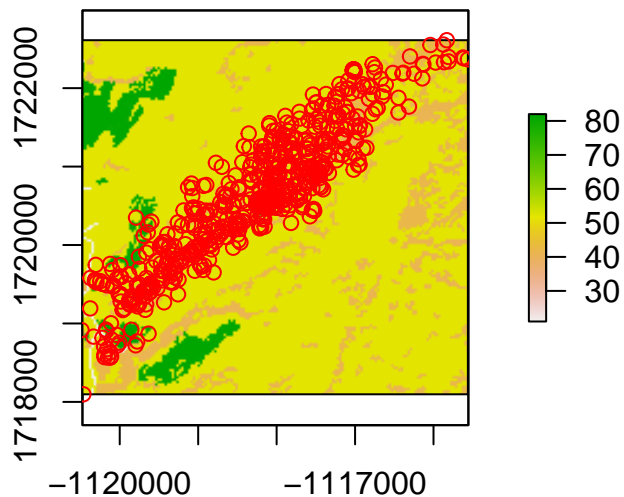
8. Alternatively, load the vegetation raster layer textfile clipped in ArcMap to be within several counties around the mule deer locations. Plot the points and bounding box over the vegetation layer and notice they are barely visible due to the large extent of the raster layer.

```
veg <- raster("extentnlcd2.txt")
#plot(veg)
plot(AlbersSP)
points(deer.albers, col="red")
```



9. We can clip the vegetation raster and plot the bounding box polygon and locations on the raster. Notice that the locations are nearly off the extent of the raster.

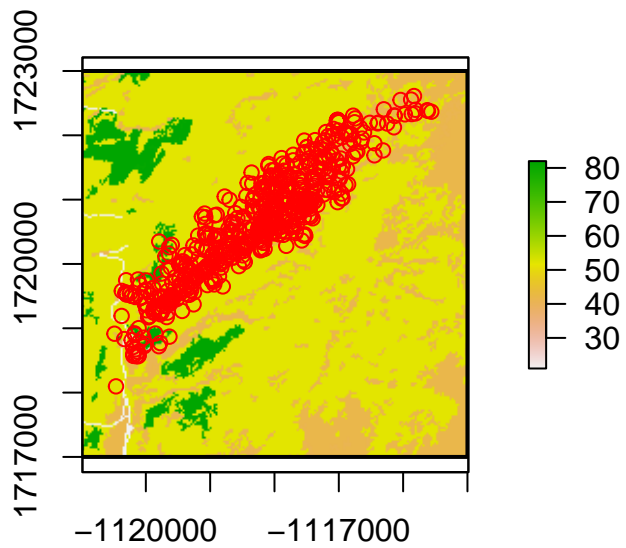
```
bbclip <- crop(veg, AlbersSP)
plot(bbclip)
plot(AlbersSP, add=T)
points(deer.albers, col="red")
```



10. So let us create a new bounding box that encompass mule deer 8 locaitons but also extends beyond the periphery of the outermost locations. Then clip the large vegetation raster again so it is within the newly created bounding box polygon

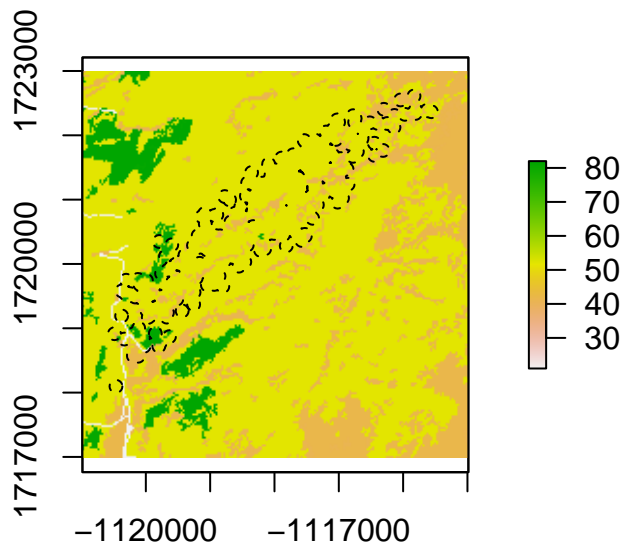
```
bb1 <- cbind(x=c(-1115000,-1115000,-1121000,-1121000, -1115000),
             y=c(1717000,1723000,1723000,1717000,1717000))
AlbersSP <- SpatialPolygons(list(Polygons(list(Polygon(bb1)),"1")),
                             proj4string=CRS(proj4string(deer.albers)))

bbclip <- crop(veg, AlbersSP)
plot(bbclip)
plot(AlbersSP,lwd=2, add=T)
points(deer.albers, col="red")
```



11. To conduct some analyses, let us create 100 m buffered circles around all the locations and extract vegetation that occurs in each buffered circle

```
settbuff=gBuffer(deer.albers,width=100)
plot(bbclip)
plot(settbuff, add=T, lty=2)
```



```
table(extract(bbclip, settbuff))
```

```
##
##    21    41    42    52    81    82
##    37   288   532  4725    56   157
```

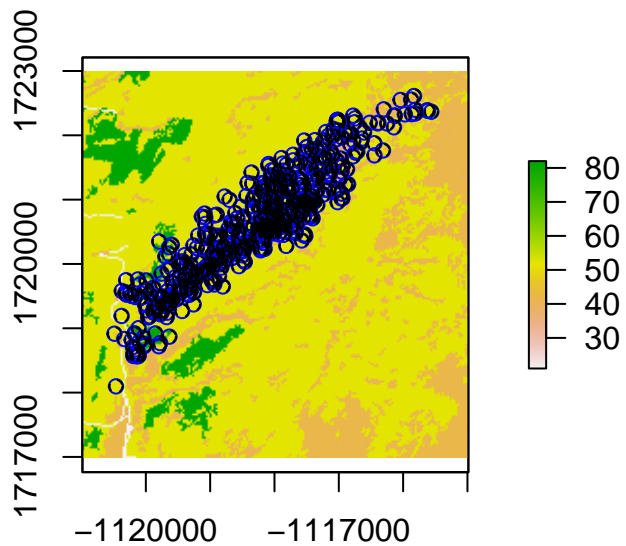
```
#Cell size of raster layer
res(bbclip)
```

```
## [1] 30 30
```

```
# 30^2
# 900*37
# (900*37)/1000000
```

12. Most efforts will want percent habitat or area of each habitat defined individually for each location (i.e., within each buffered circle). To do this we only need to specify in the gBuffer function to create unique buffered circles with the byid=TRUE command.

```
settbuff=gBuffer(deer.albers, width=100, byid=TRUE)
plot(bbclip)
points(deer.albers, col="blue")
plot(settbuff, add=TRUE, lty=8)
```



```
#Extract the amount of vegetation in each buffer and place it in a table by buffer ID
```

```
e= extract(bbclip,settbuff)
```

```
et=lapply(e,table)
```

```
#Example below identifies buffered circles number 328
```

```
et[[328]]
```

```
##
```

```
## 41 42 52
```

```
##  4  7 24
```

```
#Buffer ID 328 has 3 vegetation categories 41, 42, and 52 of 4, 7, and 24 cells, respectively
```