

Anna Roser

Homework 4: Generative Model for Species Distribution

Study Organism: Lupin

Predictor Variable: Number of pollinators

- Lupin distribution are likely to be predicted by the number of pollinators in an area because lupin rely on many pollinators for reproduction and fertilization. The plants will have a higher likelihood of reproductive success in dense pollinator areas.
- My phi value is 0.5 because I would expect that pollinators are likely to prefer some areas over others so there will not be an even distribution of pollinator density across a landscape.
- The number of points that I can sample is constrained by the number of plots which I can visit. I've chosen to visit 100 plots because lupin plants can be counted quickly.

Distribution of Pollinators with sample sites

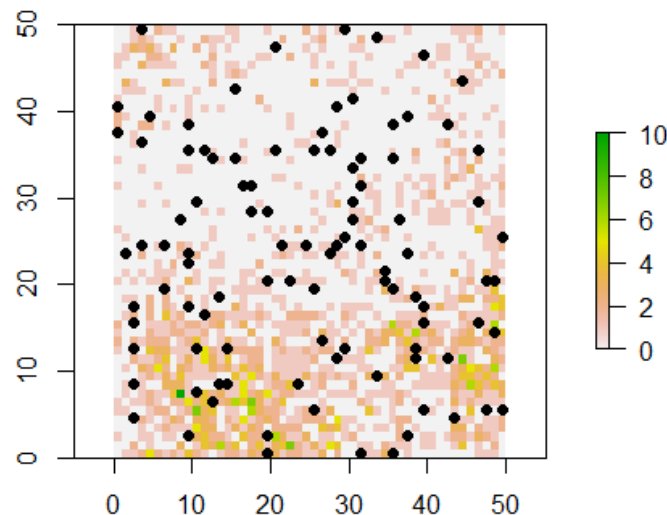


Figure 1. Generated map of pollinator density across an assumed landscape. Sample sites for lupin counts are displayed in black (n=100).

- We observe a hurdle model because it matches the presence/absence binomial model which are plotted with PA term in code. A hurdle model allows us to better

f. My landscape has high spatial autocorrelation because pollinators are not evenly distributed, so I would expect that lupin presence is also unevenly distributed over the site because of plan reliance on pollinators. I assume that the amount of plots with no lupin will be high (0's) but that some plots will have high counts of lupin, resulting in a high variance for the data set.



I was not able to successfully capture the true slope and intercept of Megan's dragons—Is this an issue of small sample size? Also, I'm not sure if I've interpreted my model outputs correctly.

My Estimates:

plogis(-21.8)= 3.407064e-10

#PA slope= 2.7

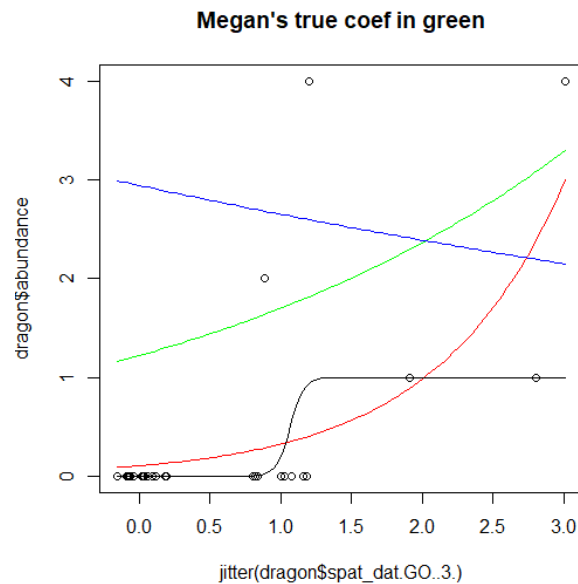
#count int= .2

#count slope= .33

$\text{plogis}(-21.800+20.414)-\text{plogis}(-21.800) = 0.20$

$\exp(1.0799) = 2.944$

$\exp(1.0799-0.1044)-\exp(1.0799) = -0.291$



```
curve(exp(.2 + .33*x), add = T, col = "green") #megan's true coef
```

```
curve(exp(-2.226 + 1.104*x), add = T, col = "red") #my estimates of megan's coef
```

```
curve(exp(1.08 - 0.1044*x), add = T, col = "blue") #my estimates of megan's coef
```

```
curve(plogis(-21.800+20.414*x), add = T, col = "black")
```

```
> PA1=ifelse(dragon$abundance>0,1,0) #separate zeros from ones  
> glm(PA1~dragon$spat_dat.GO..3., family = "binomial")
```

```
call: glm(formula = PA1 ~ dragon$spat_dat.GO..3., family = "binomial")
```

Coefficients:

```
(Intercept)  dragon$spat_dat.GO..3.  
-21.80      20.41
```

Degrees of Freedom: 29 Total (i.e. Null); 28 Residual

Null Deviance: 27.03

Residual Deviance: 10.01 AIC: 14.01

```
> plogis(-21.800+20.414)-plogis(-21.800) #difference of PA for dragons
```

```
[1] 0.2000471 #You are 20% more likely to see a dragon if there's a castle?
```

```

> abundance2<-dragon$abundance[which(dragon$abundance>0)] #model only
those greater than zero
> castle<-dragon$spat_dat.GO..3.[which(dragon$abundance>0)] #make dat
a frames the same length
> glm(abundance2~castle, family= "poisson") #hurdle model is a good
way to model data if you think drivers can be seperated.

```

```

Call:  glm(formula = abundance2 ~ castle, family = "poisson")

```

```

Coefficients:

```

```

(Intercept)      castle
      1.0800      -0.1044

```

```

Degrees of Freedom: 4 Total (i.e. Null);  3 Residual

```

```

Null Deviance:      3.942

```

```

Residual Deviance: 3.838    AIC: 20.98

```

```

> exp(1.0799-0.1044)-exp(1.0799)

```

```

[1] -0.291892

```

- i. I would plot the autocorrelation of response variable and make a spatial autocorrelation map. If I plotted lupin counts and locations, then I could get an estimate of phi from my lupin density distribution.