Advanced Stats - Bank Swallow Movement

2023-04-24

## BIO8940 Final Project

### Bank swallow movements to roosting habitat

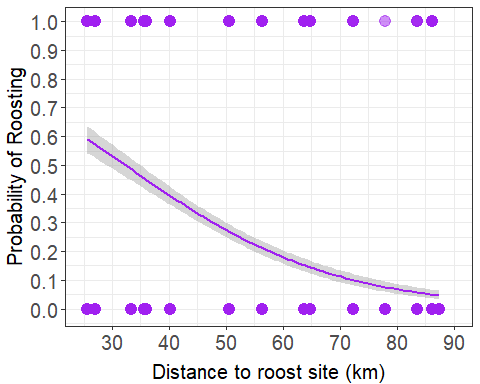
### By: Manon Veselovsky - 8259387

### Introduction:

#### Various animals across taxa are known to form aggregate groups during their lifecycle. This phenomenon can become problematic when faced with rapid environmental change and the alteration of suitable habitats where this clustering behaviour is centered. For example, during the winter, the eastern migratory monarch butterfly population forms a single roosting colony of millions of individuals in a very small region of oyamel forest in Mexico. While many factors are contributing to declining monarch butterfly populations, one of the most concerning is the human alteration of the oyamel forests which provide this roosting habitat (\_\_\_\_\_\_\_\_\_\_\_\_\_). Today, only \_\_\_\_\_\_\_\_\_\_\_ remains of the original \_\_\_\_\_\_\_\_\_\_ which could house these overwintering insects. Unfortunately, habitat alteration and loss is only projected to increase as human infrastructure expands, which is likely to continue to threaten certain habitats and species that utilize these habitats. For conservation of habitats to be effective, it is important to understand the degree to which these habitats are being used by endangered species, especially when endangered species aggregate in these areas.

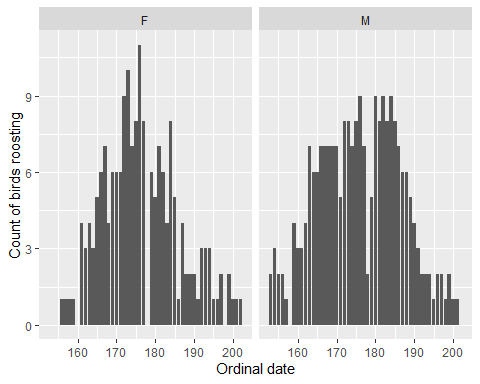
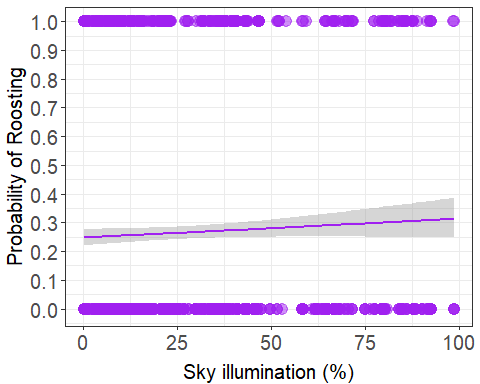
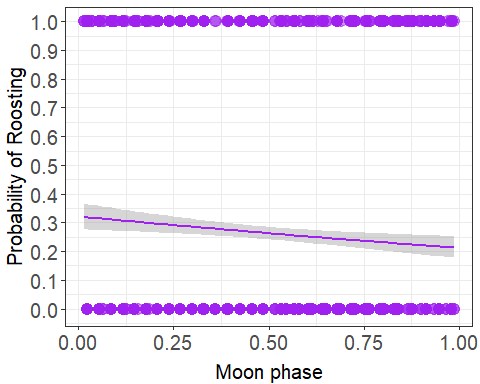
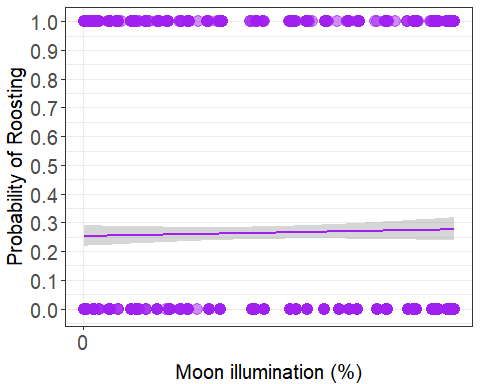
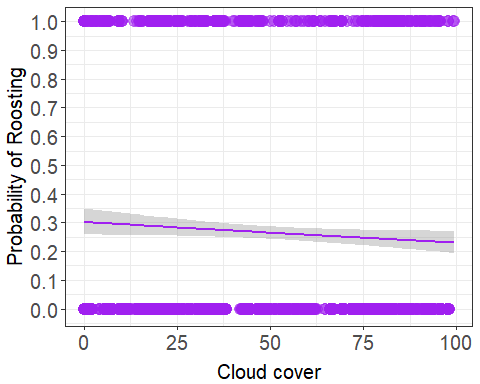
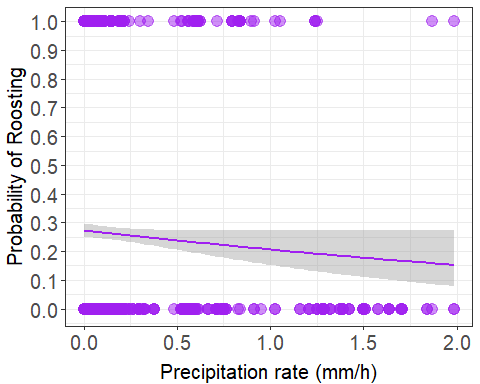
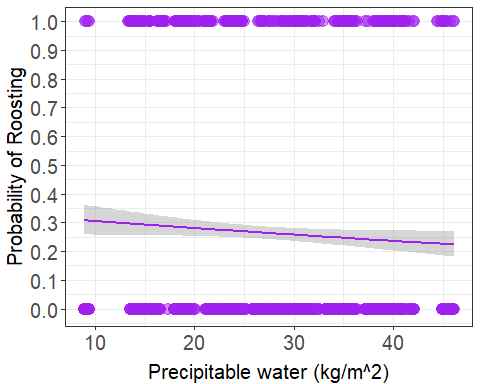
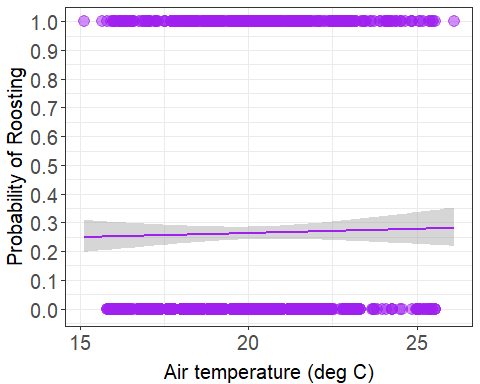
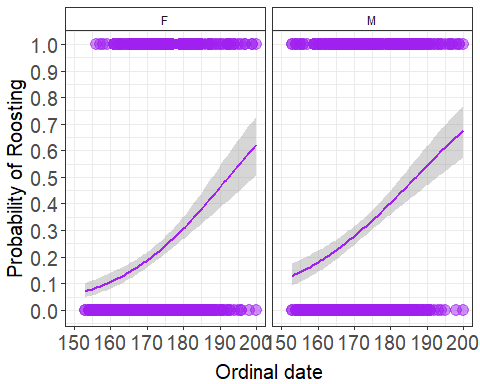
#### One highly threatened species whose aggregation ecology requries greater study is the bank swallow (Riparia riparia). The North American bank swallow has declined by \_\_\_\_\_\_\_\_\_. Much of its behavioural ecology remains unknown, a shortcoming that must be addressed if this species is to be conserved. Bank swallows form breeding colonies on the banks of lakes and in gravel pits across North America. yet much about its recently been discovered as using wetland habitats habitat that has faced significant alteration is that of wetlands in Ontario. In the 1800s, Ontario was composed of over \_\_\_\_\_\_\_\_ hectares of wetland habitats, but only \_\_\_\_\_\_\_\_\_\_ of this area remains. Wetlands are home to a host of threatened and endangered species. more surprising is that some aggregation behaviours are only just being in North America. One such example is the bank swallow (Riparia riparia), a bird native to and threatened in North America (\_\_\_\_\_\_\_). The North American bank swallow

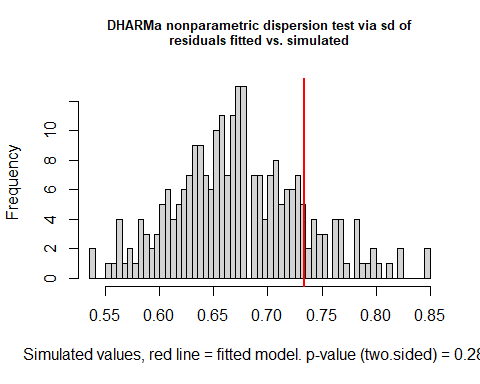
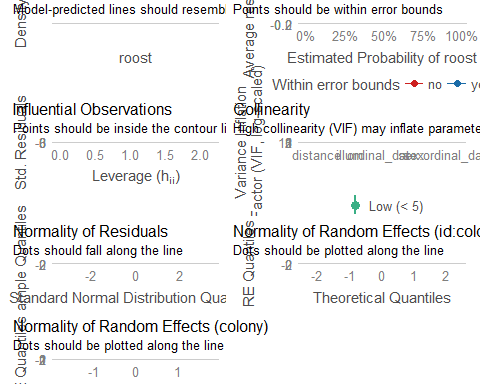
#################### SECTION 1.2 VARIABLE MODIFICATIONS + SCALED DATABASE ################  
  
# convert air temperature from Kelvin to degrees Celsius  
depart\_final$temp = depart\_final$air\_temp - 273  
  
#get lunar illumination (fraction of the moon that is illuminated) and moon phase at the time the bird was observed (movement to roost could be linked to availability of light)  
depart\_final$moon = getMoonIllumination(depart\_final$time\_departure,keep=c("fraction","phase"))  
  
# create a variable for sky illumination by combining cloud cover and illumination of the moon (moon fraction) --> a full moon has a moon fraction of 1; illum will be maximum (100%) when the moon is full and cloud cover is 0  
depart\_final$illum = depart\_final$moon.fraction\*(100-depart\_final$cloud\_cover)  
  
#convert precipitation rate from mm/s (= kg/m^2/s) to mm/h  
depart\_final$precip\_mmh = depart\_final$precip\_rate\*60\*60  
  
# make bird ID read as a factor, not integer  
depart\_final$id = as.factor(depart\_final$id)  
  
#set up a scaled database using standardize from data\_wizard (reduces problems in glmer compared to scale())  
df.scale = standardize(depart\_final,select=c("distance","ordinal\_date"))  
  
scale\_dist = scale(depart\_final$distance)  
scaleList\_dist = list(scale = attr(scale\_dist, "scaled:scale"),  
 center = attr(scale\_dist, "scaled:center"))  
  
scale\_date = scale(depart\_final$ordinal\_date)  
scaleList\_date = list(scale = attr(scale\_date, "scaled:scale"),  
 center = attr(scale\_date, "scaled:center"))



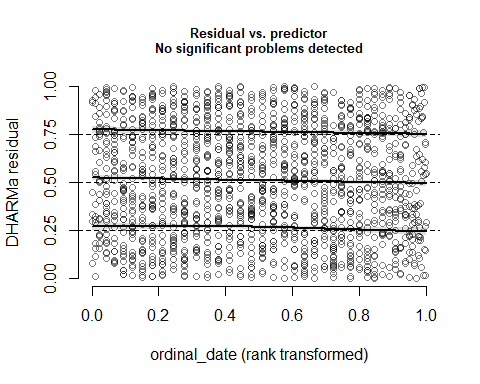
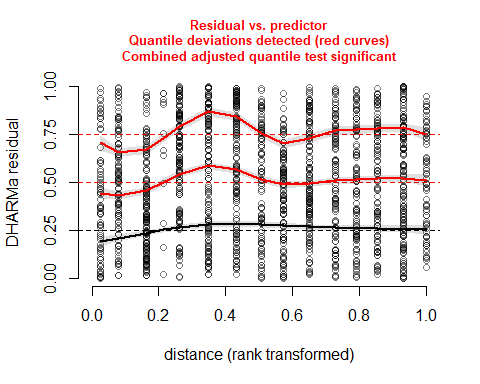
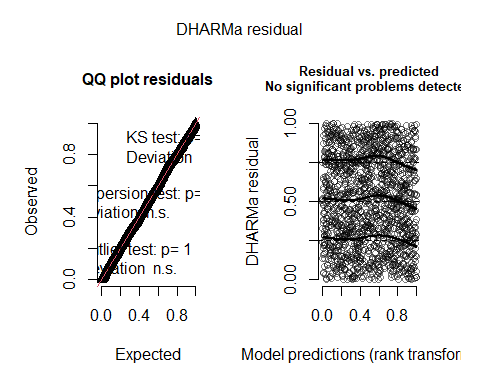
## Warning: Removed 5 rows containing non-finite values (`stat\_smooth()`).

## Warning: Removed 5 rows containing missing values (`geom\_point()`).

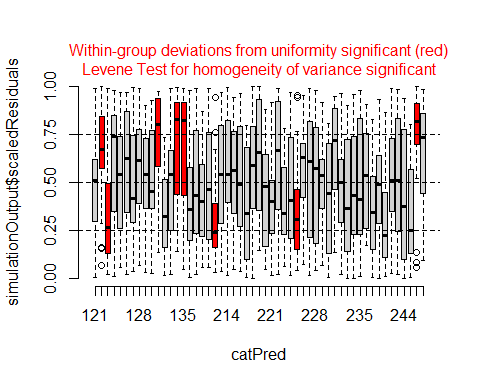
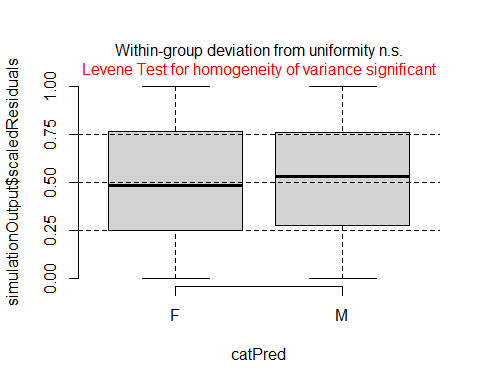




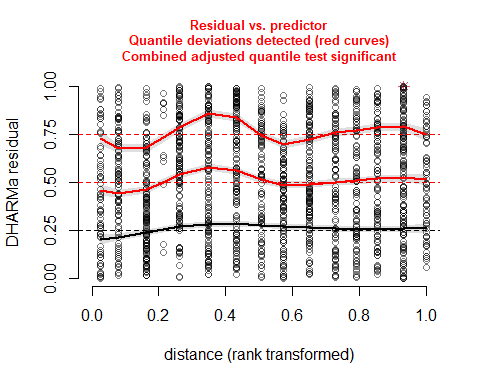
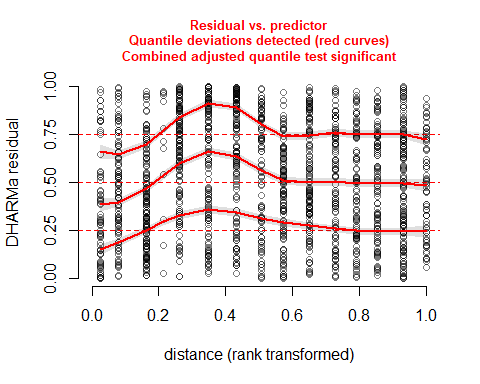
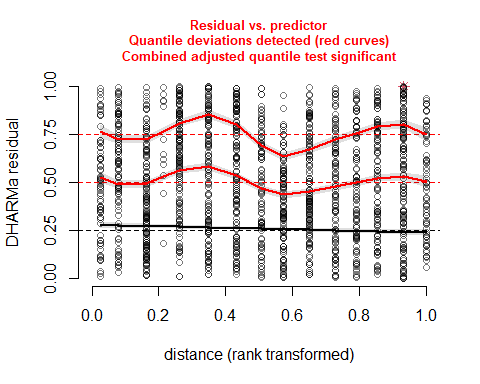
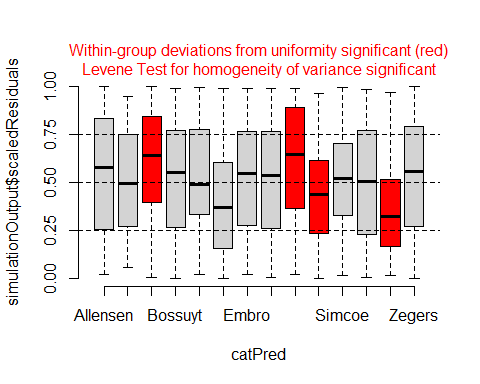
##   
## DHARMa nonparametric dispersion test via sd of residuals fitted vs.  
## simulated  
##   
## data: simulationOutput  
## dispersion = 1.0895, p-value = 0.288  
## alternative hypothesis: two.sided



## Warning in ensurePredictor(simulationOutput, form): DHARMa:::ensurePredictor:  
## character string was provided as predictor. DHARMa has converted to factor  
## automatically. To remove this warning, please convert to factor before  
## attempting to plot with DHARMa.

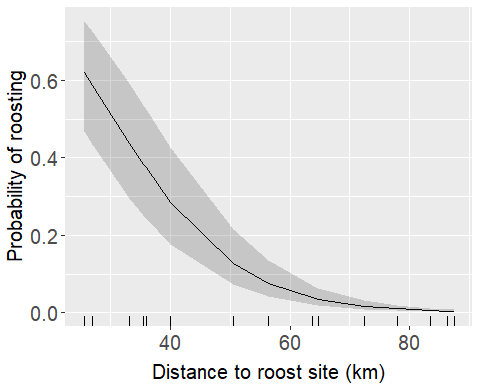


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#### Translations of distance did not help the fit of my model, however, plots are alright (per \_\_\_\_\_\_\_\_). Therefore, I will continue with

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: roost ~ distance + sex + ordinal\_date + sex:ordinal\_date + illum +   
## (1 | colony/id)  
## Data: df.scale  
##   
## AIC BIC logLik deviance df.resid   
## 1068.6 1111.6 -526.3 1052.6 1571   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -12.1991 -0.3228 -0.1231 0.1793 14.6400   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## id:colony (Intercept) 1.6419 1.2814   
## colony (Intercept) 0.6189 0.7867   
## Number of obs: 1579, groups: id:colony, 54; colony, 14  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.489848 0.383874 -6.486 8.81e-11 \*\*\*  
## distance -2.019687 0.315909 -6.393 1.62e-10 \*\*\*  
## sexM 0.724532 0.427975 1.693 0.0905 .   
## ordinal\_date 1.630949 0.160221 10.179 < 2e-16 \*\*\*  
## illum -0.003178 0.003160 -1.006 0.3146   
## sexM:ordinal\_date -0.455592 0.207049 -2.200 0.0278 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) distnc sexM ordnl\_ illum   
## distance 0.214   
## sexM -0.517 -0.067   
## ordinal\_dat -0.168 -0.173 0.120   
## illum -0.202 -0.022 -0.014 -0.116   
## sxM:rdnl\_dt 0.108 0.058 -0.128 -0.727 0.004



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