Untitled

```r
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --
```

```
## v ggplot2 3.3.5      v purrr   0.3.4
## v tibble  3.1.6      v dplyr   1.0.7
## v tidyr   1.1.4      v stringr 1.4.0
## v readr   2.1.1      v forcats 0.5.1
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```r
library(lme4)
```

```
## Loading required package: Matrix
```

```
##
## Attaching package: 'Matrix'
```

```
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
```

```r
library(lmerTest)
```

```
##
## Attaching package: 'lmerTest'
```

```
## The following object is masked from 'package:lme4':
##
##     lmer
```

```
## The following object is masked from 'package:stats':
##
##     step
```

```r
library(MASS)
```

```
##
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':
##
##     select
```

```
library(DHARMa)
```

```
## This is DHARMa 0.4.5. For overview type '?DHARMa'. For recent changes, type news(package = 'D
HARMa')
```

```
library(ggplot2)
library(effectsize)
```

```
## Warning: package 'effectsize' was built under R version 4.1.3
```

```
## Registered S3 method overwritten by 'parameters':
##   method                         from
##   format.parameters_distribution datawizard
```

```
library(EMAtools)
```

```
## Warning: package 'EMAtools' was built under R version 4.1.3
```

```
data <- read.csv("Z:/home/ryanh/projects/ripple_heterogeneity/replay_participation_df.csv")

data$basepath = factor(data$basepath)
data$animal = factor(data$animal)
data$deepSuperficial = factor(data$deepSuperficial)
data$epoch  = factor(data$epoch)
data$replay_type  = factor(data$replay_type)
data$replay_layer  = factor(data$replay_layer)

summary(data)
```

```
##        X            participation      rip_par         epoch        n_replays
## Min.   :  0.00   Min.   :0.0000   Min.   :0.0000   post:544   Min.   :  0.0
## 1st Qu.: 32.00   1st Qu.:0.1333   1st Qu.:0.0889   pre :544   1st Qu.: 11.0
## Median : 67.00   Median :0.2657   Median :0.1444   task:544   Median : 23.0
## Mean   : 80.76   Mean   :0.3085   Mean   :0.1819              Mean   : 30.7
## 3rd Qu.:115.00   3rd Qu.:0.4444   3rd Qu.:0.2388              3rd Qu.: 43.0
## Max.   :267.00   Max.   :1.0000   Max.   :0.8489              Max.   :107.0
##                  NA's   :24
##       UID          deepSuperficial deepSuperficialDistance
## Min.   :  1.0   Deep       :1200   Min.   :-214.29
## 1st Qu.: 24.0   Superficial: 432   1st Qu.: -90.17
## Median : 46.0                      Median : -42.50
## Mean   : 75.1                      Mean   : -36.32
## 3rd Qu.: 84.0                      3rd Qu.:  30.13
## Max.   :280.0                      Max.   : 285.87
##
##                                           basepath       replay_type
## Z:\\Data\\GrosmarkAD\\Achilles\\Achilles_11012013:294   forward:816
## Z:\\Data\\Kenji\\ec014.459_480                   :276   reverse:816
## Z:\\Data\\GrosmarkAD\\Achilles\\Achilles_10252013:210
## Z:\\Data\\GrosmarkAD\\Cicero\\Cicero_09102014    :186
## Z:\\Data\\HMC1\\day8                             :174
## Z:\\Data\\GrosmarkAD\\Gatsby\\Gatsby_08282013    :144
## (Other)                                          :348
##          replay_layer        animal
## forwardDeep       :600   Achilles:504
## forwardSuperficial:216   Buddy   : 24
## reverseDeep       :600   Cicero  :372
## reverseSuperficial:216   ec014   :276
##                          Gatsby  :282
##                          HMC1    :174
##
```

```
m1 = glmer(participation ~ deepSuperficial + epoch + (1|basepath/replay_type), weights=n_replay
s, data=data,family="binomial")

summary(m1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: participation ~ deepSuperficial + epoch + (1 | basepath/replay_type)
##     Data: data
## Weights: n_replays
##
##      AIC      BIC   logLik deviance df.resid
##  12803.0  12835.3  -6395.5  12791.0     1602
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -5.571 -1.558 -0.235  1.279 10.776
##
## Random effects:
##  Groups               Name        Variance  Std.Dev.
##  replay_type:basepath (Intercept) 0.0007366 0.02714
##  basepath             (Intercept) 0.1135207 0.33693
## Number of obs: 1608, groups:  replay_type:basepath, 18; basepath, 9
##
## Fixed effects:
##                            Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -0.78062    0.11381  -6.859 6.94e-12 ***
## deepSuperficialSuperficial  0.15107    0.02402   6.288 3.21e-10 ***
## epochpre                   -0.28561    0.02318 -12.323  < 2e-16 ***
## epochtask                   0.19288    0.03093   6.235 4.52e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) dpSprS epchpr
## dpSprfclSpr -0.065
## epochpre    -0.072 -0.003
## epochtask   -0.056  0.002  0.257
```

```
testDispersion(m1)
```

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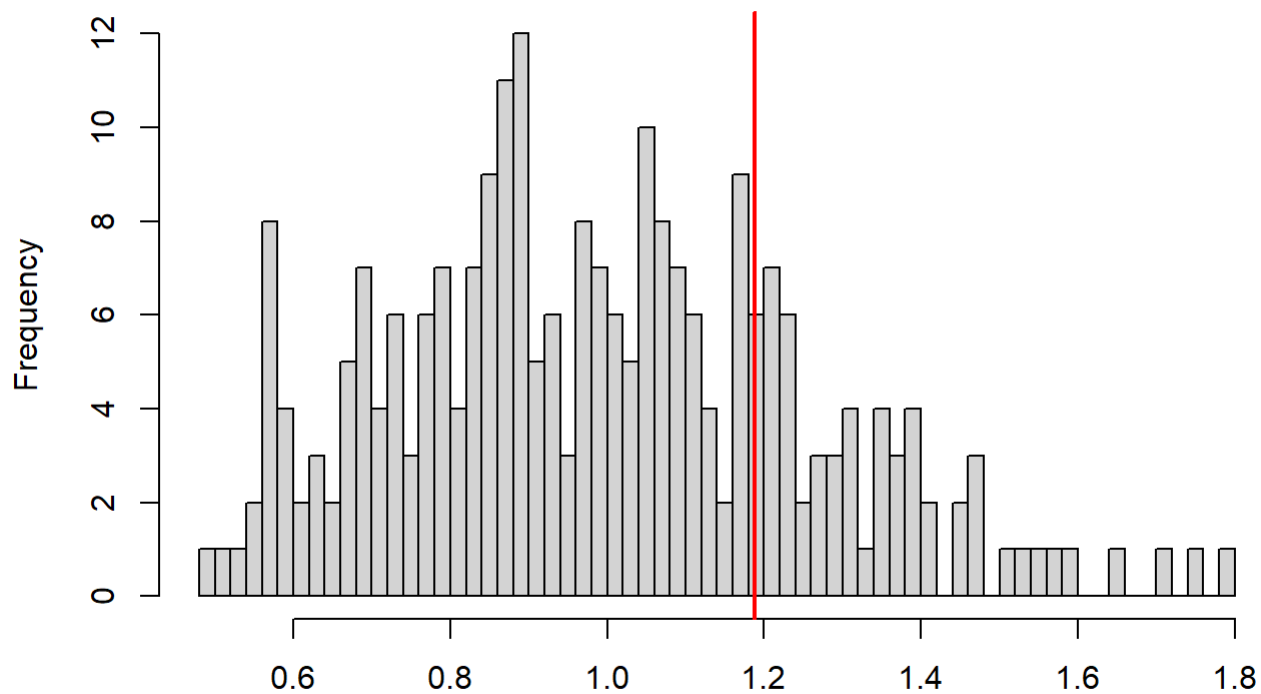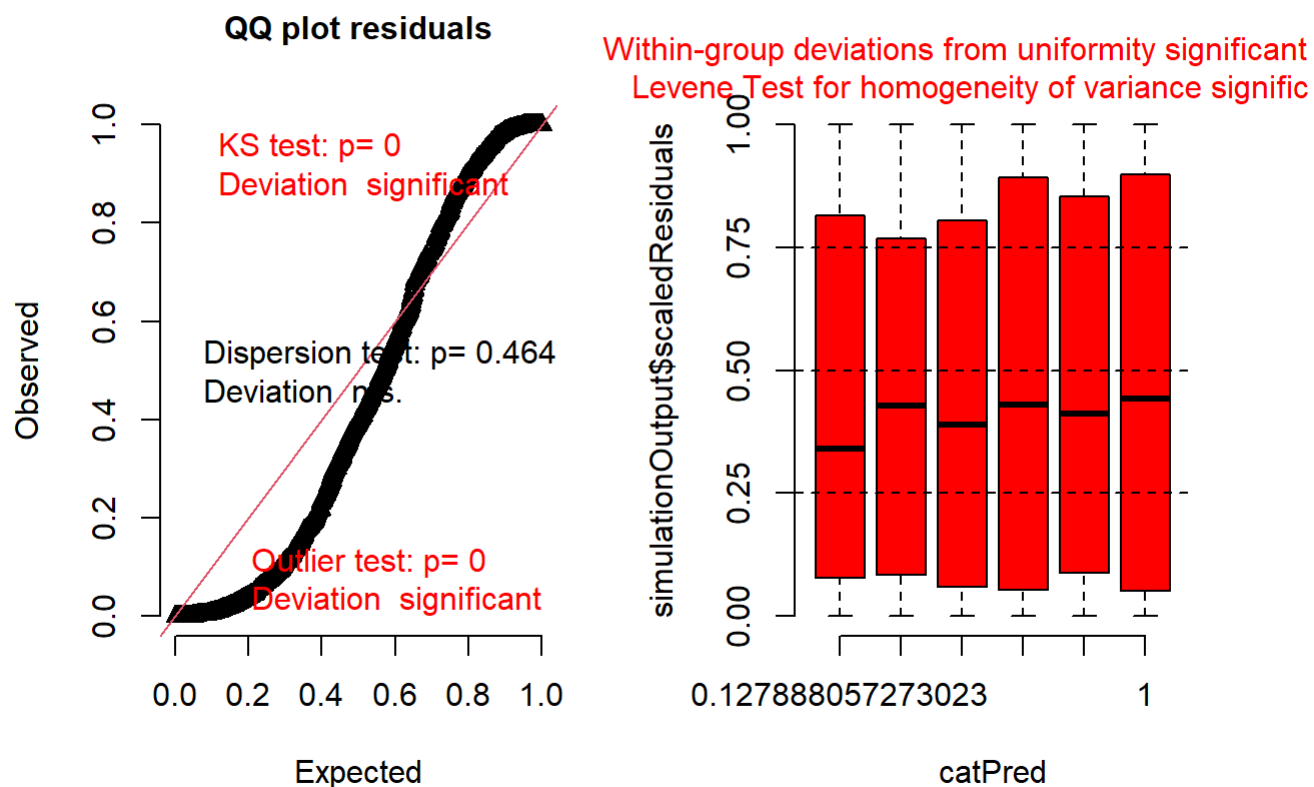

Simulated values, red line = fitted model. p-value (two.sided) = 0.464

```
## 
##  DHARMa nonparametric dispersion test via sd of residuals fitted vs.
##  simulated
## 
## data:  simulationOutput
## dispersion = 1.1983, p-value = 0.464
## alternative hypothesis: two.sided
```
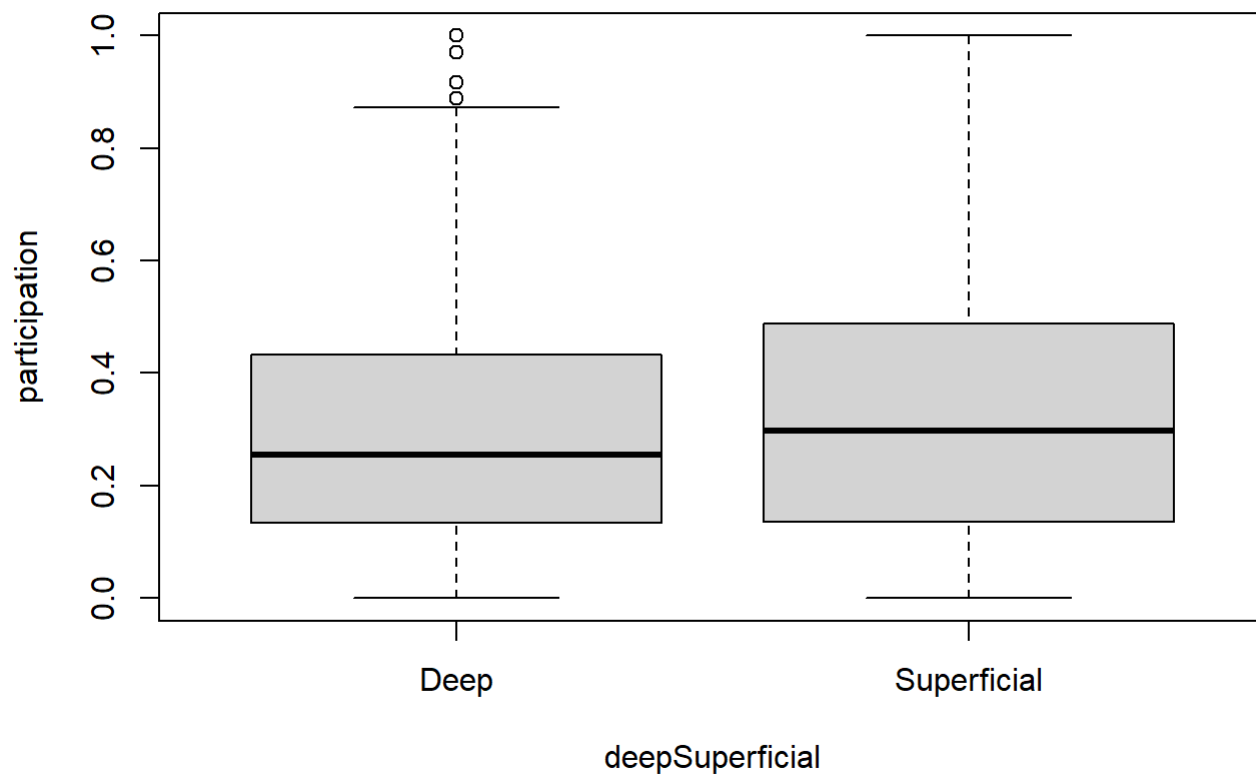
```
simulationOutput <- simulateResiduals(fittedModel = m1, plot = F)
plot(simulationOutput)
```

```
## DHARMa:testOutliers with type = binomial may have inflated Type I error rates for integer-val
ued distributions. To get a more exact result, it is recommended to re-run testOutliers with typ
e = 'bootstrap'. See ?testOutliers for details
```

DHARMa residual

QQ plot residuals

KS test: p= 0
Deviation significant

Dispersion test: p= 0.464
Deviation n.s.

Outlier test: p= 0
Deviation significant

Observed (y-axis), Expected (x-axis)

Within-group deviations from uniformity significant
Levene Test for homogeneity of variance signific

simulationOutput$scaledResiduals (y-axis)

0.127888057273023   1

catPred

```
#
# lme.dscore(m1,data=temp_data,type="lme4")
plot(participation ~ deepSuperficial, data = data)
```

```
m1 = glmer(participation ~ deepSuperficial + (1|basepath/replay_type), weights=n_replays, data=d
ata[data$epoch == "pre",],family="binomial")
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary(m1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: participation ~ deepSuperficial + (1 | basepath/replay_type)
##     Data: data[data$epoch == "pre", ]
## Weights: n_replays
##
##      AIC      BIC   logLik deviance df.resid
##   4056.9   4074.0  -2024.4   4048.9      532
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.3172 -1.5247 -0.2357  1.1584  9.3032
##
## Random effects:
##  Groups               Name        Variance Std.Dev.
##  replay_type:basepath (Intercept) 0.00000  0.0000
##  basepath             (Intercept) 0.05357  0.2315
## Number of obs: 536, groups:  replay_type:basepath, 18; basepath, 9
##
## Fixed effects:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)              -1.07534    0.08175  -13.15  < 2e-16 ***
## deepSuperficialSuperficial  0.14632    0.04750    3.08  0.00207 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr)
## dpSprfclSpr -0.180
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
testDispersion(m1)
```

DHARMa nonparametric dispersion test via sd of
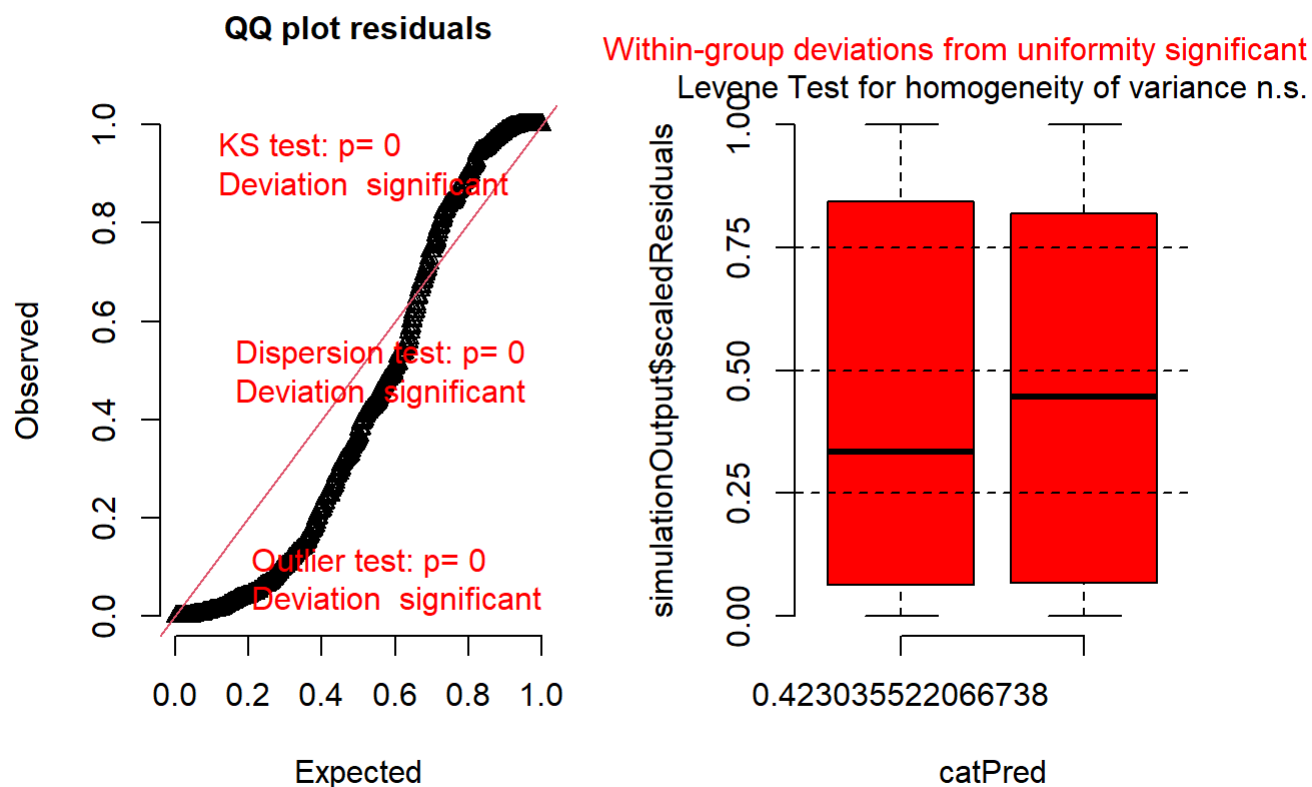## residuals fitted vs. simulated
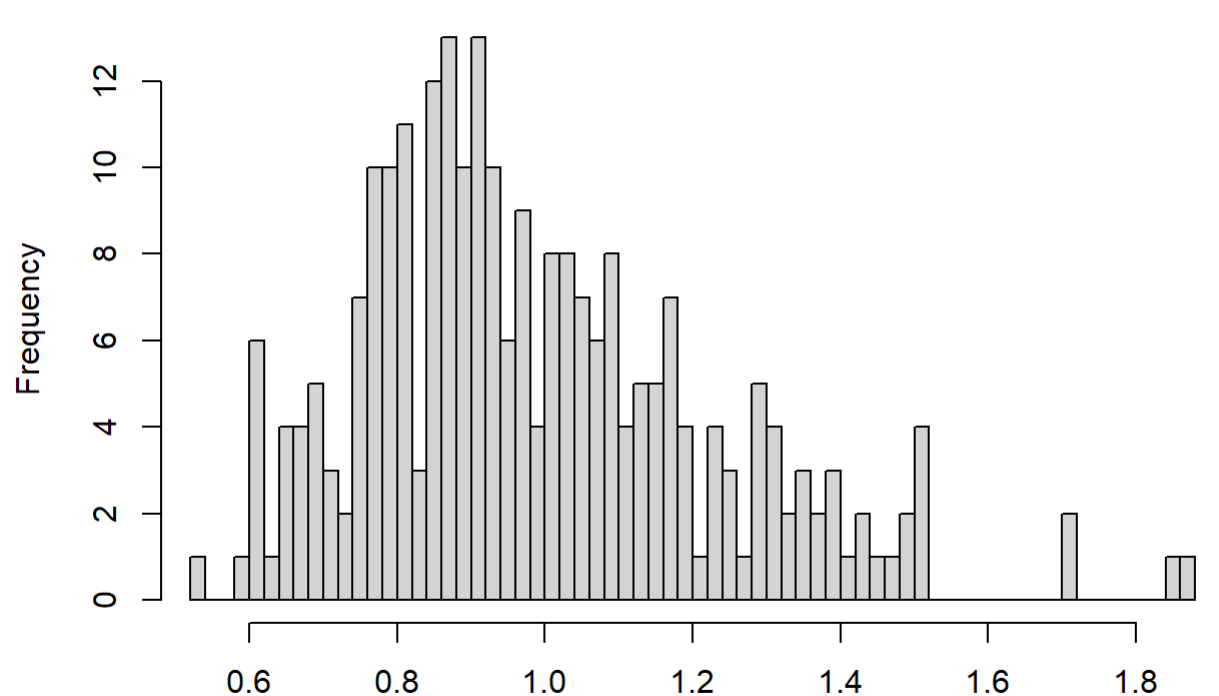
Simulated values, red line = fitted model. p-value (two.sided) = 0

```
##
##  DHARMa nonparametric dispersion test via sd of residuals fitted vs.
##  simulated
##
## data:  simulationOutput
## dispersion = 1.9458, p-value < 2.2e-16
## alternative hypothesis: two.sided
```
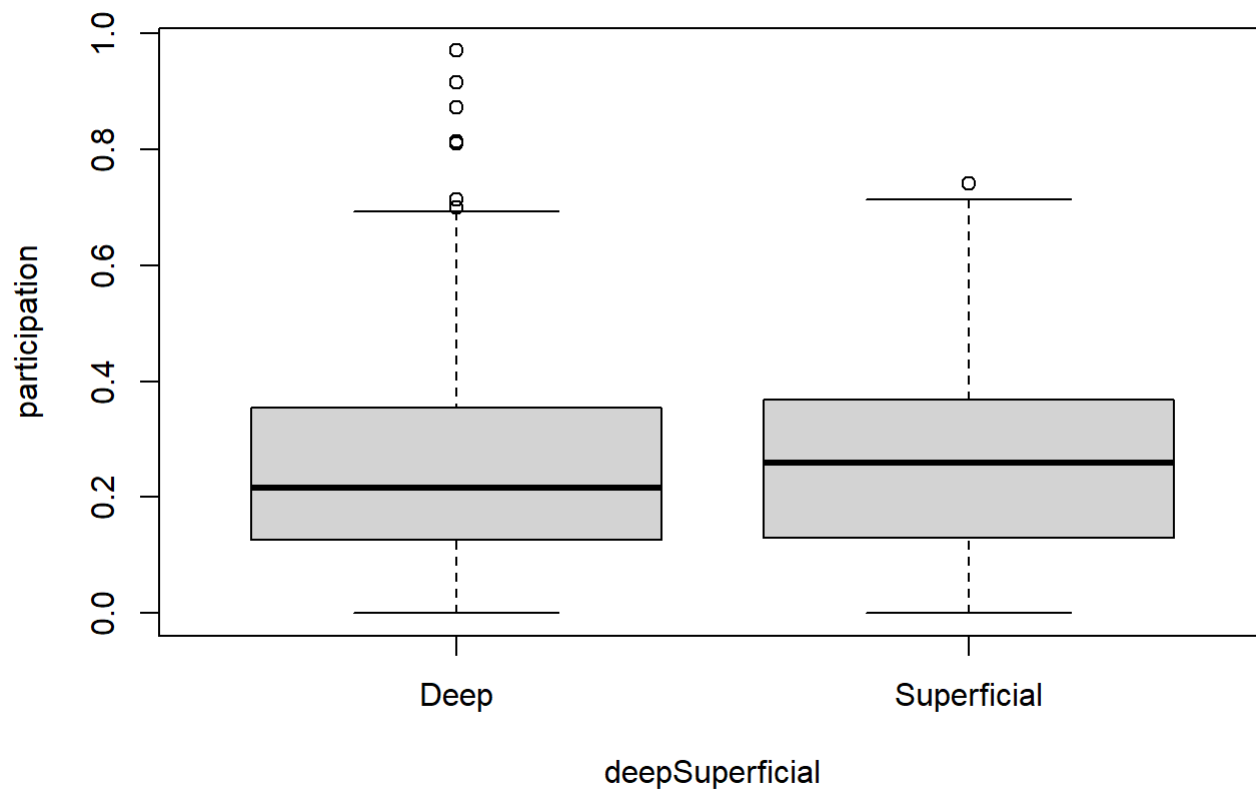
```
simulationOutput <- simulateResiduals(fittedModel = m1, plot = F)
plot(simulationOutput)
```

```
## DHARMa:testOutliers with type = binomial may have inflated Type I error rates for integer-val
ued distributions. To get a more exact result, it is recommended to re-run testOutliers with typ
e = 'bootstrap'. See ?testOutliers for details
```

DHARMa residual

QQ plot residuals

KS test: p= 0
Deviation significant

Dispersion test: p= 0
Deviation significant

Outlier test: p= 0
Deviation significant

Observed

Expected

Within-group deviations from uniformity significant
Levene Test for homogeneity of variance n.s.

simulationOutput$scaledResiduals

0.423035522066738

catPred

```
#
# lme.dscore(m1,data=temp_data,type="lme4")
plot(participation ~ deepSuperficial, data = data[data$epoch == "pre",])
```

```
m1 = glmer(participation ~ deepSuperficial + (1|basepath/animal/replay_type), weights=n_replays,
data=data[data$epoch == "task",],family="binomial")

summary(m1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: participation ~ deepSuperficial + (1 | basepath/animal/replay_type)
##     Data: data[data$epoch == "task", ]
## Weights: n_replays
##
##      AIC       BIC    logLik deviance df.resid
##   2847.4    2868.8   -1418.7   2837.4       531
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.8960 -1.3186 -0.2305  1.2677  5.8985
##
## Random effects:
##  Groups                        Name        Variance Std.Dev.
##  replay_type:(animal:basepath) (Intercept) 0.009646 0.09821
##  animal:basepath               (Intercept) 0.152319 0.39028
##  basepath                      (Intercept) 0.092207 0.30366
## Number of obs: 536, groups:
## replay_type:(animal:basepath), 18; animal:basepath, 9; basepath, 9
##
## Fixed effects:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)              -0.50254    0.17180  -2.925  0.00344 **
## deepSuperficialSuperficial  0.04584    0.06215   0.737  0.46083
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr)
## dpSprfclSpr -0.109
```

```
testDispersion(m1)
```

**DHARMa nonparametric dispersion test via sd of
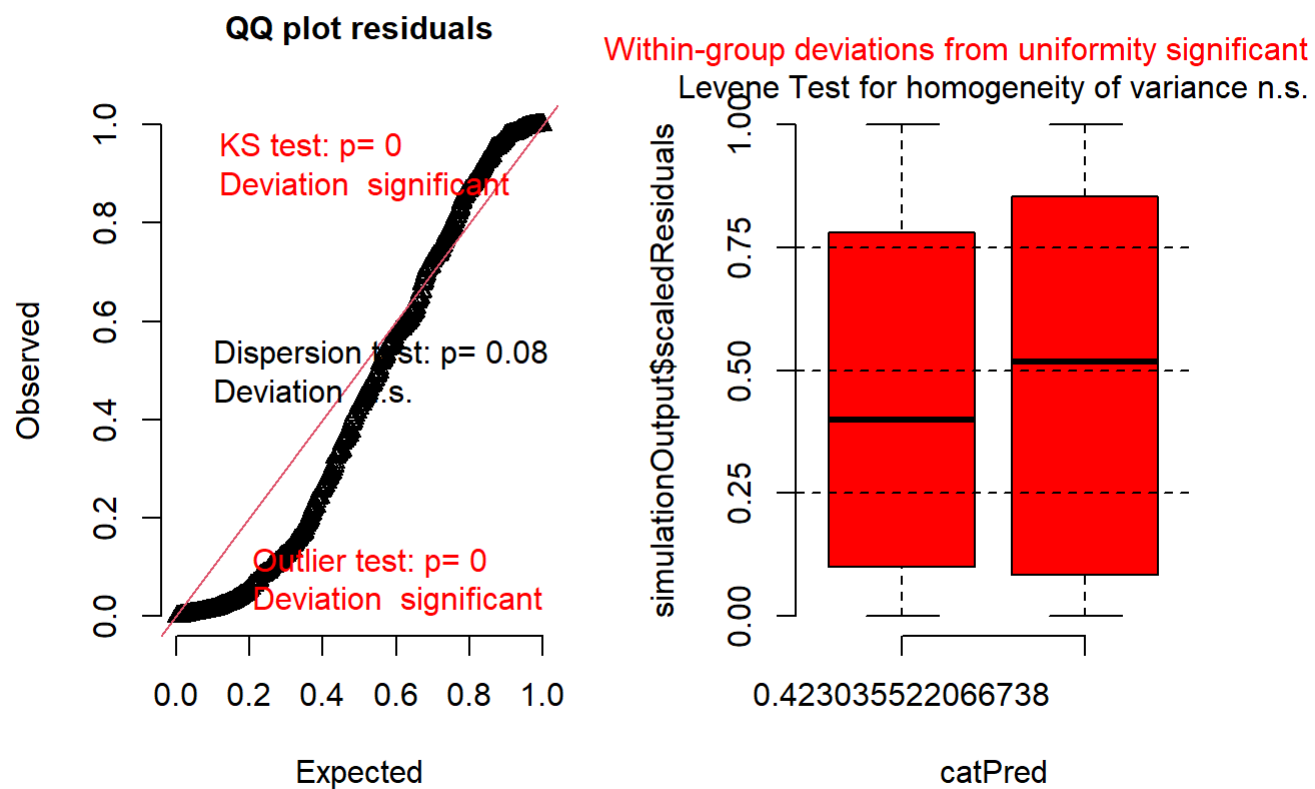residuals fitted vs. simulated**
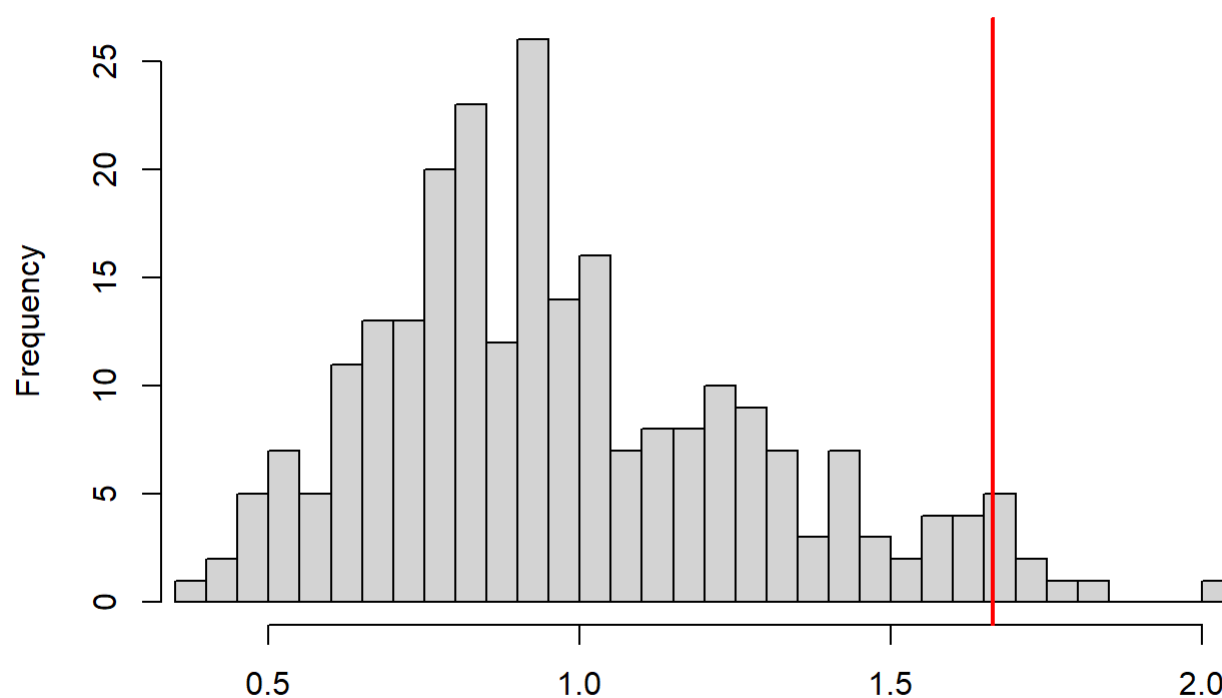
Simulated values, red line = fitted model. p-value (two.sided) = 0.08

```
## 
##  DHARMa nonparametric dispersion test via sd of residuals fitted vs.
##  simulated
## 
## data:  simulationOutput
## dispersion = 1.6948, p-value = 0.08
## alternative hypothesis: two.sided
```
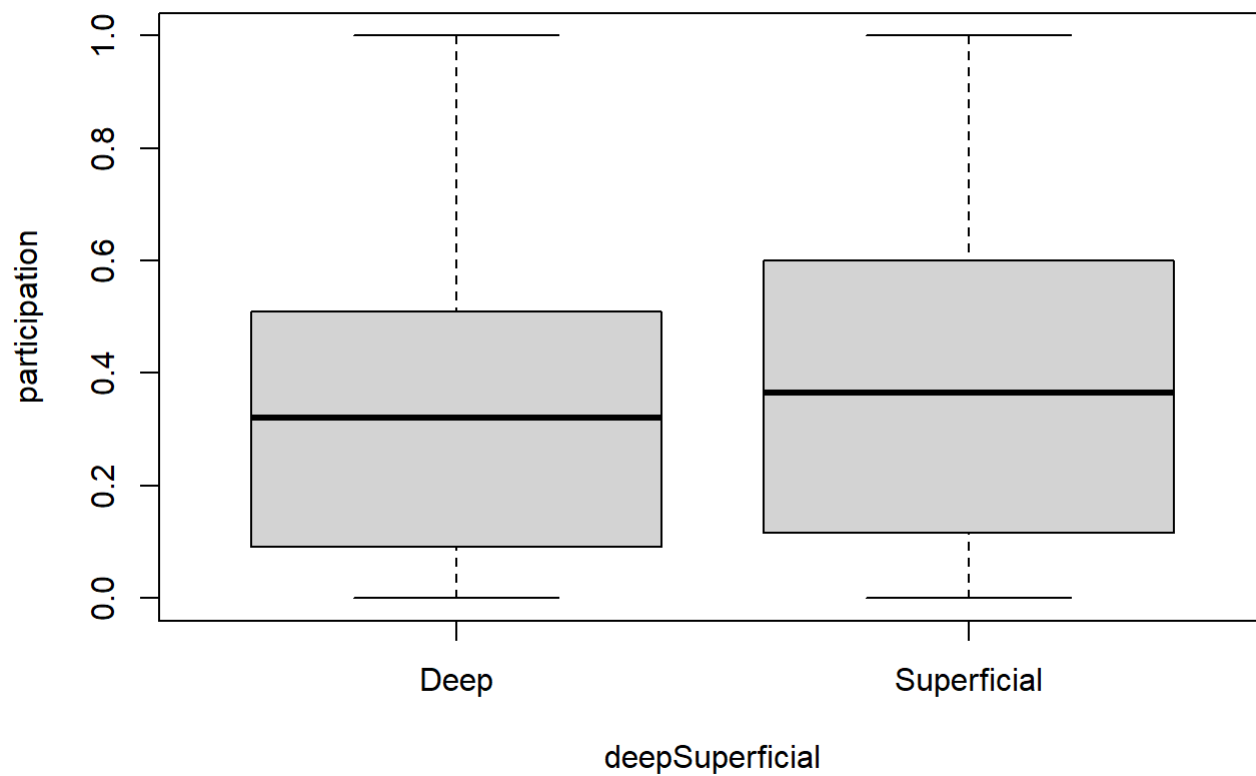
```
simulationOutput <- simulateResiduals(fittedModel = m1, plot = F)
plot(simulationOutput)
```

```
## DHARMa:testOutliers with type = binomial may have inflated Type I error rates for integer-val
ued distributions. To get a more exact result, it is recommended to re-run testOutliers with typ
e = 'bootstrap'. See ?testOutliers for details
```

DHARMa residual

QQ plot residuals

KS test: p= 0
Deviation significant

Dispersion test: p= 0.08
Deviation n.s.

Outlier test: p= 0
Deviation significant

Observed

Expected

Within-group deviations from uniformity significant
Levene Test for homogeneity of variance n.s.

simulationOutput$scaledResiduals

0.423035522066738

catPred

```
plot(participation ~ deepSuperficial, data = data[data$epoch == "task",])
```

```
m1 = glmer(participation ~ deepSuperficial + (1|basepath/animal/replay_type), weights=n_replays,
data=data[data$epoch == "post",],family="binomial")

summary(m1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: participation ~ deepSuperficial + (1 | basepath/animal/replay_type)
##     Data: data[data$epoch == "post", ]
## Weights: n_replays
##
##      AIC      BIC   logLik deviance df.resid
##   5812.6   5834.0  -2901.3   5802.6      531
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -5.9375 -1.8068 -0.1889  1.5841 10.1397
##
## Random effects:
##  Groups                       Name        Variance Std.Dev.
##  replay_type:(animal:basepath) (Intercept) 0.006482 0.08051
##  animal:basepath              (Intercept) 0.078615 0.28038
##  basepath                     (Intercept) 0.048463 0.22014
## Number of obs: 536, groups:
## replay_type:(animal:basepath), 18; animal:basepath, 9; basepath, 9
##
## Fixed effects:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)              -0.81858    0.12202  -6.709 1.97e-11 ***
## deepSuperficialSuperficial  0.18168    0.03119   5.825 5.71e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr)
## dpSprfclSpr -0.079
```

```
testDispersion(m1)
```

DHARMa nonparametric dispersion test via sd of
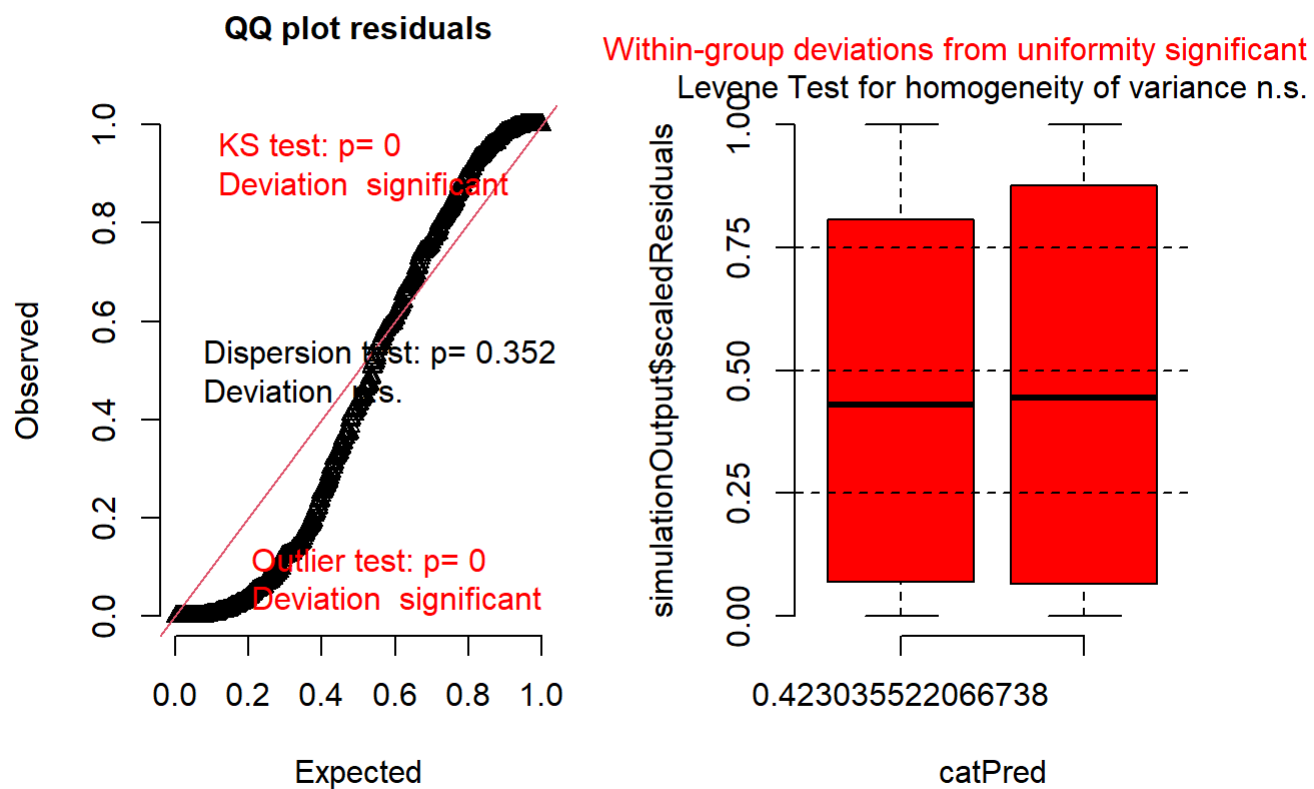## residuals fitted vs. simulated
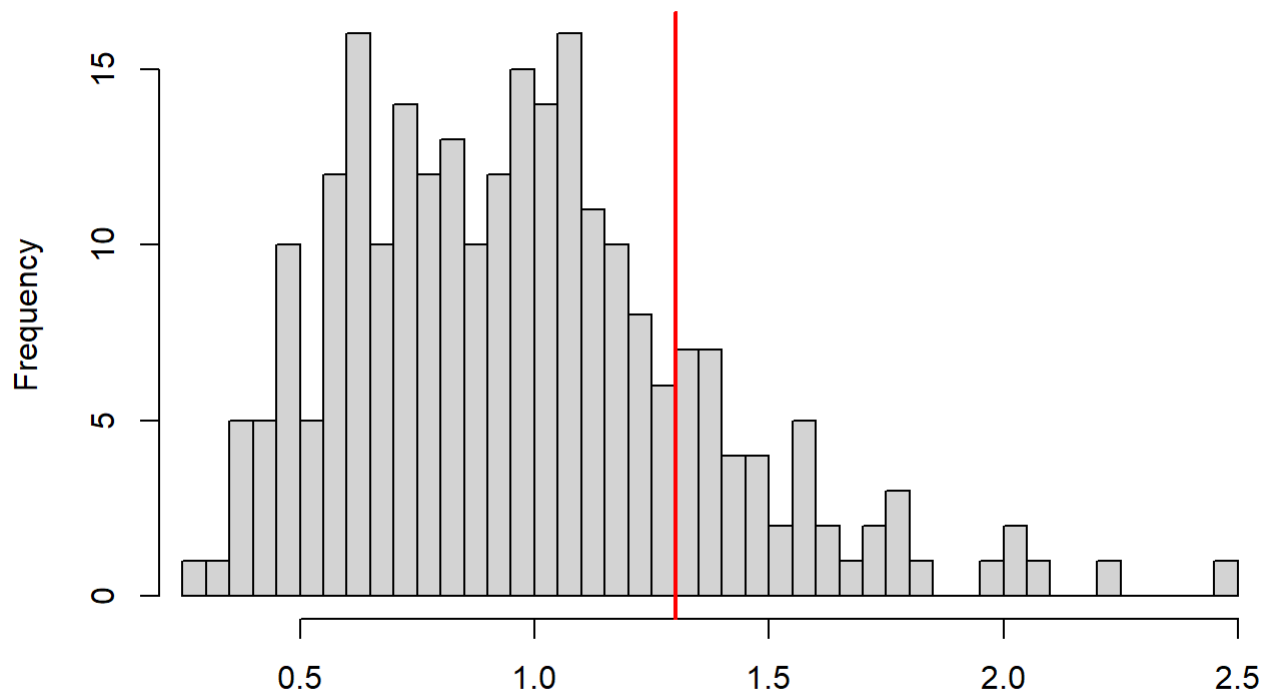
Simulated values, red line = fitted model. p-value (two.sided) = 0.352

```
##
##  DHARMa nonparametric dispersion test via sd of residuals fitted vs.
##  simulated
##
## data:  simulationOutput
## dispersion = 1.3353, p-value = 0.352
## alternative hypothesis: two.sided
```
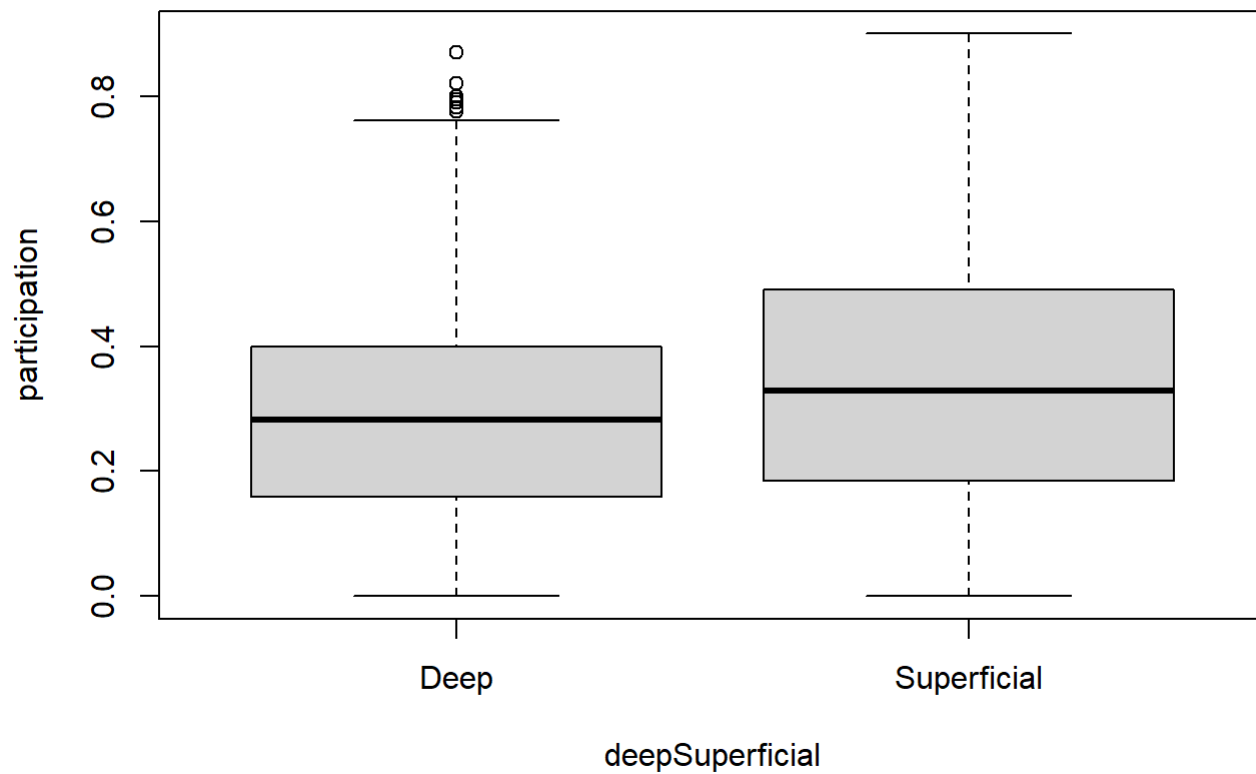
```
simulationOutput <- simulateResiduals(fittedModel = m1, plot = F)
plot(simulationOutput)
```

```
## DHARMa:testOutliers with type = binomial may have inflated Type I error rates for integer-val
ued distributions. To get a more exact result, it is recommended to re-run testOutliers with typ
e = 'bootstrap'. See ?testOutliers for details
```

DHARMa residual

QQ plot residuals

KS test: p= 0
Deviation significant

Dispersion test: p= 0.352
Deviation n.s.

Outlier test: p= 0
Deviation significant

Observed

Expected

Within-group deviations from uniformity significant
Levene Test for homogeneity of variance n.s.

simulationOutput$scaledResiduals

0.423035522066738

catPred

```
plot(participation ~ deepSuperficial, data = data[data$epoch == "post",])
```
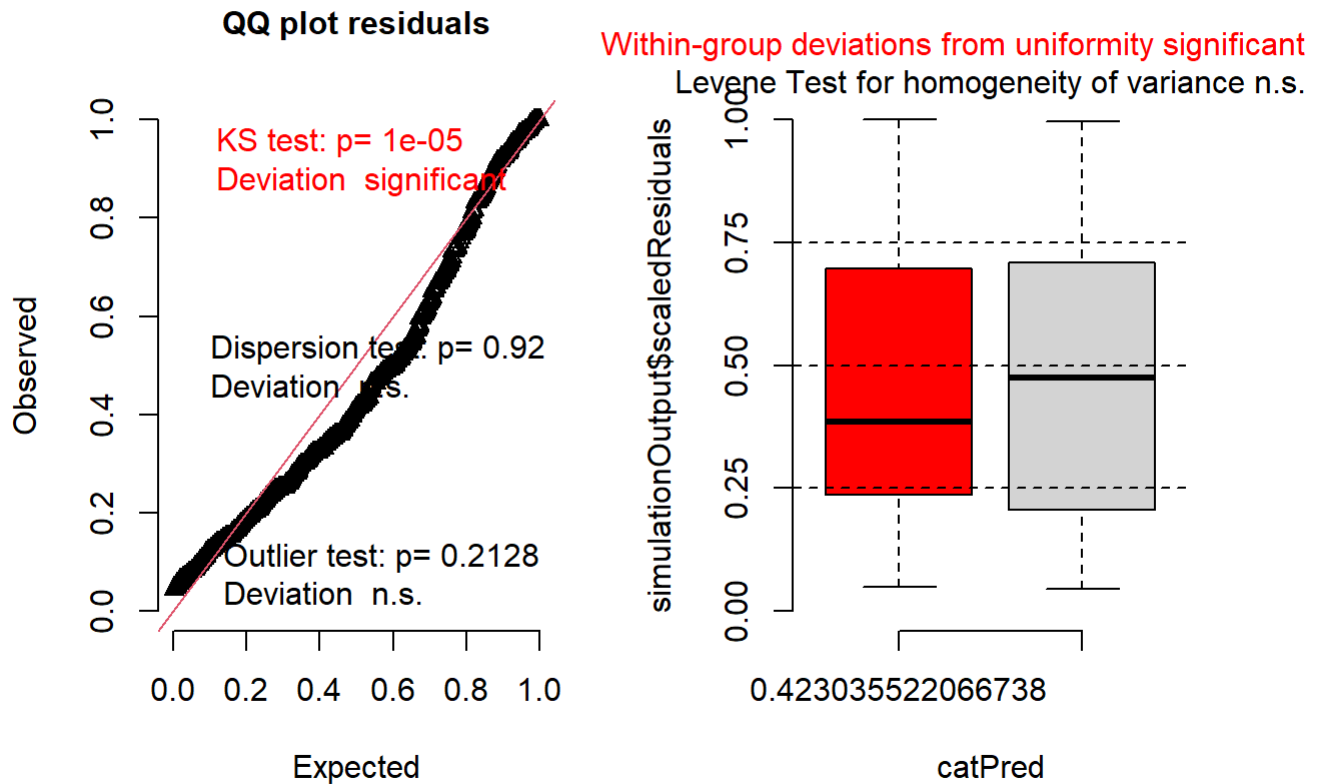
Same with lmer

```
temp_data <- data[data$epoch == "pre",]

# temp_data$y_trans <- log(temp_data$participation+1)

m1 = lmer(participation ~ deepSuperficial + (1 | animal/basepath), data = temp_data,REML=FALSE)
summary(m1)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: participation ~ deepSuperficial + (1 | animal/basepath)
##    Data: temp_data
##
##      AIC      BIC   logLik deviance df.resid
##   -323.5   -302.1    166.8   -333.5      531
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.8308 -0.7594 -0.1599  0.5926  4.0599
##
## Random effects:
##  Groups          Name        Variance  Std.Dev.
##  basepath:animal (Intercept) 0.0008235 0.02870
##  animal          (Intercept) 0.0007306 0.02703
##  Residual                    0.0307537 0.17537
## Number of obs: 536, groups:  basepath:animal, 9; animal, 5
##
## Fixed effects:
##                           Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)                0.25906    0.01827   5.78144  14.182 1.04e-05 ***
## deepSuperficialSuperficial 0.01827    0.01815 493.54016   1.007    0.314
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr)
## dpSprfclSpr -0.269
```

```
simulationOutput <- simulateResiduals(fittedModel = m1, plot = F)
plot(simulationOutput)
```

DHARMa residual

QQ plot residuals

KS test: p= 1e-05
Deviation significant

Dispersion test: p= 0.92
Deviation n.s.

Outlier test: p= 0.2128
Deviation n.s.

Within-group deviations from uniformity significant
Levene Test for homogeneity of variance n.s.

```
a1 = anova(m1)
F_to_eta2(a1$`F value`, a1$NumDF, a1$DenDF)
```

```
## Eta2 (partial) |        95% CI
## ----------------------------
## 2.05e-03        | [0.00, 1.00]
##
## - One-sided CIs: upper bound fixed at (1).
```

```
lme.dscore(m1,data=temp_data,type="lme4")
```

```
##                              t       df        d
## deepSuperficialSuperficial 1.011418 493.745 0.09103523
```
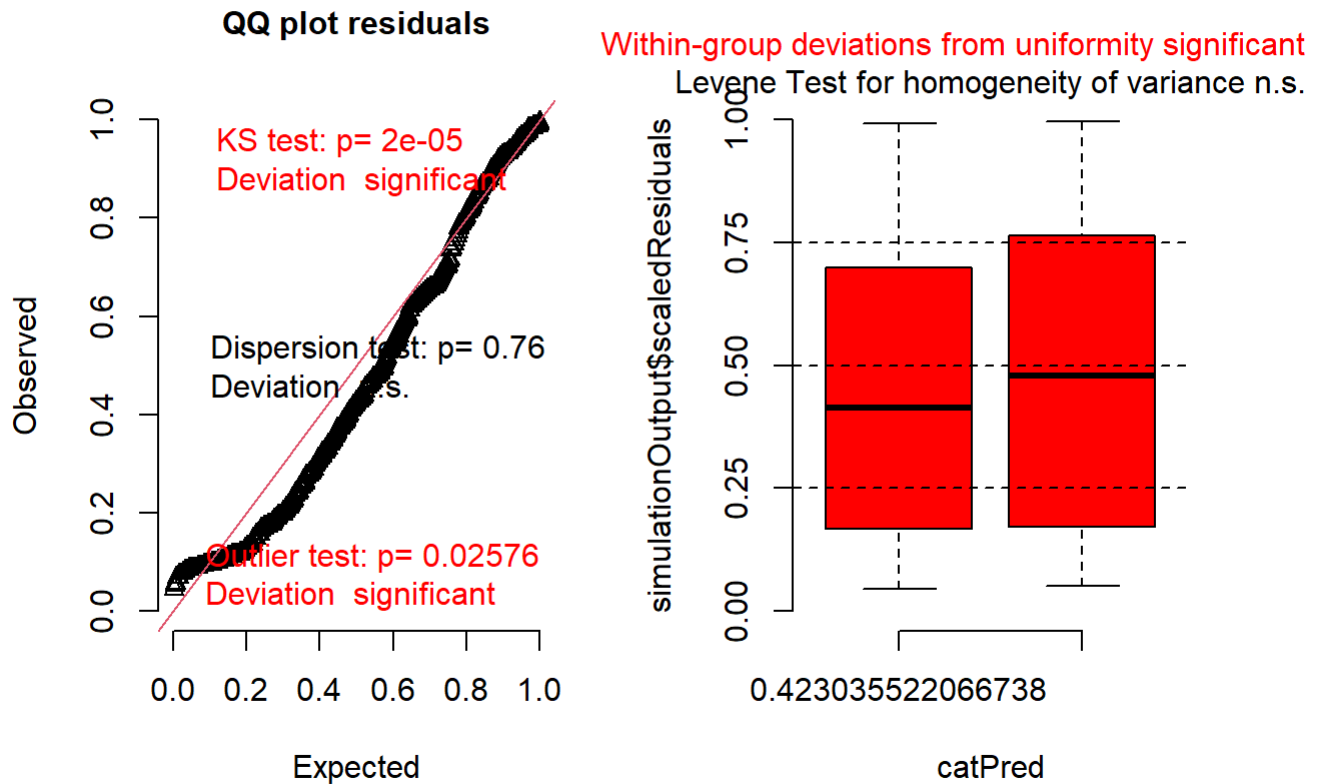
```
# data$y_trans <- log(data$participation+1)

temp_data <- data[data$epoch == "task",]

m1 = lmer(participation ~ deepSuperficial + (1 | basepath), data = temp_data,REML=FALSE)
summary(m1)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: participation ~ deepSuperficial + (1 | basepath)
##    Data: temp_data
##
##      AIC      BIC   logLik deviance df.resid
##    168.5    185.6    -80.3    160.5      532
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.0700 -0.7367 -0.1025  0.6367  2.5171
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  basepath (Intercept) 0.01170  0.1081
##  Residual             0.07605  0.2758
## Number of obs: 536, groups:  basepath, 9
##
## Fixed effects:
##                           Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)              3.824e-01  3.919e-02 1.016e+01   9.759 1.76e-06 ***
## deepSuperficialSuperficial 4.643e-03  2.902e-02 5.358e+02   0.160    0.873
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr)
## dpSprfclSpr -0.219
```

```
simulationOutput <- simulateResiduals(fittedModel = m1, plot = F)
plot(simulationOutput)
```

DHARMa residual

QQ plot residuals

KS test: p= 2e-05
Deviation significant

Dispersion test: p= 0.76
Deviation n.s.

Outlier test: p= 0.02576
Deviation significant

Observed / Expected

Within-group deviations from uniformity significant
Levene Test for homogeneity of variance n.s.

simulationOutput$scaledResiduals

0.423035522066738

catPred

```
a1 = anova(m1)
F_to_eta2(a1$`F value`, a1$NumDF, a1$DenDF)
```

```
## Eta2 (partial) |        95% CI
## -----------------------------
## 4.78e-05        | [0.00, 1.00]
##
## - One-sided CIs: upper bound fixed at (1).
```

```
lme.dscore(m1,data=temp_data,type="lme4")
```

```
##                              t        df         d
## deepSuperficialSuperficial 0.1466217 533.8323 0.01269188
```
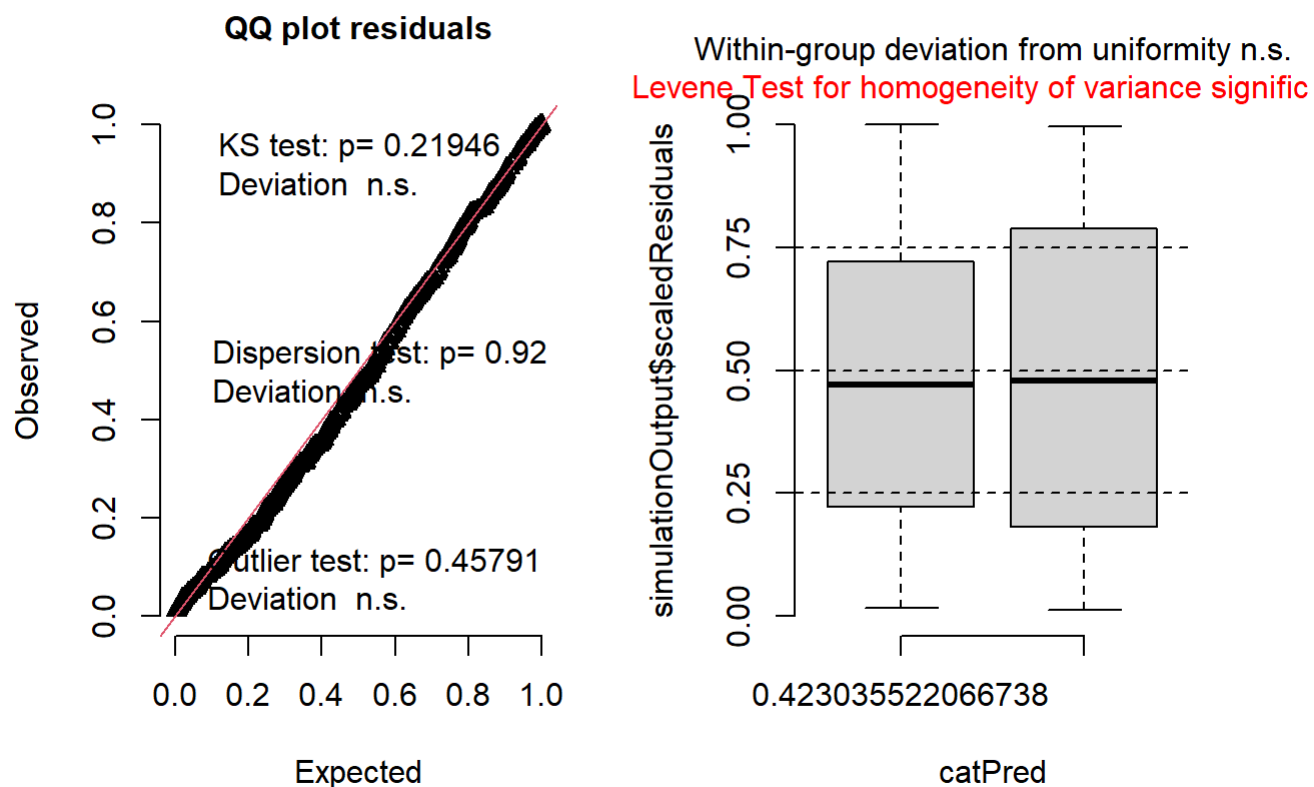
```
data$y_trans <- log(data$participation+1)

temp_data <- data[data$epoch == "post",]

m1 = lmer(y_trans ~ deepSuperficial + (1 | basepath), data = temp_data,REML=FALSE)
summary(m1)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: y_trans ~ deepSuperficial + (1 | basepath)
##    Data: temp_data
##
##      AIC      BIC   logLik deviance df.resid
##   -674.0   -656.9    341.0   -682.0      532
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.2288 -0.6847 -0.0070  0.7067  2.7606
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  basepath (Intercept) 0.003183 0.05642
##  Residual             0.015727 0.12541
## Number of obs: 536, groups:  basepath, 9
##
## Fixed effects:
##                           Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)                0.26035    0.02007   9.67184   12.97 1.96e-07 ***
## deepSuperficialSuperficial 0.02883    0.01322 535.90179    2.18   0.0297 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr)
## dpSprfclSpr -0.195
```

```
simulationOutput <- simulateResiduals(fittedModel = m1, plot = F)
plot(simulationOutput)
```

DHARMa residual

QQ plot residuals

KS test: p= 0.21946
Deviation n.s.

Dispersion test: p= 0.92
Deviation n.s.

Outlier test: p= 0.45791
Deviation n.s.

Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance signific

0.423035522066738

catPred

```
a1 = anova(m1)
F_to_eta2(a1$`F value`, a1$NumDF, a1$DenDF)
```

```
## Eta2 (partial) |       95% CI
## ----------------------------
## 8.79e-03       | [0.00, 1.00]
##
## - One-sided CIs: upper bound fixed at (1).
```

```
lme.dscore(m1,data=temp_data,type="lme4")
```

```
##                              t       df        d
## deepSuperficialSuperficial 2.172703 533.9144 0.1880592
```