Advanced Stats - Bank Swallow Movement

2023-04-24

## BIO8940 Final Project

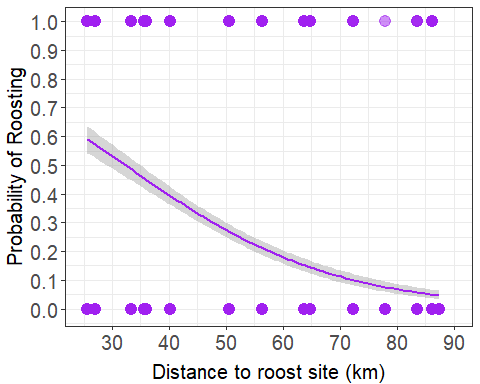
### Bank swallow movements to roosting habitat

### By: Manon Veselovsky - 8259387

### Introduction:

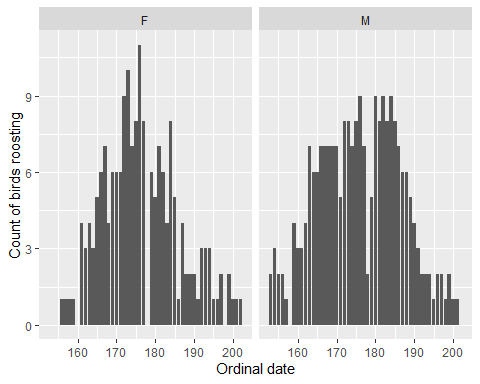
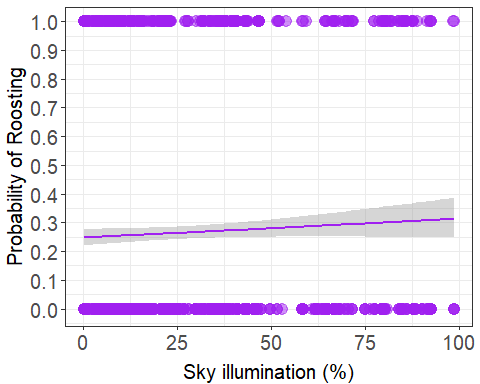
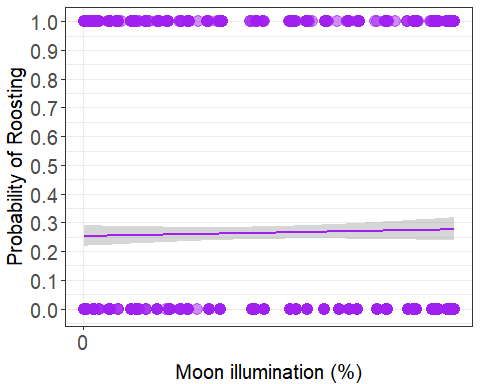
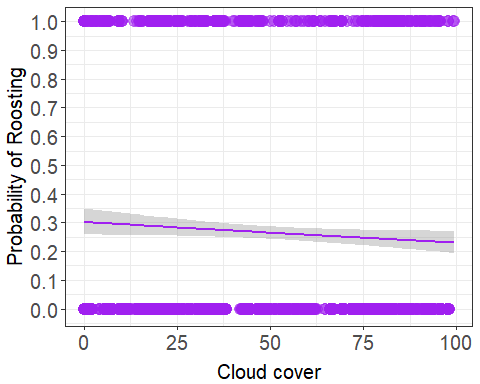
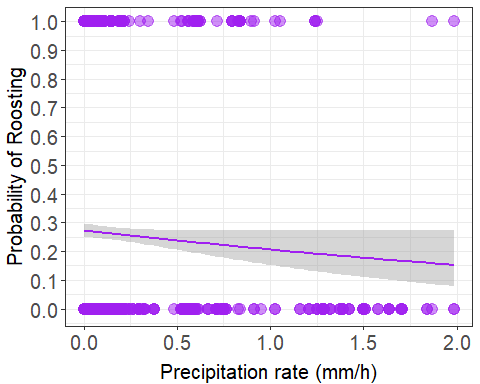
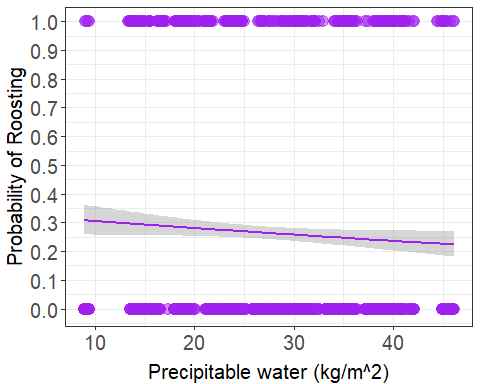
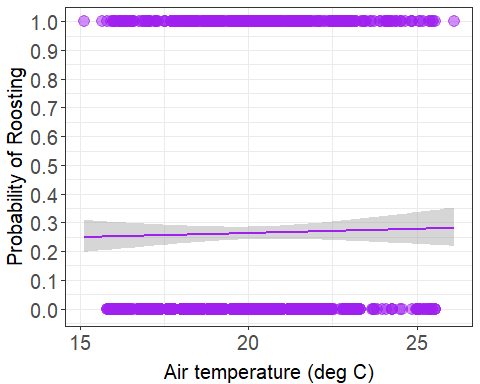
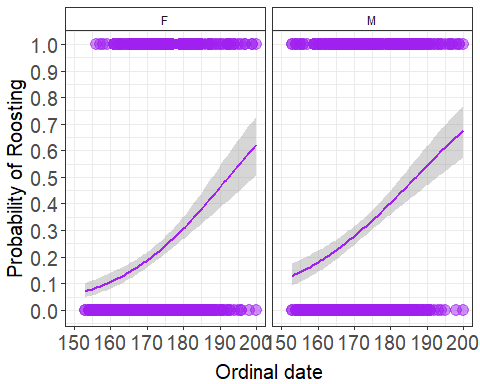
### Various animals across taxa are known to form aggregate groups during their lifecycle. This phenomenon can become problematic when faced with rapid environmental change and the alteration of suitable habitats where this clustering behaviour is centered. For example, during the winter, the eastern 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



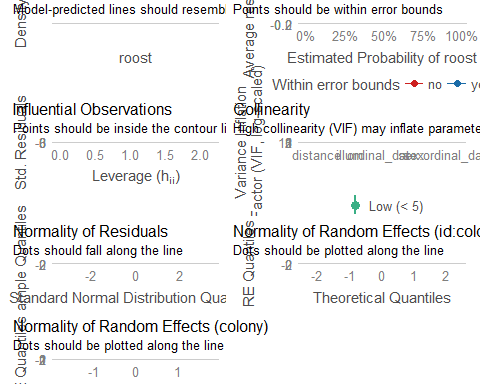
## Warning: Removed 5 rows containing non-finite values (`stat\_smooth()`).

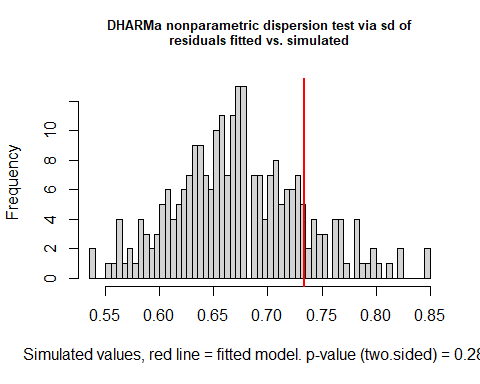
## Warning: Removed 5 rows containing missing values (`geom\_point()`).



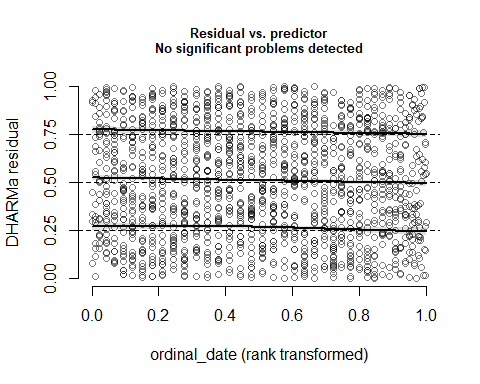
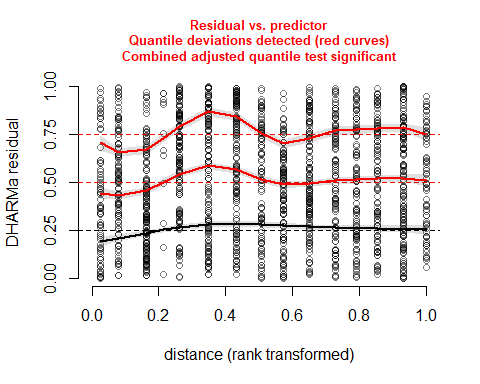
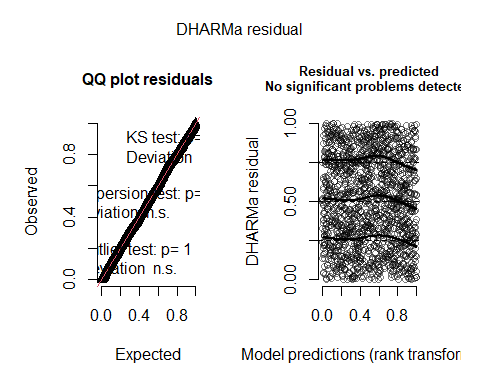
################### SECTION 1.4 MODEL BUILDING AND DIAGNOSTIC PLOTS ####################  
# model has problems using unscaled data, use df.scale (df where distance and ordinal date were scaled and centered)  
m = glmer(roost ~ distance + sex + ordinal\_date + sex:ordinal\_date + illum + (1|colony/id), data=df.scale, family="binomial",na.action=na.omit)

### First, I will examine the normality of the residuals from the random variables using the performance package check\_model() function.

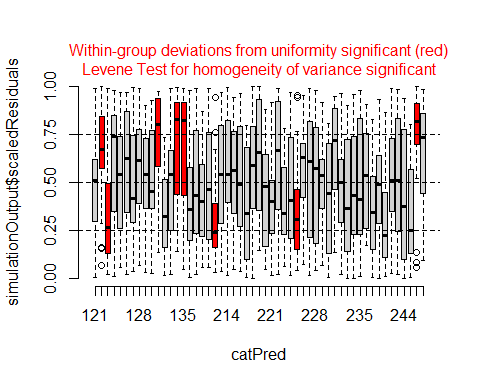
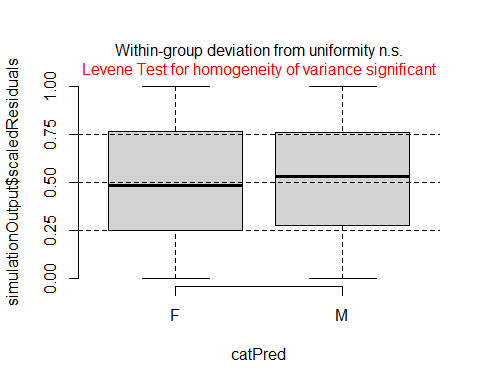




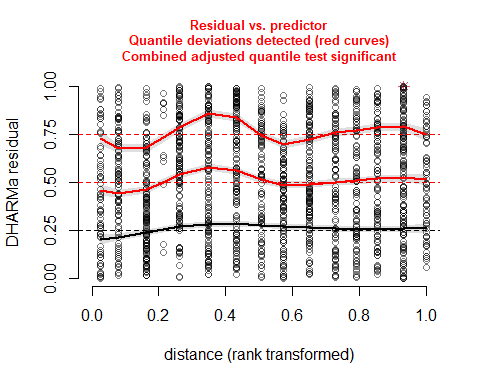
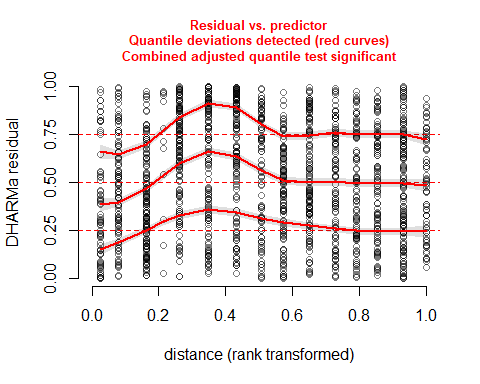
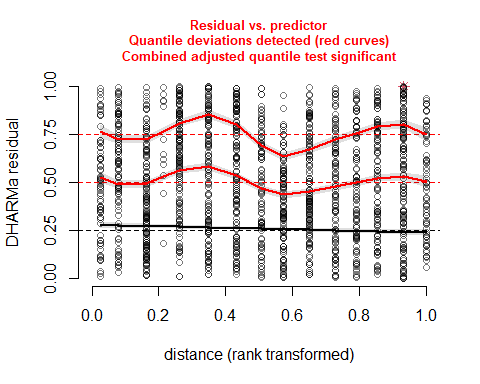
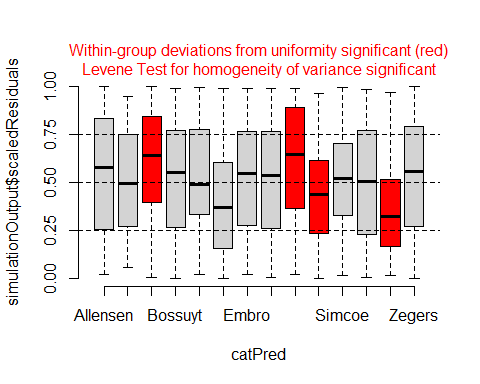
##   
## DHARMa nonparametric dispersion test via sd of residuals fitted vs.  
## simulated  
##   
## data: simulationOutput  
## dispersion = 1.0895, p-value = 0.288  
## alternative hypothesis: two.sided



## 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.

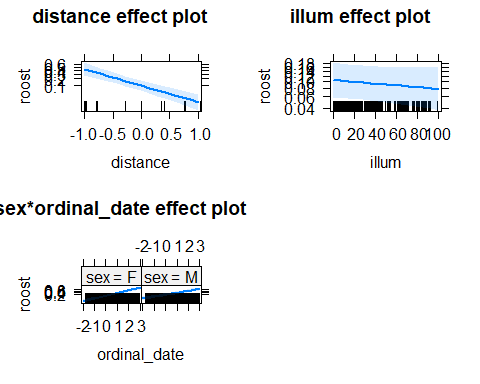


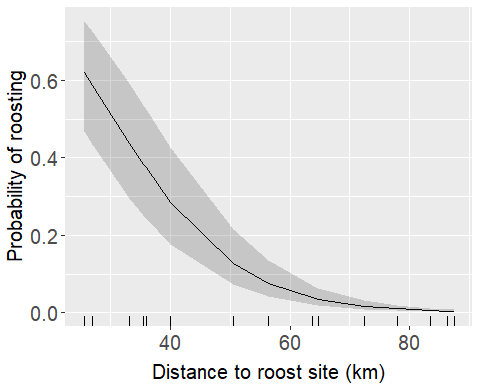
## Warning in ensurePredictor(simulationOutput, form): DHARMa:::ensurePredictor:  
## character string was provided as predictor. DHARMa has converted to factor  
## automatically. To remove this warning, please convert to factor before  
## attempting to plot with DHARMa.



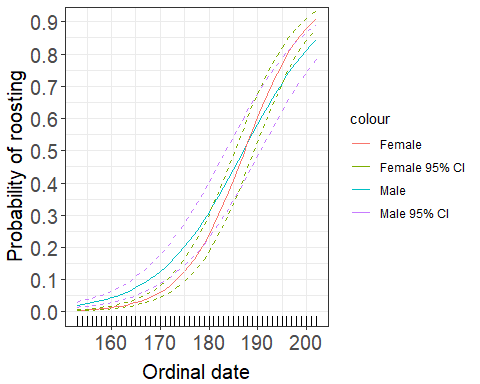
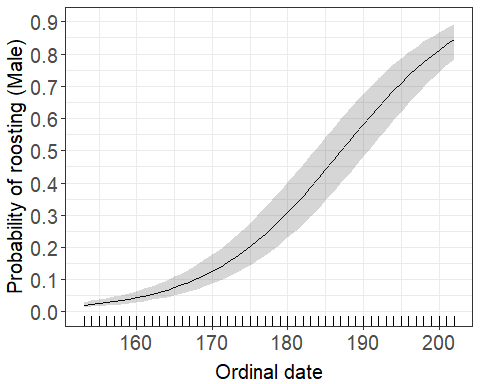
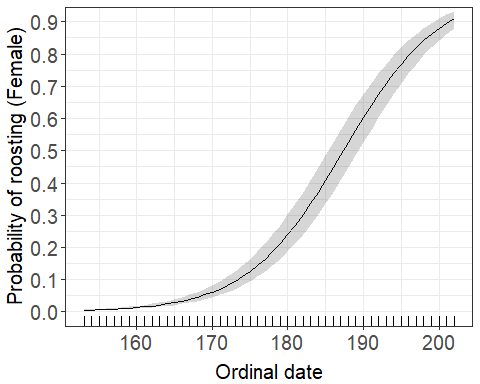
### Translations of distance did not help the fit of my model, however, plots are alright (per \_\_\_\_\_\_\_\_). Therefore, I will continue with my original model. I will now look at the effects of the model, first on the logit scale.

## 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   
## -12.1989 -0.3228 -0.1231 0.1793 14.6402   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## id:colony (Intercept) 1.6418 1.2813   
## 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) -2.489846 0.383877 -6.486 8.81e-11 \*\*\*  
## distance -2.019681 0.315913 -6.393 1.63e-10 \*\*\*  
## sexM 0.724513 0.427978 1.693 0.0905 .   
## ordinal\_date 1.630962 0.160222 10.179 < 2e-16 \*\*\*  
## illum -0.003178 0.003160 -1.006 0.3146   
## sexM:ordinal\_date -0.455616 0.207049 -2.201 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

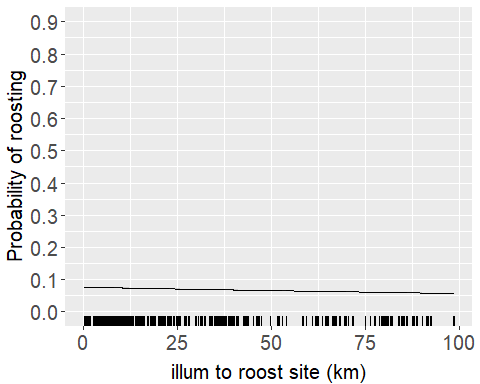
 ### There is a significant relationship with each variable except for the night sky illumination % (illum). However, the effect size is hard to elucidate here as these estimates are on a logistic scale, and on variables that have been scaled (ordinal date and distance). Below I will back-transform these to the observed scale.

 ### Here, we can see that the distance to the wetland site has a significant effect on whether the wetland roost will be used. If the wetland habitat is within 10 km, the swallows are estimated to use them to roost at night 50%-60% of the time. There is a significant drop in roosting use with distance to the wetland. At >50 km from the colony, the birds will only use the roost at an estimated mean of ~13% of the time (with 95% confidence interval maximum being ~22%), 1/4th the use of wetlands within 10 km. Beyond this, the wetland begins to be used <10% of the time. ### I will continue with my exploration of effects, looking at the interaction of the bird’s sex and the ordinal date of the season next.

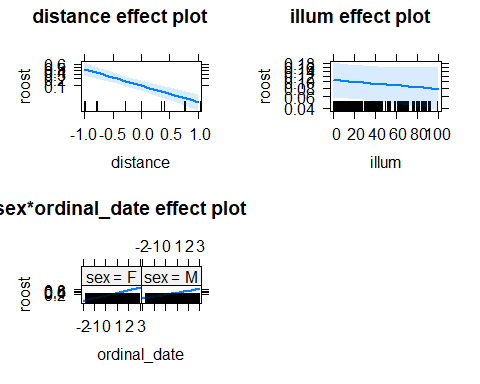
## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
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## Groups Name Variance Std.Dev.  
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## Number of obs: 1579, groups: id:colony, 54; colony, 14  
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## sexM:ordinal\_date -0.455616 0.207049 -2.201 0.0278 \*   
## ---  
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##   
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## (Intr) distnc sexM ordnl\_ illum   
## distance 0.214   
## sexM -0.517 -0.067   
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## sxM:rdnl\_dt 0.108 0.058 -0.128 -0.727 0.004

 ### Here we can see the effect of the interaction sex and ordinal date. Before the ordinal date of 171, there is no overlap of 95% CIs between the two sexes. During this early breeding season period, males use wetlands to roost significantly more often. At ordinal date 170, it’s estimated that ~12.5% of males are using the wetlands to roost at night, in contrast to only ~6% of females. This shows twice as many males using the wetlands compared to females in the early breeding period. This greater use of roosts by males was previously observed in a small sample of bank swallows (n = 12) in this same study system (@Falconer2016). It is hypothesized that this difference could be due to females having to provide warmth to their young. Before 8 days old, chicks are unable to regulate their own body temperature, and rely on the warmth from their mother (@Marsh1979). Thus, females likely cannot leave the colony to roost before this period is over. ### We see that this greater use of wetlands by males compared to females continues for the majority of the breeding season, although after day 171 this difference is not as significant (overlap of the 95% CIs). Interestingly, it seems that males and females could be swapping their overall use of the wetland late in the season, with the mean estimate for females beginning to exceed that of males around ordinal date 187. After this, the estimated use of wetlands by females is about 1/10th greater than males. However, the 95% CIs do overlap here, indicating this observation could be due to chance.

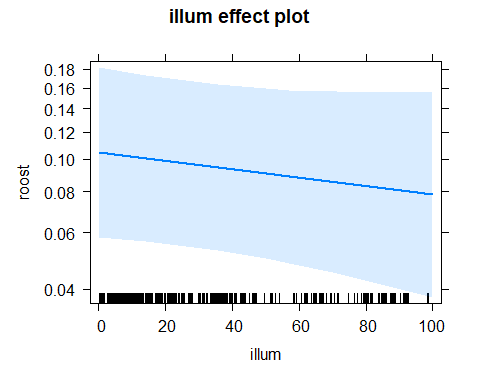
#get the same plot for males (this is the interaction component of sex:ordinal\_date)  
df.scale$illum\_logit\_ypred = -2.489848 - 0.003178\*depart\_final$illum #get the predicted value on the logit scale  
df.scale$illum\_logit\_upper = df.scale$illum\_logit\_ypred+0.003160\*1.96 #get upper confidence interval on logit  
df.scale$illum\_logit\_lower = df.scale$illum\_logit\_ypred-0.003160\*1.96 #get lower CI on logit  
  
#convert these values to the observed scale  
depart\_final$illum\_ypred = 1 / (1 + exp(-df.scale$illum\_logit\_ypred))  
depart\_final$illum\_upper = 1 / (1 + exp(-df.scale$illum\_logit\_upper))  
depart\_final$illum\_lower = 1 / (1 + exp(-df.scale$illum\_logit\_lower))  
  
ggplot(depart\_final,aes(illum,illum\_ypred,  
 ymin=illum\_lower,ymax=illum\_upper,legend="FALSE",  
 ))+  
 geom\_line()+theme(legend.position="none")+  
 geom\_ribbon(alpha=0.2,colour=NA)+ylab("Probability of roosting")+xlab("illum to roost site (km)")+  
 geom\_rug(sides="b") + theme(strip.background = element\_rect(fill="white"),axis.title.x=element\_text(size=15, vjust=-0.4), axis.title.y=element\_text(size=15, vjust=1.5),axis.text.x=element\_text(size=15), axis.text.y=element\_text(size=15))+ scale\_y\_continuous(breaks=c(0,0.10,0.20,0.30,0.40,0.50,0.60,0.70,0.80,0.90,1))+coord\_cartesian(ylim = c(0, 0.9))



plot(allEffects(m))



plot(effect("illum",m))



effects\_m = allEffects(m)  
effect\_dist = as.data.frame(effects\_m$distance)  
effect\_dist\_unscaled = effect\_dist  
effect\_dist\_unscaled$distance = effect\_dist$distance\*scaleList\_dist$scale + scaleList\_dist$center  
effect\_dist\_unscaled

## distance fit se lower upper  
## 1 35.52936 0.44901959 0.098708260 0.271580043 0.64045865  
## 2 41.79056 0.30777605 0.074088290 0.183604316 0.46780508  
## 3 56.50440 0.09670252 0.027862518 0.054187969 0.16669416  
## 4 71.00954 0.02562842 0.010592600 0.011323578 0.05696309  
## 5 77.27075 0.01414713 0.006881899 0.005426037 0.03637273

ggplot(effect\_dist\_unscaled,aes(distance,fit,  
 ymin=lower,ymax=upper,legend="FALSE",  
 ))+  
 geom\_line()+theme(legend.position="none")+  
 geom\_ribbon(alpha=0.2,colour=NA)+ylab("Probability of roosting")+xlab("Distance to roost site (km)")+  
 geom\_rug(sides="b") + theme(strip.background = element\_rect(fill="white"),axis.title.x=element\_text(size=15, vjust=-0.4), axis.title.y=element\_text(size=15, vjust=1.5), axis.text.x=element\_text(size=15), axis.text.y=element\_text(size=15))

