

Homework 4

Clara Buchholtz

3/4/2019

```
#Setup
```

```
library("raster")
```

```
## Warning: package 'raster' was built under R version 3.5.2
```

```
## Loading required package: sp
```

```
library("rgeos")
```

```
## rgeos version: 0.4-2, (SVN revision 581)
```

```
## GEOS runtime version: 3.6.1-CAPI-1.10.1
```

```
## Linking to sp version: 1.3-1
```

```
## Polygon checking: TRUE
```

```
library("rgdal")
```

```
## Warning: package 'rgdal' was built under R version 3.5.2
```

```
## rgdal: version: 1.3-9, (SVN revision 794)
```

```
## Geospatial Data Abstraction Library extensions to R successfully loaded
```

```
## Loaded GDAL runtime: GDAL 2.1.3, released 2017/20/01
```

```
## Path to GDAL shared files: /Library/Frameworks/R.framework/Versions/3.5/Resources/library/rgdal/gdal
```

```
## GDAL binary built with GEOS: FALSE
```

```
## Loaded PROJ.4 runtime: Rel. 4.9.3, 15 August 2016, [PJ_VERSION: 493]
```

```
## Path to PROJ.4 shared files: /Library/Frameworks/R.framework/Versions/3.5/Resources/library/rgdal/pj
```

```
## Linking to sp version: 1.3-1
```

```
library("MASS")
```

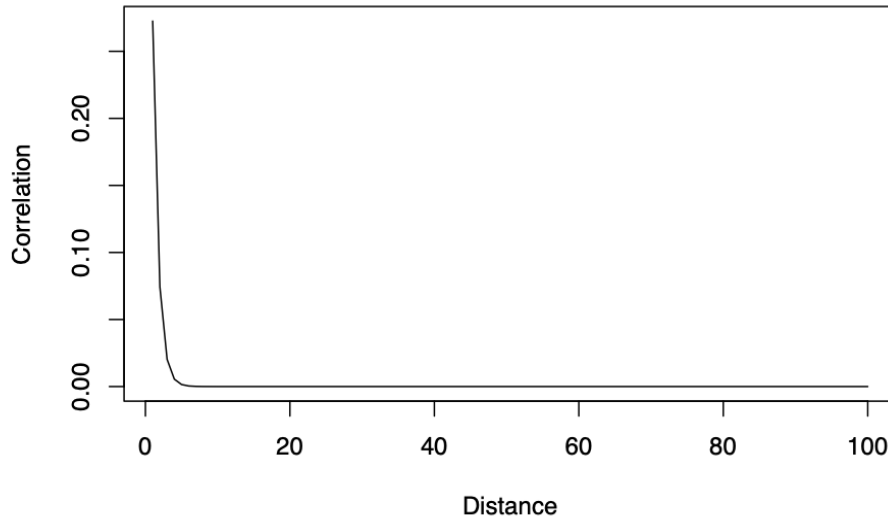
```
##
```

```
## Attaching package: 'MASS'
```

```
## The following objects are masked from 'package:raster':
```

```
##
```

```
##      area, select
```



a) The distribution of ptarmigan is likely to correspond to the patterns in ice cover. Vegetation access is a major life or death factor for arctic resident herbivores, especially in winter, so we are likely to see them clustering around large or continuous areas of low ice cover, and almost entirely absent from areas of high ice cover.

b) I chose $\phi=1.3$ because the rugged terrain of the arctic landscape has a lot of variation to it, and only spots that are pretty close to one another- say circa 10 to 50 meters from one another, are consistently likely to be similar in ice cover. For e.g. a large low flat area with lots of snow and ice is likely to have small rugged ridge protrusions that are devoid of ice, and which may have exposed veg for the animals to eat.

```
#Using a beta distribution, because this is about % cover
#r beta args: (n, shape1, shape2, ncp = 0)
#n was set above as the number of pixels
XXX<-plogis(rmvn(1, rep(0, n),exp(-phi * distance))) #our mean from the random multivariate draw
X<-rbeta(n,shape1=XXX*.5,shape2=(1-XXX)*.5)

# Visualize results
Xraster <- rasterFromXYZ(cbind(simgrid[, 1:2] - 0.5, X))

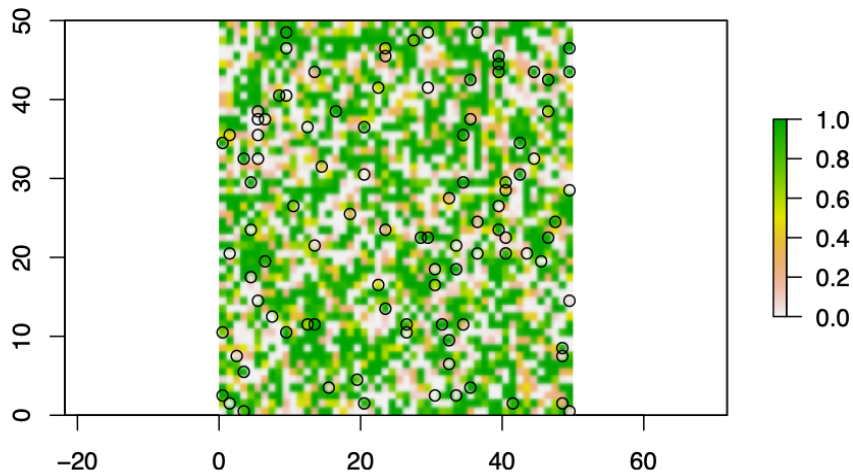
plot(Xraster) #As we can see, there's a lot of ice,
#and the patches of high autocorrelation are small and localized,
#but also follow along narrow continuous areas as well. This is a good simulation
#of the rugged arctic landscape at its stage in early spring--ice and snow areas are
#still abundant, but are growing more patchy, and their distribution is
#very revealing of the landscape underneath them

#Converting raster to a dataframe
spat_dat=rasterToPoints(Xraster)

#how many points can you sample? Choose a set of sample points
#that is realistic for your sample organism
G0=sample(x=c(1:nrow(spat_dat)),size=100)

#Then we overlay those random sample points on our landscape (and put on graph)
```

```
points(spat_dat[G0,c(1:2)])
```



c) The landscape, weather conditions, time, and money largely restrict the number of points we can sample. If each pixel is 30m^2 , the total area represented by the matrix above is 2.25 square kilometers. Within this area, over the course of my 6 weeks of sampling, it would be realistic to sample somewhere around 100 sites (approximately 2-3 per day, while allowing for difficult travel, and storms to reduce field time.) d) see plot above

```
#Presence/Absence component:
#How rare is it for the ptarmigan to be on any of these pixels?
presence_intercept=.2 #baseline chance of seeing ptarmigan at any pixel is pretty low
presence_slope=-10 #for every % increase in ice cover the
#likelihood of seeing ptarmigan decreases by ~2.5% (which is 10/4)

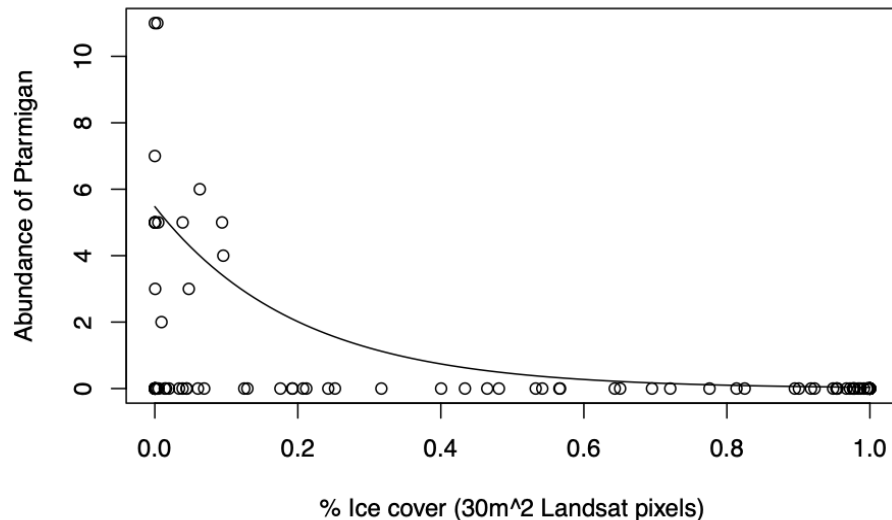
PA=rbinom(100,plogis(presence_intercept+spat_dat[G0,3]*presence_slope),
          size=1)

#Count/Abundance component:
#if you do find ptarmigan at a place with ice, how many will you find

count_intercept=1.7
count_slope=-5
over_dispersion=10

abundance=PA*rbinom(100,mu=
exp(count_intercept+count_slope*spat_dat[G0,3]),
size=over_dispersion)

plot(abundance~spat_dat[G0,3],
      xlab="% Ice cover (30m^2 Landsat pixels)", ylab="Abundance of Ptarmigan")
curve(exp(1.7+-5*x), add=T)
```



The probability of seeing ptarmigan anywhere on the landscape, even without ice cover, is already relatively low. So a lot of zero counts might be a product of that rarity, and not a product of ice cover. For one thing, we are assuming that the distributions are modeling the same set of variables- in this case the same landscape and the same birds. g) see plot above

```
#Juliette's data:
batdata<- read.csv("fake_data.csv")
#Note: I edited the data she sent me because the generative model produced
#only zeros for abundance of bats, so I couldn't recapture parameters from a no bats scenario
```

```
#Get the parameters for presence/absence of bats
BATpresabs<- ifelse(batdata$abundance>0,1,0)
presmod <-glm(BATpresabs~batdata$spat_dat.G0..3., family="binomial")
coef(presmod) #these should be her pres abs values she originally put in
```

```
##          (Intercept) batdata$spat_dat.G0..3.
##          -1.3121043          -0.2523883
plogis(-1.3121043) #intercept
```

```
## [1] 0.2121349
-0.2523883 /4 #max slope
```

```
## [1] -0.06309708
```

This would suggest a baseline probability of seeing a bat is about 21%, and that there is a very modest decrease in the chance of seeing one with each increase in the predictor variable.

```
#Get rid of the zeros
NEWBATZ <- subset(batdata, batdata$abundance>0)
#Capture parameters for abundance i.e. how many bats are there when you actually see some
NEWBATZ.mod <- glm(NEWBATZ$abundance~NEWBATZ$spat_dat.G0..3., family="poisson")
coef(NEWBATZ.mod)
```

```
##          (Intercept) NEWBATZ$spat_dat.G0..3.
```

```
##              1.427116              -1.427116
#OR
NEWBATZ.modNB <- glm.nb(NEWBATZ$abundance~NEWBATZ$spat_dat.G0..3.)
coef(NEWBATZ.modNB)

##              (Intercept) NEWBATZ$spat_dat.G0..3.
##              1.427116              -1.427116
exp(1.427116)

## [1] 4.166665
exp(-1.427116)-exp(1.427116+-1.427116)

## [1] -0.7599999
```

I ran the data on abundance using both a poisson and a negative binomial estimation, and both produced essentially the same results. This would suggest you see around 4 bats at baseline when you do see any bats, and that with each increase in the predictor variable you see ~ 0.76 fewer bats.

- h) I was able to capture parameters, but I will re-run this if we can generate non-zero data. When I ran with the data that was only zeros, all of my estimates were either near zeros or errors, so in a way I suppose that did capture the original data.
- i) I might want to see if autocorrelation in the landscape is predictive of patterns in my response variable. I also might want to see if I could bring some version of the phi value into my glm to account for autocorrelation in the predictor variable