script4-markdown

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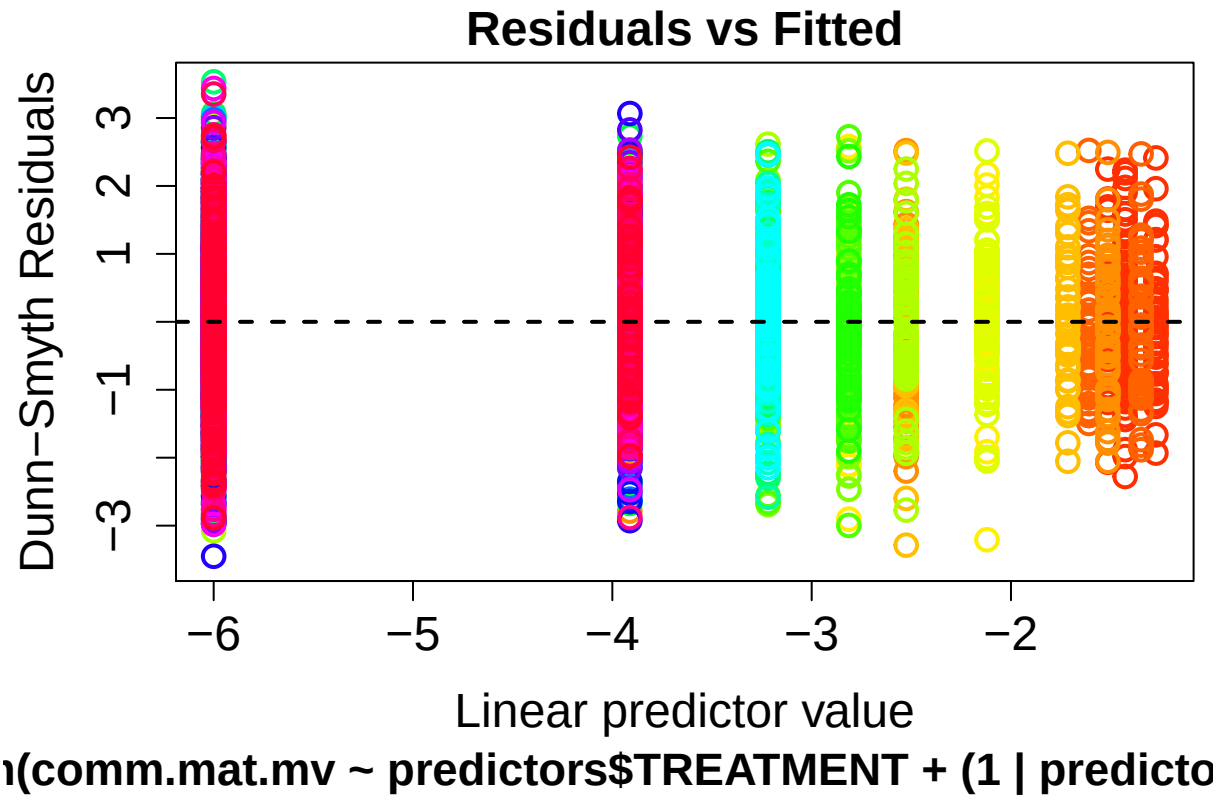
Conducting manyGLMs with the full community matrix

Run the nested model

```
m4 <- manyglm(comm.mat.mv ~ predictors$TREATMENT + (1|predictors$BLOCK/predictors$DATE.ORD),
              family = "negative_binomial")

plot(m4)
```




```
anova(m4, p.uni = "adjusted")
```

```
## Time elapsed: 0 hr 2 min 16 sec
```

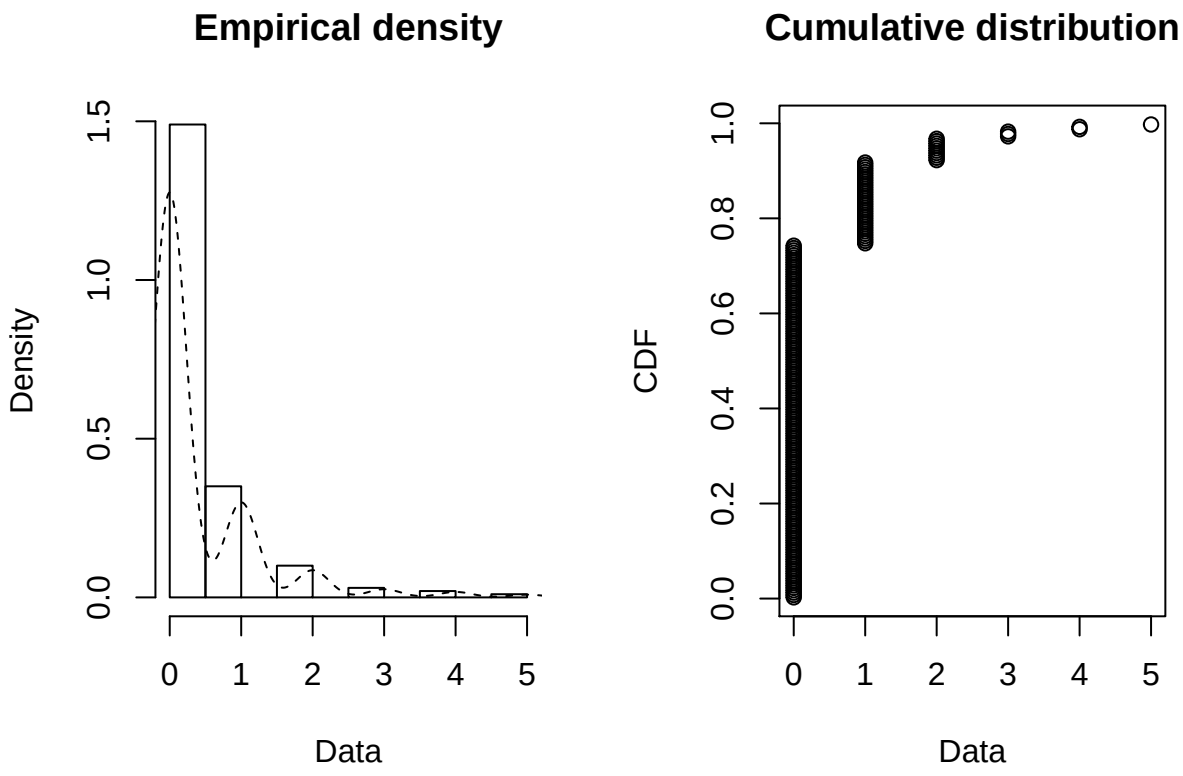
```
## Analysis of Deviance Table
##
## Model: manyglm(formula = comm.mat.mv ~ predictors$TREATMENT + (1 | predictors$BLOCK/predictors$DATE.(
## Model:     family = "negative_binomial")
##
## Multivariate test:
##                      Res.Df Df.diff   Dev Pr(>Dev)
## (Intercept)             199
## predictors$TREATMENT    196       3 99.39    0.051 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Univariate Tests:
##                      ACORN           ASTER1           ASTER2           DESMO
##                        Dev Pr(>Dev)     Dev Pr(>Dev)     Dev Pr(>Dev)   Dev
## (Intercept)
## predictors$TREATMENT 2.772    0.995  2.772    0.987  2.772    0.995 2.796
##                                DICO           CONVULV           BRASS
##                      Pr(>Dev)  Dev Pr(>Dev)     Dev Pr(>Dev)   Dev Pr(>Dev)
## (Intercept)
## predictors$TREATMENT    0.981  4.4    0.956   2.772    0.995 2.772    0.995
##                      NYJER           PINE           PIZZA           RHUS
##                        Dev Pr(>Dev)  Dev Pr(>Dev)   Dev Pr(>Dev)   Dev Pr(>Dev)
## (Intercept)
## predictors$TREATMENT 2.772    0.995  0.1    0.995 2.845    0.981 3.244    0.981
##                      LRHUS           SMLBLK           SMILAX           SORG
##                        Dev Pr(>Dev)     Dev Pr(>Dev)     Dev Pr(>Dev)  Dev
## (Intercept)
## predictors$TREATMENT 2.772    0.995  5.545    0.824  5.778    0.680 5.65
##                                  SUN           RUBIAC           PLANTAG
##                      Pr(>Dev)   Dev Pr(>Dev)     Dev Pr(>Dev)     Dev Pr(>Dev)
## (Intercept)
## predictors$TREATMENT    0.692 2.772    0.995  1.726    0.995   3.688    0.981
##                      MILLET.           PLANTAG2           UNK6           UNK7
##                          Dev Pr(>Dev)      Dev Pr(>Dev)   Dev Pr(>Dev)   Dev
## (Intercept)
## predictors$TREATMENT   2.796    0.987    2.772    0.995 2.796    0.987 2.772
##                                 UNK8           UNK9           UNK10
##                      Pr(>Dev)   Dev Pr(>Dev)   Dev Pr(>Dev)   Dev Pr(>Dev)
## (Intercept)
## predictors$TREATMENT    0.995 2.772    0.995 2.772    0.995 2.772    0.995
##                      UNK11           UNK12           UNK13           UNK14
##                        Dev Pr(>Dev)   Dev Pr(>Dev)   Dev Pr(>Dev)   Dev
## (Intercept)
## predictors$TREATMENT 5.997    0.669 4.879    0.902 2.772    0.995 2.772
##                                UNK15           PARTH
##                      Pr(>Dev)   Dev Pr(>Dev)   Dev Pr(>Dev)
## (Intercept)
## predictors$TREATMENT    0.995 2.772    0.995 2.796    0.987
## Arguments:
##  Test statistics calculated assuming uncorrelated response (for faster computation)
## P-value calculated using 999 resampling iterations via PIT-trap resampling (to account for correlati
```

Model for seed richness time series

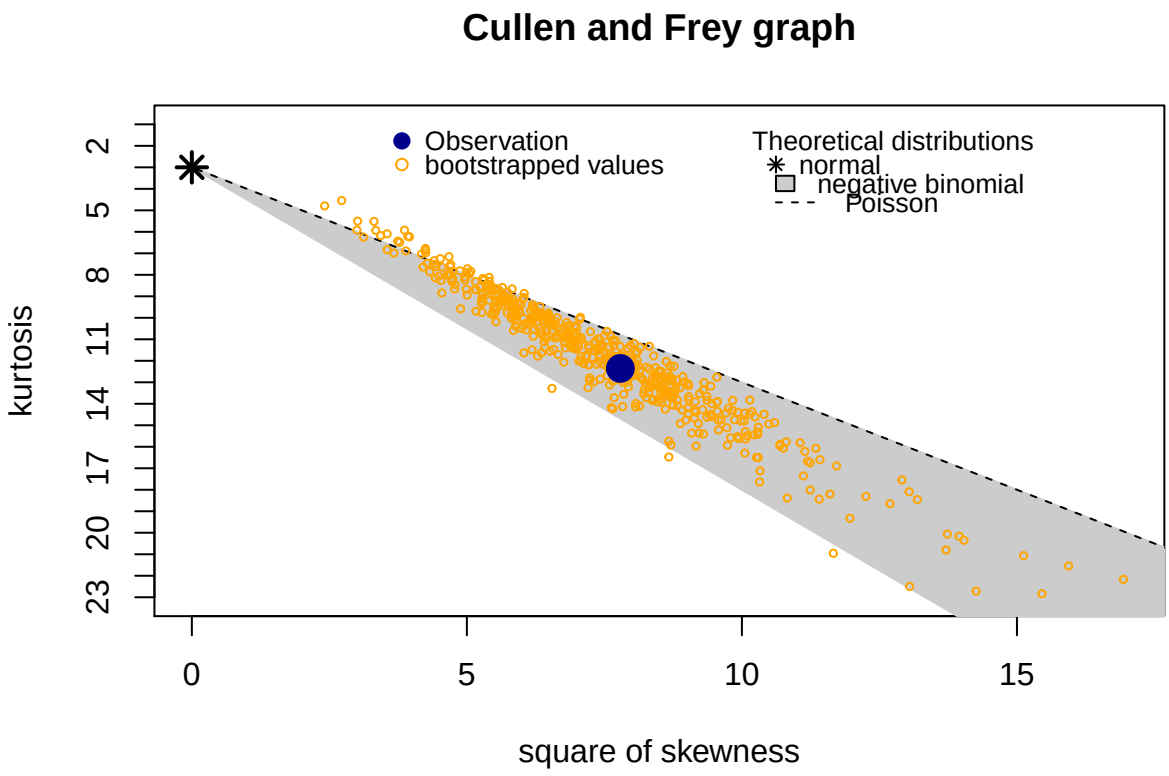
First calculate richness

Plot distribution

```
plotdist(seeds$RICH, histo = TRUE, demp = TRUE)
```



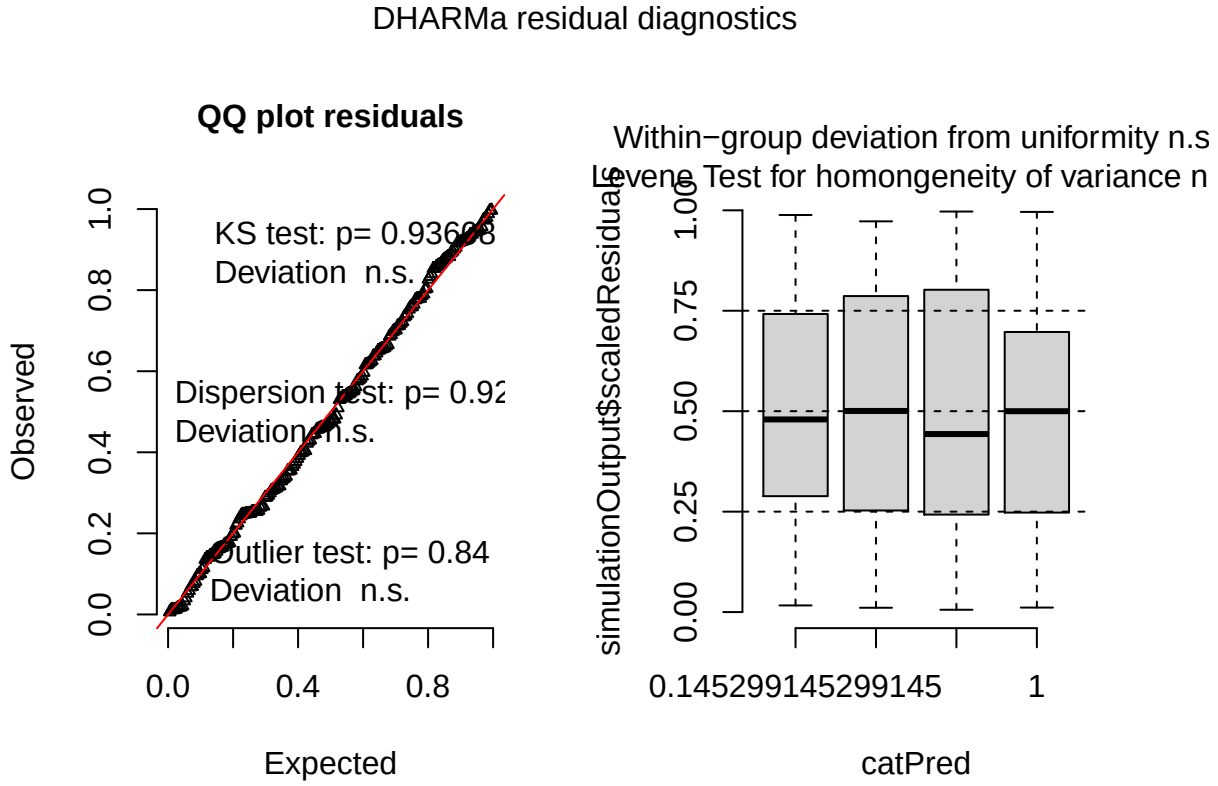

```
descdist(seeds$RICH, discrete=TRUE, boot=500) # NB
```




```
## summary statistics
## ------
## min:  0   max:  5
## median:  0
## mean:  0.385
## estimated sd:  0.8062414
## estimated skewness:  2.791148
## estimated kurtosis:  12.35535
```

Run model

```
m6 <- glmmTMB(RICH ~ TREATMENT.NUMB + (1|BLOCK/DATE.ORD),
              data = seeds, family = nbinom2(link = "log"))
sim_m6 <- simulateResiduals(fittedModel = m6, n = 250)
plot(sim_m6)
```




```
car::Anova(m6)
```

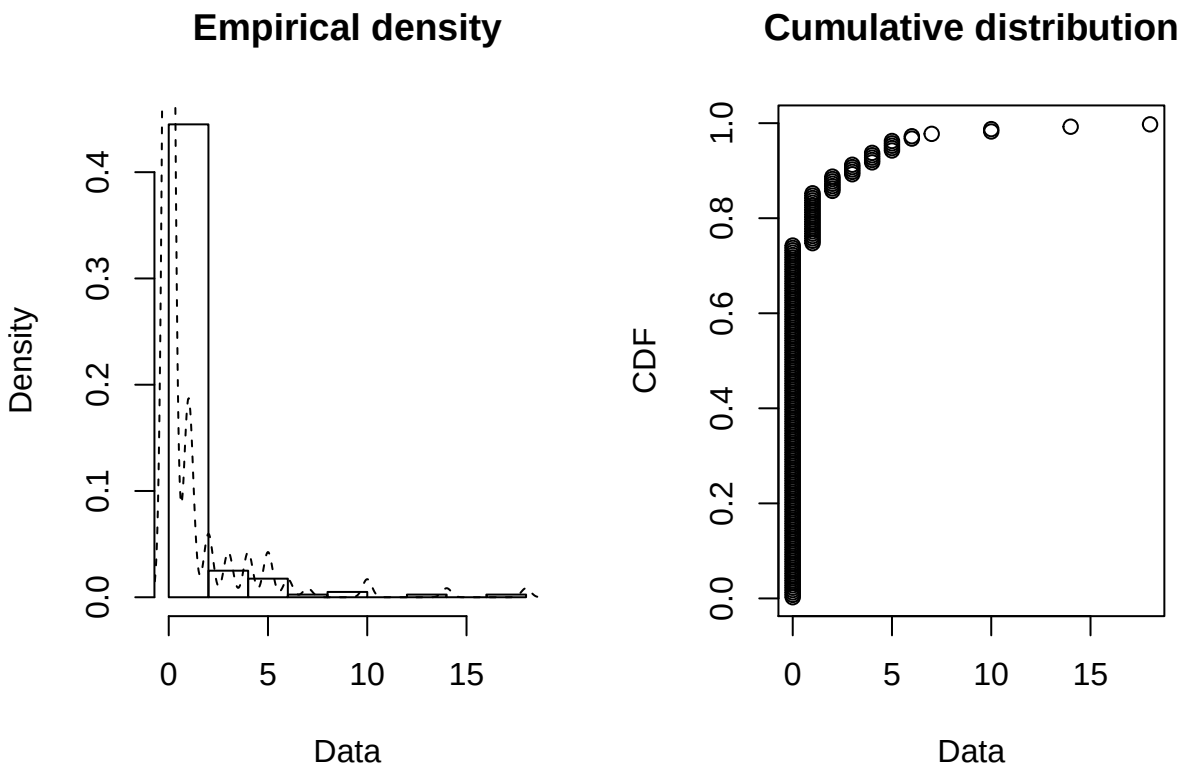
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: RICH
##                  Chisq Df Pr(>Chisq)
## TREATMENT.NUMB 3.1464  1    0.07609 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model for seed detections time series

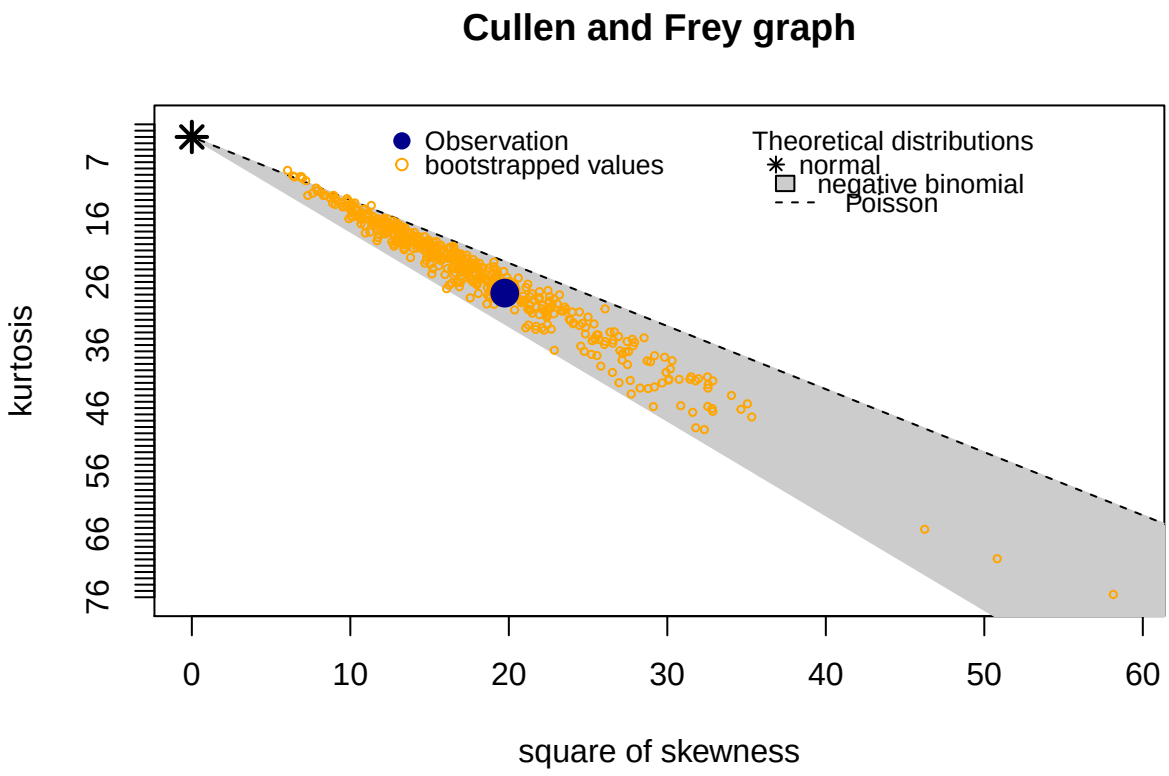
First calculate detections

Plot distribution

```
plotdist(seeds$DETECTIONS, histo = TRUE, demp = TRUE)
```



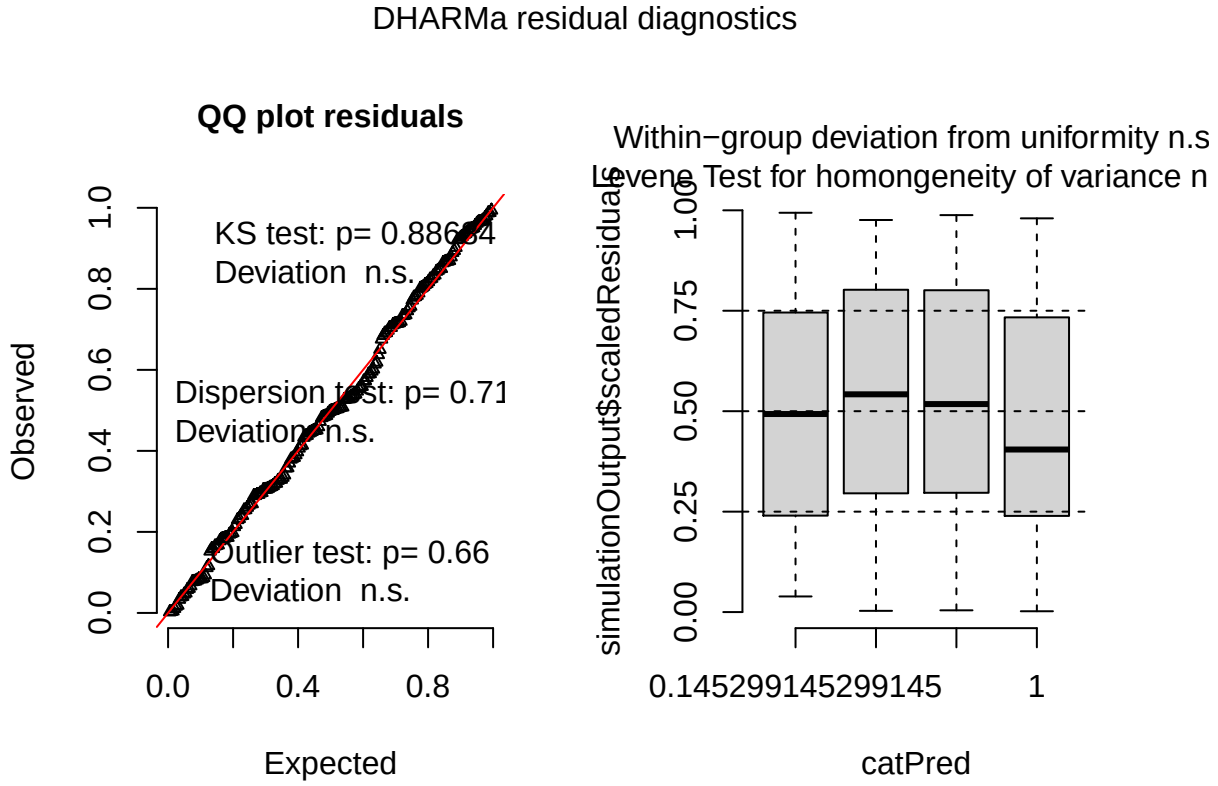

```
descdist(seeds$DETECTIONS, discrete=TRUE, boot=500) # NB
```




```
## summary statistics
## ------
## min:  0   max:  18
## median:  0
## mean:  0.835
## estimated sd:  2.243421
## estimated skewness:  4.443215
## estimated kurtosis:  27.76637
```

Run model

```
m7 <- glmmTMB(DETECTIONS ~ TREATMENT.NUMB + (1|BLOCK/DATE.ORD),
              data = seeds, family = nbinom2(link = "log"))
sim_m7 <- simulateResiduals(fittedModel = m7, n = 250)
plot(sim_m7)
```




```
car::Anova(m7)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: DETECTIONS
##                  Chisq Df Pr(>Chisq)
## TREATMENT.NUMB 1.7453  1     0.1865
```