

Noise distracts foraging bats - supplement

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```
##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

```
#reordering 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
```

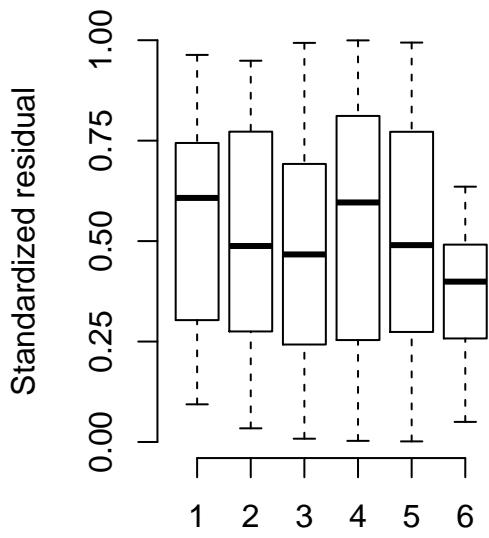
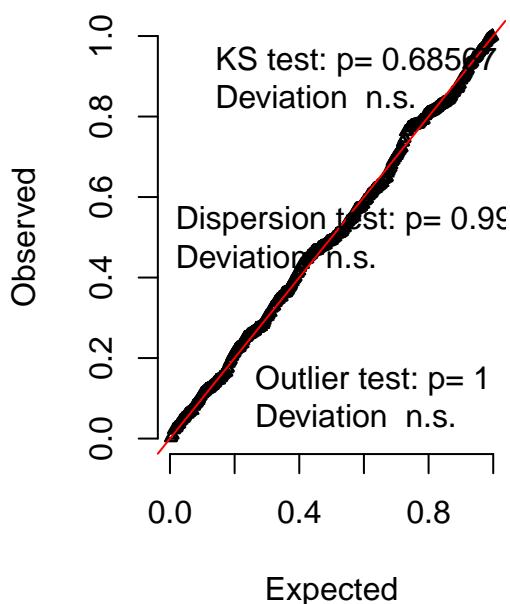
```

## 
## (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)

```

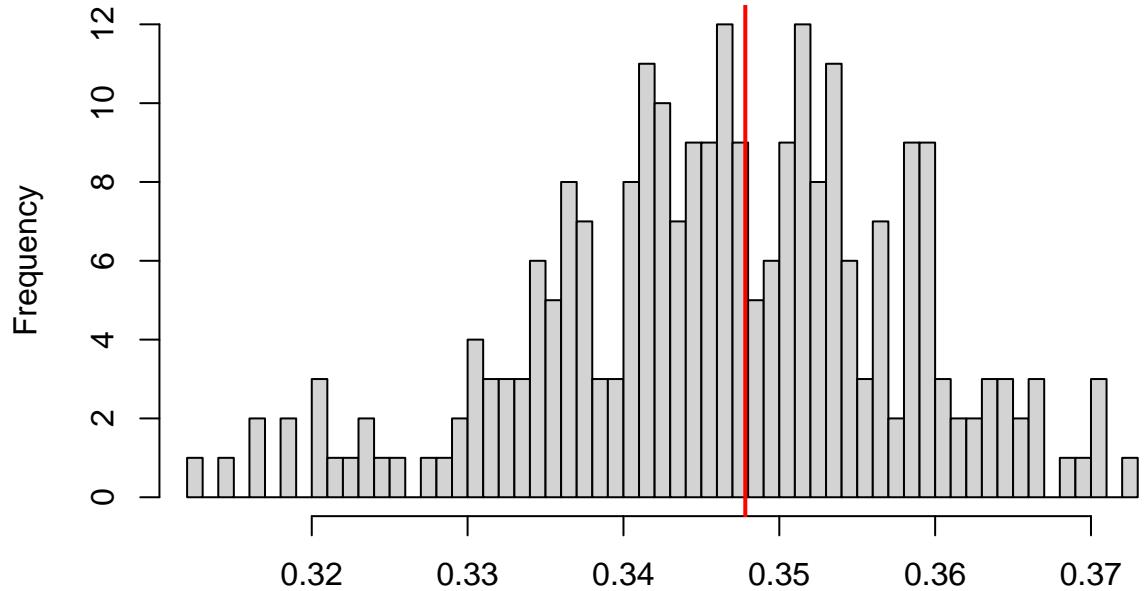
DHARMA residual diagnostics

QQ plot residuals



```
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="Figure S1. Interaction between treatment and presence of a prey reward.
  There is no difference in probability of attempting capture with or without a prey item.", title=element_blank())+theme(axis.title.x=element_blank())

```

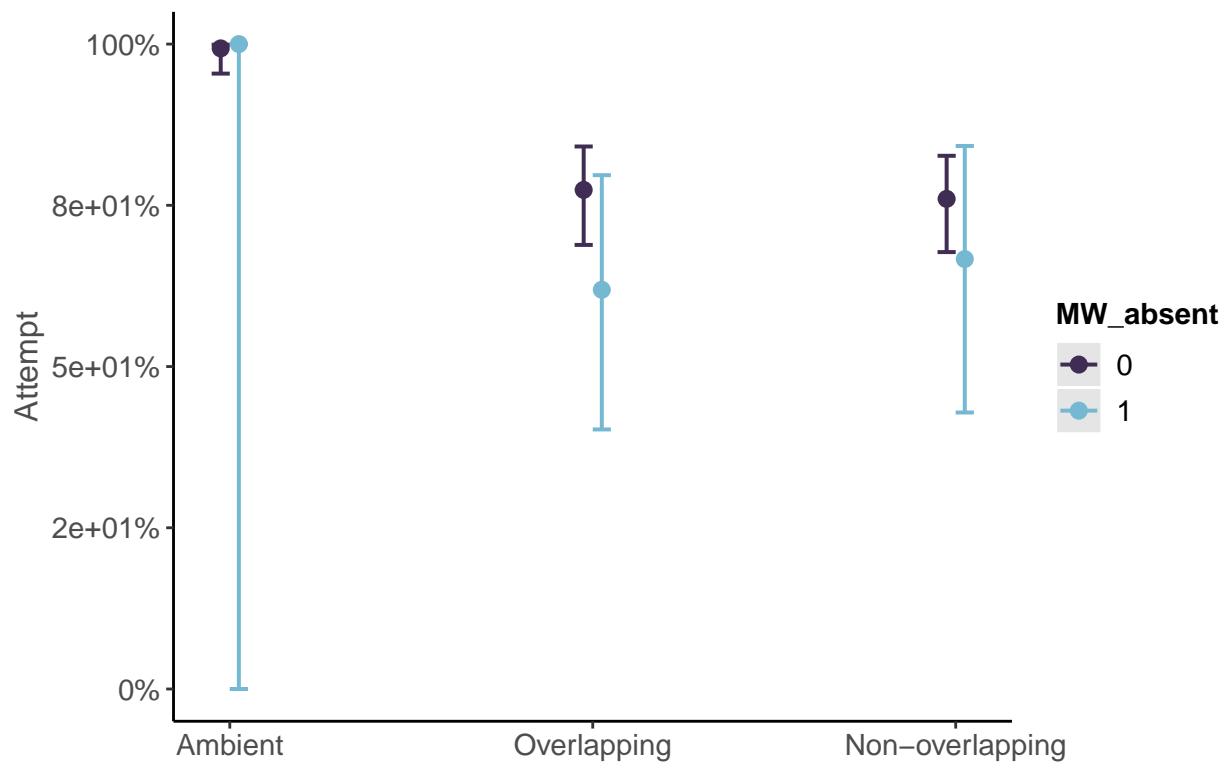


Figure S1. Interaction between treatment and presence of a prey reward.
There is no difference in probability of attempting capture with or without a prey item.

```
###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)
```

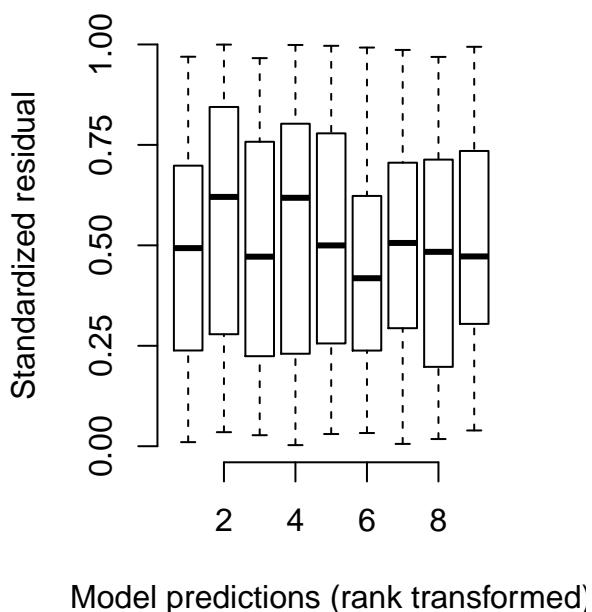
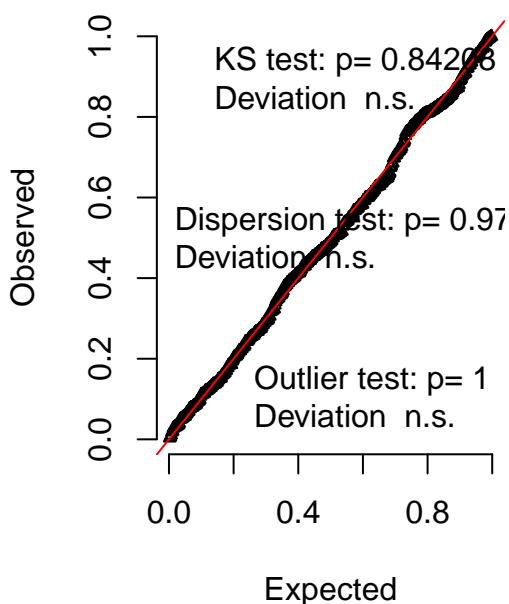
```

## 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)

```

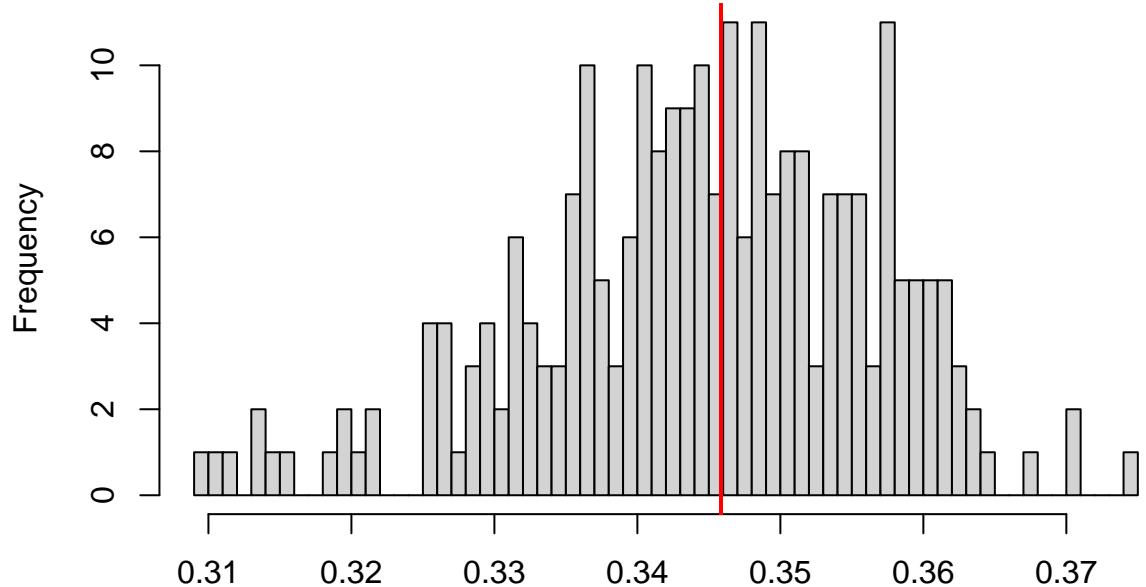
DHARMA residual diagnostics

QQ plot residuals



```
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="Figure S2. Interaction between treatment type and bat ID. Bats do not differ from  
  each other across treatments.",  
  title=element_blank())+theme(axis.title.x=element_blank())
```

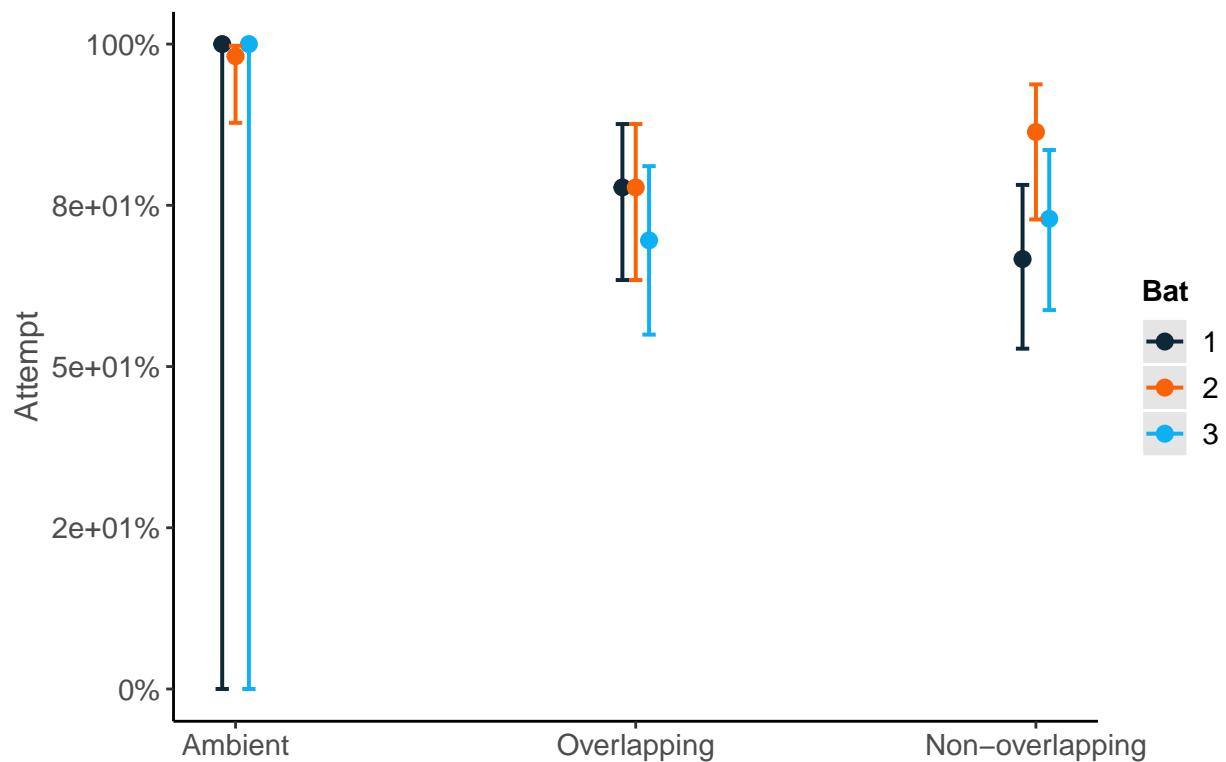


Figure S2. Interaction between treatment type and bat ID. Bats do not differ from each other across treatments.

```
###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
```

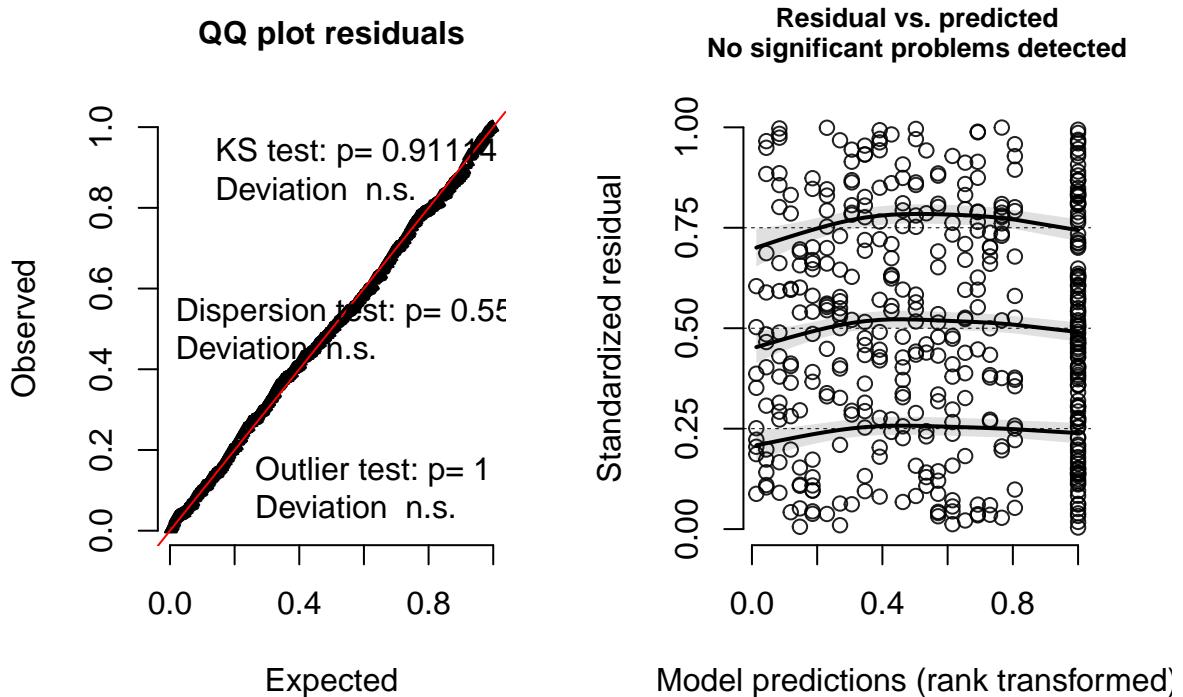
```

## Residual deviance: 276.08 on 432 degrees of freedom
## AIC: 288.08
##
## Number of Fisher Scoring iterations: 21
#Getting confidence intervals
CI_attempt<-emmeans(Attempt_mod3, "Treatment", transform="log", type="response", level=0.95)

#checking model fit
check_mod_AT3 <- simulateResiduals(fittedModel = Attempt_mod3, n=1000, plot=T)

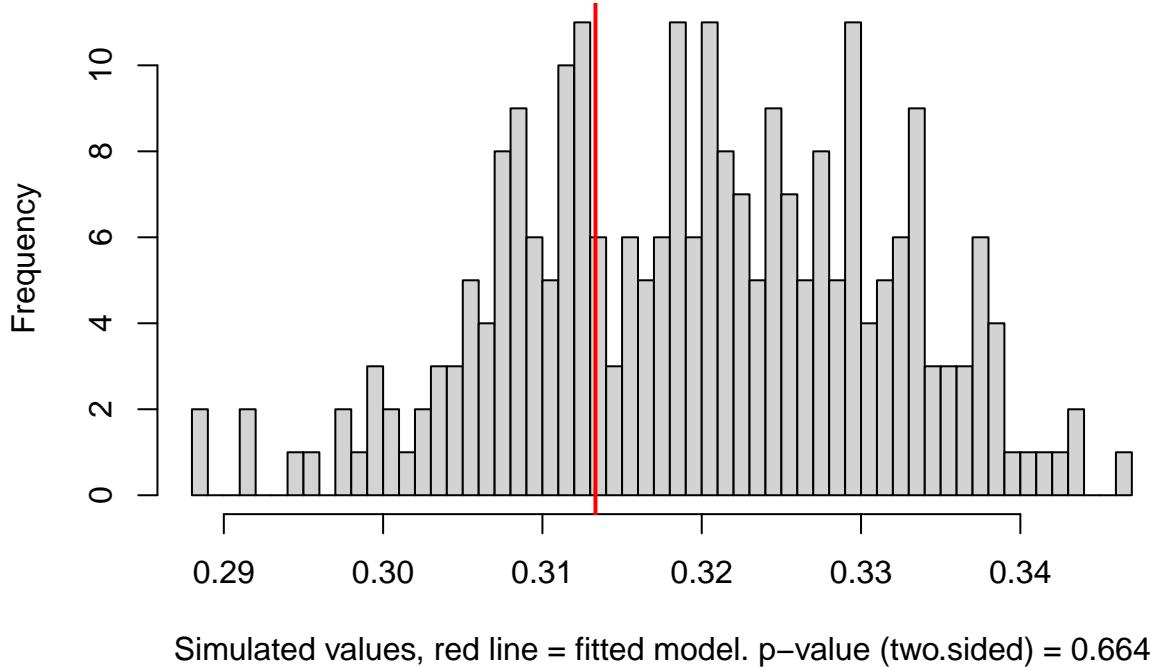
```

DHARMA residual diagnostics



```
testDispersion(Attempt_mod3)
```

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



```
##  
## 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)
```

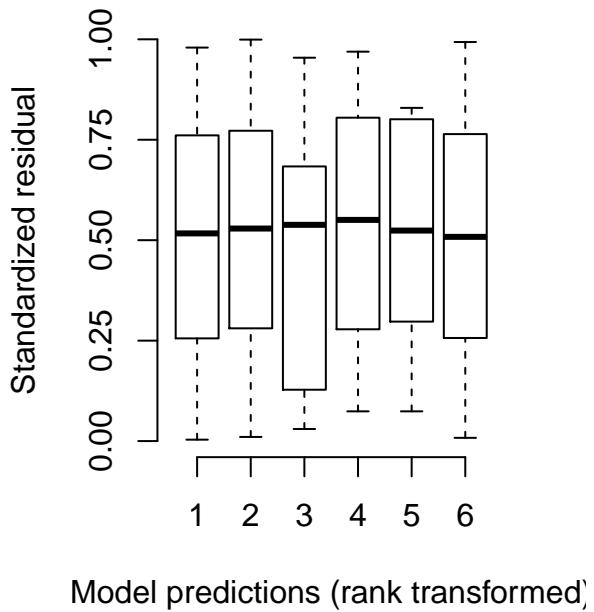
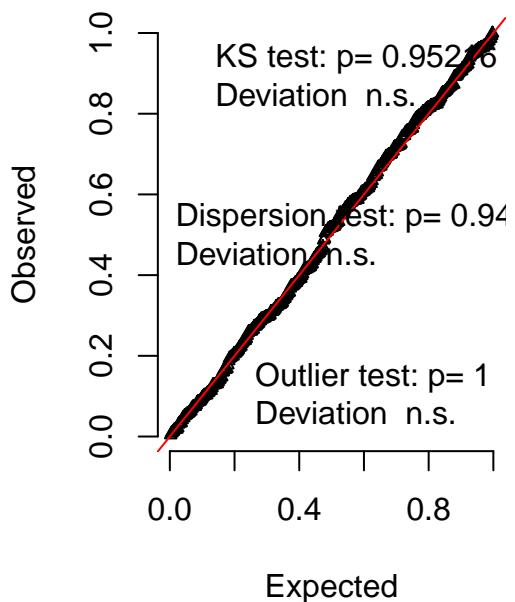
```

##      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_
## Trtmnt0vrlp -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)

```

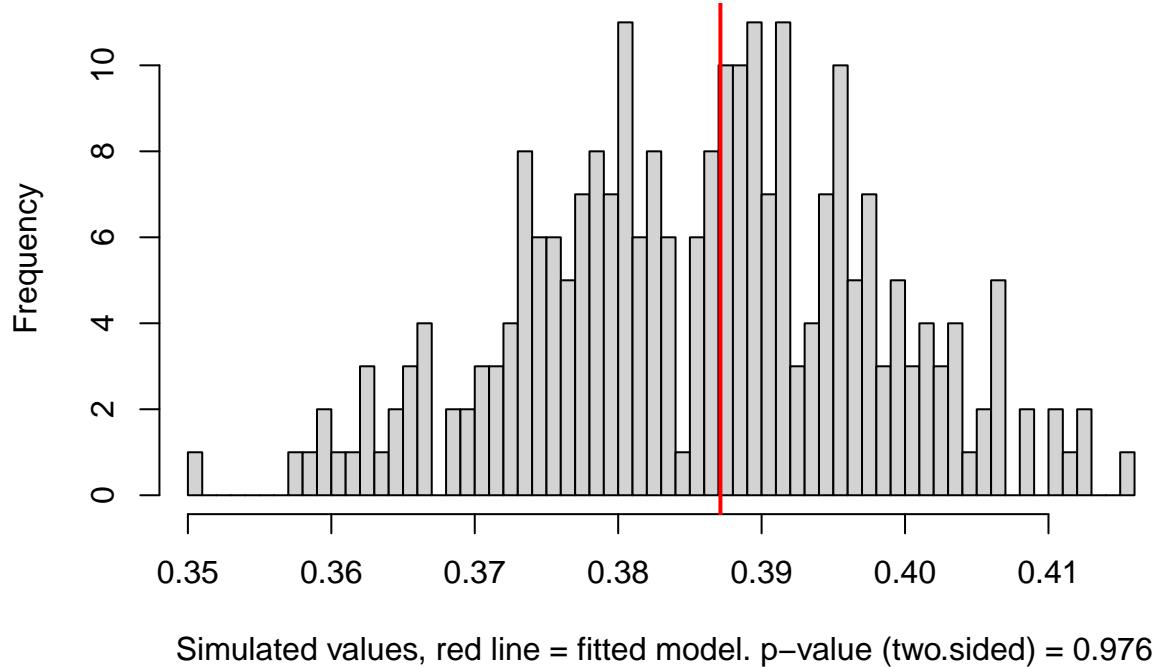
DHARMA residual diagnostics

QQ plot residuals



```
testDispersion(success_mod1)
```

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



```

## 
## 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="Figure S3. Interaction between treatment type and presence of a prey reward.
  There is no difference in probability of success with or without a prey item.", title=element_

```

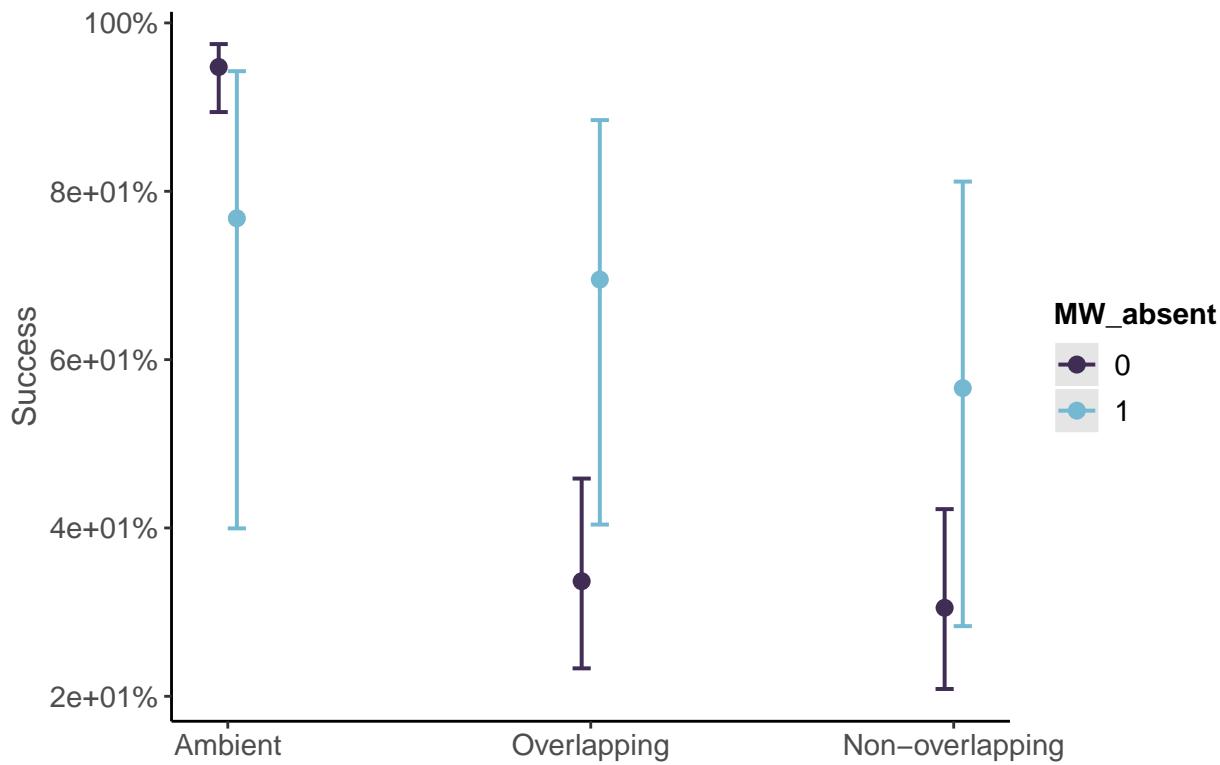


Figure S3. Interaction between treatment type and presence of a prey reward.
There is no difference in probability of success with or without a prey item.

```
### 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)
```

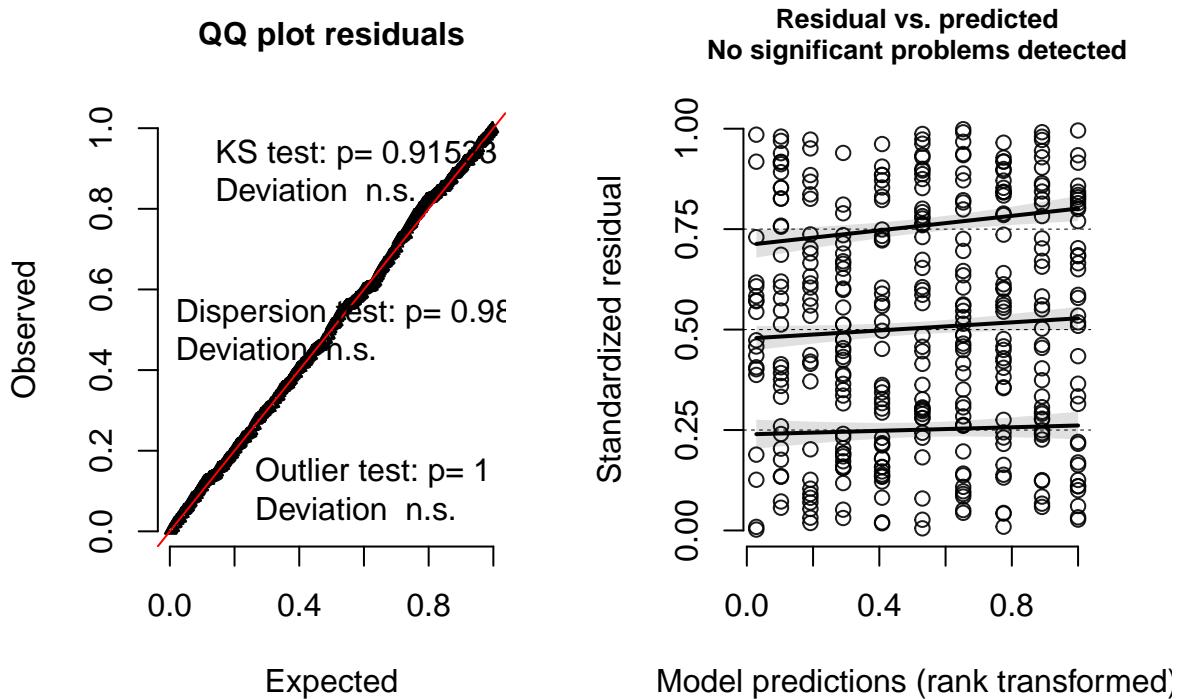
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Success ~ Night + (1 | Bat)
## Data: dat2
##
##      AIC      BIC  logLik deviance df.resid
##      497.3    509.0   -245.7     491.3     364
##
## Scaled residuals:
##      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)

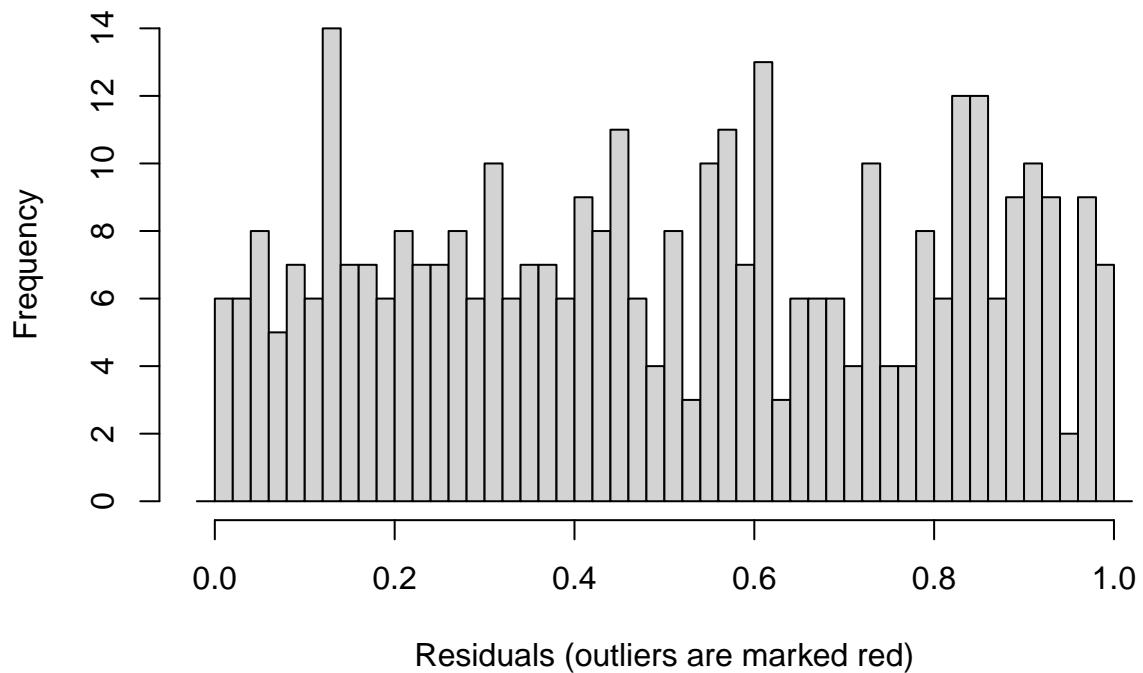
```

DHARMA residual diagnostics



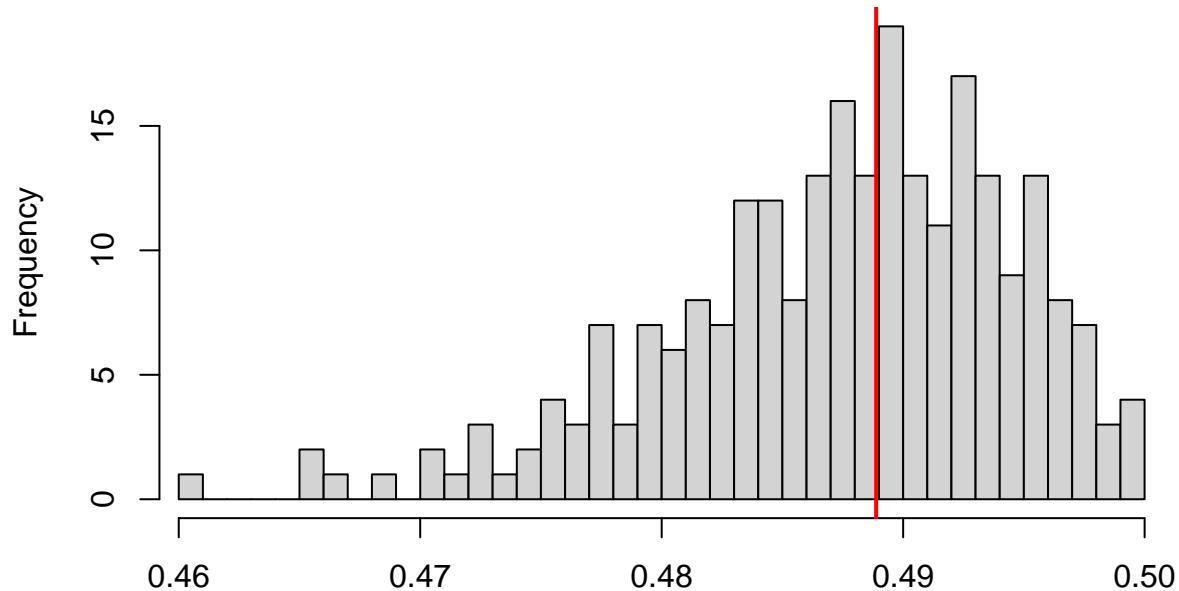
```
hist(check_mod_Suc2)
```

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),
```

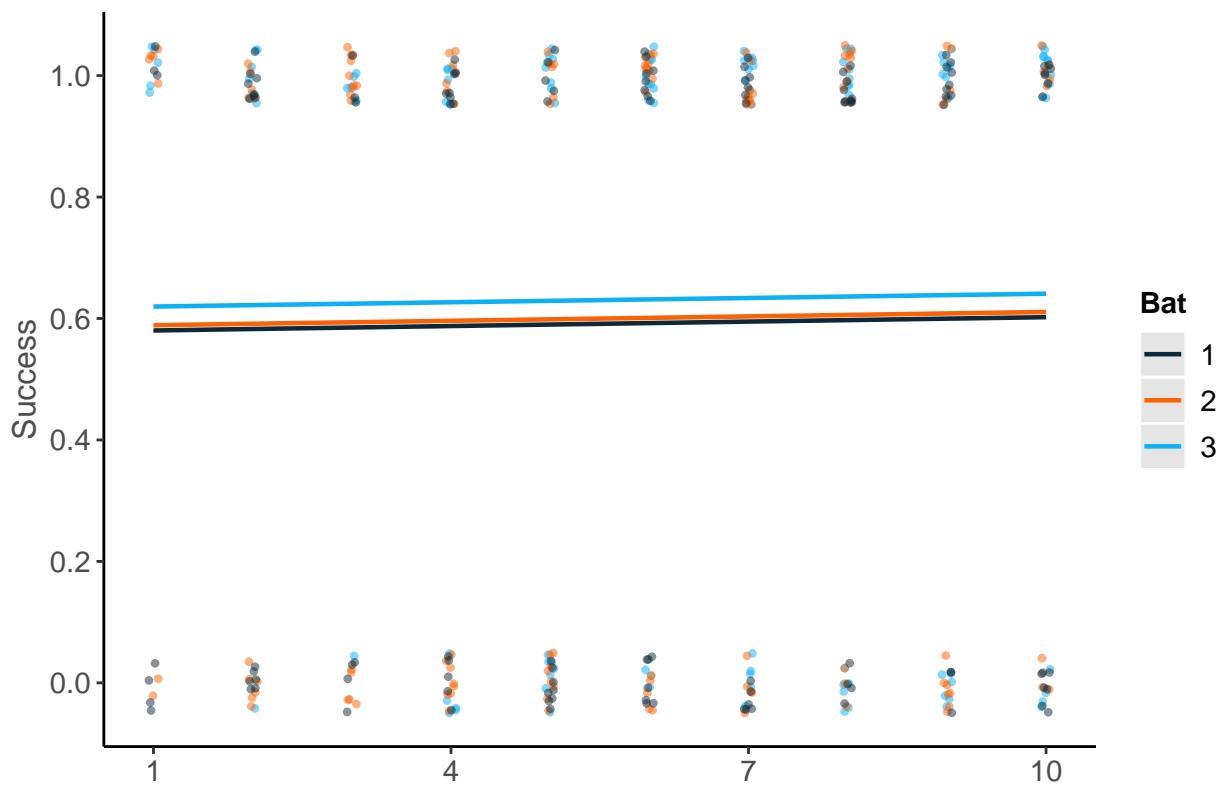


Figure S4. Probability of success does not change across experimental night for all bats

```
### 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 ***
```

```

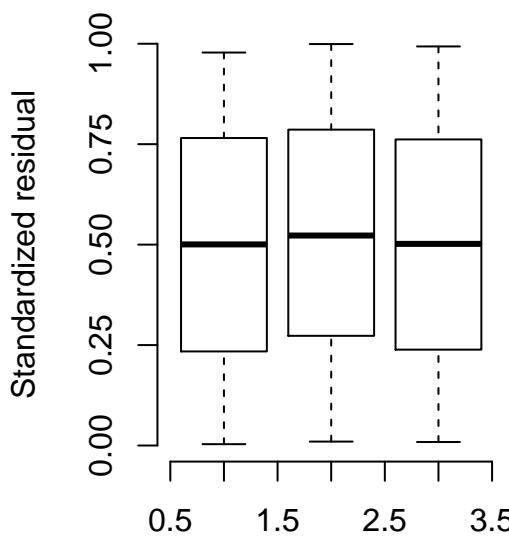
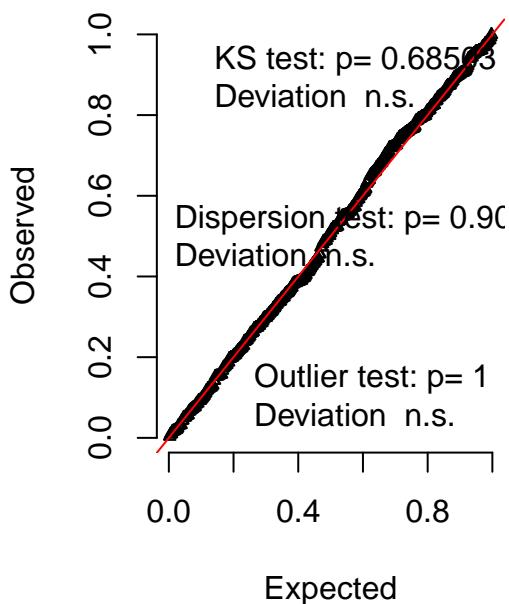
## TreatmentOverlapping      -3.1976      0.3879   -8.243 < 2e-16 ***
## TreatmentNon-overlapping -3.4067      0.3894   -8.749 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) Trtmn0
## TrtmntOvrlp -0.784
## TrtmntNn-vr -0.783  0.720
#
#Getting confidence intervals
CI_success<-emmeans(success_mod3, "Treatment", transform="log", type="response", level=0.95)

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

```

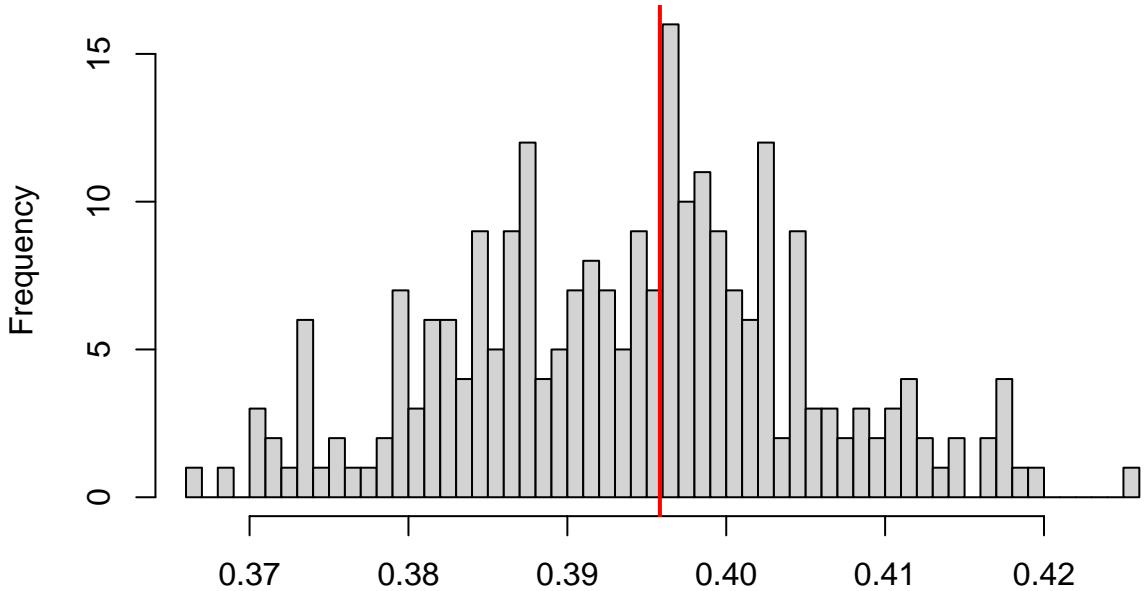
DHARMA residual diagnostics

QQ plot residuals



```
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]
```

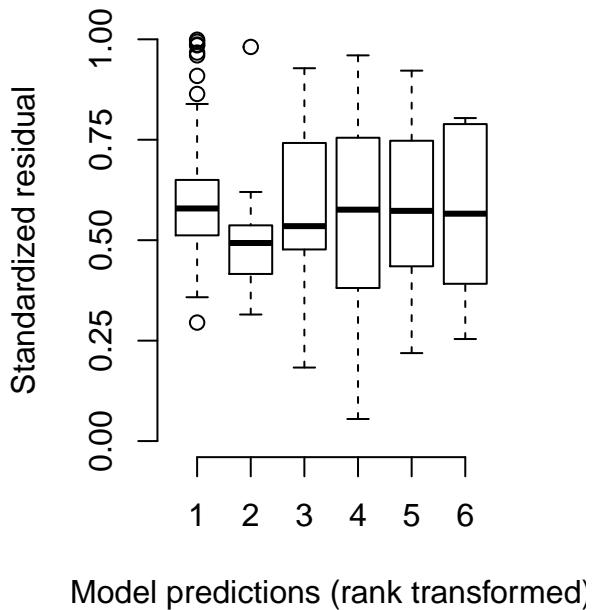
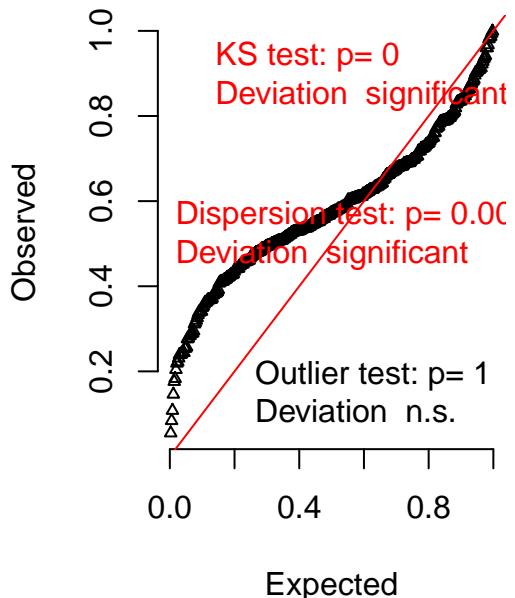
```

## 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 T0:MW_
## TrtmntOvrlp -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)

```

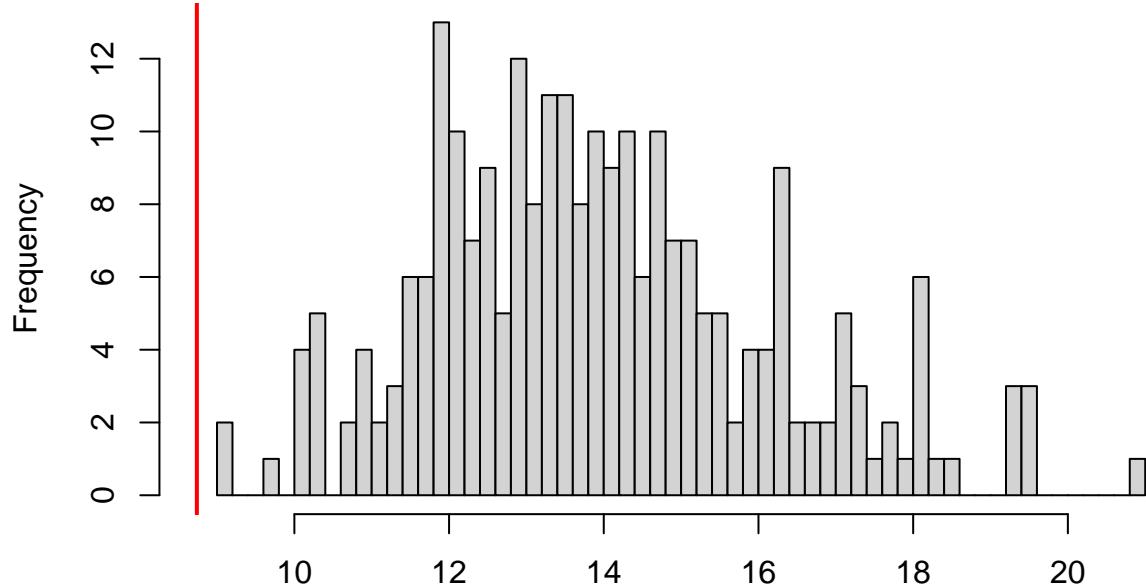
DHARMA residual diagnostics

QQ plot residuals



```
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="Figure S5. Interaction between treatment type and presence of a prey reward.  
  There is no difference in search time across treatment treatments with or without a prey item.",  
    ylab("Search time (ms)"))
```

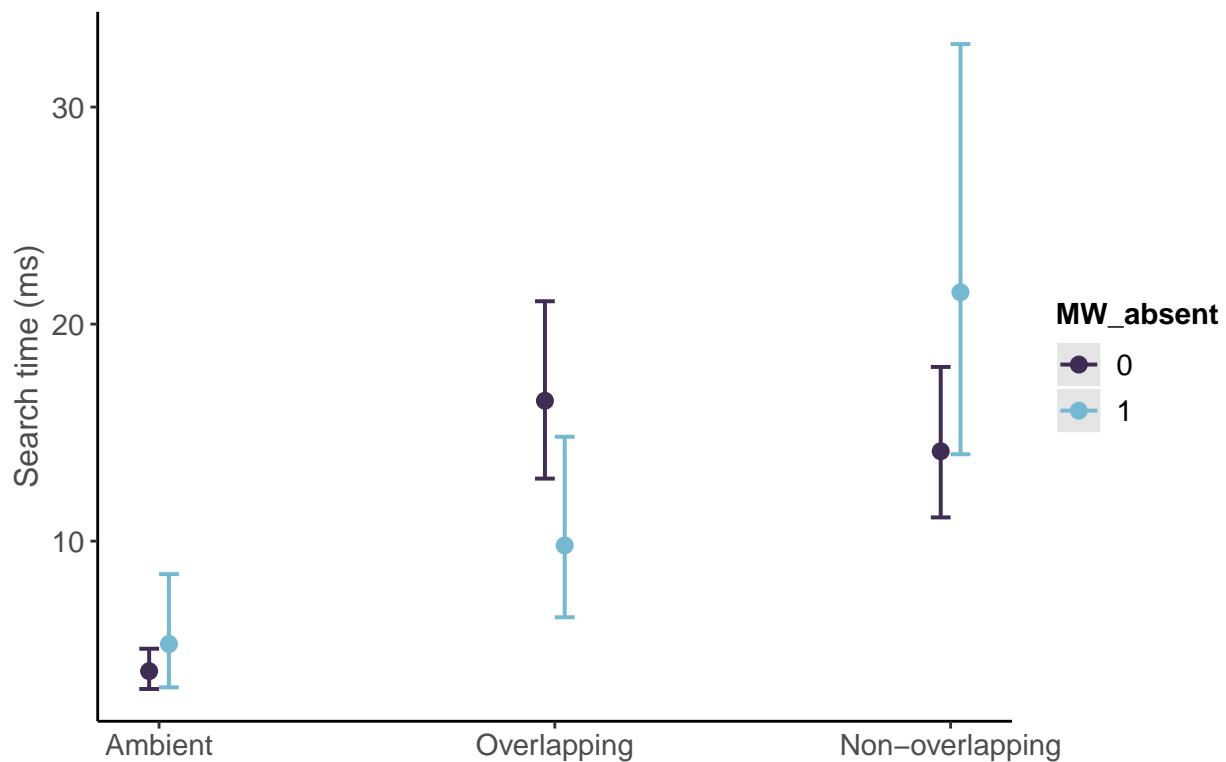


Figure S5. Interaction between treatment type and presence of a prey reward.
There is no difference in search time across treatment treatments with or without a prey item.

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

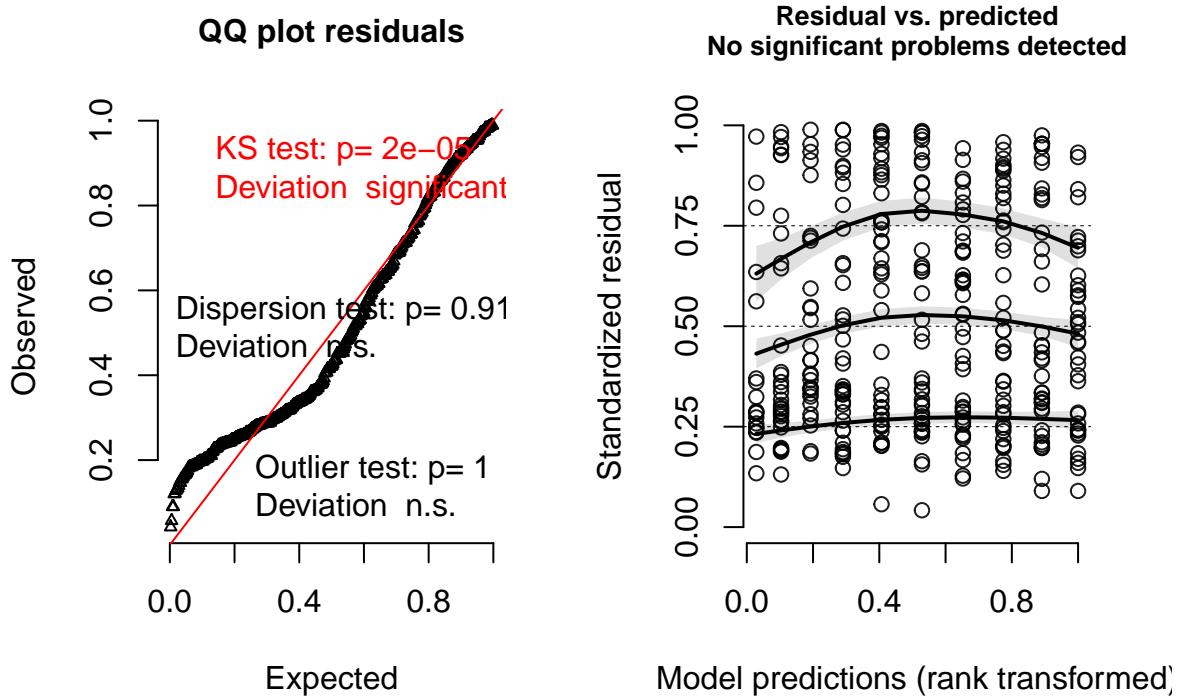
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: Gamma ( log )
## Formula: Search_time ~ Night + (1 | Bat)
## Data: dat2
##
##      AIC      BIC  logLik deviance df.resid
##  2453.9  2469.5 -1222.9   2445.9     362
##
## Scaled residuals:
##      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)

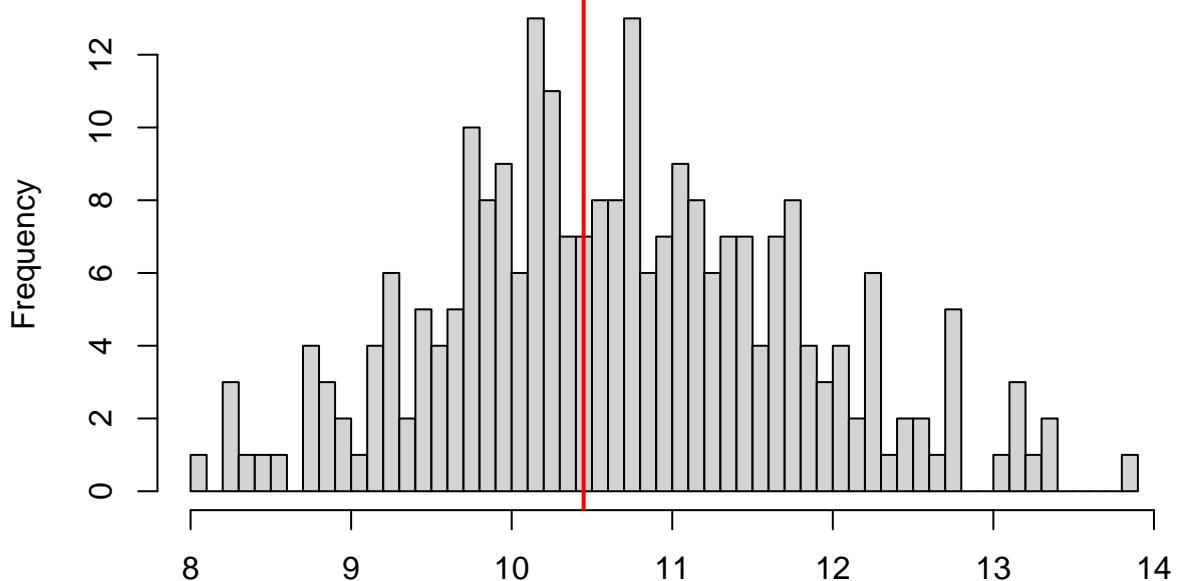
```

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
```

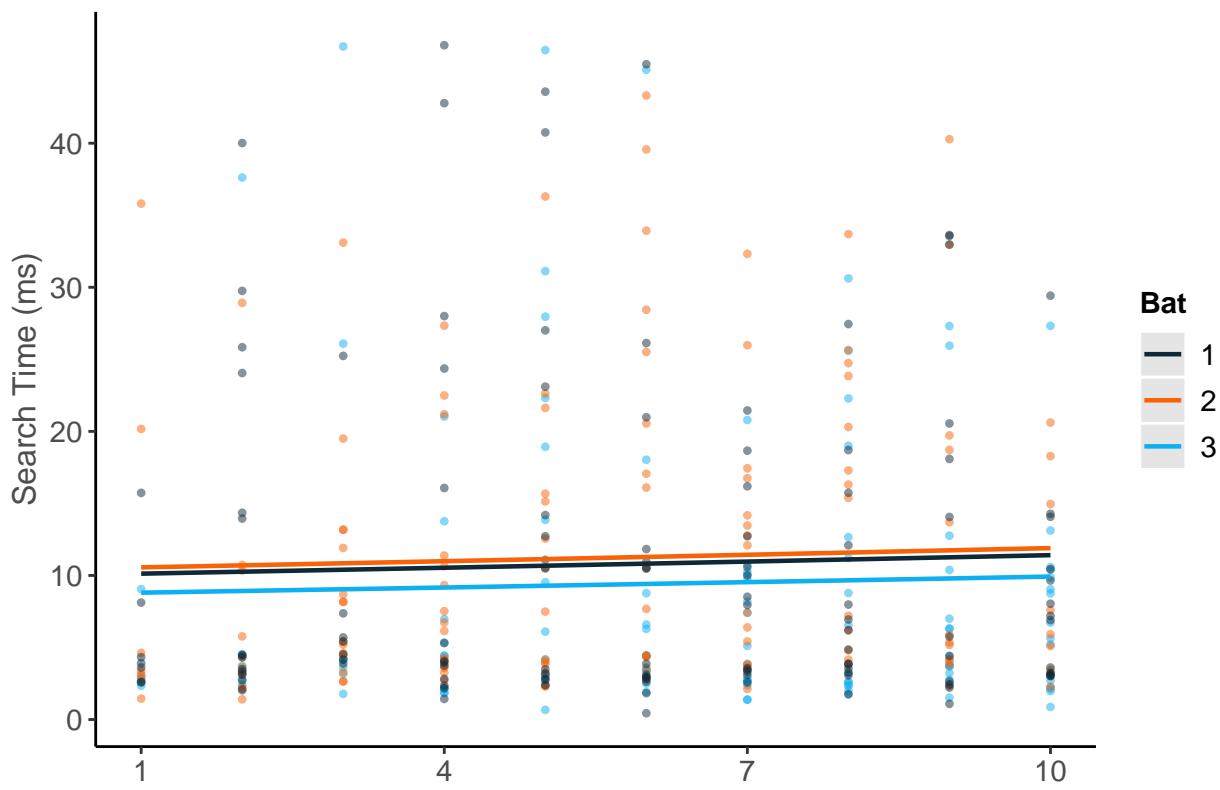


Figure S6. Search time does not change across experimental night for all bats

One bat (bat 2) in particular began taking longer to make a foraging decision (i.e., land on a speaker) in ambient conditions beginning on Night 7, and eventually refused to land at all in the final ambient trial on the final night. This could have been due to increasing experimental fatigue, but as he continued to forage in all treatments, we preserved his data in our final set.

In general, bats displayed slight behavioral differences from each other that were internally consistent across treatments and did not have an effect on the outcome of the study. For example, one of the bats (bat 3) took less time on average to make a foraging decision than the other bats, however, this was not drastic and she followed the same trend as the others, i.e., her search time increased in both noise conditions.

###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
##
```

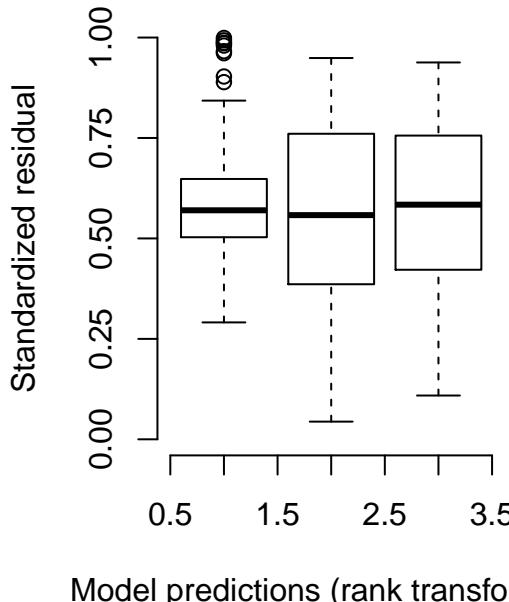
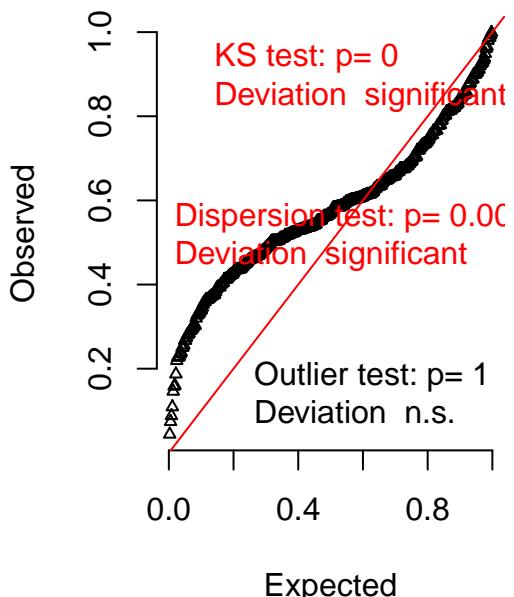
```

## 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)

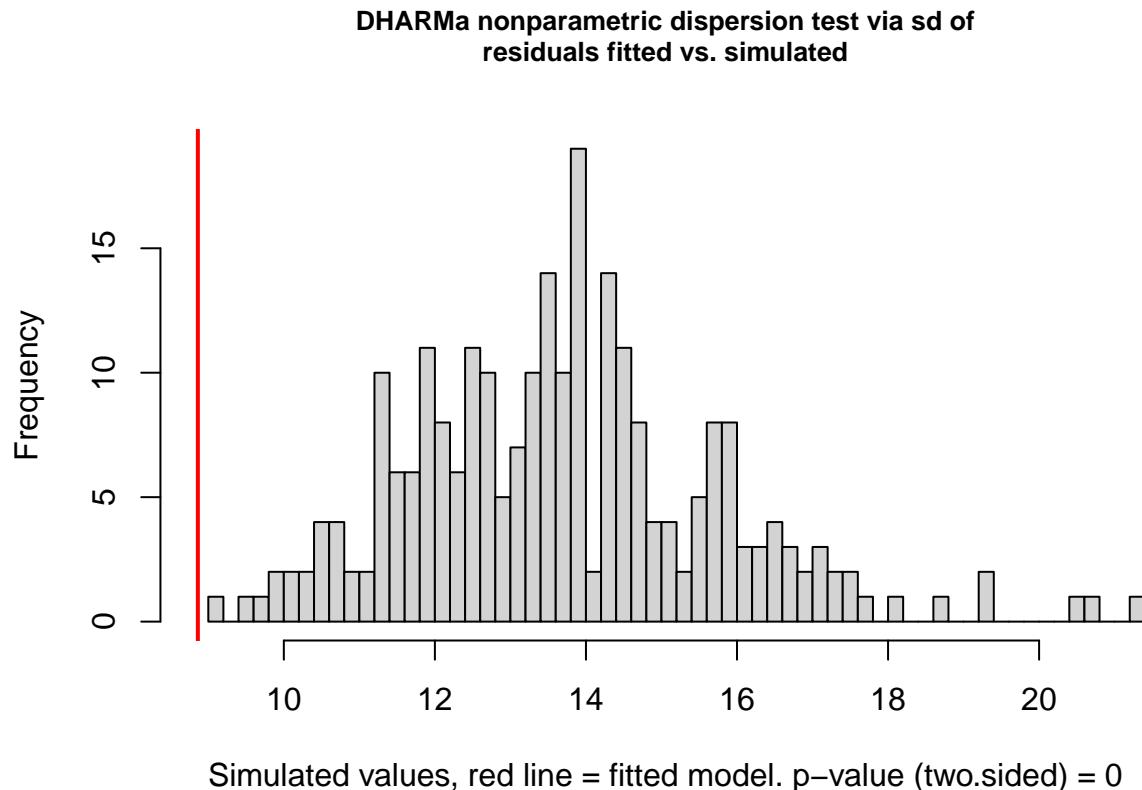
```

DHARMA residual diagnostics

QQ plot residuals



```
testDispersion(ST_mod3)
```



```
##  
## 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  
CI_ST<-emmeans(ST_mod3, "Treatment", transform="log", type="response", level=0.95)
```

Some of these models display evidence of underdispersion in our DHARMA check, however, we found that our parameter estimates were robust to model distribution selection and random intercept inclusion and we therefore chose to maintain our initial model structure. Additionally, underdispersion is less problematic than overdispersion, as it leads to statistical conservatism and low type I errors [1].

Echolocation models

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

```
#reordering 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)

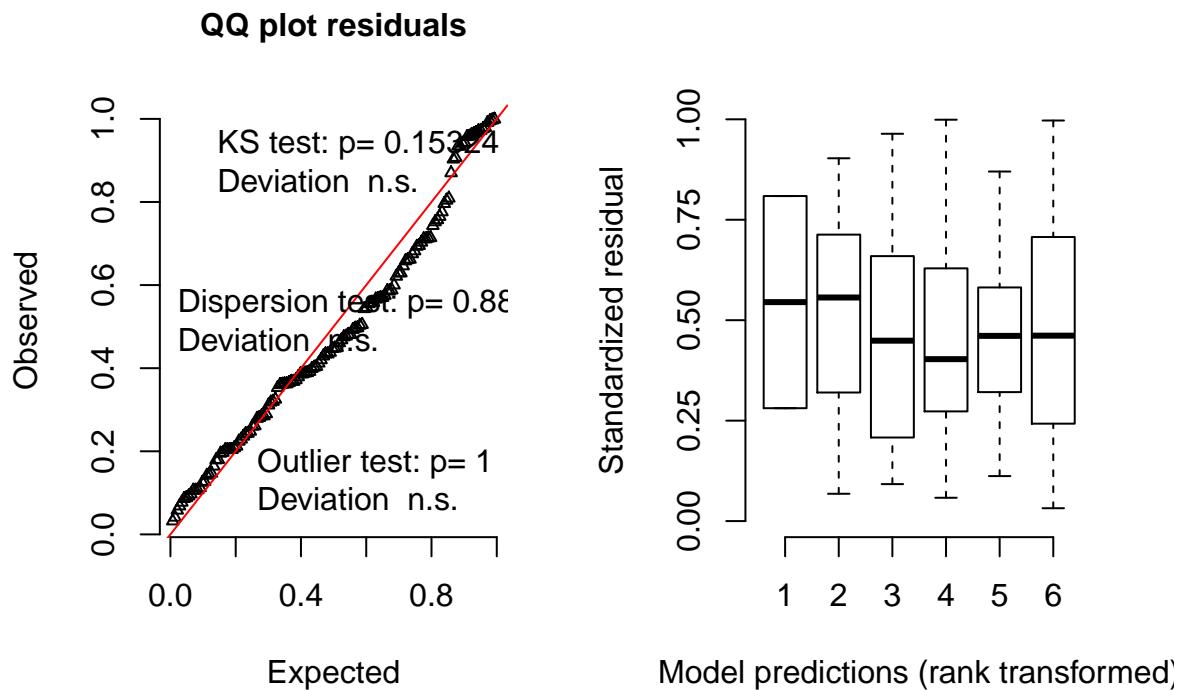
## Linear mixed model fit by REML ['lmerMod']
## Formula: avg_IPI ~ Treatment * MW_absent + (1 | Bat)
##   Data: acous
##
## REML criterion at convergence: 1270.4
##
```

```

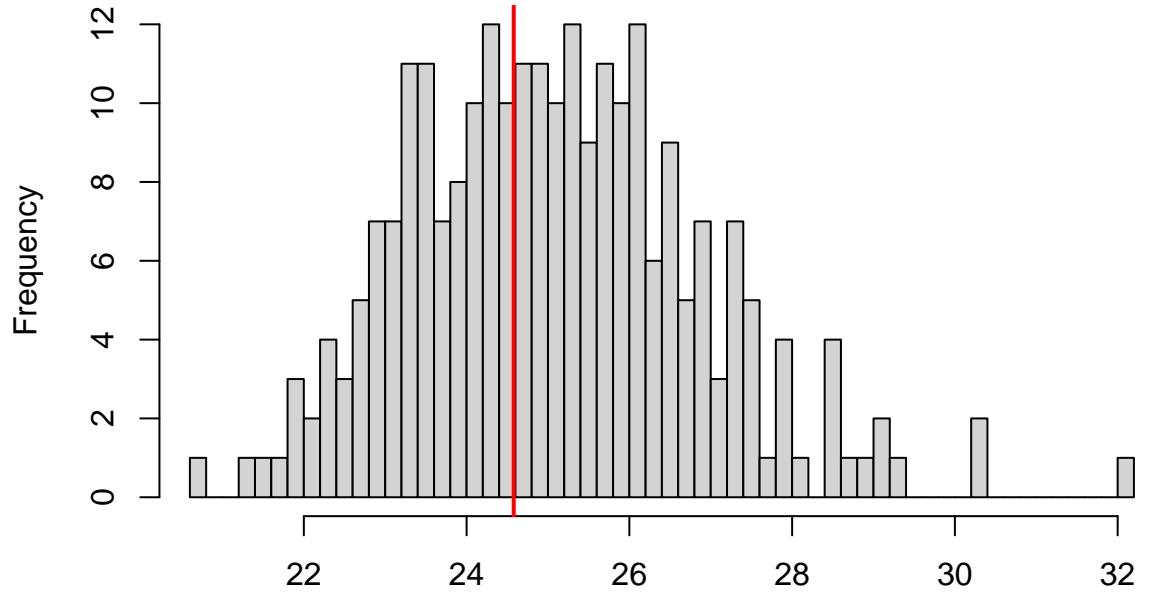
## Scaled residuals:
##      Min     1Q Median     3Q    Max
## -1.8183 -0.6449 -0.1462  0.4195  2.7271
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   Bat       (Intercept) 79.11    8.894
##   Residual             576.56   24.012
##   Number of obs: 142, groups: Bat, 3
##
## Fixed 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_
##   TrtmntOvrlp -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



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="Figure S7. Interaction of treatment and presence of a prey reward.  
  There is no difference in average IPI across treatments with or without a prey item.", title=element
```

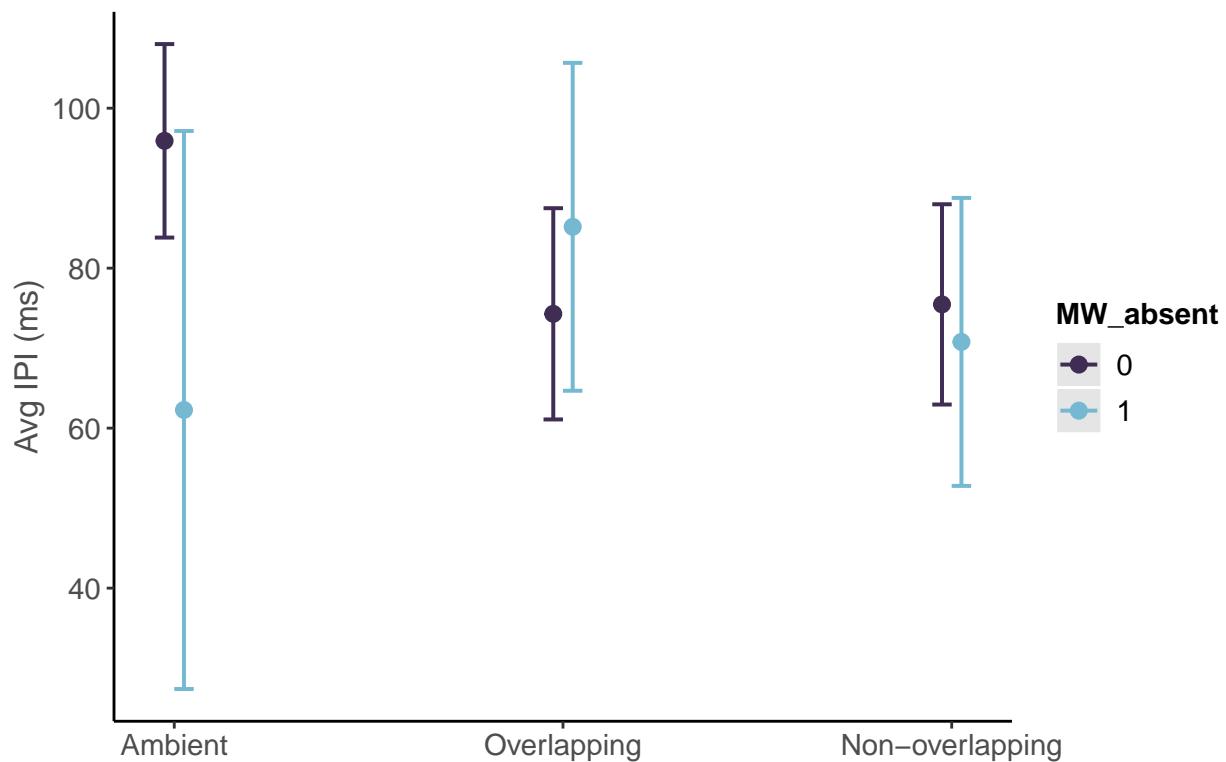


Figure S7. Interaction of treatment and presence of a prey reward.
There is no difference in average IPI across treatments with or without a prey item.

```
###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 ***

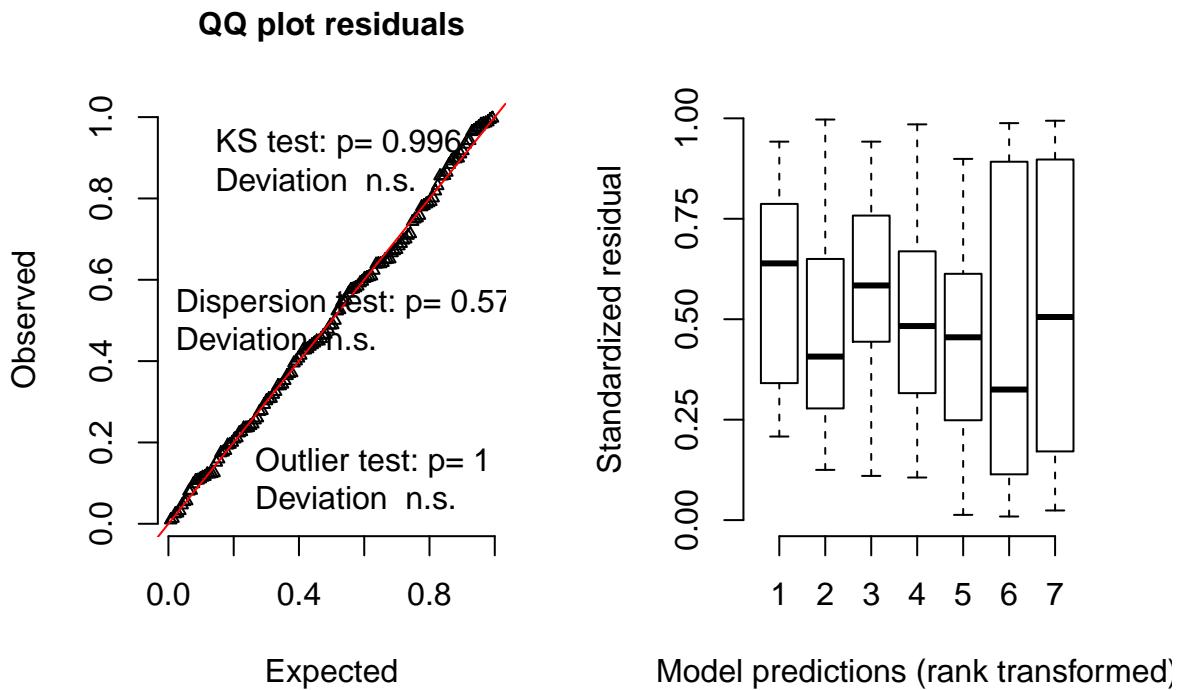
```

```

## 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)

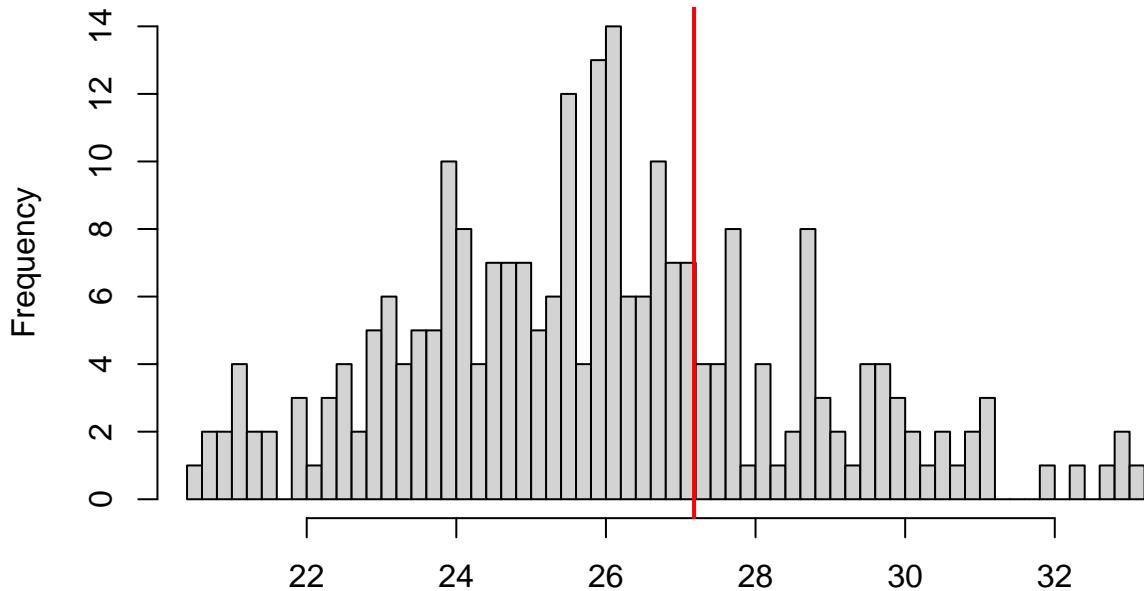
```

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="Figure S8. 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())
```

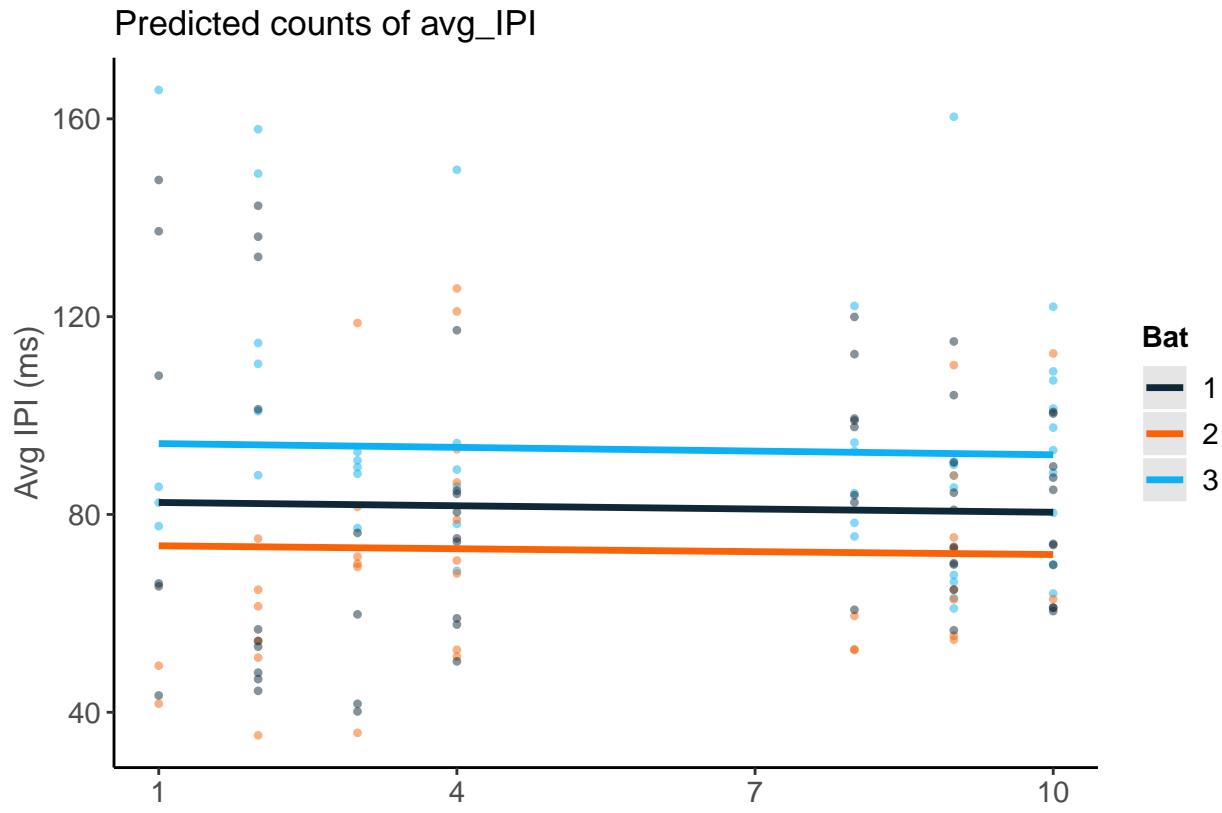


Figure S8. IPI does not change across experimental night for all bats

```
###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
```

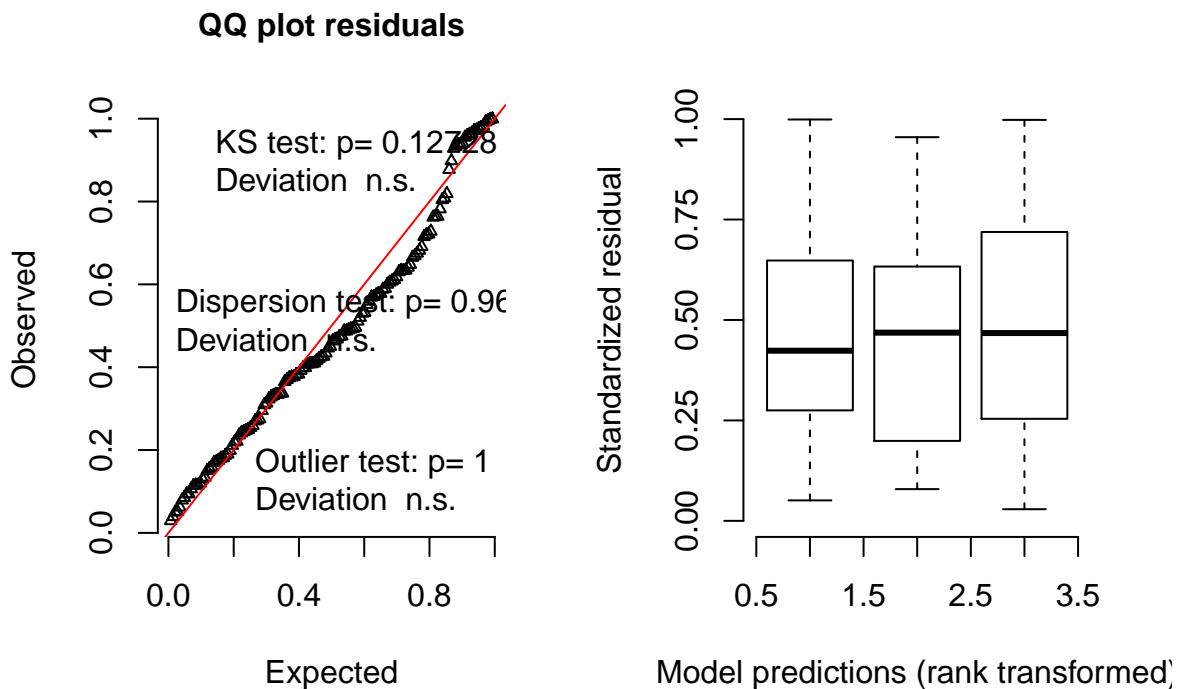
```

## TreatmentNon-overlapping -20.308      4.816   -4.217
##
## Correlation of Fixed Effects:
##           (Intr) Trtmn0
## TrtmntOvrlp -0.373
## TrtmntNn-vr -0.402  0.461
#
#getting confidence intervals
CI_IPI<-emmeans(IPI_mod3, "Treatment", type="response", level=0.95)

#checking model fit
check_IPI_mod3<-simulateResiduals(fittedModel = IPI_mod3, n=1000, plot=T)

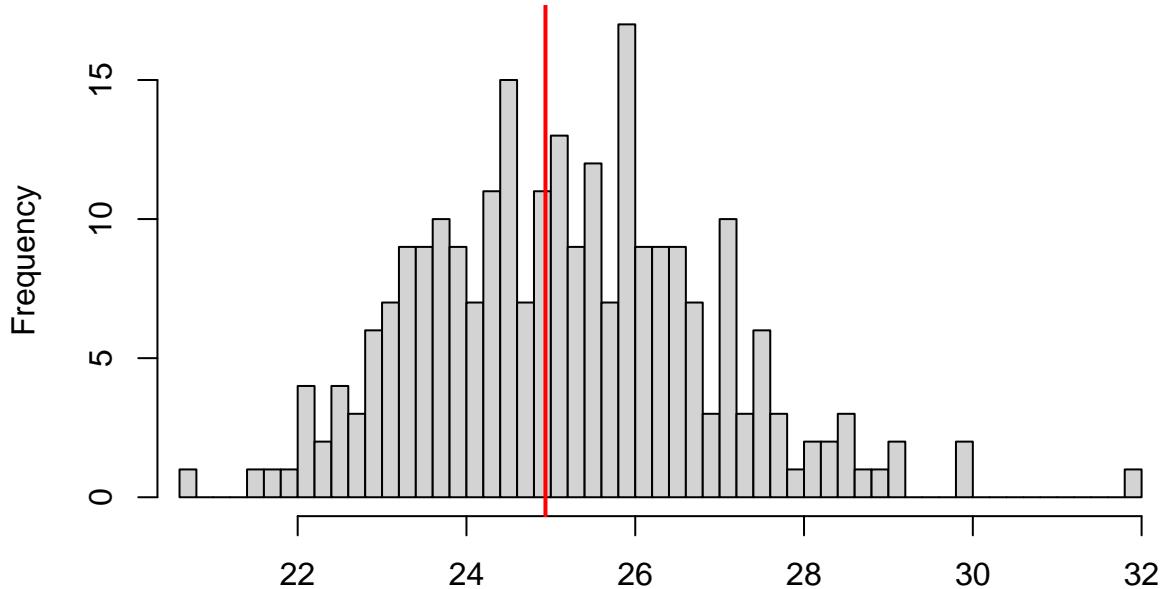
```

DHARMA residual diagnostics



```
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.
## 
```

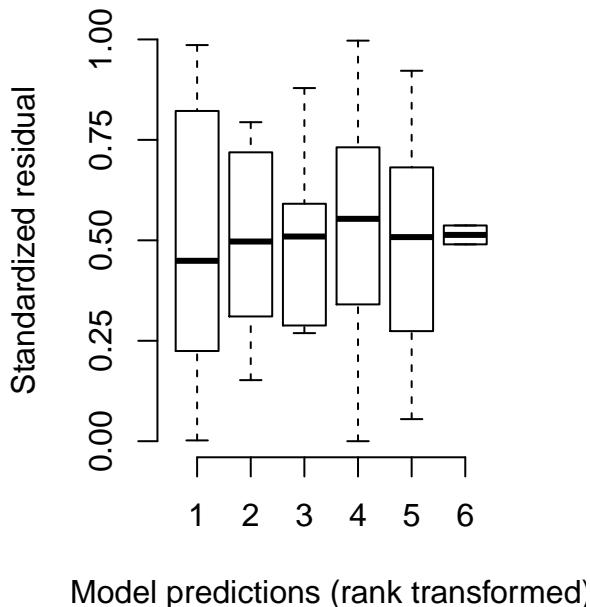
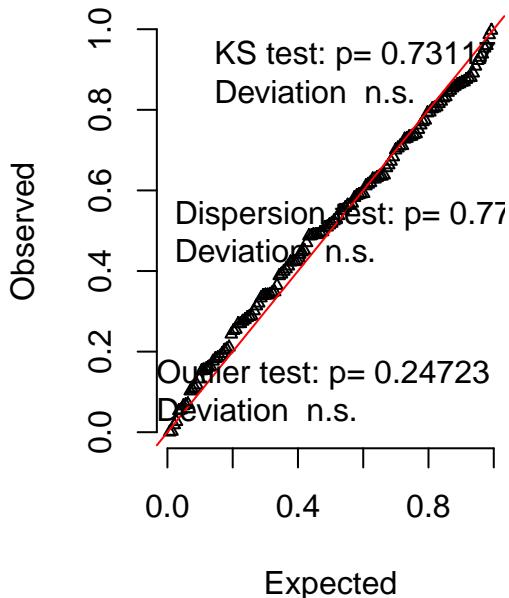
```

##  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_
## TrtmntOvrlp -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)

```

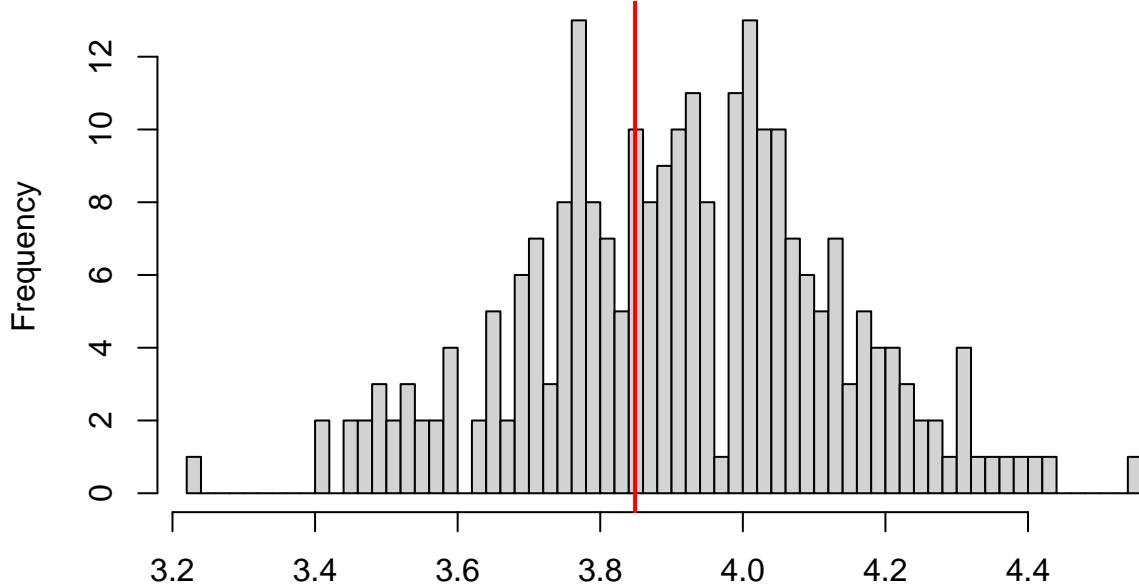
DHARMA residual diagnostics

QQ plot residuals



```
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="Figure S9. Interaction of treatment and presence of a prey item. There is no difference in dominant frequency with or without a prey item.", title=element_blank())+theme(axis.title.x=element_blank())
```

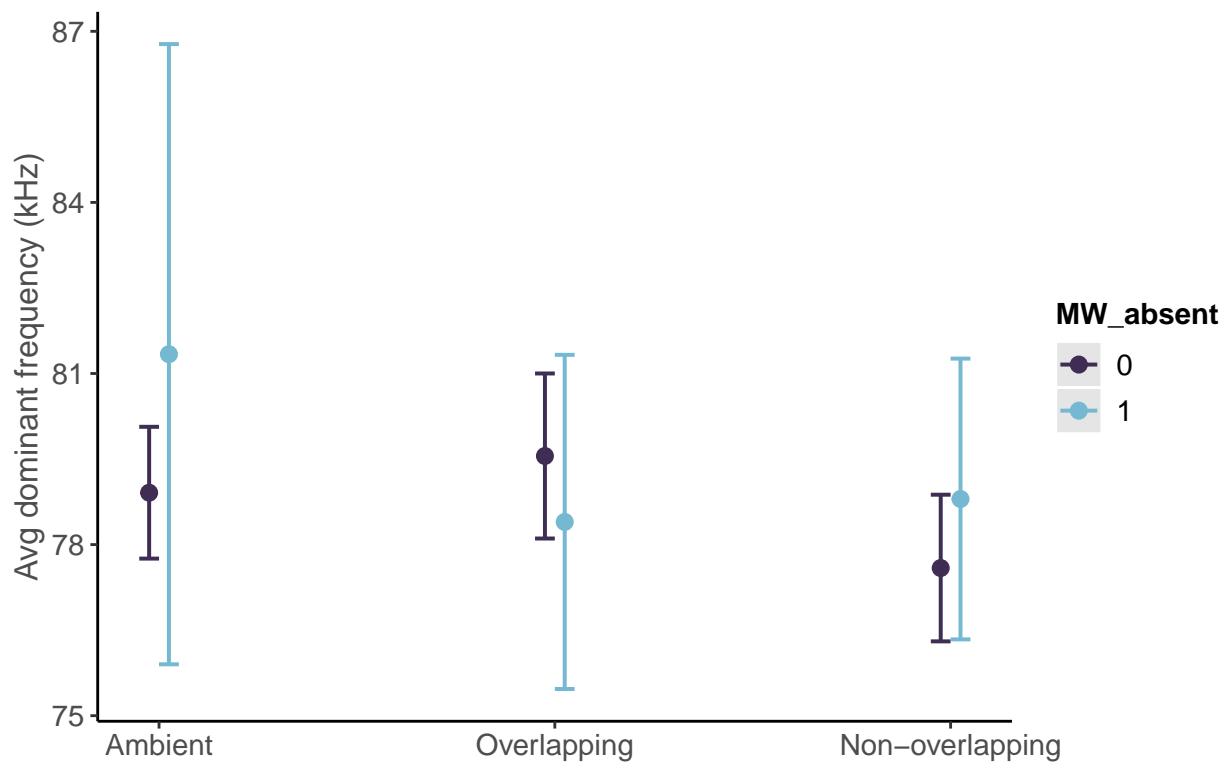


Figure S9. Interaction of treatment and presence of a prey reward.
There is no difference in dominant frequency with or without a prey item.

```
###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
```

```

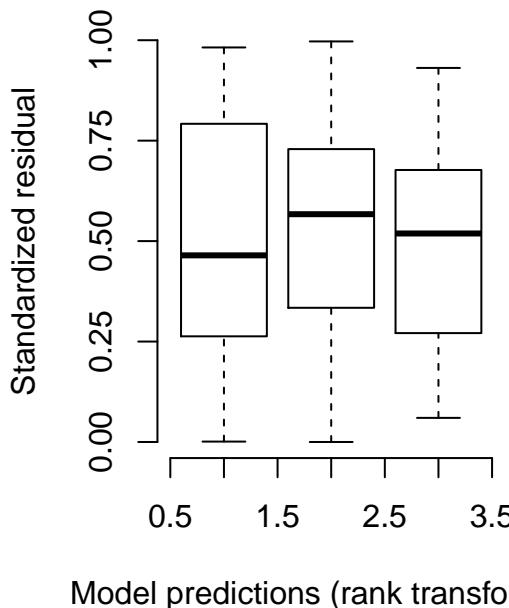
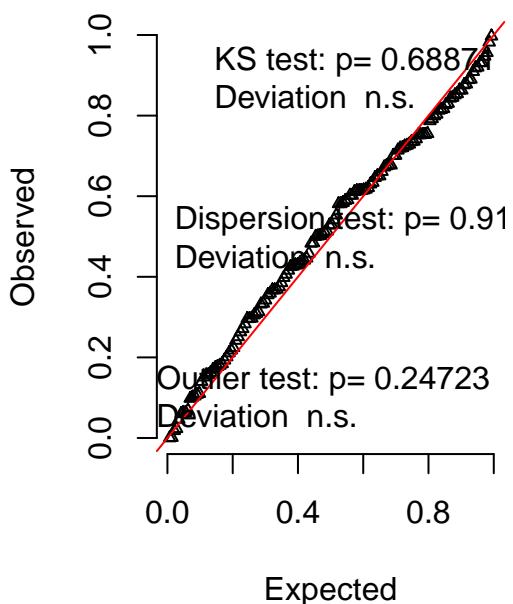
## TreatmentNon-overlapping -1.1507      0.7674   -1.499
##
## Correlation of Fixed Effects:
##           (Intr) Trtmn0
## TrtmntOvrlp -0.582
## TrtmntNn-vr -0.628  0.452
#getting confidence intervals
CI_df<-emmeans(dfreq_mod2, "Treatment", type="response")

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

```

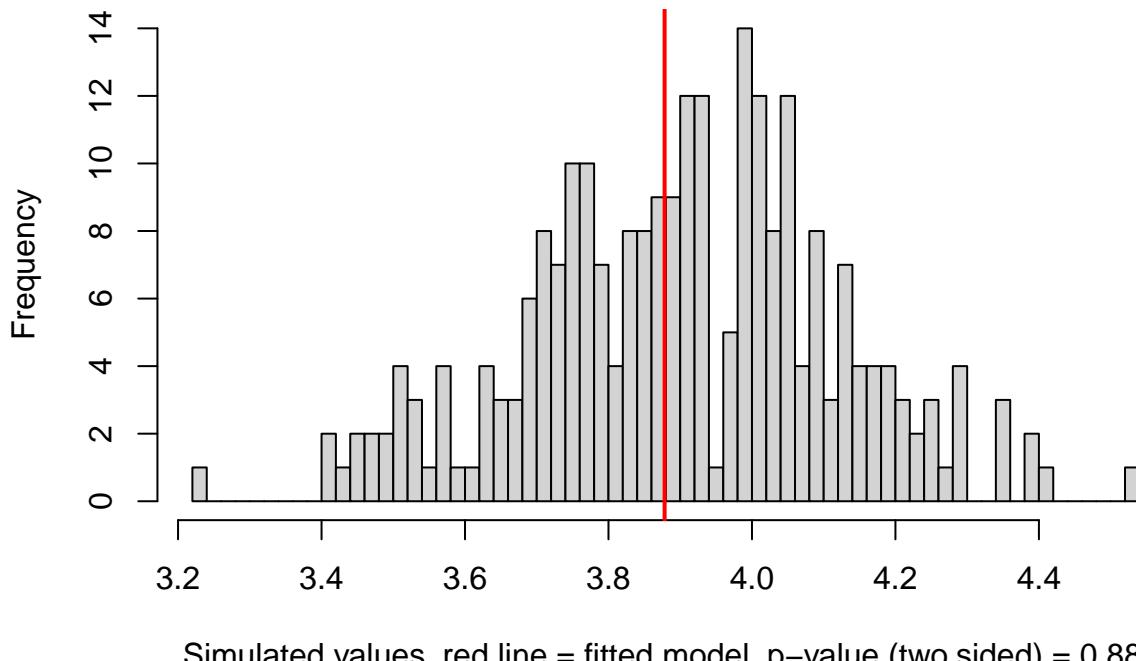
DHARMA residual diagnostics

QQ plot residuals



```
testDispersion(dfreq_mod2)
```

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



```
##  
## 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=
```

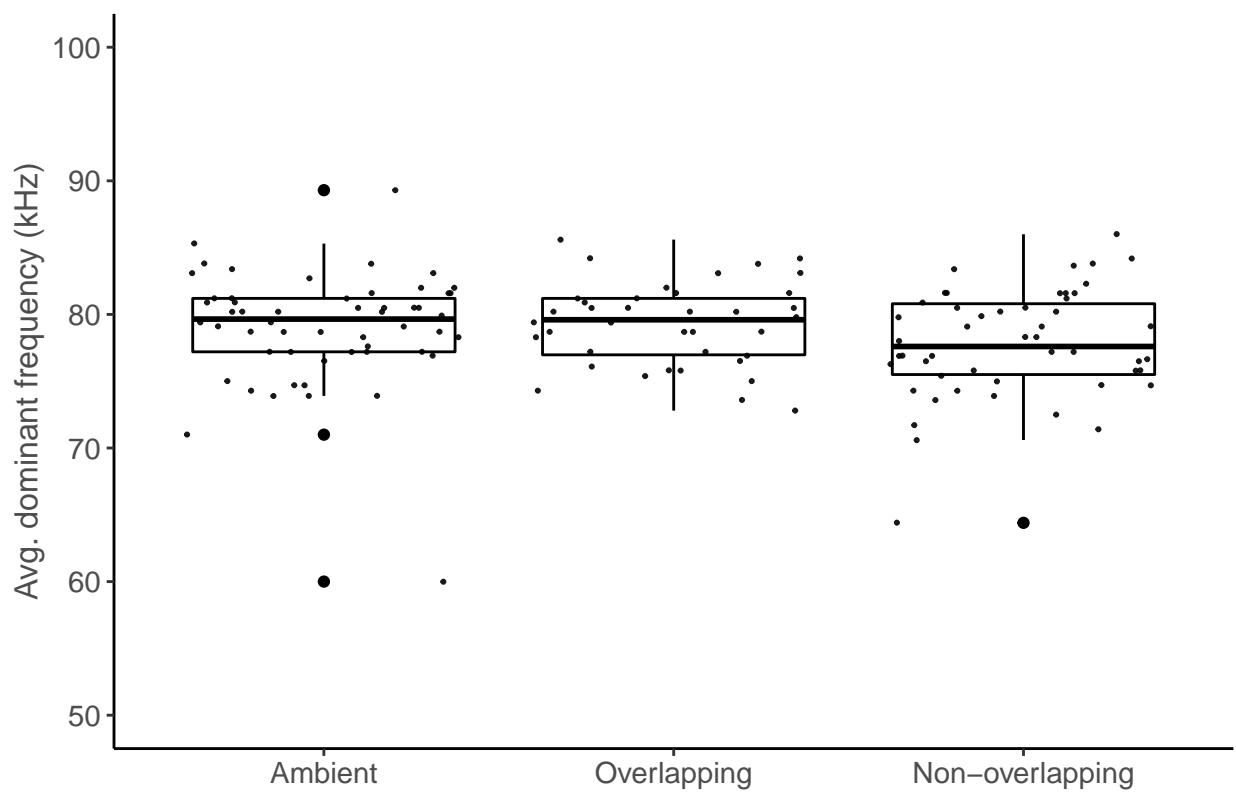


Figure S10. Treatment type does not affect dominant frequency of bat sonar

References

1. Schielzeth, H. et al. 2020 Robustness of linear mixed-effects models to violations of distributional assumptions. *Methods in Ecology and Evolution* **11**, 1141–1152.