

# Pallids in Noise Supplement

8/9/2020

```
##reading in video data
dat1<-read.csv("BatsInNoise_8-5.csv")
dat1$Bat<-as.factor(dat1$Bat)

###reading in audio data
dat3<-read.csv("Echolocation_BatsInNoise_8-5.csv")
dat3$Bat<-as.factor(dat3$Bat)
dat3<-droplevels(subset(dat3, Attempt!="0"))
```

## Attempt models

The following models test the effect of noise on bats' willingness to make a foraging attempt

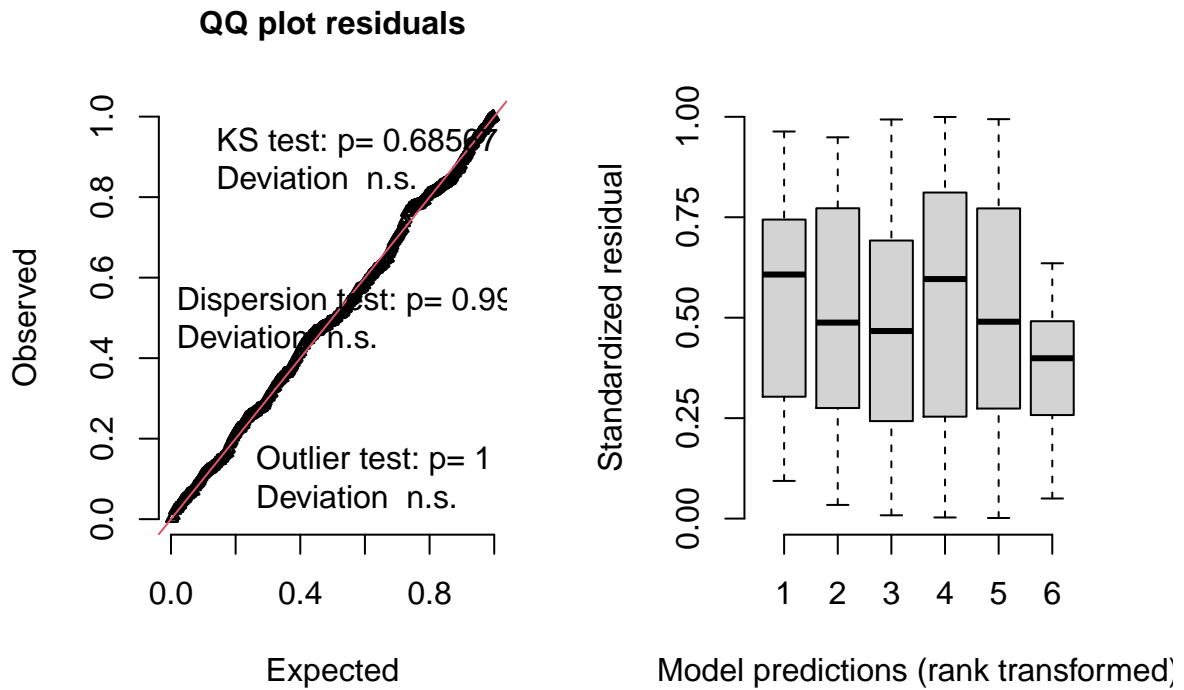
```
##reording levels of Treatment
dat1$Treatment<-factor(dat1$Treatment, levels=c("Ambient", "Overlapping", "Non-overlapping"))

###Model testing the effect of prey reward on trial outcome###
Attempt_mod1<-glm(Attempt~Treatment*MW_absent, family=binomial(link="logit"), data=dat1)
summary(Attempt_mod1)
```

```
##
## Call:
## glm(formula = Attempt ~ Treatment * MW_absent, family = binomial(link = "logit"),
##      data = dat1)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.1656   0.1157   0.1157   0.7409   0.9794
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)         5.004      1.003   4.987 6.12e-07 ***
## TreatmentOverlapping    -3.773      1.028  -3.671 0.000241 ***
## TreatmentNon-overlapping -3.851      1.025  -3.757 0.000172 ***
## MW_absent             11.562     799.849   0.014 0.988467
## TreatmentOverlapping:MW_absent -12.307     799.849  -0.015 0.987724
## TreatmentNon-overlapping:MW_absent -12.022     799.849  -0.015 0.988008
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 388.19  on 437  degrees of freedom
## Residual deviance: 323.55  on 432  degrees of freedom
```

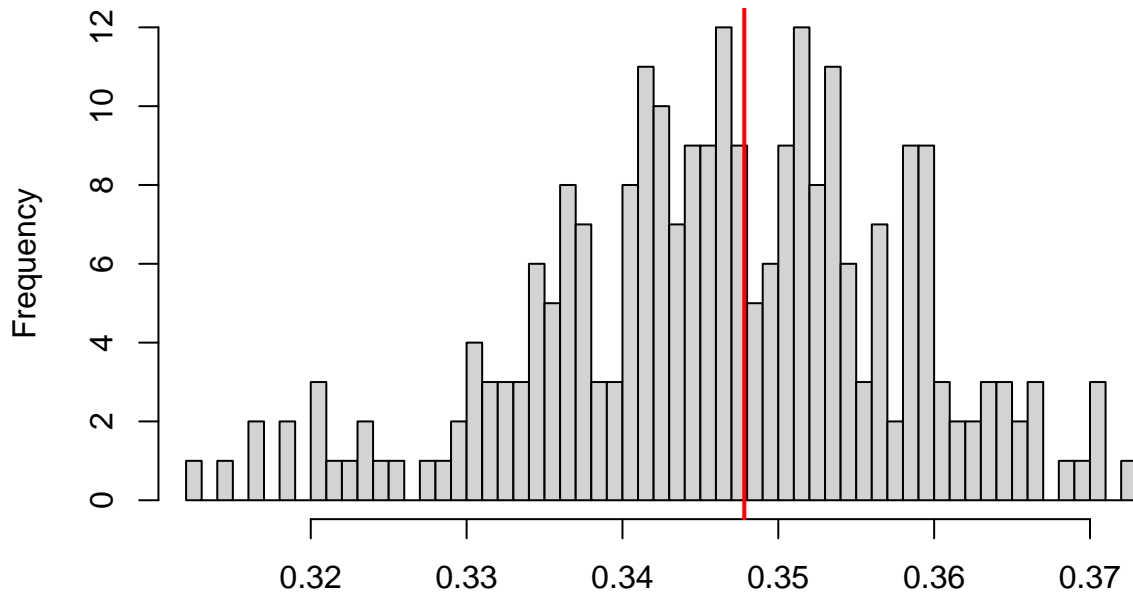
```
## AIC: 335.55
##
## Number of Fisher Scoring iterations: 15
#checking model fit
check_mod_AT1 <- simulateResiduals(fittedModel = Attempt_mod1, n=1000, plot=T)
```

### DHARMA residual diagnostics



```
testDispersion(Attempt_mod1)
```

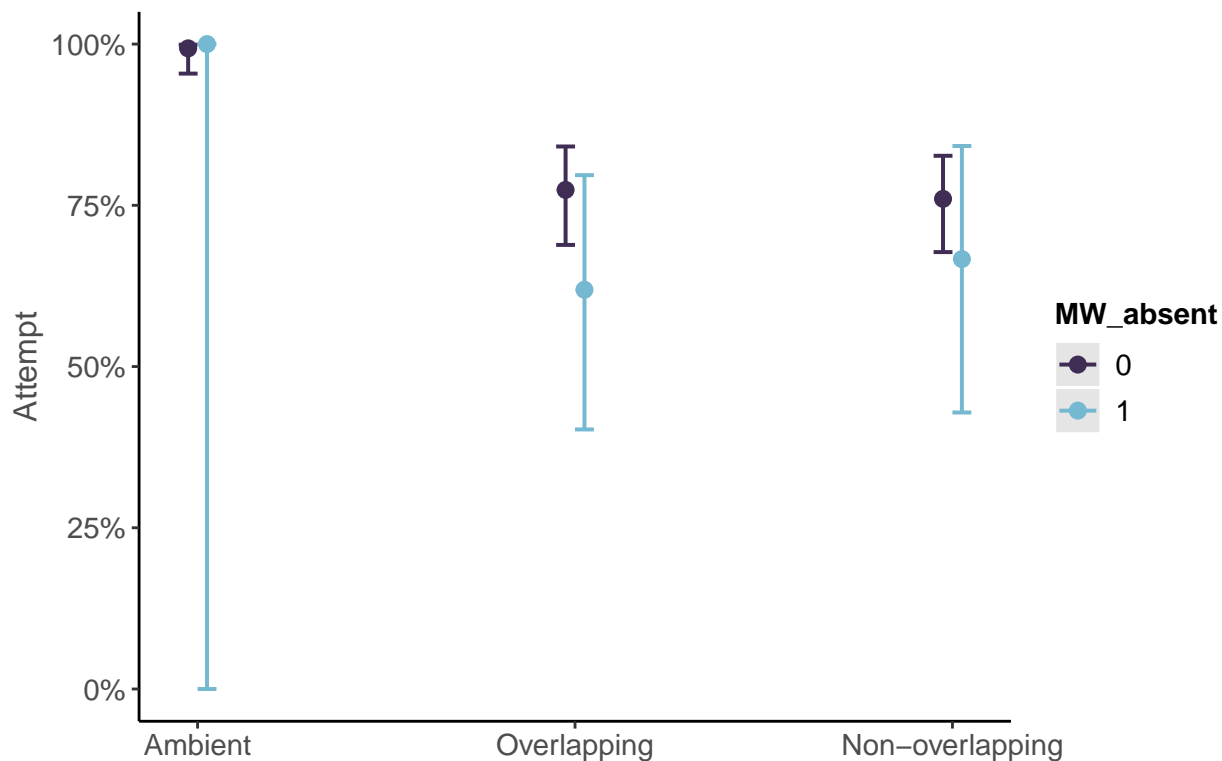
DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.912

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## ratioObsSim = 1.0045, p-value = 0.912
## alternative hypothesis: two.sided

#Interaction plot for prey reward --> perfect separation in Ambient condition
set_theme(base=theme_classic())
plot_model(Attempt_mod1, type="int", transform="plogis", colors="ipsum")+
labs(caption="Interaction between treatment and the presence of a prey reward on the board. We find
no difference in probability of attempting capture across treatments with or without a prey item.",
title=element_blank()+theme(axis.title.x=element_blank()))
```



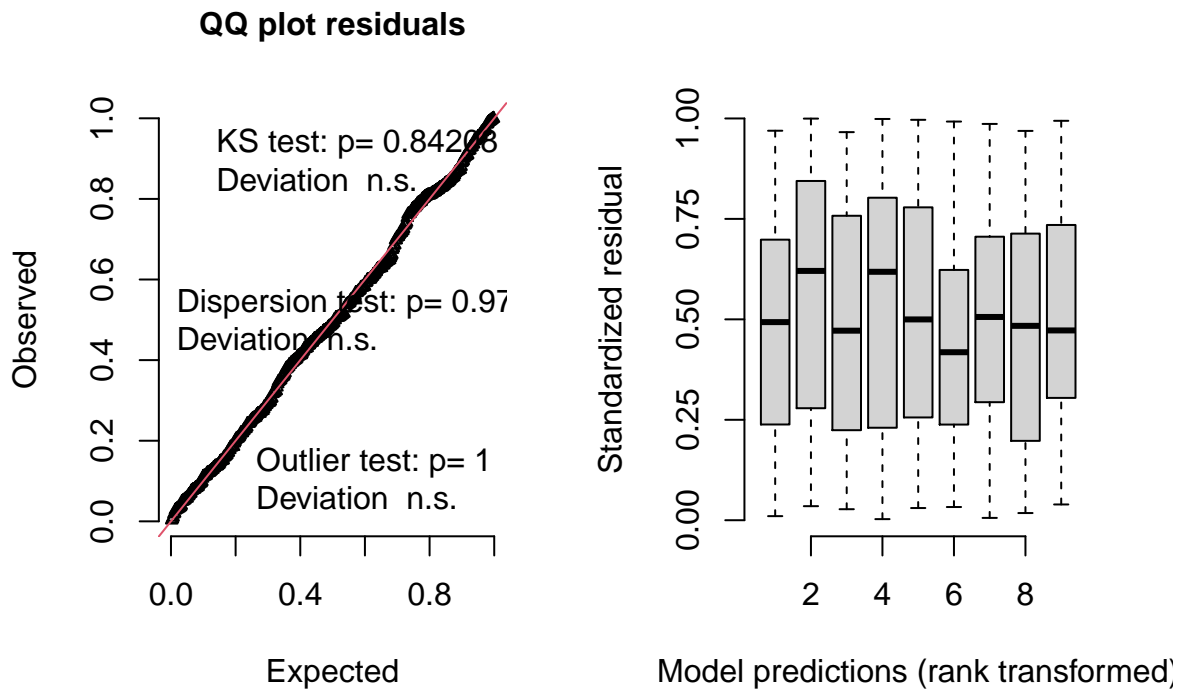
Interaction between treatment and the presence of a prey reward on the board. We find no difference in probability of attempting capture across treatments with or without a prey item.

```
###Model testing the effect of bat ID on trial outcome###
Attempt_mod2<-glm(Attempt~Treatment*Bat, family=binomial(link="logit"), data=dat1)
summary(Attempt_mod2)
```

```
##
## Call:
## glm(formula = Attempt ~ Treatment * Bat, family = binomial(link = "logit"),
## data = dat1)
##
## Deviance Residuals:
## Min 1Q Median 3Q Max
## -2.81790 0.00013 0.19518 0.70896 0.90052
##
## Coefficients:
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) 1.857e+01 8.960e+02 0.021 0.983
## TreatmentOverlapping -1.731e+01 8.960e+02 -0.019 0.985
## TreatmentNon-overlapping -1.787e+01 8.960e+02 -0.020 0.984
## Bat2 -1.461e+01 8.960e+02 -0.016 0.987
## Bat3 1.628e-08 1.267e+03 0.000 1.000
## TreatmentOverlapping:Bat2 1.461e+01 8.960e+02 0.016 0.987
## TreatmentNon-overlapping:Bat2 1.577e+01 8.960e+02 0.018 0.986
## TreatmentOverlapping:Bat3 -4.261e-01 1.267e+03 0.000 1.000
## TreatmentNon-overlapping:Bat3 2.973e-01 1.267e+03 0.000 1.000
##
## (Dispersion parameter for binomial family taken to be 1)
```

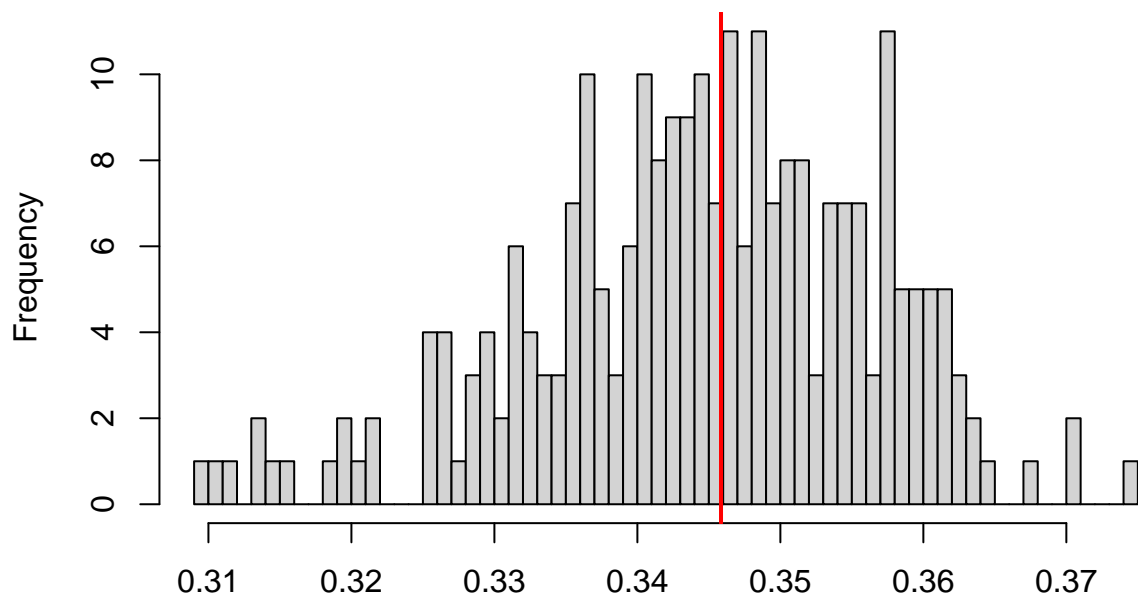
```
##
## Null deviance: 388.19 on 437 degrees of freedom
## Residual deviance: 317.85 on 429 degrees of freedom
## AIC: 335.85
##
## Number of Fisher Scoring iterations: 17
#checking model fit
check_mod_AT2 <- simulateResiduals(fittedModel = Attempt_mod2,n=1000, plot=T)
```

### DHARMA residual diagnostics



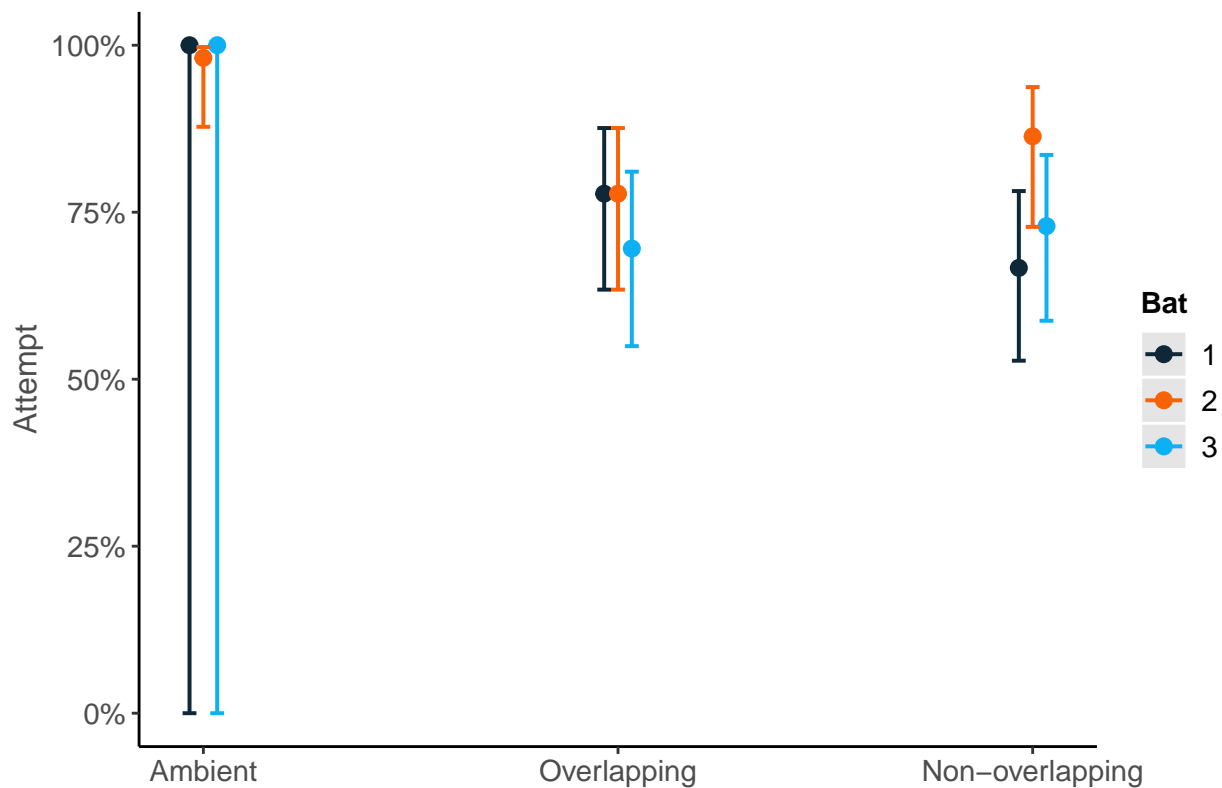
```
testDispersion(Attempt_mod2)
```

### DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.952

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## ratioObsSim = 1.004, p-value = 0.952
## alternative hypothesis: two.sided
#Interaction plot for bat ID
plot_model(Attempt_mod2, type="int", transform="plogis", colors="system", ci.lvl=0.95)+
  labs(caption="Interaction between treatment type and bat ID. Bats do not differ from each other across
         title=element_blank()+theme(axis.title.x=element_blank())
```



Interaction between treatment type and bat ID. Bats do not differ from each other across treatments.

```
###Model testing the effect of experimental Night on trial outcome###
Attempt_mod3<-glm(Attempt~Treatment*Night, family=binomial(link="logit"), data=dat1)

summary(Attempt_mod3)
```

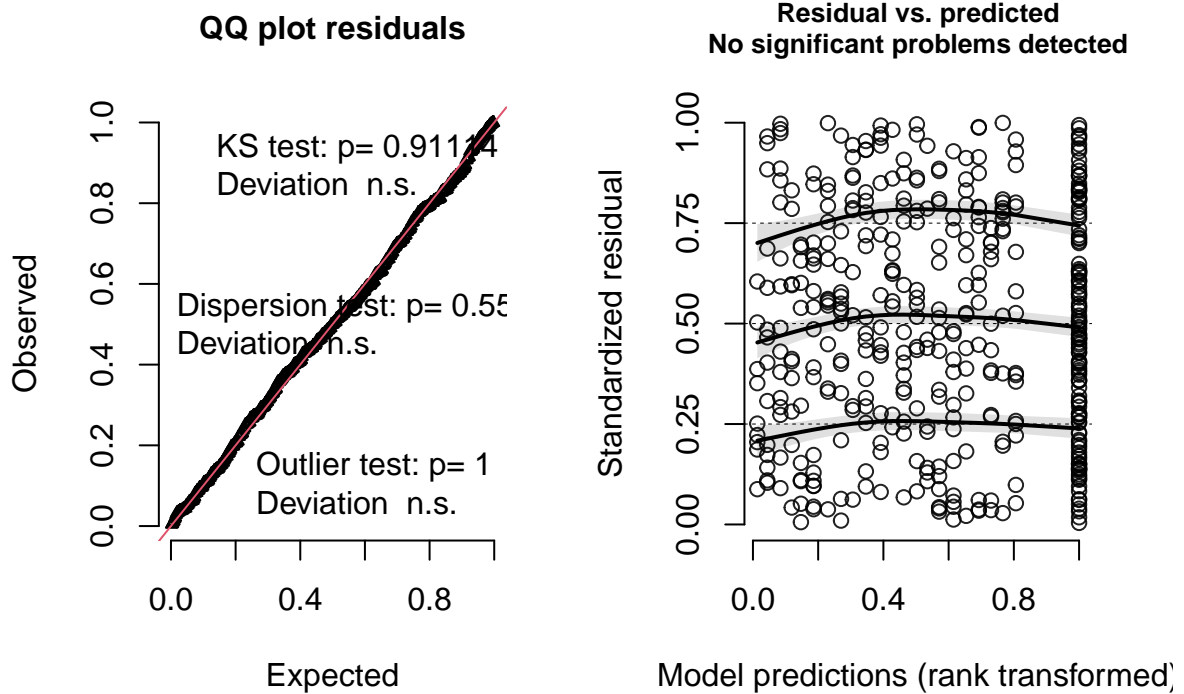
```
##
## Call:
## glm(formula = Attempt ~ Treatment * Night, family = binomial(link = "logit"),
## data = dat1)
##
## Deviance Residuals:
## Min 1Q Median 3Q Max
## -2.5308 0.0000 0.2881 0.6117 1.2516
##
## Coefficients:
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) 154.37 10817.18 0.014 0.989
## TreatmentOverlapping -155.33 10817.18 -0.014 0.989
## TreatmentNon-overlapping -154.87 10817.18 -0.014 0.989
## Night -15.18 1081.72 -0.014 0.989
## TreatmentOverlapping:Night 15.59 1081.72 0.014 0.988
## TreatmentNon-overlapping:Night 15.51 1081.72 0.014 0.989
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 388.19 on 437 degrees of freedom
```

```
## Residual deviance: 276.08 on 432 degrees of freedom
## AIC: 288.08
##
## Number of Fisher Scoring iterations: 21
```

```
#checking model fit
```

```
check_mod_AT3 <- simulateResiduals(fittedModel = Attempt_mod3, n=1000, plot=T)
```

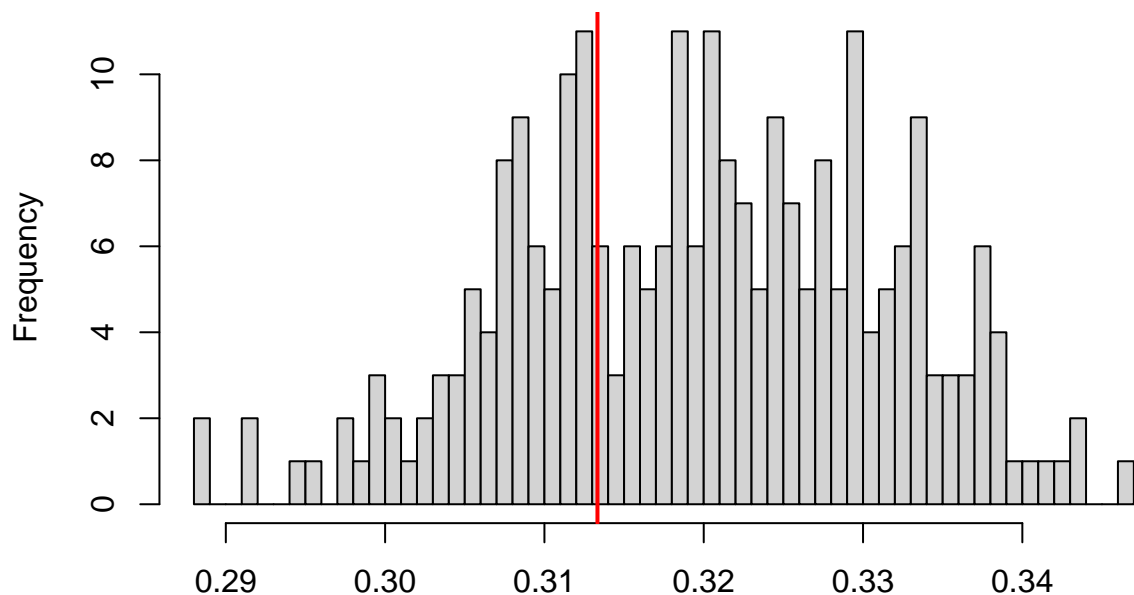
### DHARMA residual diagnostics



```
testDispersion(Attempt_mod3)
```



### DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.664

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## ratioObsSim = 0.98019, p-value = 0.664
## alternative hypothesis: two.sided

##Success Models

The following models test the effect of noise on bats' ability to successfully localize prey. That is, the
probability of landing on the correct speaker playing the prey cue

#subsetting to keep only trials where bats made an attempt
dat2 <-droplevels(subset(dat1, Attempt!="0"))

###Model testing the effect of prey reward on trial outcome###
success_mod1<-glmer(Success~Treatment*MW_absent+(1|Bat), family=binomial(link="logit"), data=dat2)
summary(success_mod1)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Success ~ Treatment * MW_absent + (1 | Bat)
## Data: dat2
##
##      AIC      BIC   logLik deviance df.resid
## 348.1    375.4  -167.0   334.1     360
```

```

##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.1653 -0.6547  0.2112  0.2557  1.6422
##
## Random effects:
##   Groups Name          Variance Std.Dev.
##   Bat      (Intercept) 0.05228  0.2287
## Number of obs: 367, groups: Bat, 3
##
## Fixed effects:
##                                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)                        2.8962    0.3891   7.444 9.8e-14 ***
## TreatmentOverlapping                -3.5742    0.4304  -8.304 < 2e-16 ***
## TreatmentNon-overlapping            -3.7192    0.4297  -8.656 < 2e-16 ***
## MW_absent                          -1.6997    0.8889  -1.912 0.05585 .
## TreatmentOverlapping:MW_absent      3.2017    1.1004   2.909 0.00362 **
## TreatmentNon-overlapping:MW_absent  2.7888    1.0864   2.567 0.01026 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Trtmn0 TrtmN- MW_bsn TO:MW_
## TrtmntOvrp -0.801
## TrtmntNn-vr -0.802  0.727
## MW_absent   -0.393  0.356  0.356
## Trtmnt0:MW_  0.319 -0.397 -0.290 -0.810
## TrtmnN-:MW_  0.316 -0.286 -0.394 -0.811  0.655

```

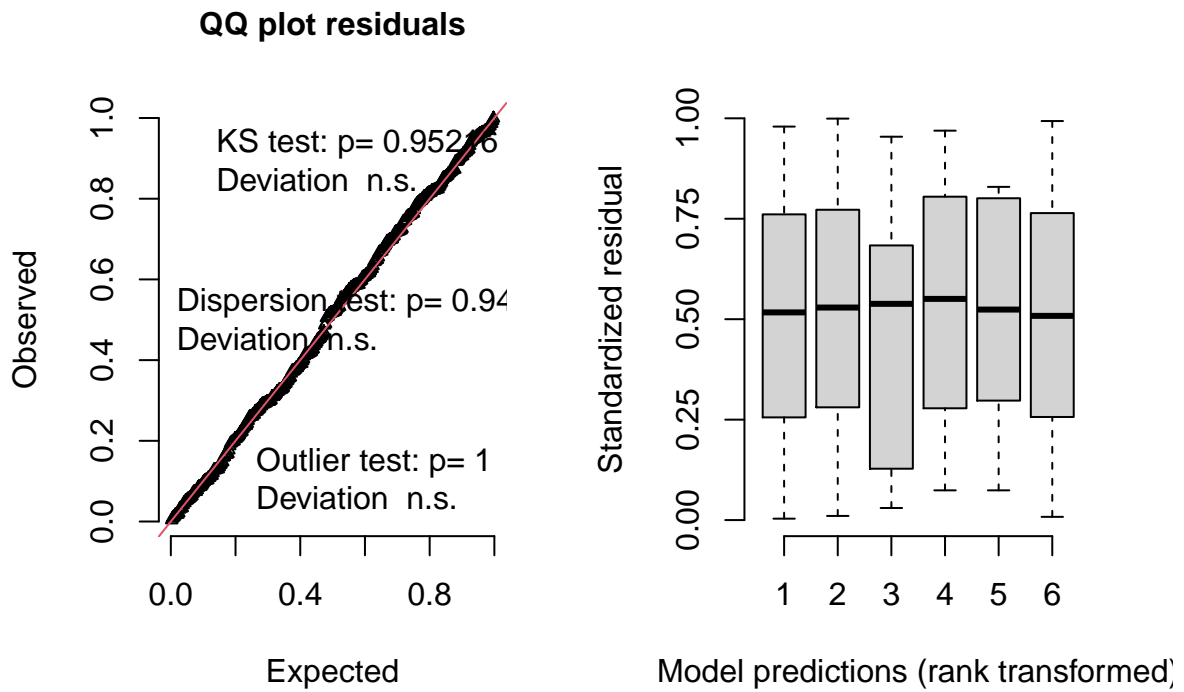
*#checking model fit*

```

check_mod_Suc1 <- simulateResiduals(fittedModel = success_mod1,n=1000, plot=T)

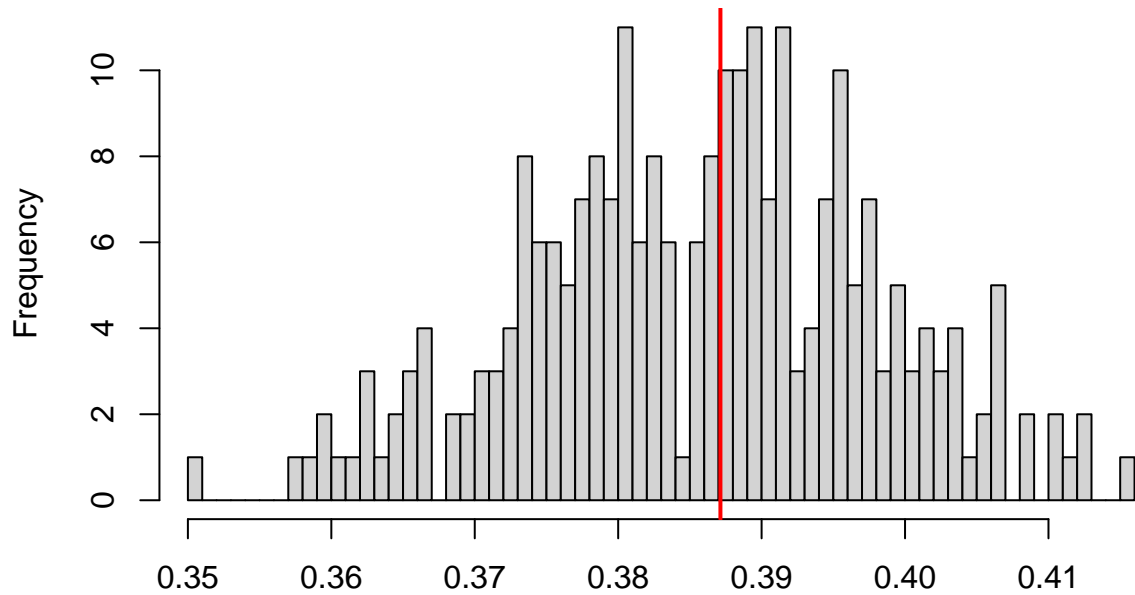
```

## DHARMA residual diagnostics



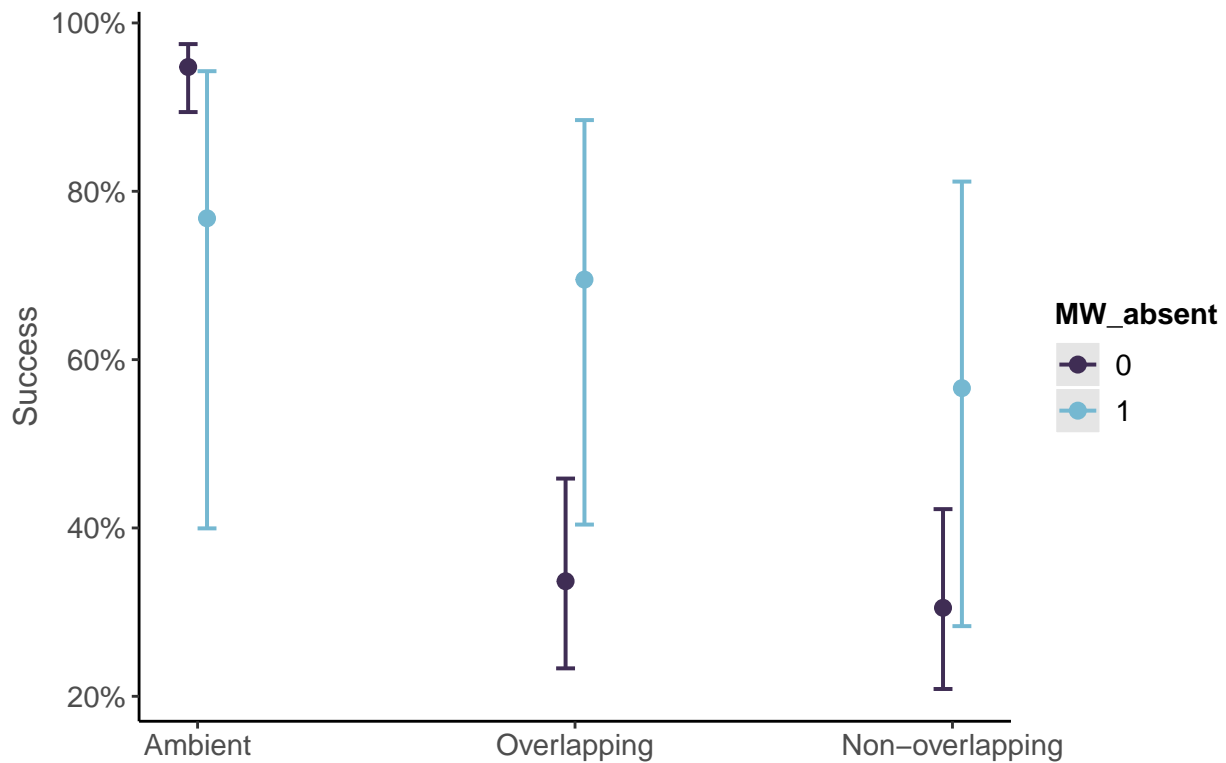
```
testDispersion(success_mod1)
```

DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.976

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## ratioObsSim = 1.0036, p-value = 0.976
## alternative hypothesis: two.sided
#Interaction plot for prey reward on Success
plot_model(success_mod1, type="int", transform="plogis", colors="ipsum")+
labs(caption="Interaction between treatment type and presence of prey reward on the board.
There is no difference in")
```



Interaction between treatment type and presence of prey reward on the board.  
There is no difference in probability of success with prey on or off the board

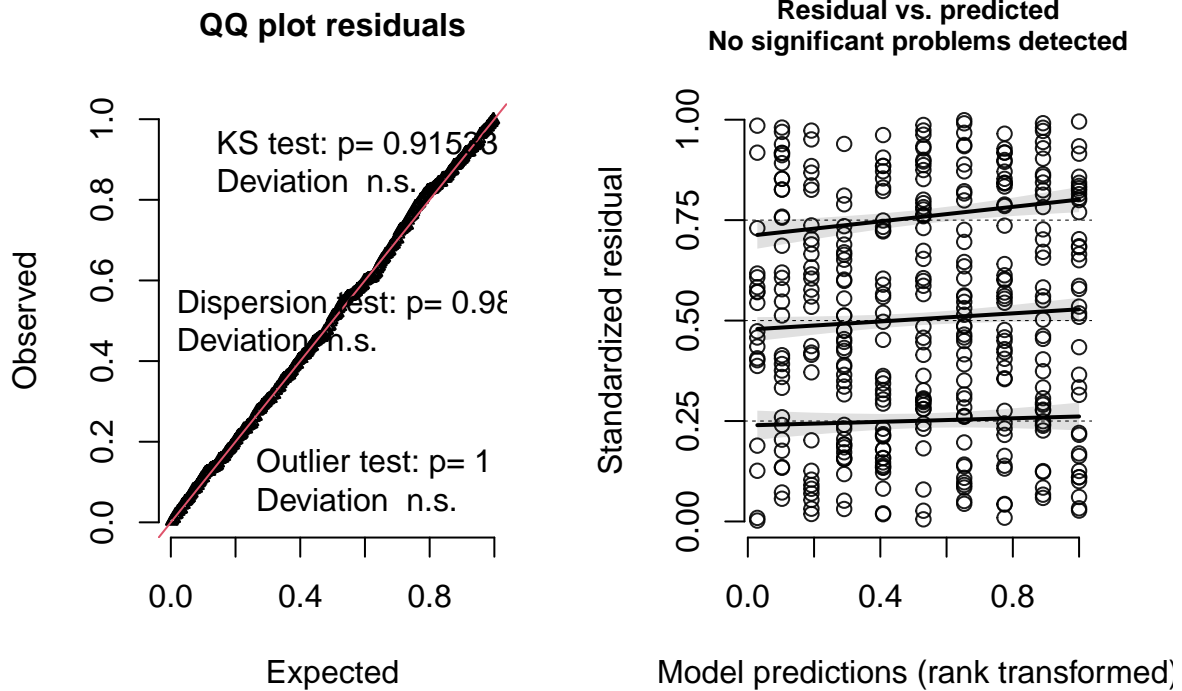
### Model testing the effect of Night and bat ID on success###

```
success_mod2<-glmer(Success~Night+(1|Bat), data=dat2, family=binomial(link="logit"))
summary(success_mod2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Success ~ Night + (1 | Bat)
## Data: dat2
##
##      AIC      BIC   logLik deviance df.resid
##  497.3    509.0  -245.7   491.3     364
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.3356 -1.2118  0.7640  0.8169  0.8505
##
## Random effects:
## Groups Name          Variance Std.Dev.
## Bat      (Intercept) 0.01581  0.1258
## Number of obs: 367, groups: Bat, 3
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.38066    0.27061   1.407   0.160
## Night        0.01009    0.04042   0.250   0.803
```

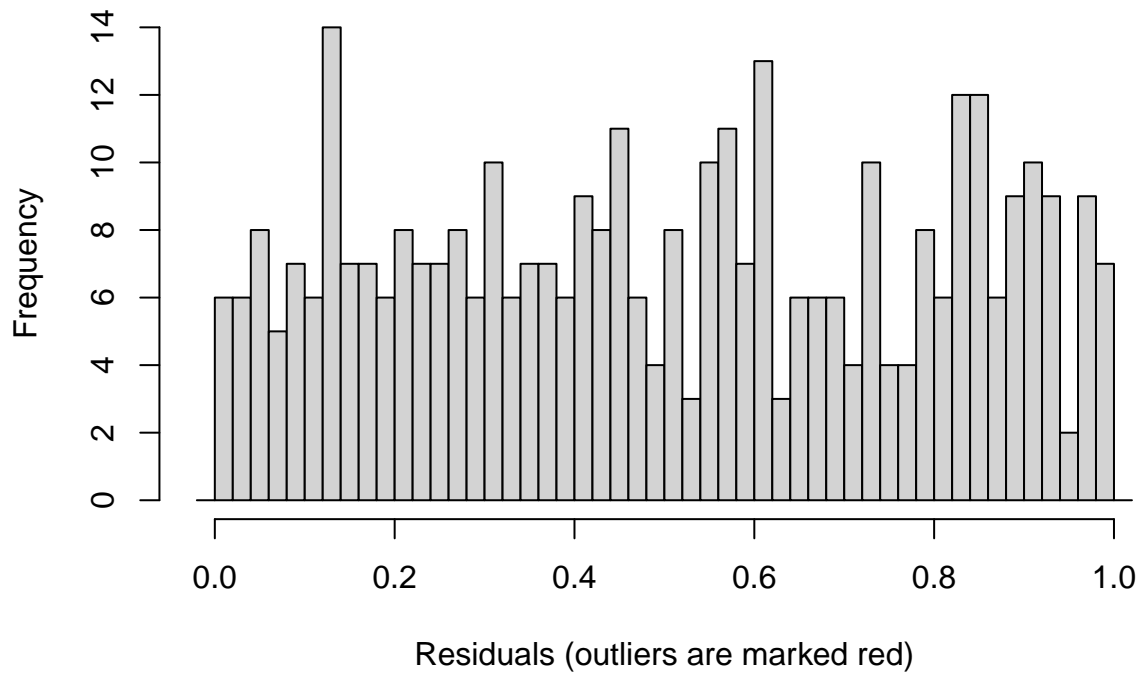
```
##
## Correlation of Fixed Effects:
##      (Intr)
## Night -0.878
#checking model fit
check_mod_Suc2 <- simulateResiduals(fittedModel = success_mod2, n=1000, plot=T)
```

### DHARMA residual diagnostics



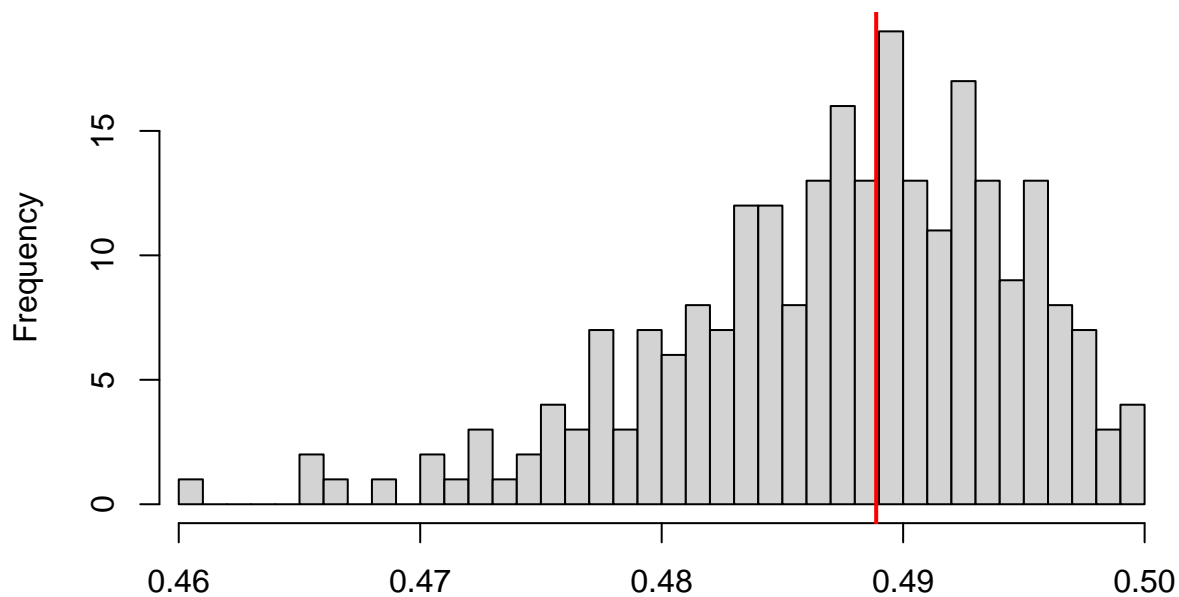
```
hist(check_mod_Suc2)
```

Hist of DHARMA residuals



```
testDispersion(success_mod2)
```

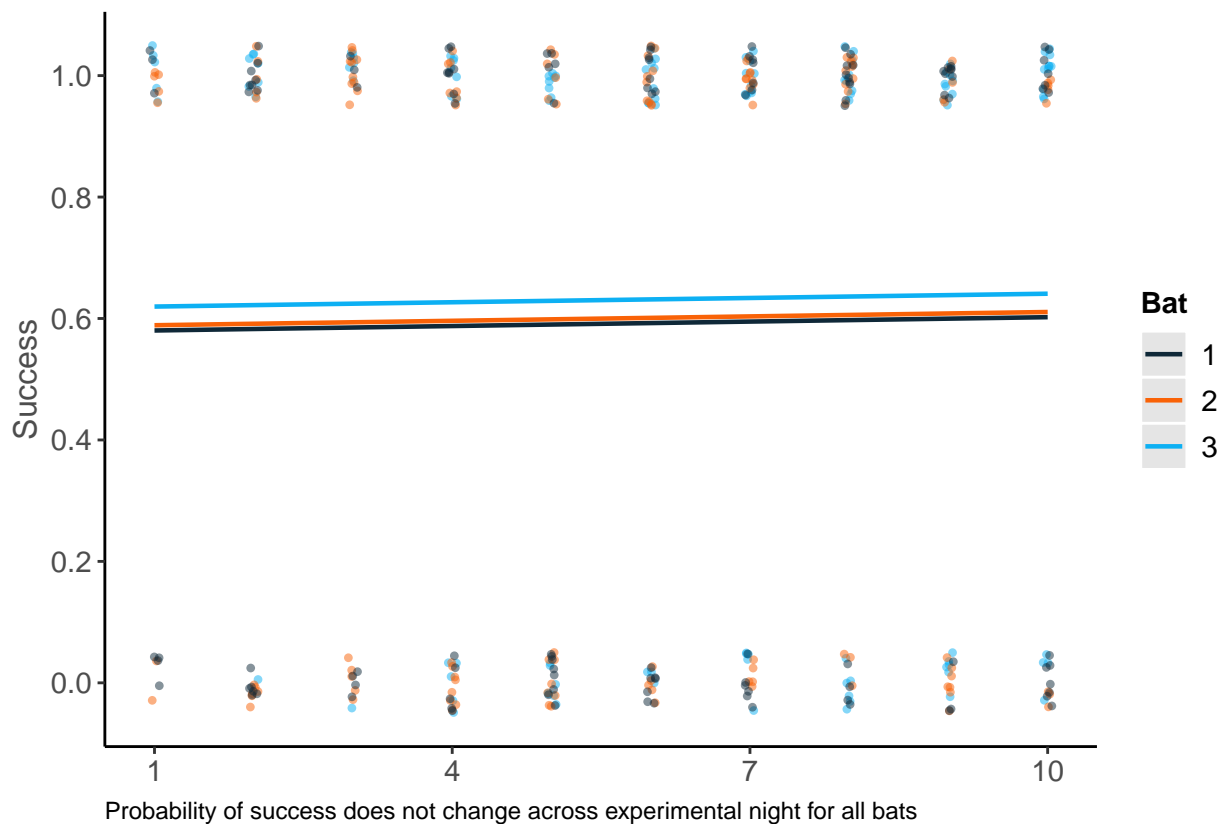
### DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.952

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## ratioObsSim = 1.0031, p-value = 0.952
## alternative hypothesis: two.sided
#Plot of the effect of Night and bat ID on success
plot_model(success_mod2, type="pred", terms=c("Night", "Bat"), pred.type="re", transform="plogis",
  colors="system",dot.size=1.2,line.size = 0.8, ci.lvl=0.95, show.data=TRUE, jitter=.05)+
  scale_y_continuous(limits=c(-.05,1.05),breaks=c(0,.2,.4,.6,.8,1))+
  scale_x_continuous(breaks=c(1, 4, 7, 10),
```





### Model testing the effect of Treatment on Success###

```
success_mod3<-glmer(Success~Treatment+(1|Bat), data=dat2, family=binomial(link="logit"))
```

```
summary(success_mod3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Success ~ Treatment + (1 | Bat)
## Data: dat2
##
##      AIC      BIC   logLik deviance df.resid
##  354.0    369.6  -173.0   346.0     363
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -3.7972 -0.7203  0.2291  0.2806  1.5412
##
## Random effects:
##  Groups Name         Variance Std.Dev.
##  Bat      (Intercept) 0.05595  0.2365
## Number of obs: 367, groups: Bat, 3
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      2.7185     0.3562   7.631 2.32e-14 ***
```

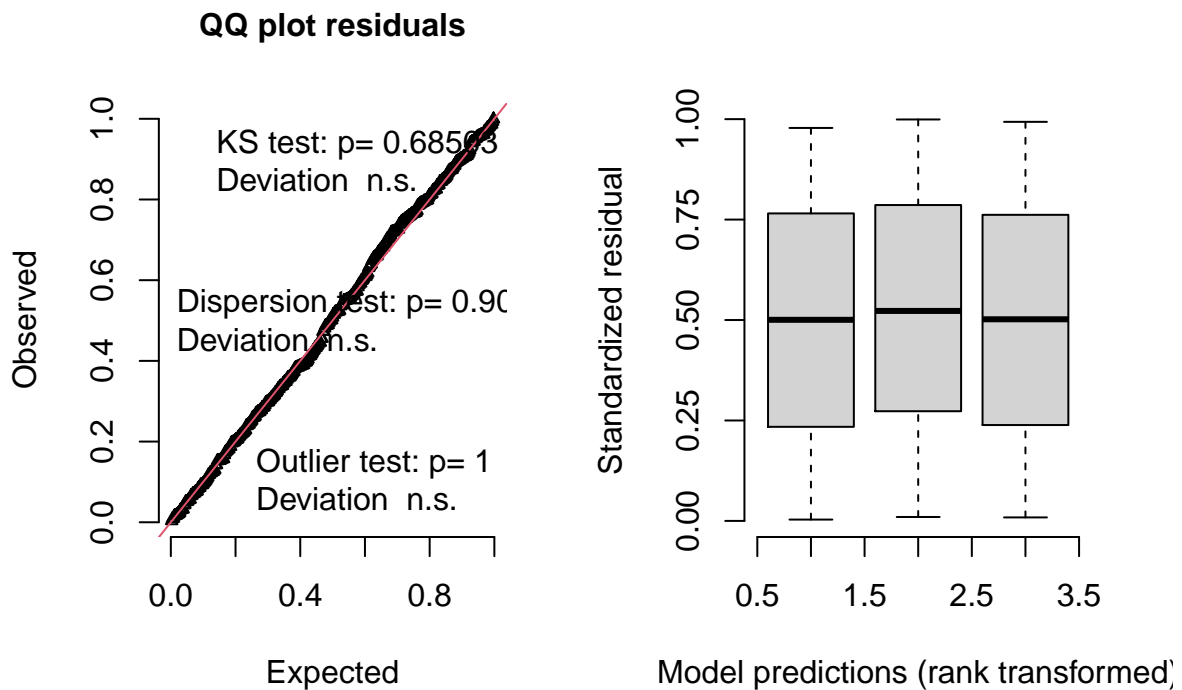
```

## TreatmentOverlapping      -3.1976      0.3879   -8.243 < 2e-16 ***
## TreatmentNon-overlapping -3.4067      0.3894   -8.749 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) Trtmn0
## TrtmntOvrlp -0.784
## TrtmntNn-vr -0.783  0.720
#Getting confidence intervals
load("easyPredCI.Rdata")
pframe <- data.frame(Treatment=factor(levels(dat2$Treatment),
                                     levels=levels(dat2$Treatment)))
cpred1 <- predict(success_mod3,re.form=NA,newdata=pframe,type="response")
cpred1.CI <- easyPredCI(success_mod3,pframe)

#checking model fit
check_mod_Suc3 <- simulateResiduals(fittedModel = success_mod3,n=1000, plot=T)

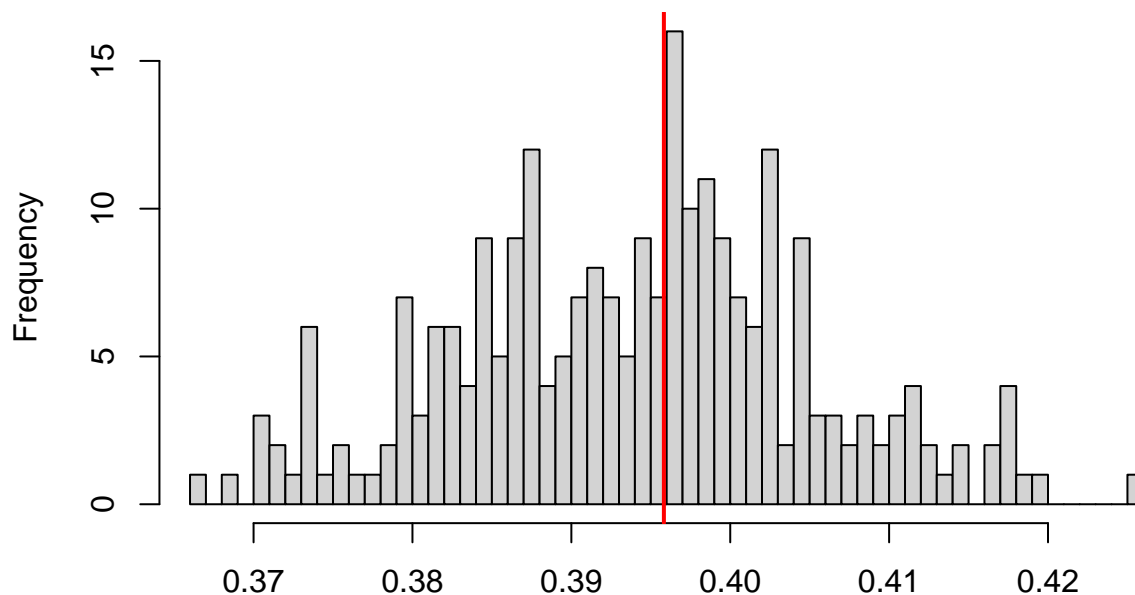
```

### DHARMA residual diagnostics



```
testDispersion(success_mod3)
```

### DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.936

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## ratioObsSim = 1.005, p-value = 0.936
## alternative hypothesis: two.sided
##Search time models
```

The following models test the effect of noise on bats' latency to make a foraging decision. That is, the time from prey signal start that it takes for the bat to land on a selected speaker on the board.

```
#cleaning the data set for search time models - i.e., getting rid of trial without start time
dat2<-droplevels(subset(dat2, Search_time!="NA"))
```

```
###Model testing the effect of prey reward on trial outcome###
```

```
ST_mod1<-glmer(Search_time~Treatment*MW_absent+(1|Bat), family=Gamma(link="log"), data=dat2)
```

```
summary(ST_mod1)
```

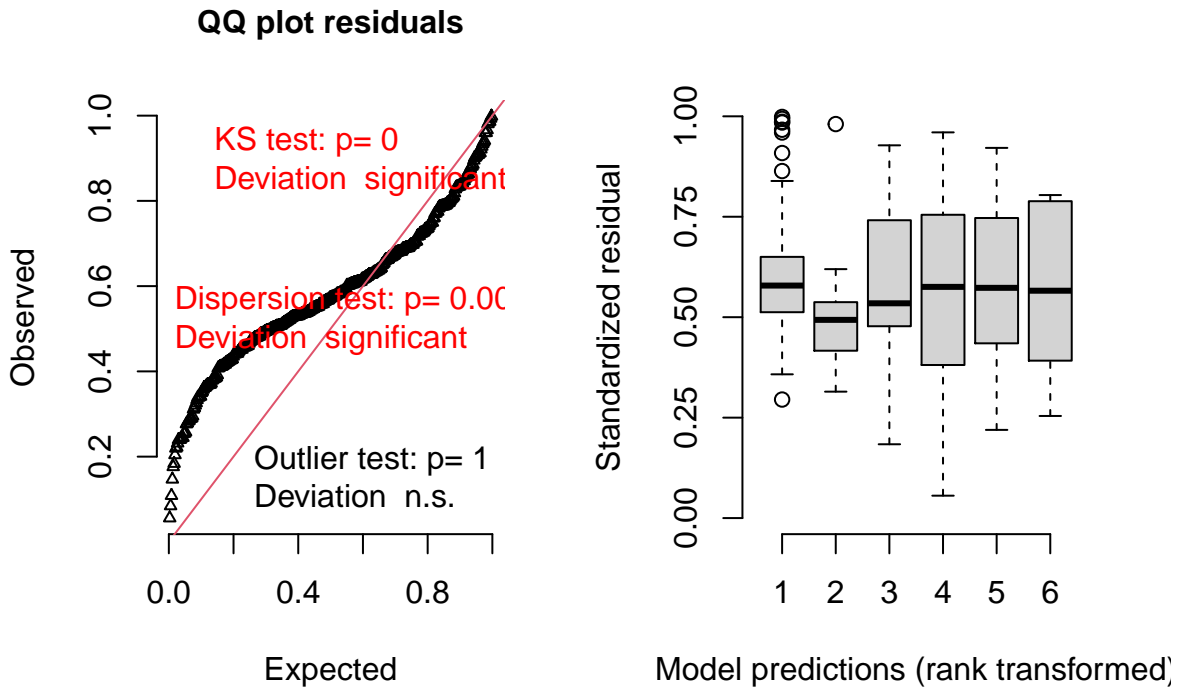
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: Gamma ( log )
## Formula: Search_time ~ Treatment * MW_absent + (1 | Bat)
## Data: dat2
##
## AIC BIC logLik deviance df.resid
```

```

## 2219.0 2250.2 -1101.5 2203.0 358
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -1.2217 -0.5599 -0.2576 0.1758 7.6221
##
## Random effects:
## Groups Name Variance Std.Dev.
## Bat (Intercept) 0.02276 0.1509
## Residual 0.62875 0.7929
## Number of obs: 366, groups: Bat, 3
##
## Fixed effects:
## Estimate Std. Error t value Pr(>|z|)
## (Intercept) 1.38837 0.11710 11.856 < 2e-16 ***
## TreatmentOverlapping 1.41304 0.08898 15.880 < 2e-16 ***
## TreatmentNon-overlapping 1.26069 0.08702 14.488 < 2e-16 ***
## MW_absent 0.27178 0.22671 1.199 0.23060
## TreatmentOverlapping:MW_absent -0.79038 0.29976 -2.637 0.00837 **
## TreatmentNon-overlapping:MW_absent 0.14559 0.30437 0.478 0.63241
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) Trtmn0 TrtmN- MW_bsn TO:MW_
## TrtmntOvrplp -0.285
## TrtmntNn-vr -0.292 0.384
## MW_absent -0.109 0.143 0.145
## Trtmnt0:MW_ 0.083 -0.295 -0.111 -0.756
## TrtmnN-:MW_ 0.079 -0.104 -0.280 -0.744 0.561
##
#model checking
check_mod_ST1 <- simulateResiduals(fittedModel = ST_mod1,n=1000, plot=T)

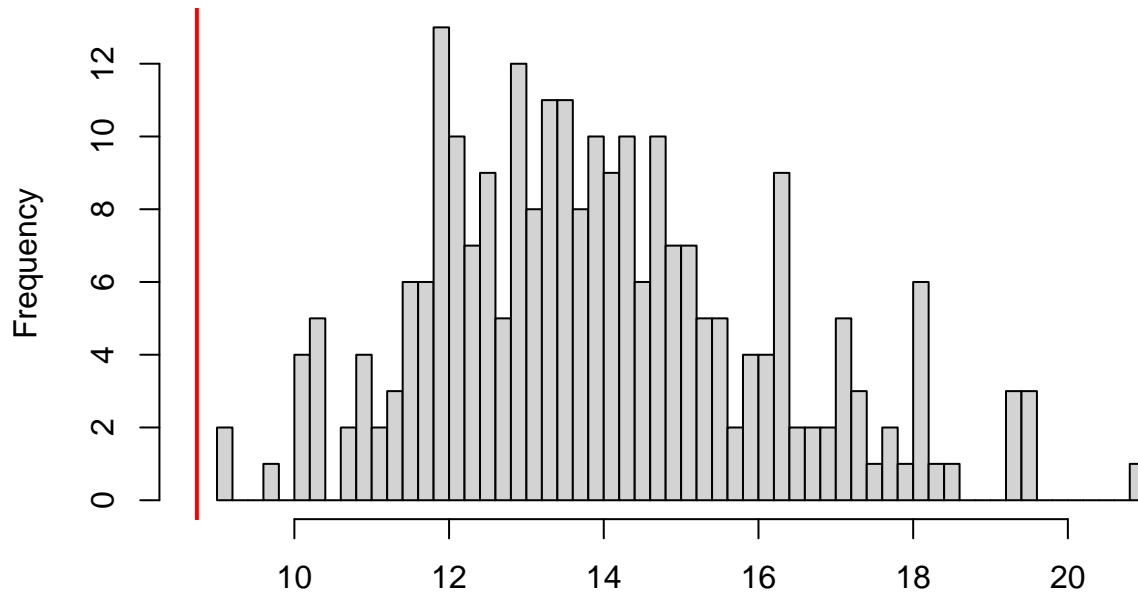
```

## DHARMA residual diagnostics



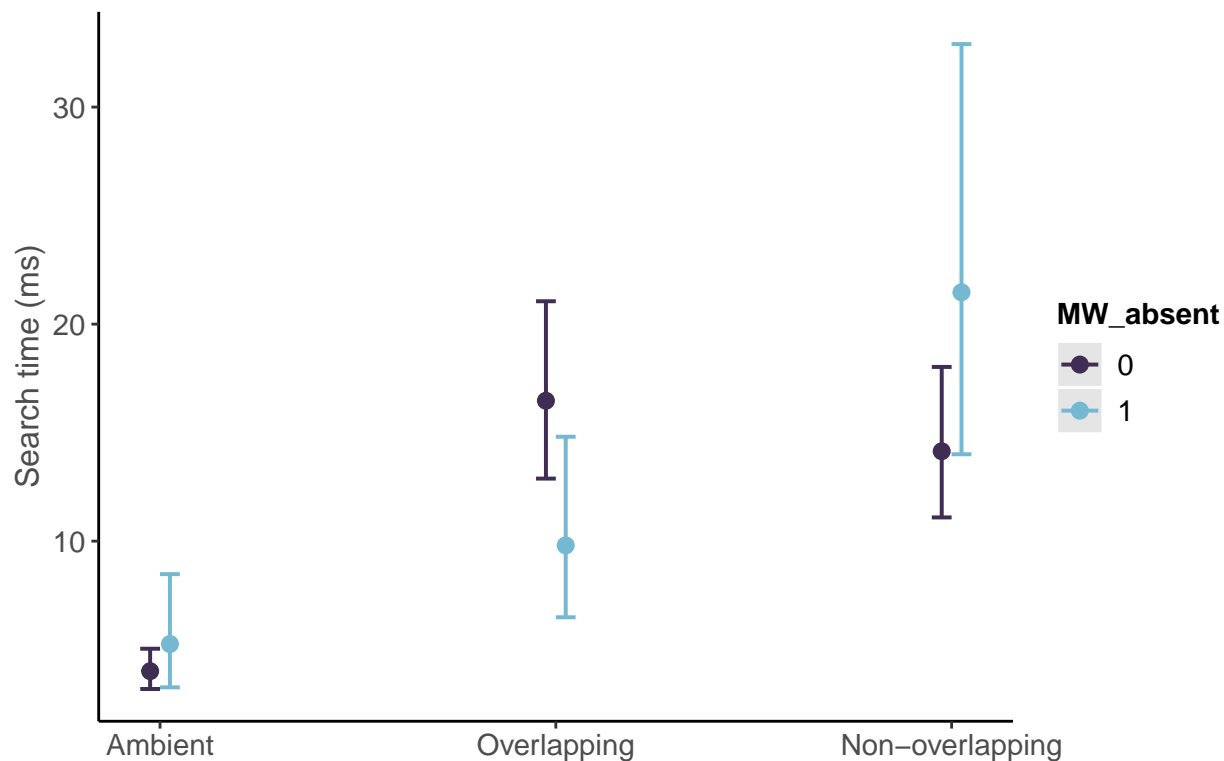
```
testDispersion(ST_mod1)
```

### DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## ratioObsSim = 0.62702, p-value < 2.2e-16
## alternative hypothesis: two.sided
#Interaction plot for prey reward on Search Time
plot_model(ST_mod1, type="int", transform="exp", colors="ipsum")+
labs(caption="Interaction of treatment and presence of prey reward on the board.
There is no difference in search
ylab("Search time (ms)")
```



Interaction of treatment and presence of prey reward on the board.  
 There is no difference in search time within treatments with prey on or off the board.

*#Testing effect of Night*

```
ST_mod2<-glmer(Search_time~Night+(1|Bat), data=dat2, family=Gamma(link="log"))
summary(ST_mod2)
```

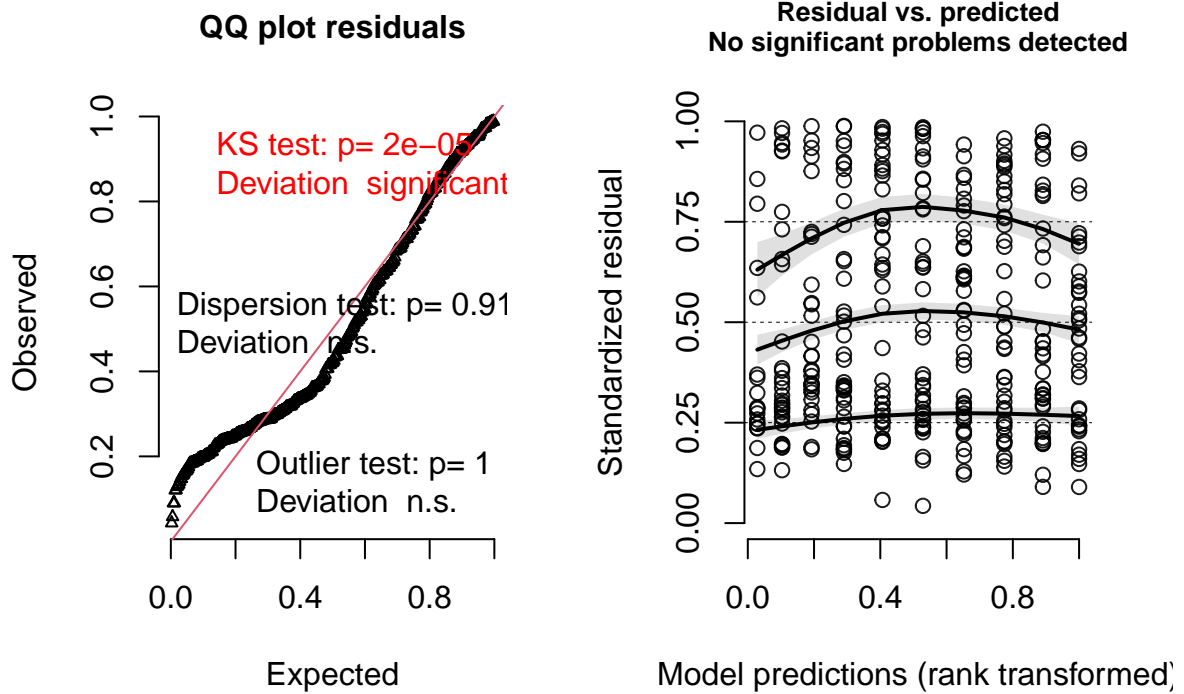
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: Gamma ( log )
## Formula: Search_time ~ Night + (1 | Bat)
## Data: dat2
##
##      AIC      BIC   logLik deviance df.resid
## 2453.9  2469.5 -1222.9  2445.9     362
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -0.9606 -0.6906 -0.4660  0.3293  4.1725
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
##  Bat      (Intercept)  0.01251  0.1119
##  Residual                    0.99737  0.9987
## Number of obs: 366, groups: Bat, 3
##
## Fixed effects:
##              Estimate Std. Error t value Pr(>|z|)
## (Intercept)  2.26879    0.13273  17.093  <2e-16 ***
```

```
## Night      0.01328    0.01815    0.732    0.464
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Night -0.807
```

```
#checking model fit
```

```
check_mod_ST2 <- simulateResiduals(fittedModel = ST_mod2,n=1000, plot=T)
```

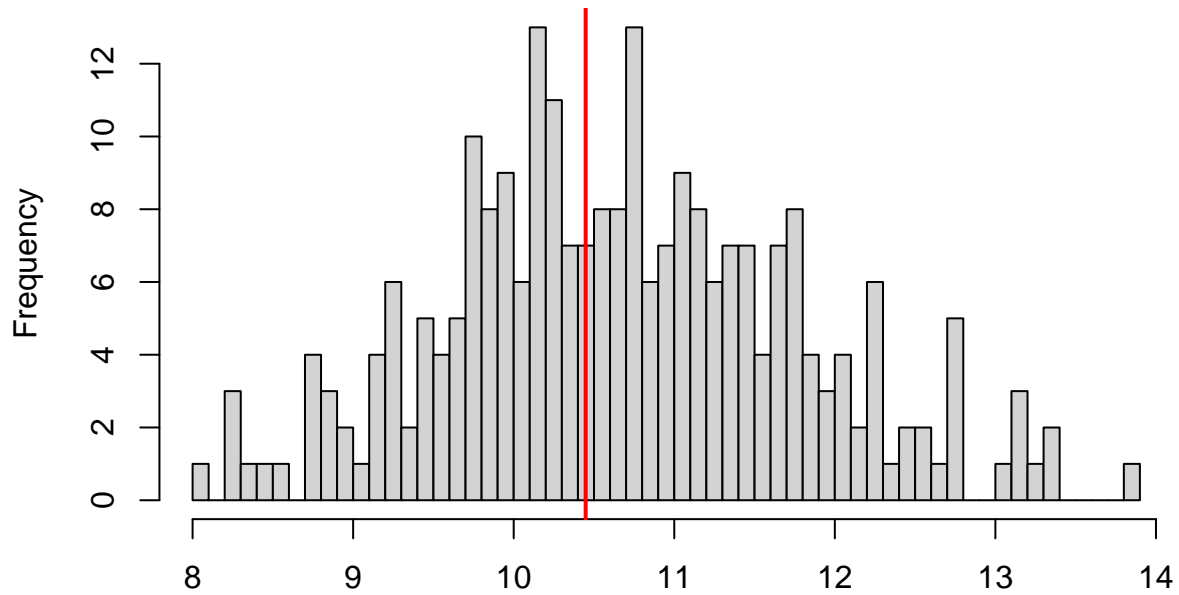
### DHARMA residual diagnostics



```
testDispersion(ST_mod2)
```

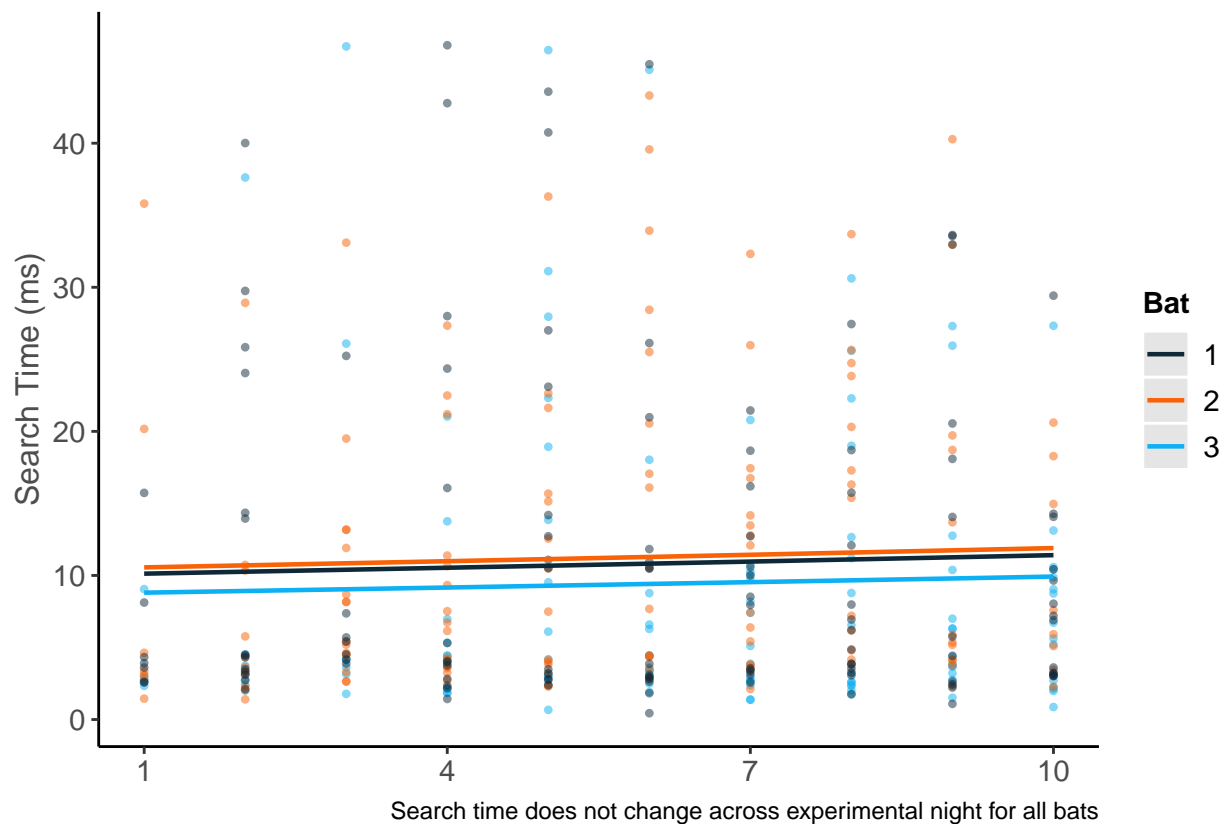


DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.896

```
##  
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.  
## simulated  
##  
## data: simulationOutput  
## ratioObsSim = 0.97804, p-value = 0.896  
## alternative hypothesis: two.sided  
  
#Plot of effect of Night and bat ID on Search time  
plot_model(ST_mod2, type="pred", terms=c("Night", "Bat"), pred.type="re", transform="exp",  
           colors="system", dot.size=1.2, line.size = .8, ci.lvl=0.95, show.data=TRUE)+labs(y="Search Time",  
                                                title="element")
```



### Model testing the effect of Treatment on Search Time ###

```
ST_mod3<-glmer(Search_time~Treatment+(1|Bat), data=dat2, family=Gamma(link="log"))
summary(ST_mod3)
```

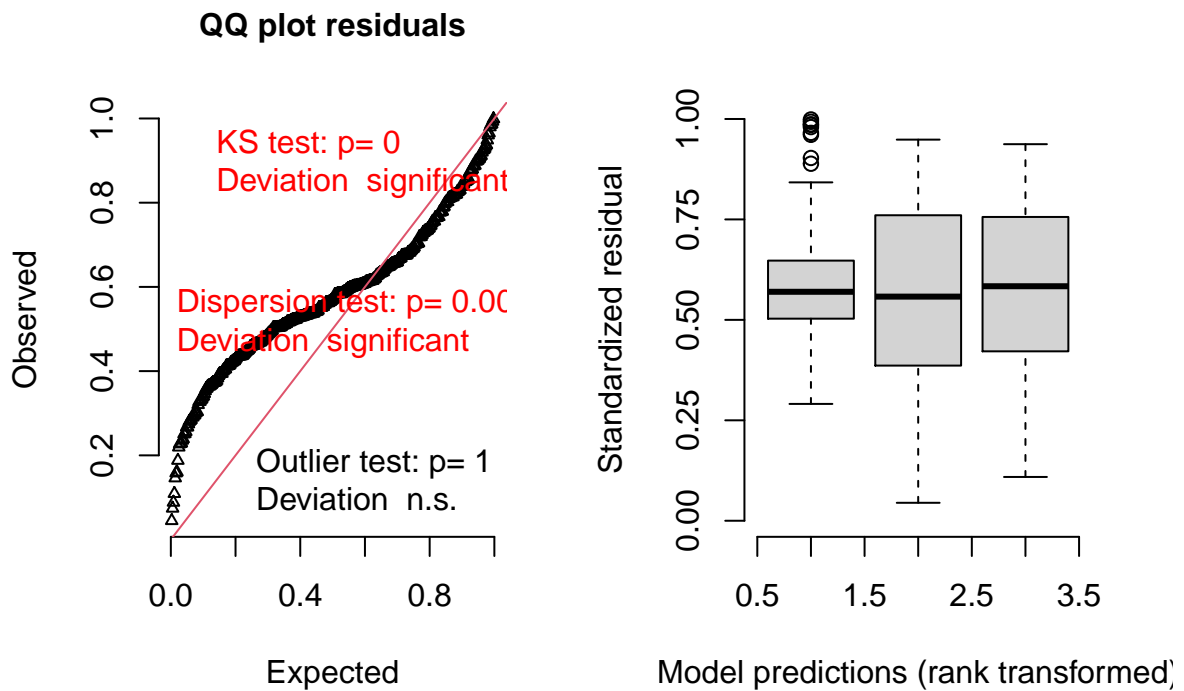
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: Gamma ( log )
## Formula: Search_time ~ Treatment + (1 | Bat)
## Data: dat2
##
##      AIC      BIC   logLik deviance df.resid
##  2225.2  2244.7  -1107.6  2215.2     361
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -1.2022 -0.5512 -0.2775  0.1436  7.4298
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
##  Bat      (Intercept)  0.02073  0.1440
##  Residual                    0.65151  0.8072
## Number of obs: 366, groups: Bat, 3
##
## Fixed effects:
##
##              Estimate Std. Error t value Pr(>|z|)
```

```
## (Intercept)          1.40714    0.11100   12.68   <2e-16 ***
## TreatmentOverlapping  1.34116    0.08561   15.67   <2e-16 ***
## TreatmentNon-overlapping 1.29780    0.08445   15.37   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) Trtmn0
## TrtmntOvrlp -0.304
## TrtmntNn-vr -0.311  0.402
```

```
#checking model fit
```

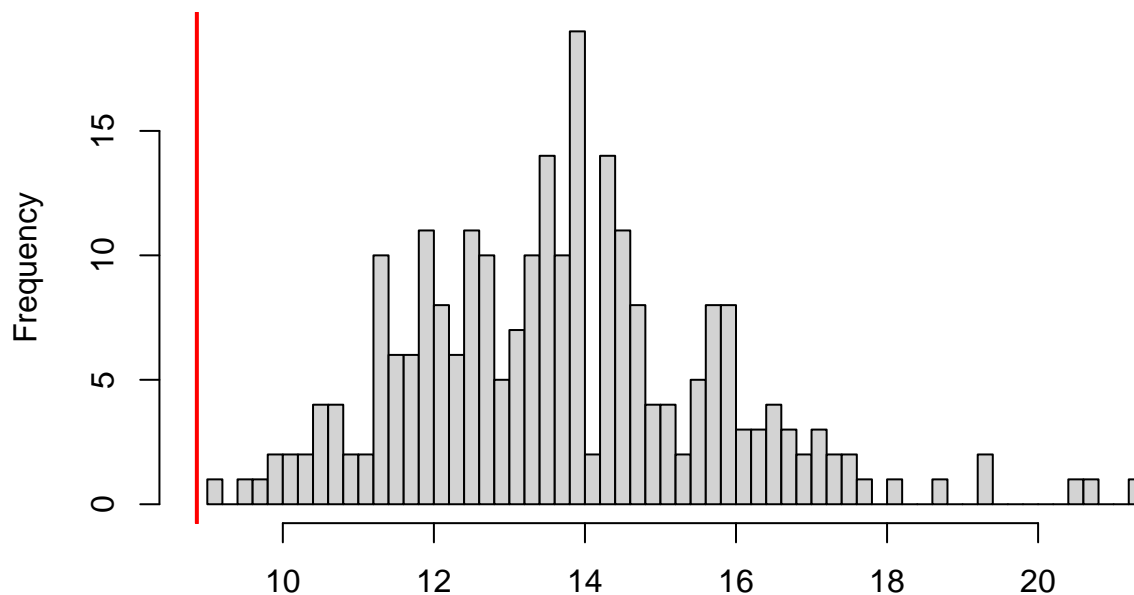
```
check_ST_mod3 <- simulateResiduals(fittedModel = ST_mod3, n=1000, plot=T)
```

### DHARMA residual diagnostics



```
testDispersion(ST_mod3)
```

### DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## ratioObsSim = 0.64686, p-value < 2.2e-16
## alternative hypothesis: two.sided
```

```
#getting confidence intervals
```

```
emmeans(ST_mod3, "Treatment", transform="log", type="response")
```

```
## Treatment      response    SE df asymp.LCL asymp.UCL
## Ambient         4.08 0.453 Inf    3.29    5.08
## Overlapping     15.62 1.839 Inf    12.40   19.67
## Non-overlapping 14.95 1.746 Inf    11.90   18.80
```

```
##
```

```
## Confidence level used: 0.95
```

```
## Intervals are back-transformed from the log scale
```

```
##Echolocation models
```

The following models test the effect of noise on bats' echolocation parameters, including average interpulse interval (IPI) and dominant frequency.

```
#reording Treatment levels
```

```
dat3$Treatment<-factor(dat3$Treatment, levels=c("Ambient", "Overlapping", "Non-overlapping"))
```

```
#making data numerical
```

```

dat3$IPI<-as.character(dat3$IPI)
dat3$IPI<-as.numeric(dat3$IPI)
dat3$freq_maxdB<-as.character(dat3$freq_maxdB)
dat3$freq_maxdB<-as.numeric(dat3$freq_maxdB)
dat3$MW_absent<-as.factor(dat3$MW_absent)

dat3 <- transform(dat3, UniqueID=match(Video, unique(Video)))

#building an empty matrix
acous <- matrix(ncol=22, nrow=0)

#running a loop to calculate the average IPI and dom freq for each trial
for (i in unique(dat3$UniqueID)){

  newdata <- dat3[which(dat3$UniqueID==i & dat3$Attempt=="1"),]
  avg_IPI<-mean(newdata$IPI, na.rm=T)
  avg_dfreq<-mean(newdata$freq_maxdB, na.rm=T)

  x=newdata[1,]

  y=cbind(x, avg_IPI, avg_dfreq)

  acous=rbind(acous,y)
}

#removing NA's
acous<-acous[!is.na(acous$avg_IPI),]
acous<-acous[!is.na(acous$avg_dfreq),]

#converting to ms
acous$avg_IPI<-acous$avg_IPI*1000

###Model testing the effect of prey reward on trial outcome###
IPI_mod1<-lmer(avg_IPI~Treatment*MW_absent+(1|Bat), data=acous)
summary(IPI_mod1)

## Linear mixed model fit by REML ['lmerMod']
## Formula: avg_IPI ~ Treatment * MW_absent + (1 | Bat)
## Data: acous
##
## REML criterion at convergence: 1270.4
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -1.8183 -0.6449 -0.1462 0.4195 2.7271
##
## Random effects:
## Groups Name Variance Std.Dev.
## Bat (Intercept) 79.11 8.894
## Residual 576.56 24.012
## Number of obs: 142, groups: Bat, 3
##

```

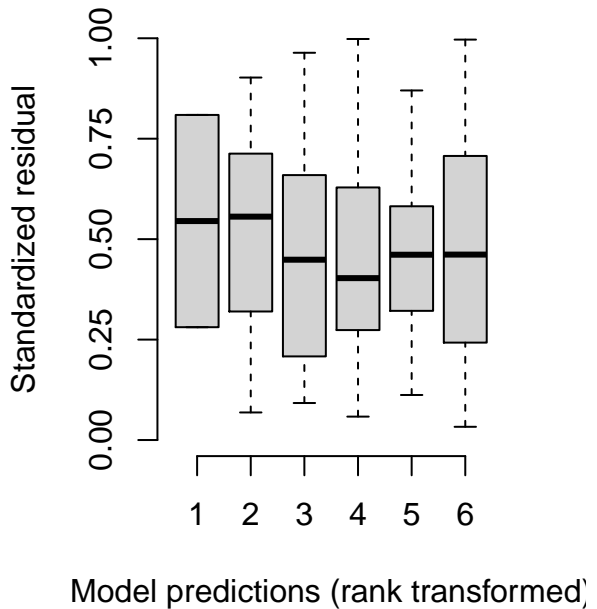
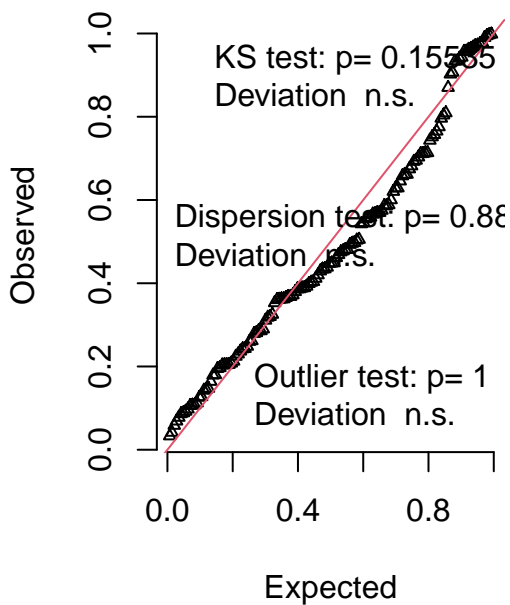
```
## Fixed effects:
##
## Estimate Std. Error t value
## (Intercept) 95.918 6.171 15.544
## TreatmentOverlapping -21.626 5.553 -3.894
## TreatmentNon-overlapping -20.446 5.127 -3.988
## MW_absent1 -33.647 17.315 -1.943
## TreatmentOverlapping:MW_absent1 44.525 20.040 2.222
## TreatmentNon-overlapping:MW_absent1 28.957 19.274 1.502
##
## Correlation of Fixed Effects:
## (Intr) Trtmn0 TrtmN- MW_bs1 TO:MW_
## TrtmntOvrp -0.343
## TrtmntNn-vr -0.372 0.418
## MW_absent1 -0.099 0.111 0.119
## Trtmn0:MW_1 0.083 -0.260 -0.099 -0.865
## TrtmN-:MW_1 0.093 -0.105 -0.258 -0.897 0.775
```

```
#checking model fit
```

```
check_IPI_mod1 <- simulateResiduals(fittedModel = IPI_mod1, n=1000, plot=T)
```

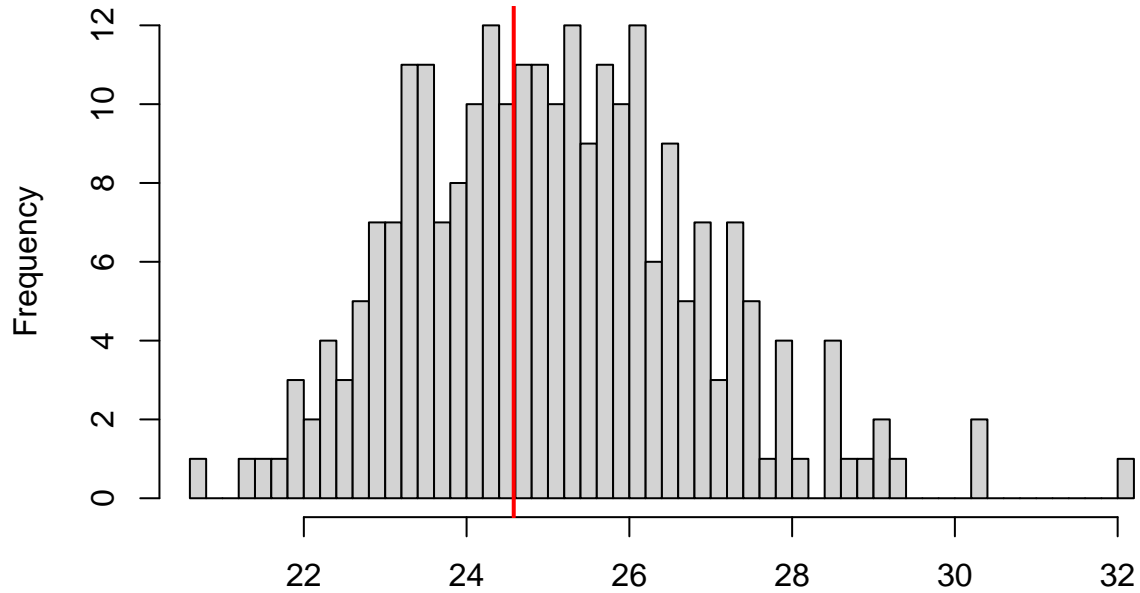
### DHARMA residual diagnostics

#### QQ plot residuals



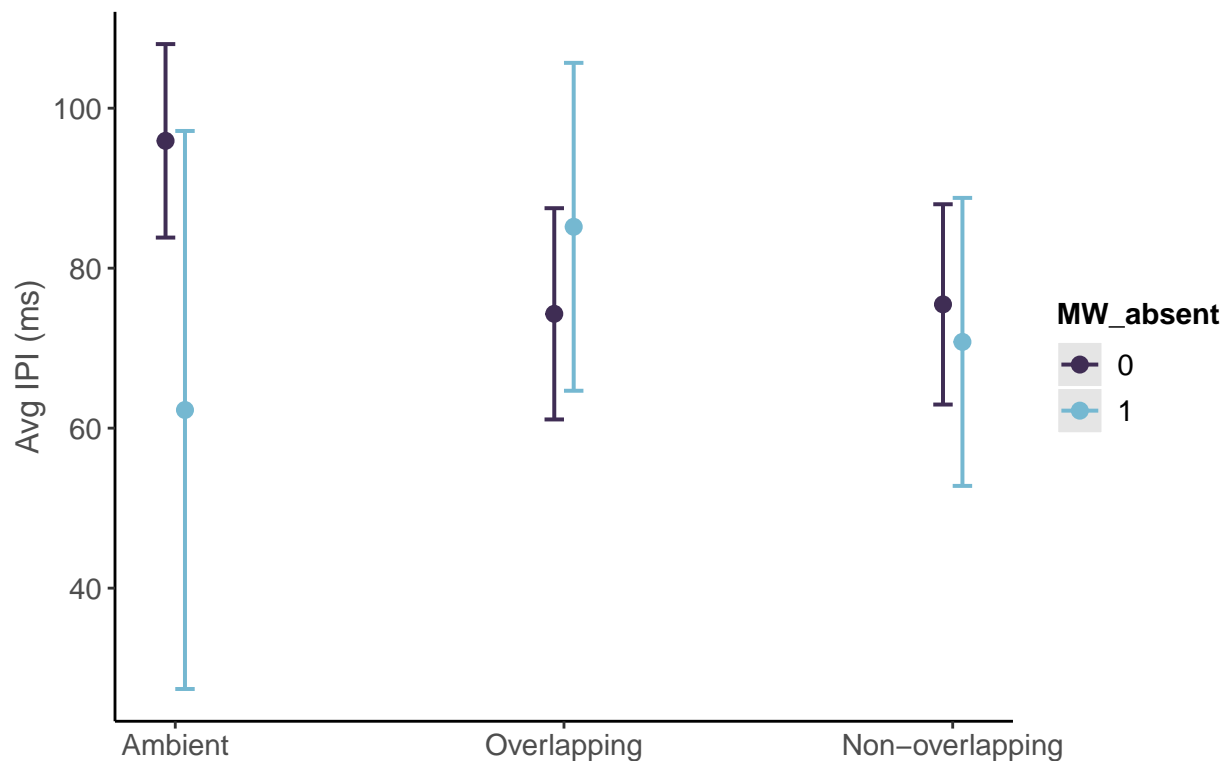
```
testDispersion(IPI_mod1)
```

DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.824

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## ratioObsSim = 0.98034, p-value = 0.824
## alternative hypothesis: two.sided
#Interaction plot for prey reward on avg IPI
plot_model(IPI_mod1, type="int", transform="exp", colors="ipsum")+
labs(y="Avg IPI (ms)",caption="Interaction of treatment and presence of prey reward on the board.
There is 1
```



Interaction of treatment and presence of prey reward on the board.  
 There is no difference of IPI within treatments with prey on or off the board.

### IPI by Night ###

```
IPI_mod2<-glmer.nb(avg_IPI~Night+(1|Bat), data=acous)
summary(IPI_mod2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: Negative Binomial(12.7612) ( log )
## Formula: avg_IPI ~ Night + (1 | Bat)
## Data: acous
##
##      AIC      BIC  logLik deviance df.resid
## 1321.4 1333.2 -656.7 1313.4    138
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -1.7111 -0.7858 -0.1679  0.5111  2.6300
##
## Random effects:
##   Groups Name          Variance Std.Dev.
##   Bat   (Intercept) 0.01192  0.1092
## Number of obs: 142, groups: Bat, 3
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  4.421999   0.080899  54.661  <2e-16 ***
```

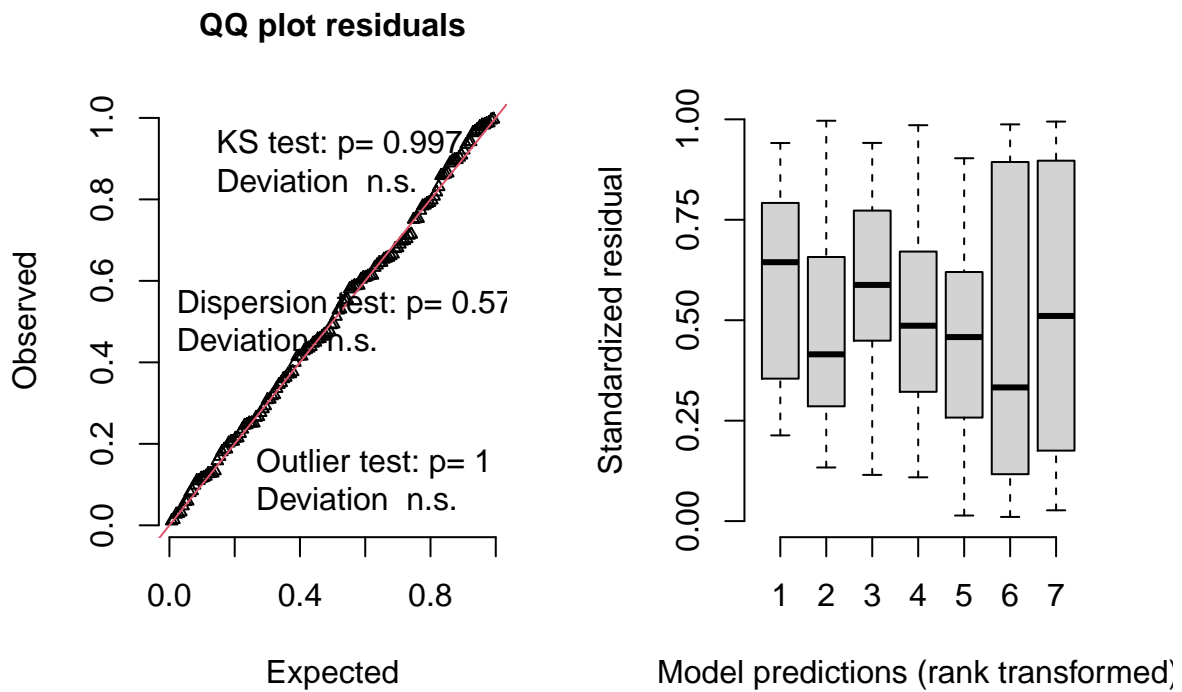


```
## Night      -0.002702  0.007591  -0.356   0.722
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Night -0.540
```

```
#checking model fit
```

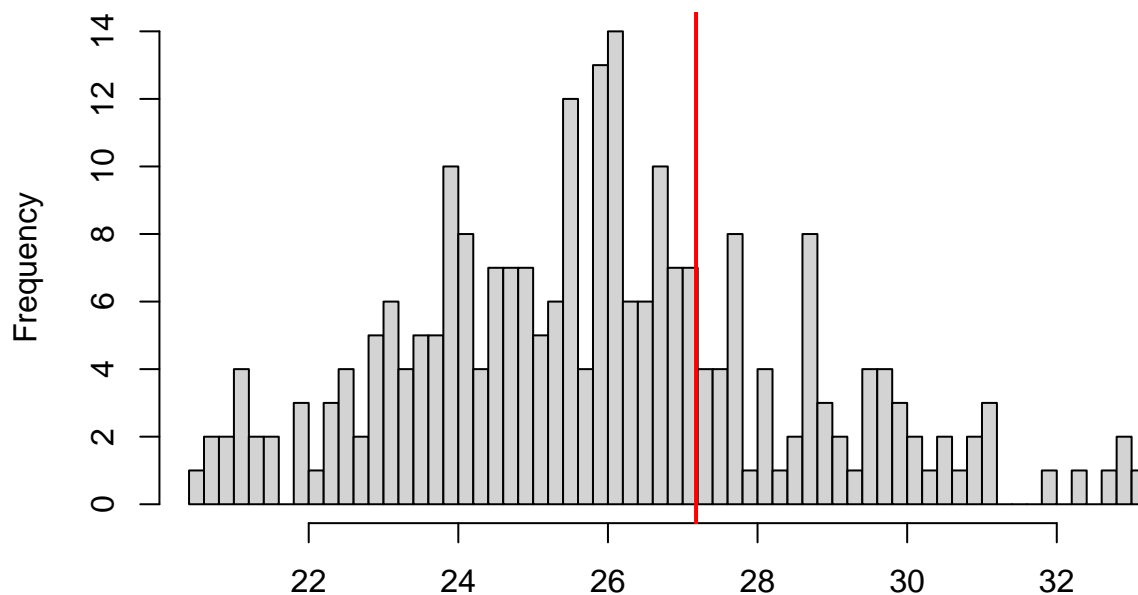
```
check_IPI_mod2 <- simulateResiduals(fittedModel = IPI_mod2, n=1000, plot=T)
```

### DHARMA residual diagnostics



```
testDispersion(IPI_mod2)
```

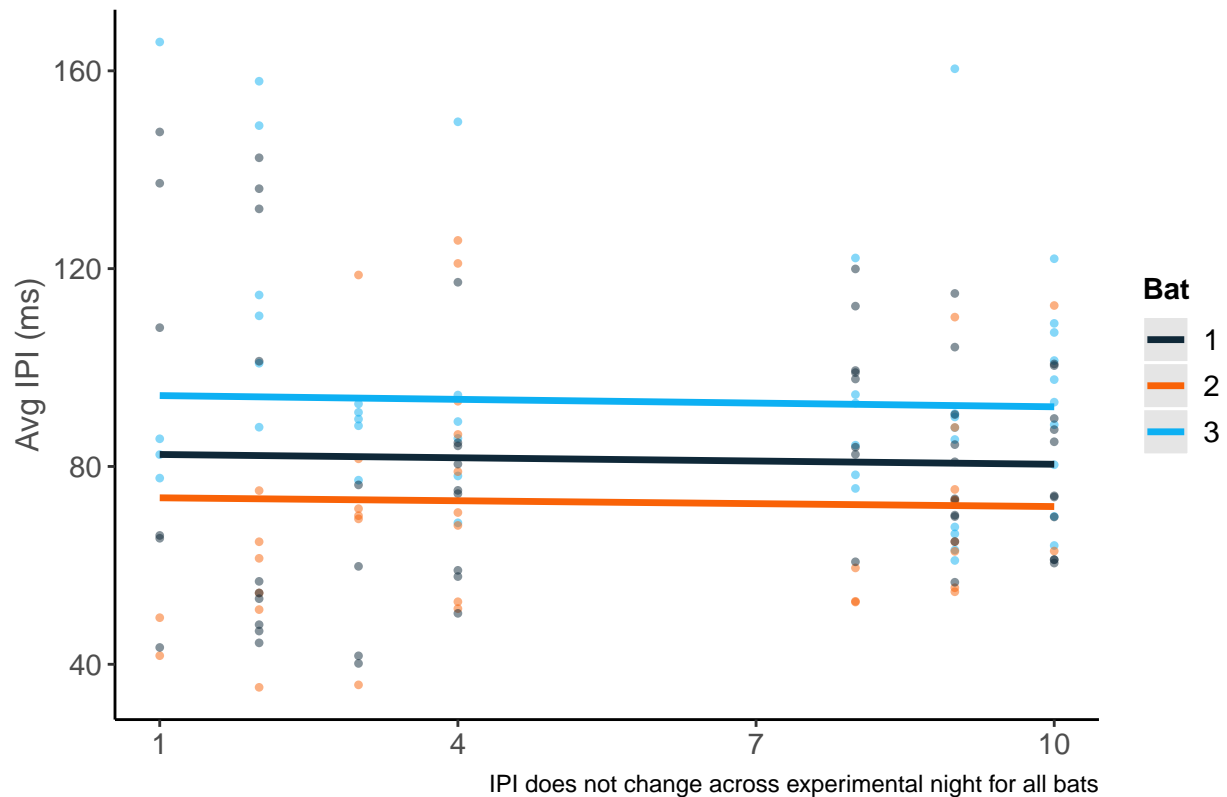
### DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.528

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## ratioObsSim = 1.0496, p-value = 0.528
## alternative hypothesis: two.sided
##plot night & bat on IPI, no effect
plot_model(IPI_mod2, type="pred", terms=c("Night", "Bat"), pred.type="re",
  transform="exp", ci.lvl=0.95, show.data=TRUE, dot.size=1.2, colors = "system", line.size=1.2)
labs(y="Avg IPI (ms)", caption="IPI does not change across experimental night for all bats")+
scale_x_continuous(breaks=c(1, 4, 7, 10), labels=scales::number_format(accuracy=1))+
theme(axis.title.x=element_blank())
```

### Predicted counts of avg\_IPI



### Model testing the effect of Treatment on Avg IPI ###

```
IPI_mod3 <- lmer(avg_IPI ~ Treatment + (1 | Bat), data = acous)
```

```
summary(IPI_mod3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: avg_IPI ~ Treatment + (1 | Bat)
## Data: acous
##
## REML criterion at convergence: 1295.8
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -1.9327 -0.6778 -0.1792  0.3582  2.7593
##
## Random effects:
##   Groups Name          Variance Std.Dev.
##   Bat    (Intercept)  71.11   8.433
##   Residual                    586.66  24.221
## Number of obs: 142, groups: Bat, 3
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    94.850    5.935  15.983
## TreatmentOverlapping -18.593    5.255  -3.538
```

```
## TreatmentNon-overlapping -20.308      4.816  -4.217
##
## Correlation of Fixed Effects:
##      (Intr) Trtmn0
## TrtmntOvrlp -0.373
## TrtmntNn-vr -0.402  0.461
```

```
confint(IPI_mod3)
```

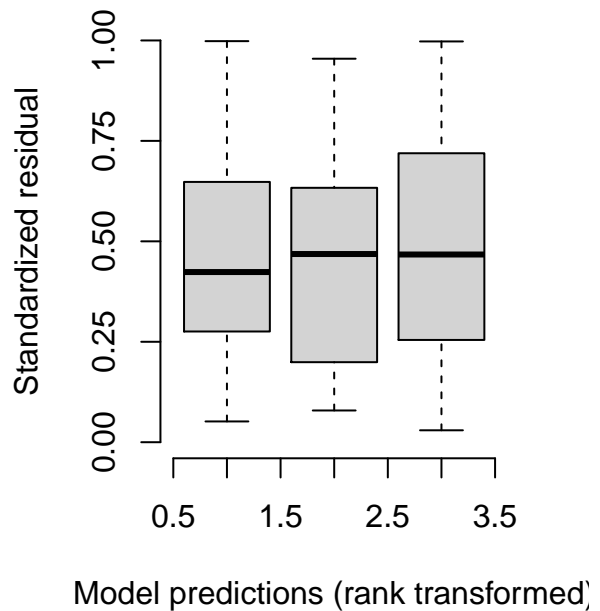
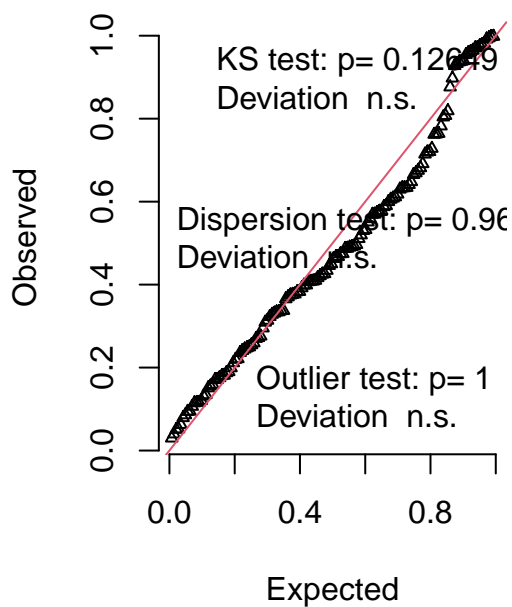
```
##                2.5 %    97.5 %
## .sig01          1.226643 21.817648
## .sigma          21.478152 27.185755
## (Intercept)     81.908427 107.283074
## TreatmentOverlapping -29.445383 -8.572017
## TreatmentNon-overlapping -30.058425 -11.069862
```

```
#checking model fit
```

```
check_IPI_mod3<-simulateResiduals(fittedModel = IPI_mod3, n=1000, plot=T)
```

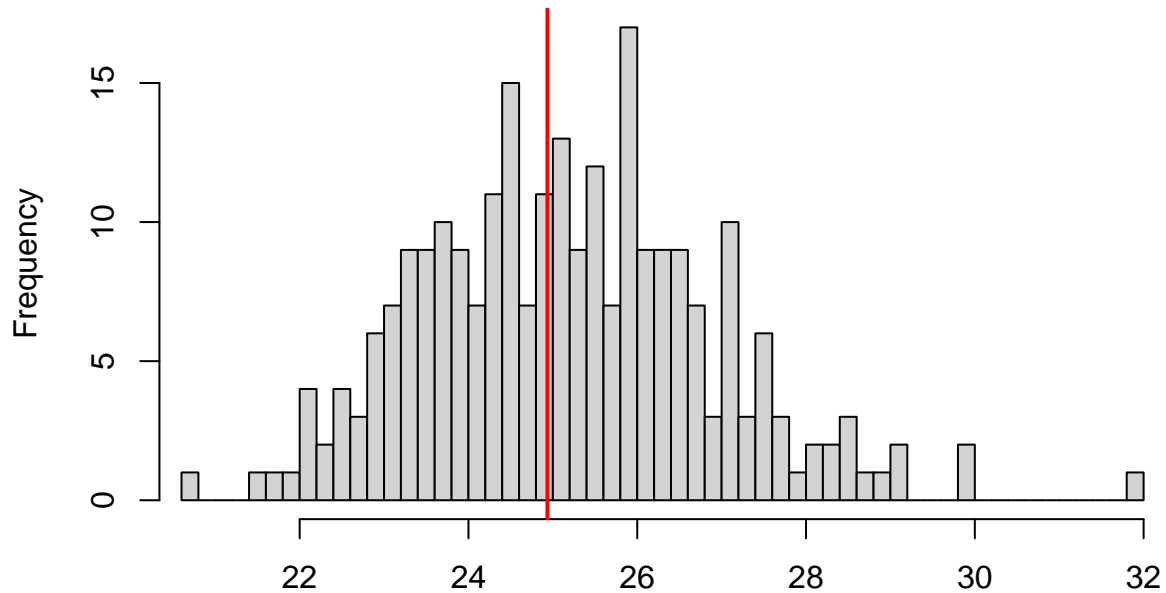
### DHARMA residual diagnostics

#### QQ plot residuals



```
testDispersion(IPI_mod3)
```

**DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated**



Simulated values, red line = fitted model. p-value (two.sided) = 0.904

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## ratioObsSim = 0.9907, p-value = 0.904
## alternative hypothesis: two.sided
```

```
###DOMINANT FREQUENCY###
```

```
###Model testing the effect of prey reward on trial outcome###
```

```
dfreq_mod1<-lmer(avg_dfreq~Treatment*MW_absent+(1|Bat), data=acous)
summary(dfreq_mod1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: avg_dfreq ~ Treatment * MW_absent + (1 | Bat)
## Data: acous
##
## REML criterion at convergence: 773.3
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -4.8104 -0.5269  0.0470  0.6491  2.5979
##
## Random effects:
## Groups Name Variance Std.Dev.
```

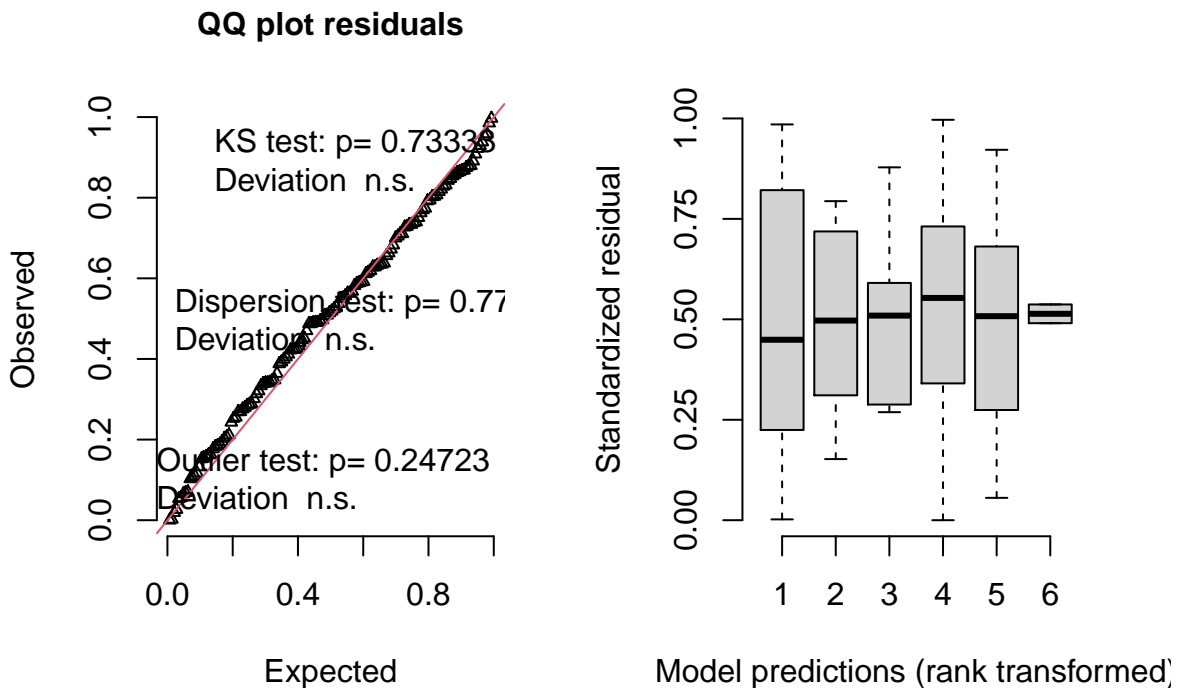
```

## Bat      (Intercept) 0.1461 0.3822
## Residual      15.2610 3.9065
## Number of obs: 142, groups: Bat, 3
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      78.9099    0.5894 133.876
## TreatmentOverlapping      0.6435    0.8921   0.721
## TreatmentNon-overlapping  -1.3208    0.8256  -1.600
## MW_absent1          2.4285    2.8156   0.862
## TreatmentOverlapping:MW_absent1  -3.5844    3.2569  -1.101
## TreatmentNon-overlapping:MW_absent1  -1.2182    3.1356  -0.389
##
## Correlation of Fixed Effects:
##      (Intr) Trtmn0 TrtmN- MW_bs1 TO:MW_
## TrtmntOvrp -0.569
## TrtmntNn-vr -0.615  0.408
## MW_absent1  -0.174  0.115  0.124
## Trtmn0:MW_1  0.149 -0.268 -0.106 -0.865
## TrtmN-:MW_1  0.159 -0.105 -0.261 -0.898  0.776

```

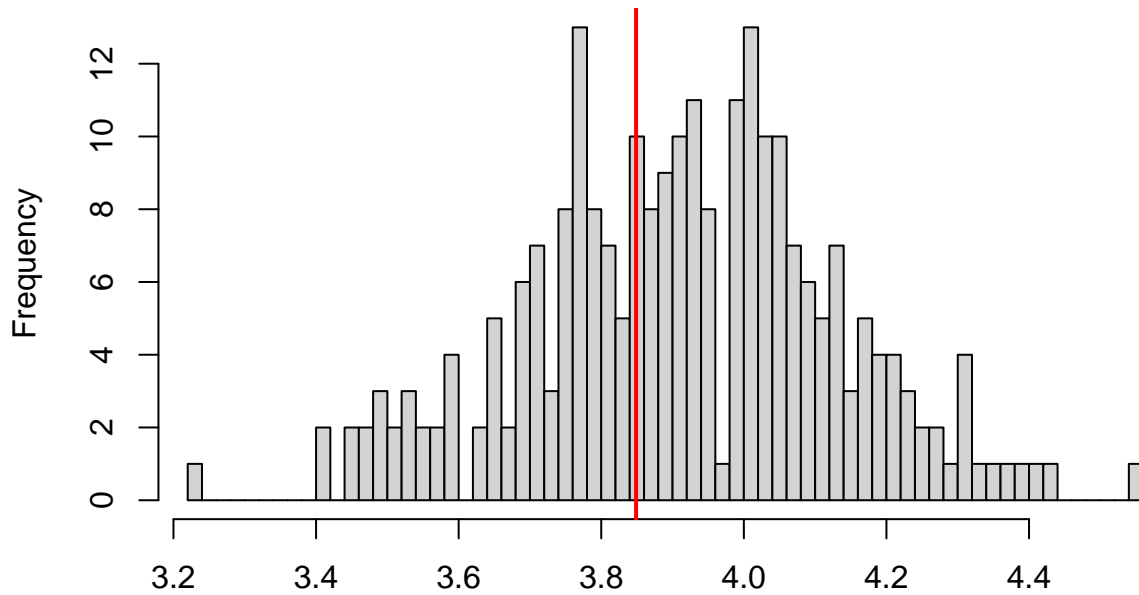
```
check_mod_dfreq1 <- simulateResiduals(fittedModel = dfreq_mod1, n=1000, plot=T)
```

### DHARMA residual diagnostics



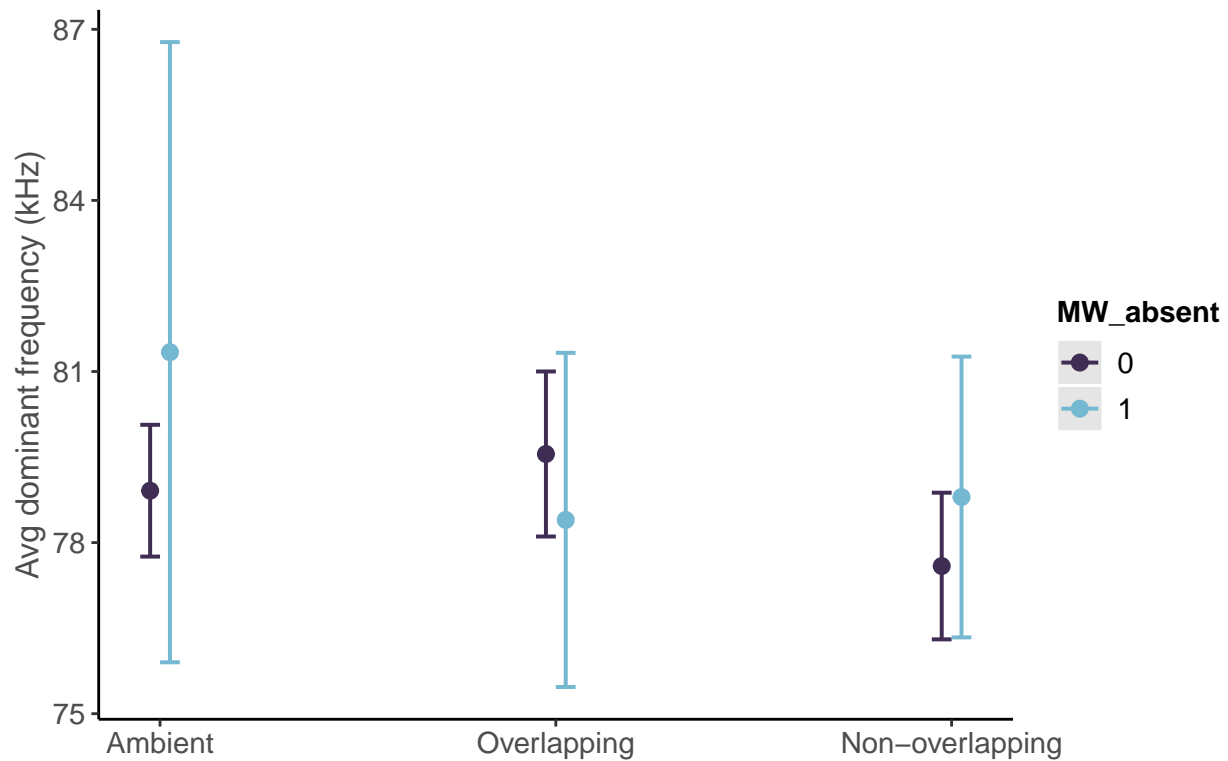
```
testDispersion(dfreq_mod1)
```

DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.752

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## ratioObsSim = 0.98315, p-value = 0.752
## alternative hypothesis: two.sided
#Interaction plot for prey reward on dominant freq.
plot_model(dfreq_mod1, type="int", colors="ipsum")+
labs(y="Avg dominant frequency (kHz)",caption="Interaction of treatment and presence of prey reward on
There is
title=element_blank()+theme(axis.title.x=element_blank())
```



Interaction of treatment and presence of prey reward on the board.  
There is no difference of dominant frequency with prey on or off the board.

### Model testing the effect of Treatment on dom. frequency ###

```
dfreq_mod2 <- lmer(avg_dfreq ~ Treatment + (1 | Bat), data = acous)
```

```
summary(dfreq_mod2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: avg_dfreq ~ Treatment + (1 | Bat)
## Data: acous
##
## REML criterion at convergence: 784.5
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -4.8465 -0.5196  0.1134  0.6153  2.5723
##
## Random effects:
## Groups Name Variance Std.Dev.
## Bat (Intercept) 0.1996 0.4467
## Residual 15.1273 3.8894
## Number of obs: 142, groups: Bat, 3
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    78.9824    0.5946 132.833
## TreatmentOverlapping 0.3713    0.8321  0.446
```



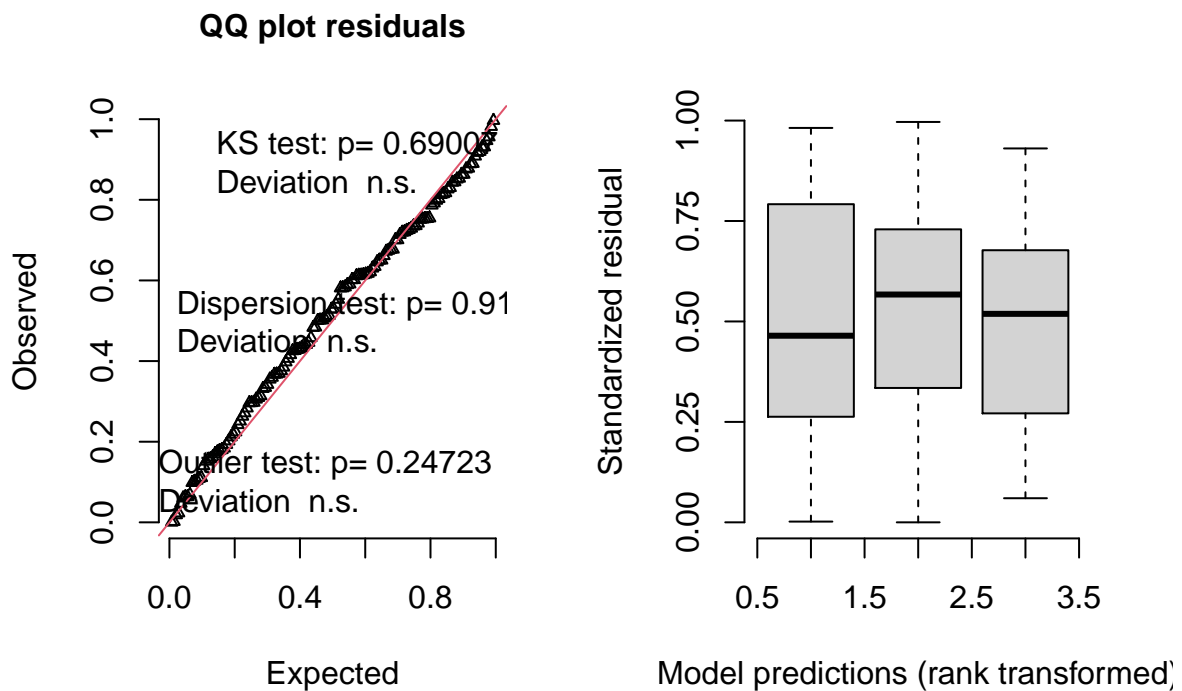
```
## TreatmentNon-overlapping -1.1507 0.7674 -1.499
##
## Correlation of Fixed Effects:
## (Intr) Trtmn0
## TrtmntOvrlp -0.582
## TrtmntNn-vr -0.628 0.452
```

```
confint(dfreq_mod2)
```

```
##                2.5 %    97.5 %
## .sig01          0.000000 1.6440113
## .sigma          3.450215 4.3612406
## (Intercept)    77.775086 80.1058443
## TreatmentOverlapping -1.368485 1.9397355
## TreatmentNon-overlapping -2.710890 0.3046862
```

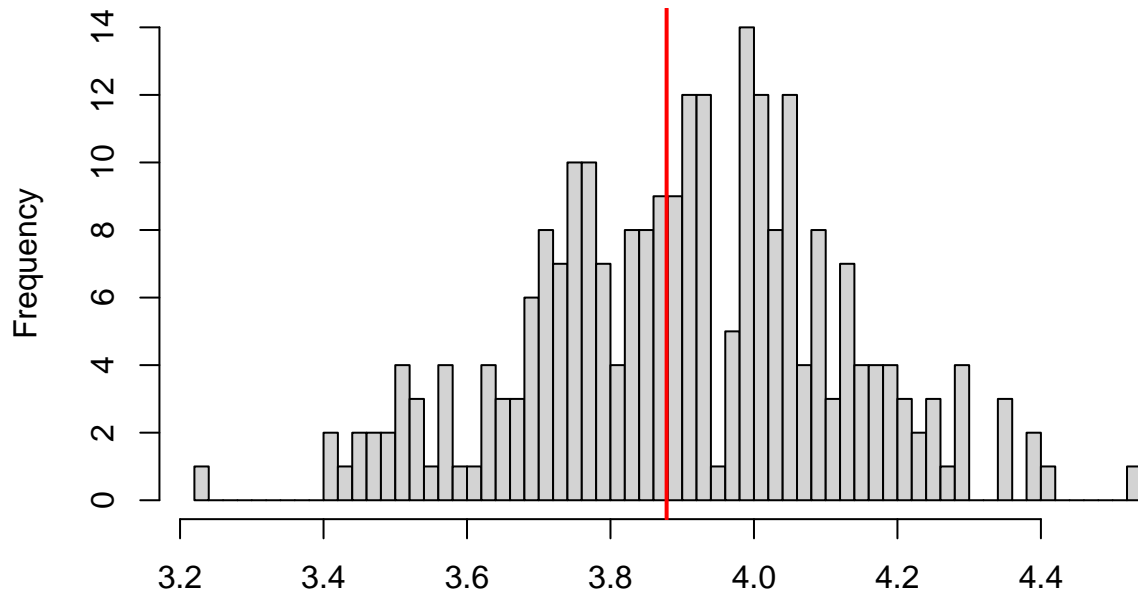
```
check_mod_dfreq2 <- simulateResiduals(fittedModel = dfreq_mod2, n=1000, plot=T)
```

### DHARMA residual diagnostics



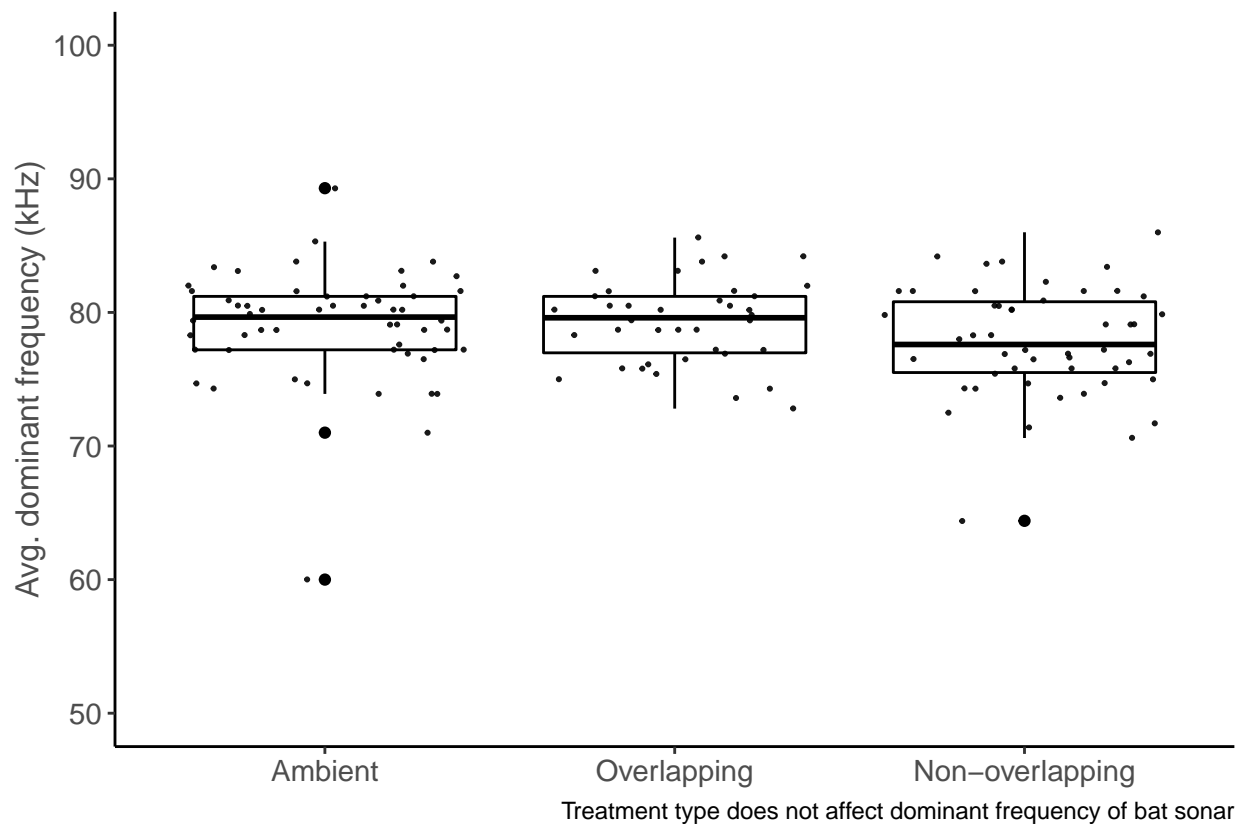
```
testDispersion(dfreq_mod2)
```

### DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.88

```
##  
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.  
## simulated  
##  
## data: simulationOutput  
## ratioObsSim = 0.99369, p-value = 0.88  
## alternative hypothesis: two.sided  
#Plot of the effect of Treatment on dom. frequency  
ggplot(acous, aes(x=Treatment, y=avg_dfreq))+geom_boxplot()+geom_jitter(color="black", size=0.4, alpha=
```



```
##Attempt plot##

#getting Attempt probabilities
dat1%>%
  mutate(pred_prob=predict(Attempt_mod3, type="response"))->pred_dat

colors1<-c("Ambient"="gray58", "Overlapping"="midnightblue", "Non-overlapping"="gold1")
Attempt_plot<-ggplot(pred_dat, aes(x=Night, y=Attempt, color=Treatment))+stat_smooth(method="glm", aes(

##Success plot##
set_theme(
  base=theme_blank(), axis.linecolor = "black", axis.ticksiz.e.y = 0.2)

me<-ggpredict(success_mod3, c("Treatment"))
Success_plot<-ggplot(me, aes(x=x, y=predicted, color=x))+geom_point(cex=2)+
  geom_errorbar(aes(ymin=conf.low, ymax=conf.high), width=0.15)+scale_color_manual(values=c("Ambient"="

##Search Time plot##
set_theme(
  base=theme_blank(), axis.linecolor = "black", axis.ticksiz.e.y = 0.2)

comparisons<-list(c("Ambient","Overlapping"),c("Ambient","Non-overlapping"),c("Non-overlapping", "Overl
ST_plot<-ggplot(dat2, aes(x=Treatment,y=Search_time, color=Treatment))+
```

```

geom_boxplot()+scale_color_manual(values=c("gray58","midnightblue","gold1"))+
geom_jitter(color="gray40", size=0.5, alpha=0.9) +
ggpubr::stat_compare_means(comparisons=comparisons, label.y=c(50, 55, 61),label="p.signif")+
theme(legend.position="none", axis.title.x=element_blank(), axis.text.x=element_text(size=15), axis.t

##Avg IPI plot##
set_theme(
  base=theme_blank(), axis.linecolor = "black", axis.ticksiz.y = 0.2)

IPI_plot<-ggplot(acous, aes(x=Treatment,y=avg_IPI, color=Treatment))+
geom_boxplot()+scale_color_manual(values=c("gray58","midnightblue","gold1"))+
geom_jitter(color="gray40", size=0.5, alpha=0.9)+
stat_compare_means(comparisons=comparisons, label.y=c(180, 190, 205),label="p.signif")+
theme(legend.position="none", axis.title.x=element_blank(), axis.text.x=element_text(size=15), axis.t

#Making combined plot
#library("useful")
#library(grid)
#png(filename="Fig2_draftb.png", width=500, height=1000, units="px", 12)
#grid.newpage()
#pushViewport(viewport(layout = grid.layout(3,1)))
#print(Success_plot, vp = vplayout(1,1))
#print(ST_plot, vp = vplayout(2,1))
#print(IPI_plot, vp = vplayout(3,1))

#dev.off()

```