MPulleyM2Q5

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2024-04-23

Download and read the orchid dataset that we used for the original logisticlab:

```
orchid=readRDS("orchid.RDS")
orchid$habitat = as.factor(orchid$habitat)
summary(orchid)
```

```
##     presence         abundance       elevation       habitat
##  Min.   :0.0000   Min.   : 0.00   Min.   : 12.00   Maple:10
##  1st Qu.:0.2500   1st Qu.: 0.25   1st Qu.: 69.25   Oak  :10
##  Median :1.0000   Median : 4.00   Median :204.50   Pine :10
##  Mean   :0.7333   Mean   :13.30   Mean   :231.83
##  3rd Qu.:1.0000   3rd Qu.:20.00   3rd Qu.:364.75
##  Max.   :1.0000   Max.   :51.00   Max.   :489.00
```

Run the following models (assume Poisson distribution):

1. Null model
2. Effect of elevation on abundance
3. Effect of elevation and habitat on abundance (additive)
4. Interactive effect of elevation and habitat on abundance
5. Effect of habitat on abundance

```
m1 <- glm(abundance ~ 1, family = poisson(link = "log"),  data = orchid)
m2 <- glm(abundance ~ elevation, family = poisson(link = "log"),  data = orchid)
m3 <- glm(abundance ~ elevation + habitat, family = poisson(link = "log"),  data = orchid)
m4 <- glm(abundance ~ elevation*habitat, family = poisson(link = "log"),  data = orchid)
m5 <- glm(abundance ~ habitat, family = poisson(link = "log"),  data = orchid)
```

Using AICc select the best model, interpret it, and plot it

```
library(MuMIn)
```

```
## Warning: package 'MuMIn' was built under R version 4.3.3
```

```
test=AICc(m1,m2,m3,m4,m5)
best = min(test$AICc)
test
```

```
##    df     AICc
## m1  1 790.1422
## m2  2 137.3474
## m3  4 141.7287
## m4  6 146.7816
## m5  3 652.6791
```

```
best
```

```
## [1] 137.3474
```

Model 2 is the best model because it has the lowest AIC. The means that for abundance of orchids, elevation is an important explanatory variable.

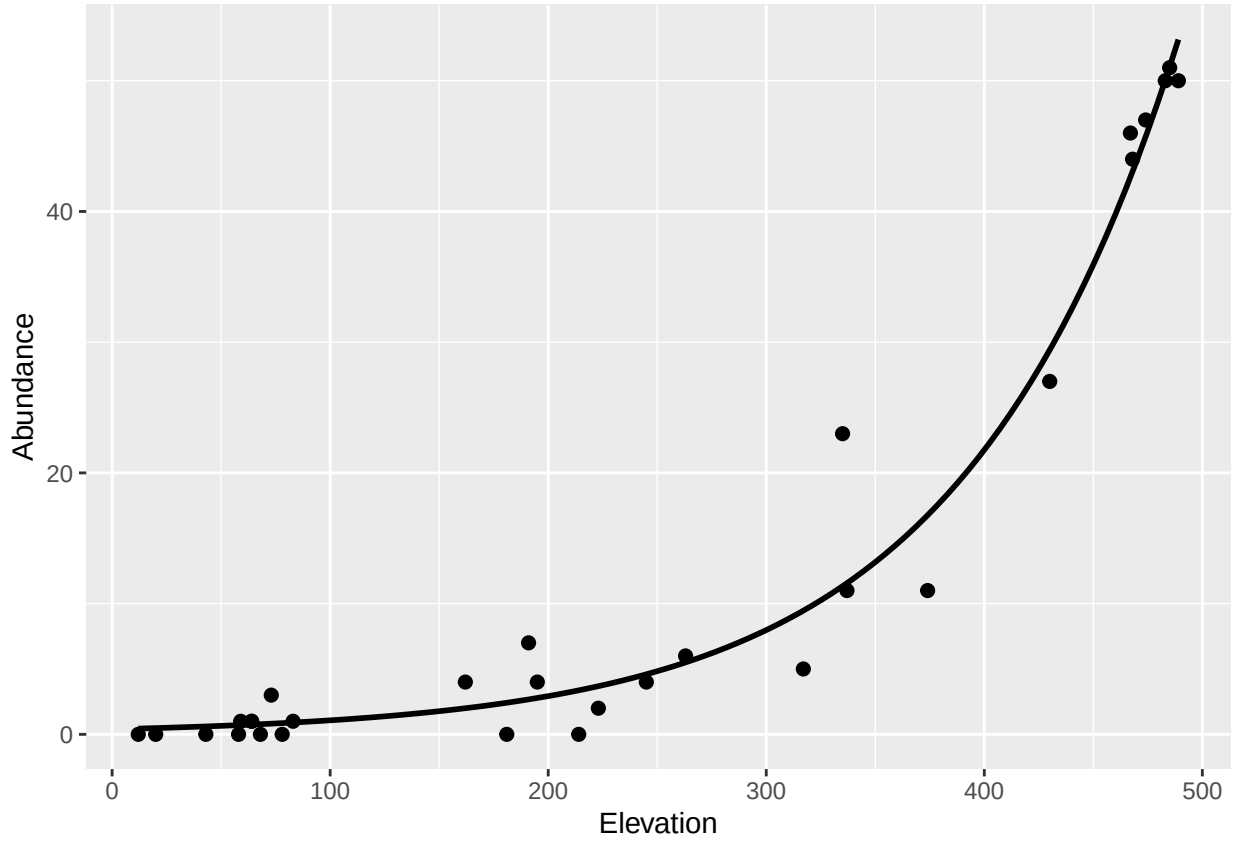
```
newdata_orchid = data.frame(abundance = seq(min(orchid$abundance),
                                            max(orchid$abundance),length=100),
                            elevation = seq(min(orchid$elevation),
                                            max(orchid$elevation),length=100),
                            show.legend = TRUE)

pred.link.full1 <- predict(m2, newdata = newdata_orchid, se.fit = TRUE)
newdata_orchid$ab <- exp(pred.link.full1$fit)

library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.3.3
```

```
ggplot() +
  geom_point(data = orchid, aes(x = elevation, y = abundance), size=2) +
  geom_path(data = newdata_orchid, aes(x = elevation, y = ab), linewidth=1) +
  xlab("Elevation") +
  ylab("Abundance")
```



Upload: AICc table, interpretation and plot.

Upload the code you used for the best model