Zero inflation in count data

Francisco Rodríguez-Sánchez

https://frodriguezsanchez.net

How many eggs in nests?

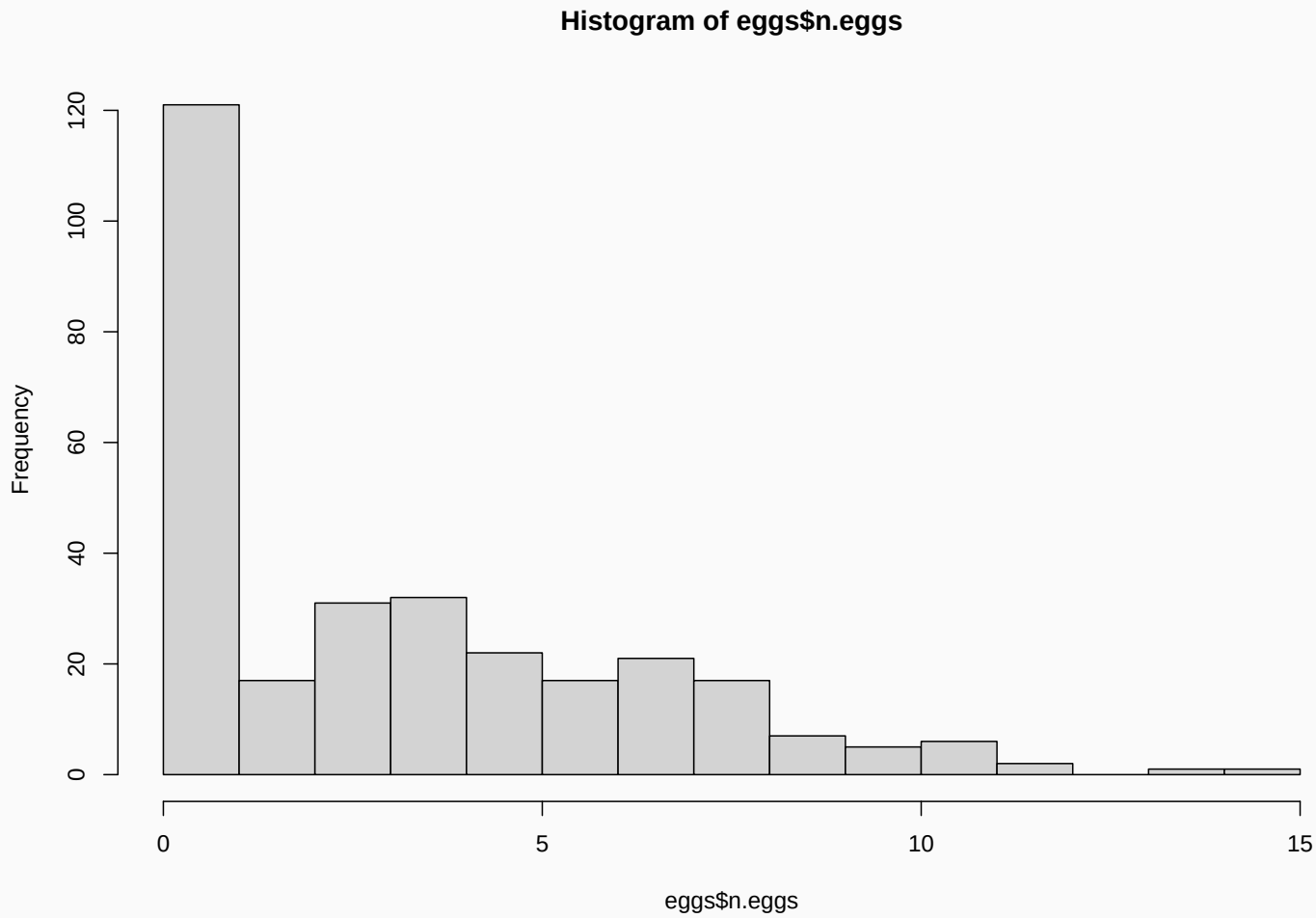
```
eggs <- read.csv("data/eggs.csv")
```

diameter	old	n.eggs
14	no	4
8	yes	0
7	yes	0

`diameter`: nest diameter (cm)

`old`: does nest look old/abandoned?

How many eggs in nests?



Many zeros does not mean you need a zero-inflated model!

Check model afterwards

How many eggs in nests?

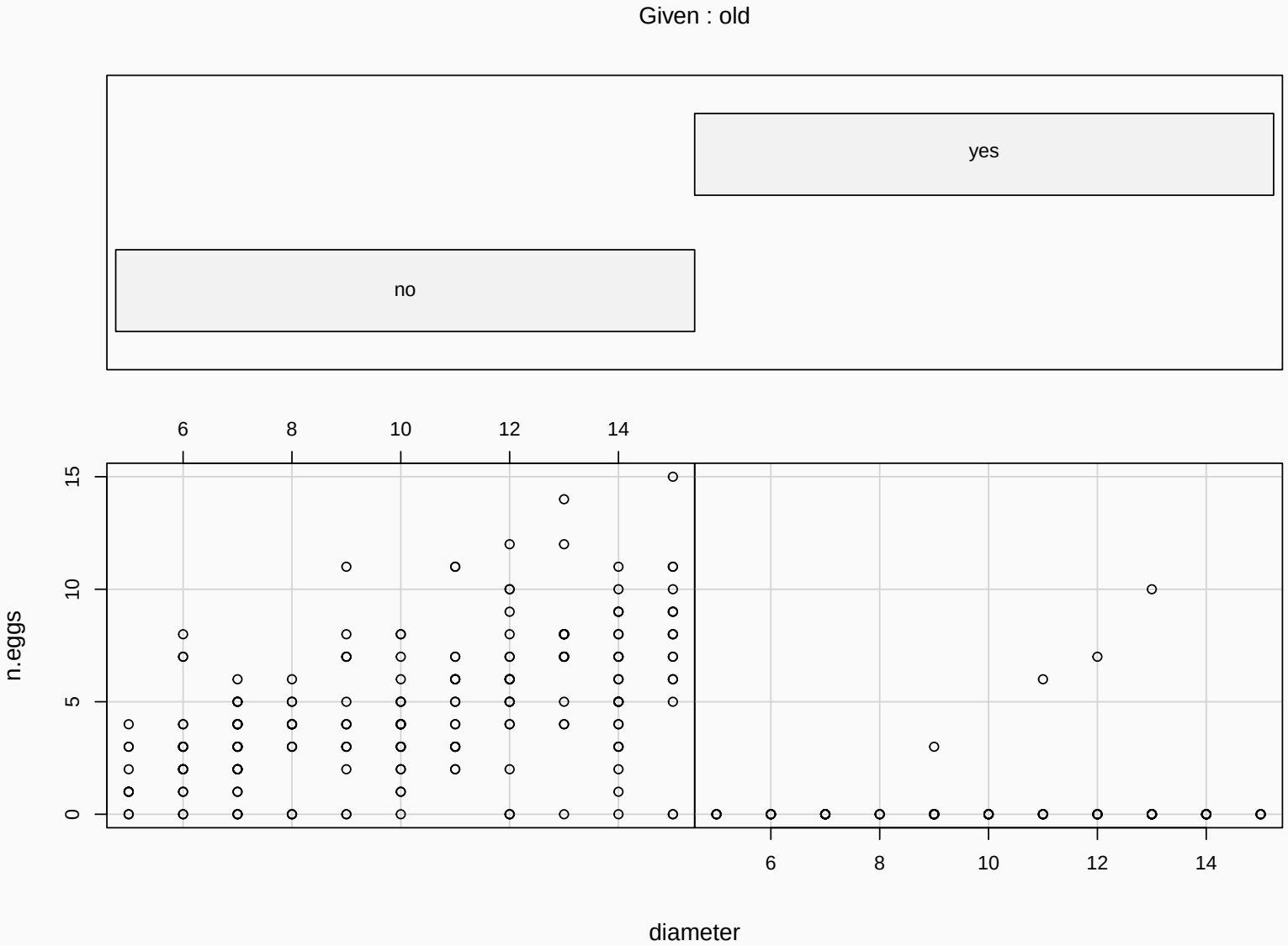
- Nests may be occupied or not

How many eggs in nests?

- Nests may be occupied or not
- Occupied nests may not have eggs (too soon, predation, etc)

Number of eggs ~ nest diameter * old appearance

```
coplot(n.eggs ~ diameter | old, data = eggs)
```



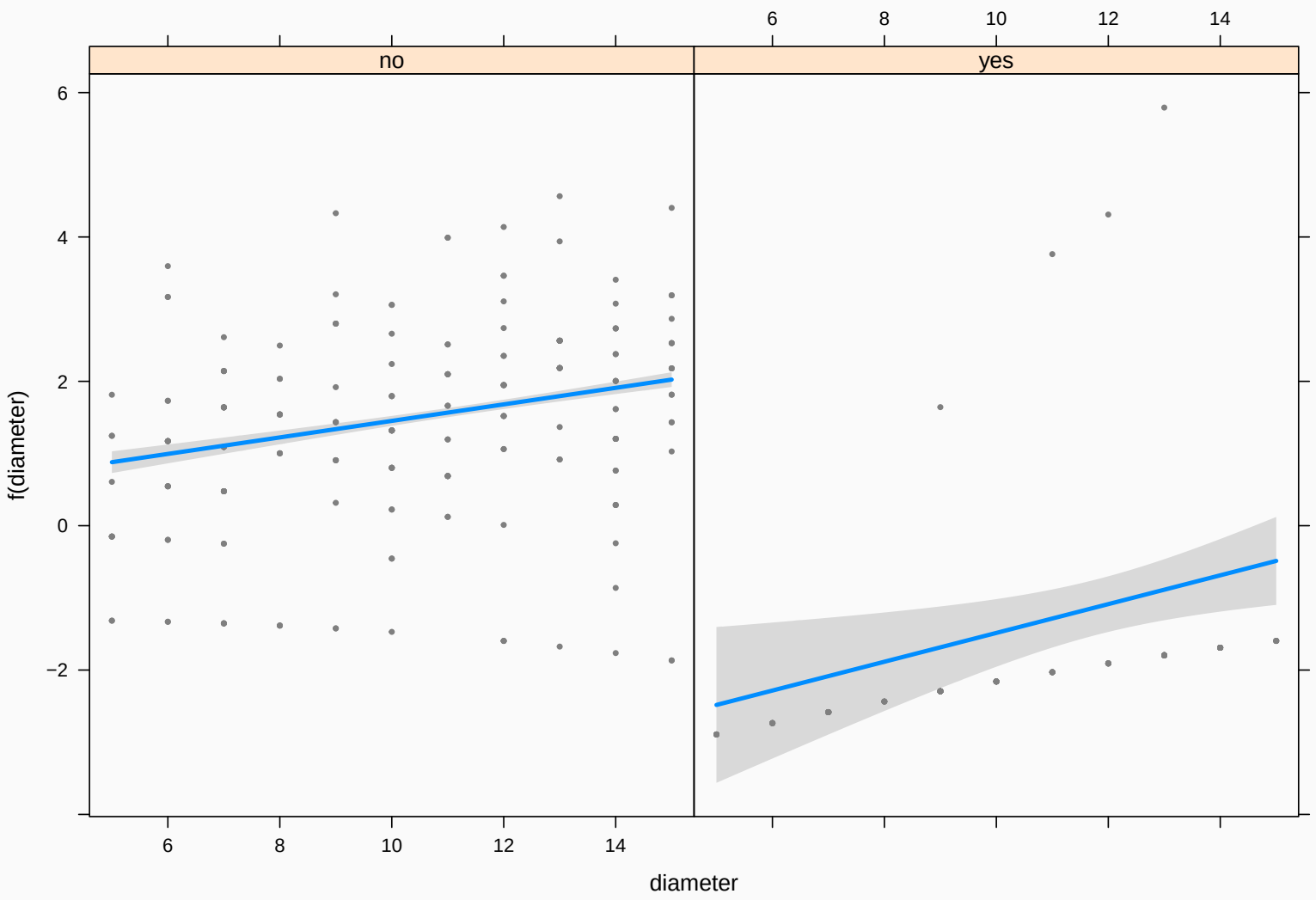
Trying Poisson GLM

```
eggs.poi <- glm(n.eggs ~ old * diameter,
                data = eggs,
                family = poisson)
```

Trying Poisson GLM

```
Call:
glm(formula = n.eggs ~ old * diameter, family = poisson, data = eggs)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.8905  -0.8784  -0.4514   0.3892   6.6795

Coefficients:
               Estimate Std. Error z value Pr(>|z|)
(Intercept)     0.30773    0.12883   2.389   0.0169 *
oldyes         -3.78879    0.92230  -4.108 3.99e-05 ***
diameter        0.11441    0.01105  10.354  < 2e-16 ***
oldyes:diameter  0.08513    0.07634   1.115   0.2648
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 1184.57  on 299  degrees of freedom
Residual deviance:  526.97  on 296  degrees of freedom
AIC: 1176.7
```

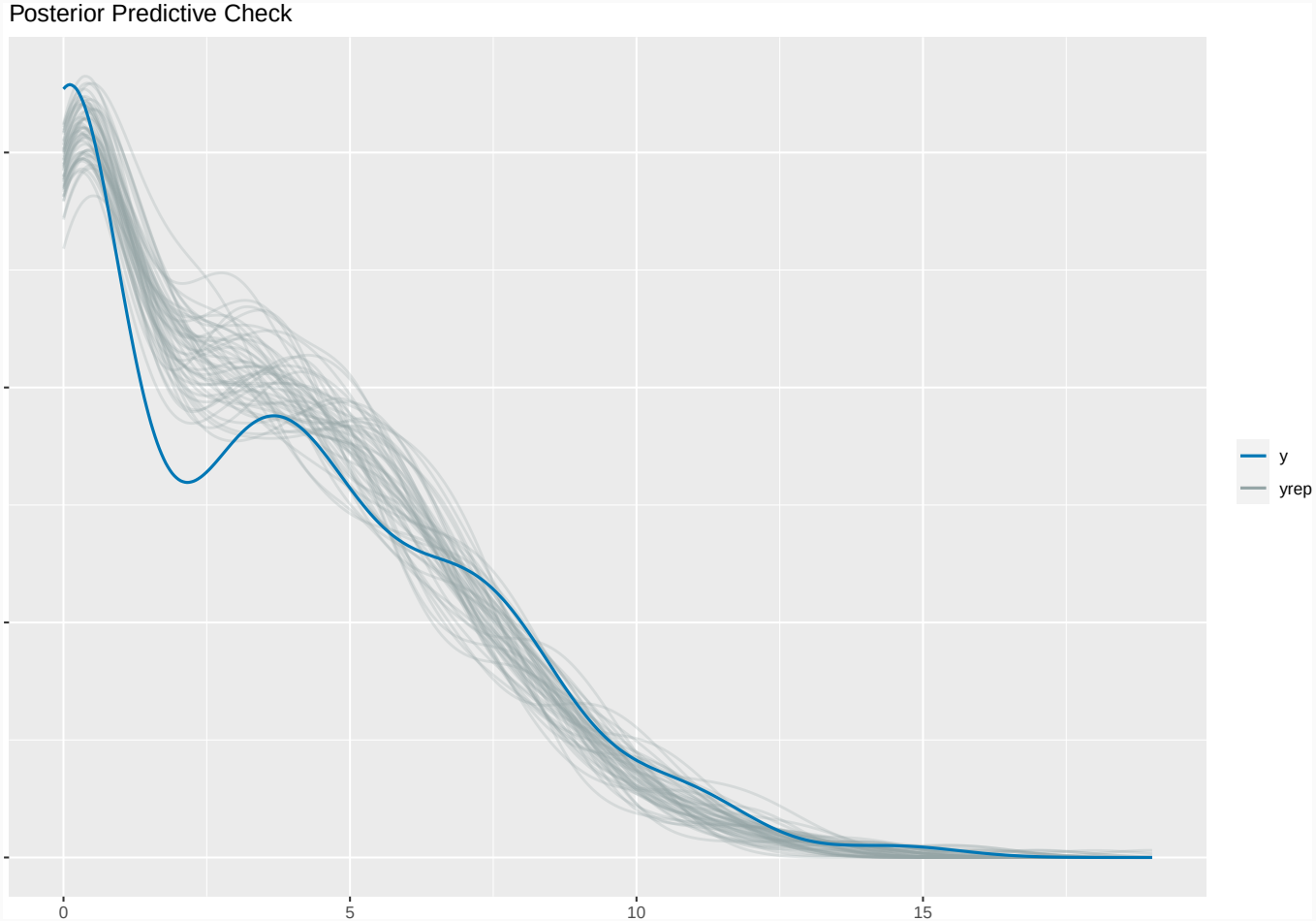
Visualising the fitted Poisson GLM



Checking Poisson GLM

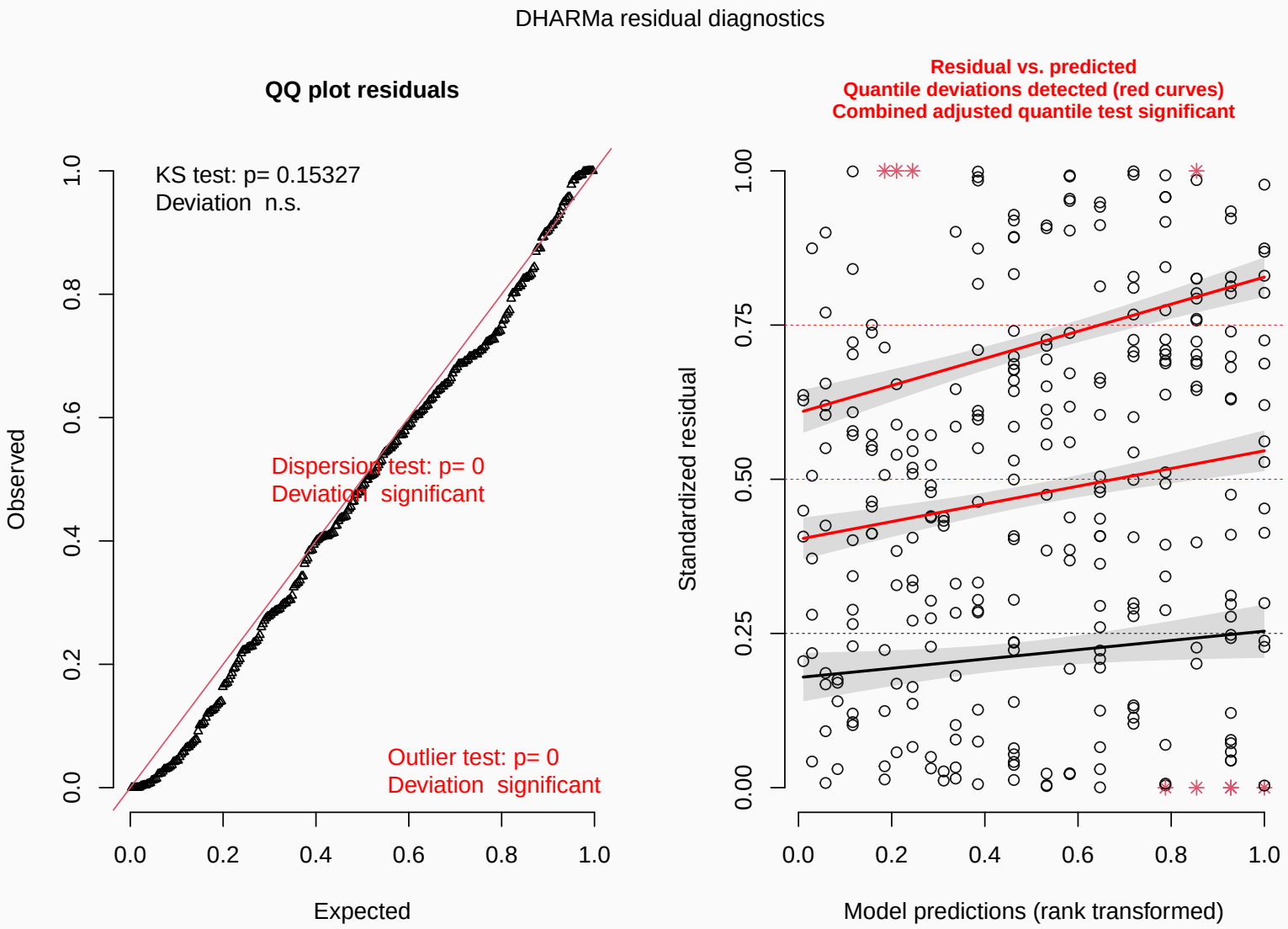
Simulate data from fitted model (**yrep**) and compare with observed data (**y**)

```
library("performance")
pp_check(eggs.poi)
```



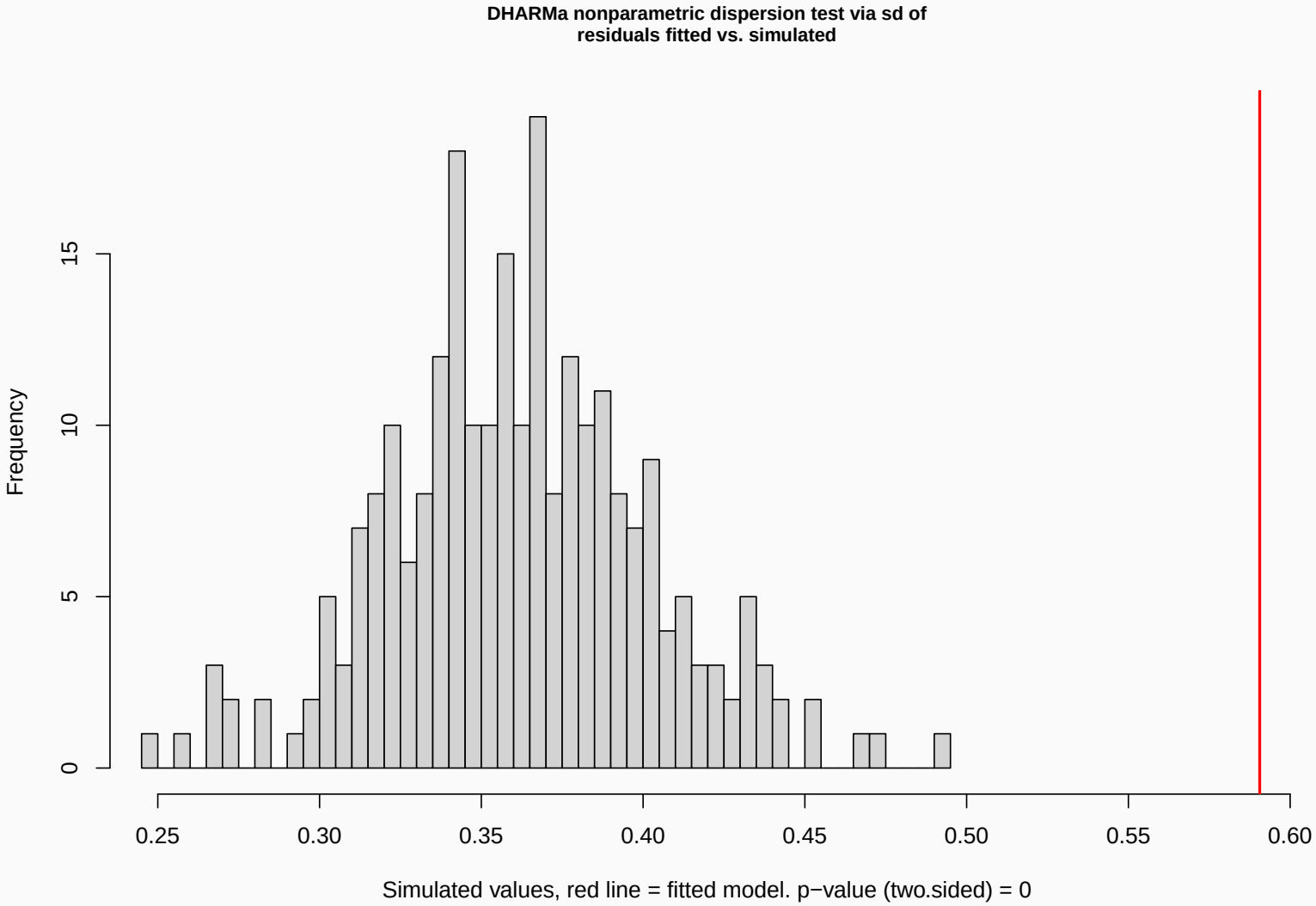
Checking Poisson GLM with DHARMa

```
library("DHARMa")
eggs.poi.res <- simulateResiduals(eggs.poi, plot = TRUE)
```



Checking overdispersion

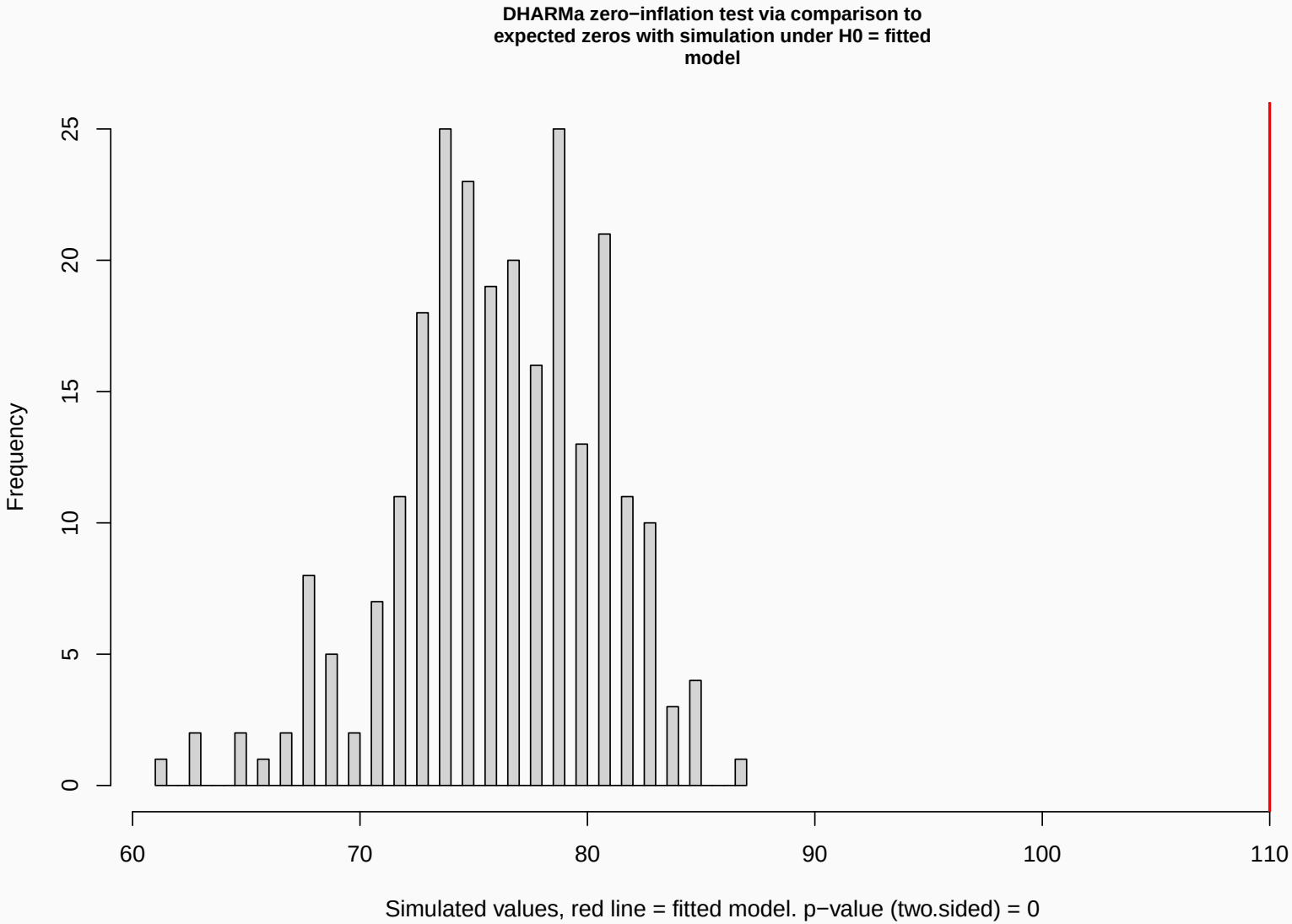
```
testDispersion(eggs.poi.res)
```




```
DHARMa nonparametric dispersion test via sd of residuals fitted
```

Checking zero inflation

```
testZeroInflation(eggs.poi.res)
```



Accounting for zero-inflation

Zero-inflated Poisson/Negative Binomial

Mixture model:

1. Model probability of 0 (`Binomial`)

Zero-inflated Poisson/Negative Binomial

Mixture model:

1. Model probability of 0 (`Binomial`)
2. Model counts (including 0) (`Poisson/Negative Binomial`)

Modelling egg number as Zero-Inflated Poisson (ZIP)

Nests may be occupied or not:

Probability nest occupied ~ old *(Binomial)*

For occupied nests:

Number of eggs ~ Nest diameter *(Poisson)*

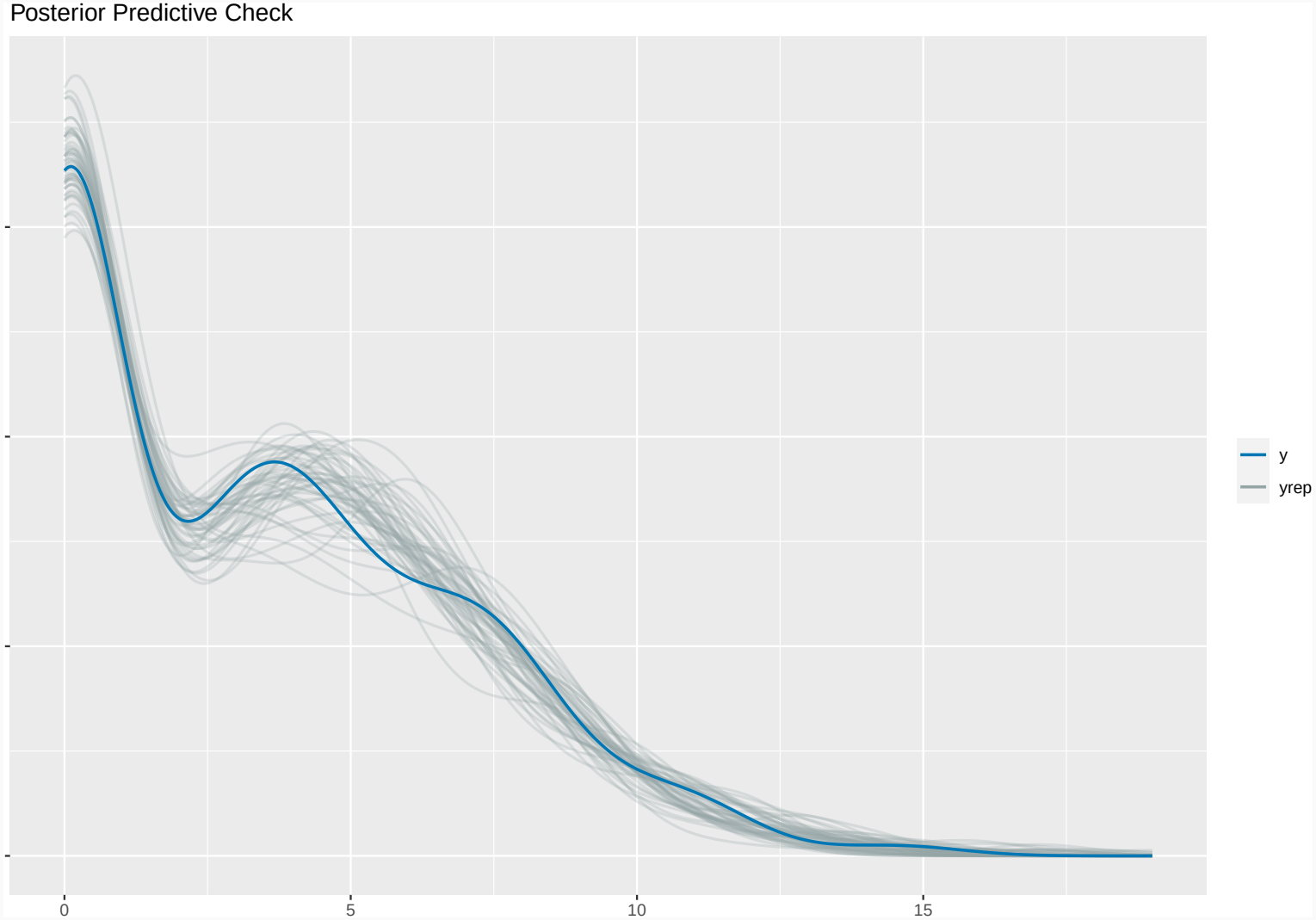
```
library("glmmTMB")
eggs.zip <- glmmTMB(n.eggs ~ diameter,
                    family = "poisson",
                    ziformula = ~ old,
                    data = eggs)
```

Modelling egg number as Zero-Inflated Poisson

```
 Family: poisson  ( log )
Formula:          n.eggs ~ diameter
Zero inflation:          ~old
Data: eggs

     AIC      BIC   logLik deviance df.resid
   993.8   1008.6   -492.9    985.8      296


Conditional model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.41622    0.13619   3.056  0.00224 **
diameter     0.11248    0.01155   9.737  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Zero-inflation model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.4054     0.2803  -8.582   <2e-16 ***
oldyes        5.4897     0.5830   9.416   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

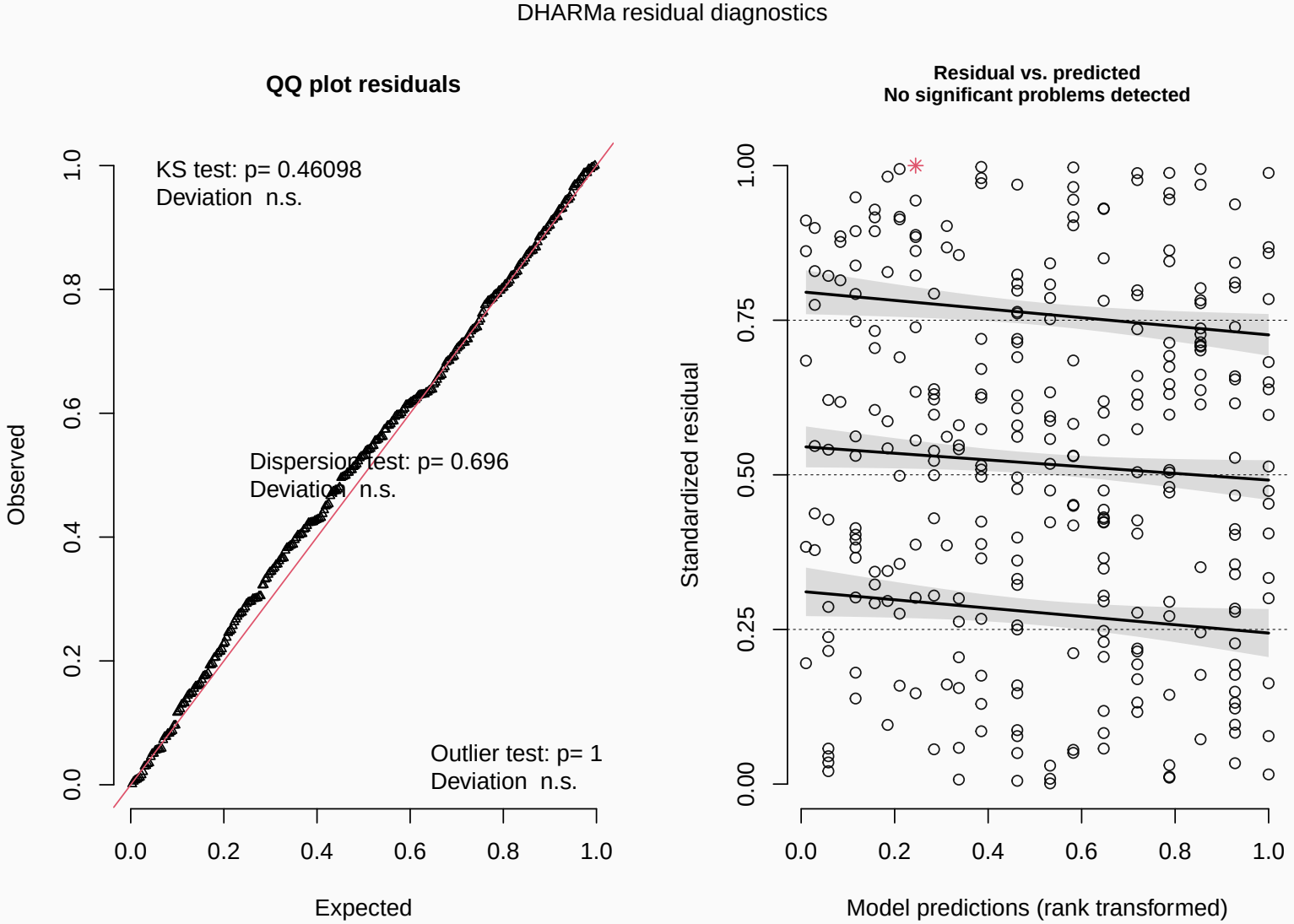
Checking ZIP model

```
pp_check(eggs.zip)
```



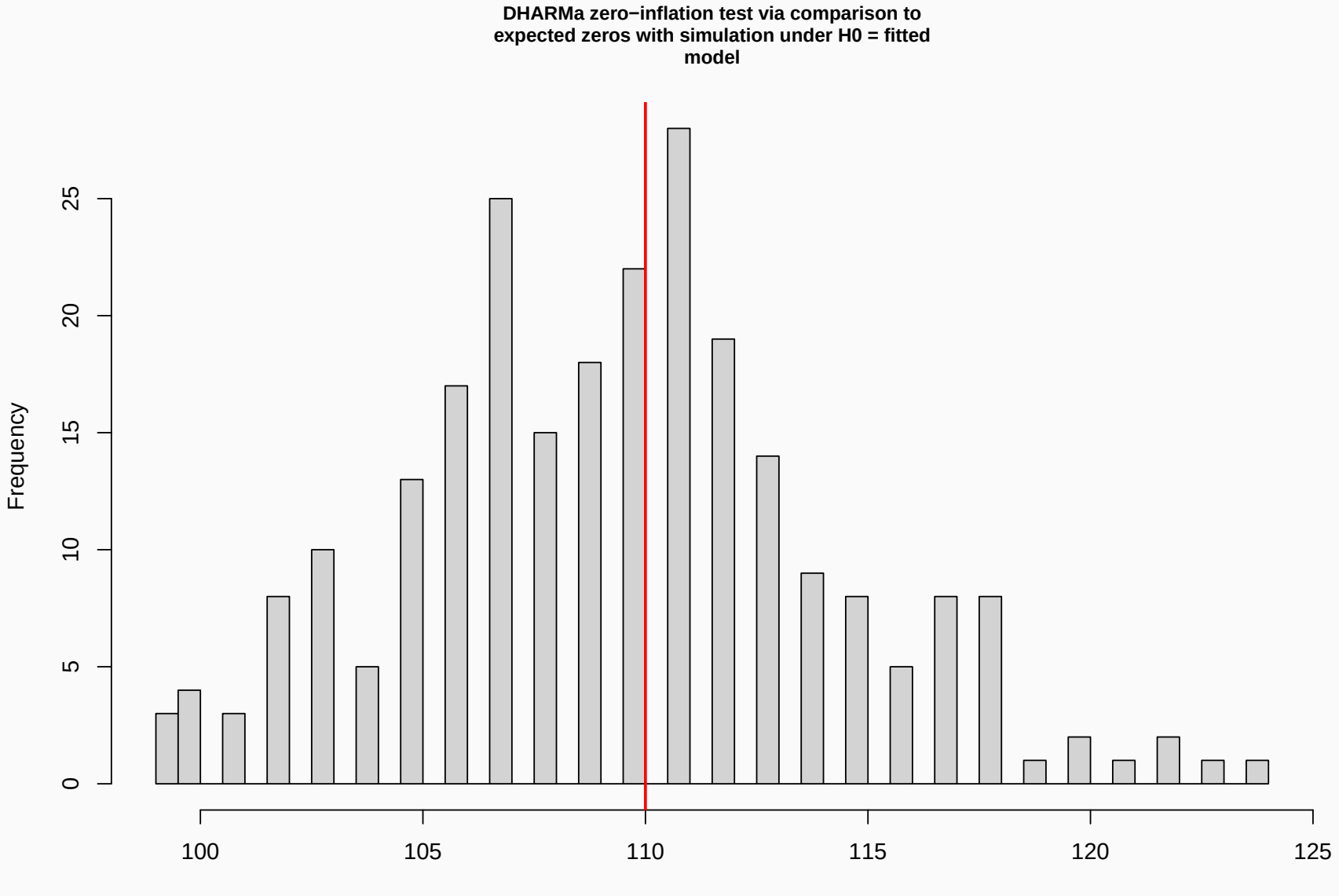
Checking ZIP model with DHARMa

```
eggs.zip.res <- simulateResiduals(eggs.zip, plot = TRUE)
```



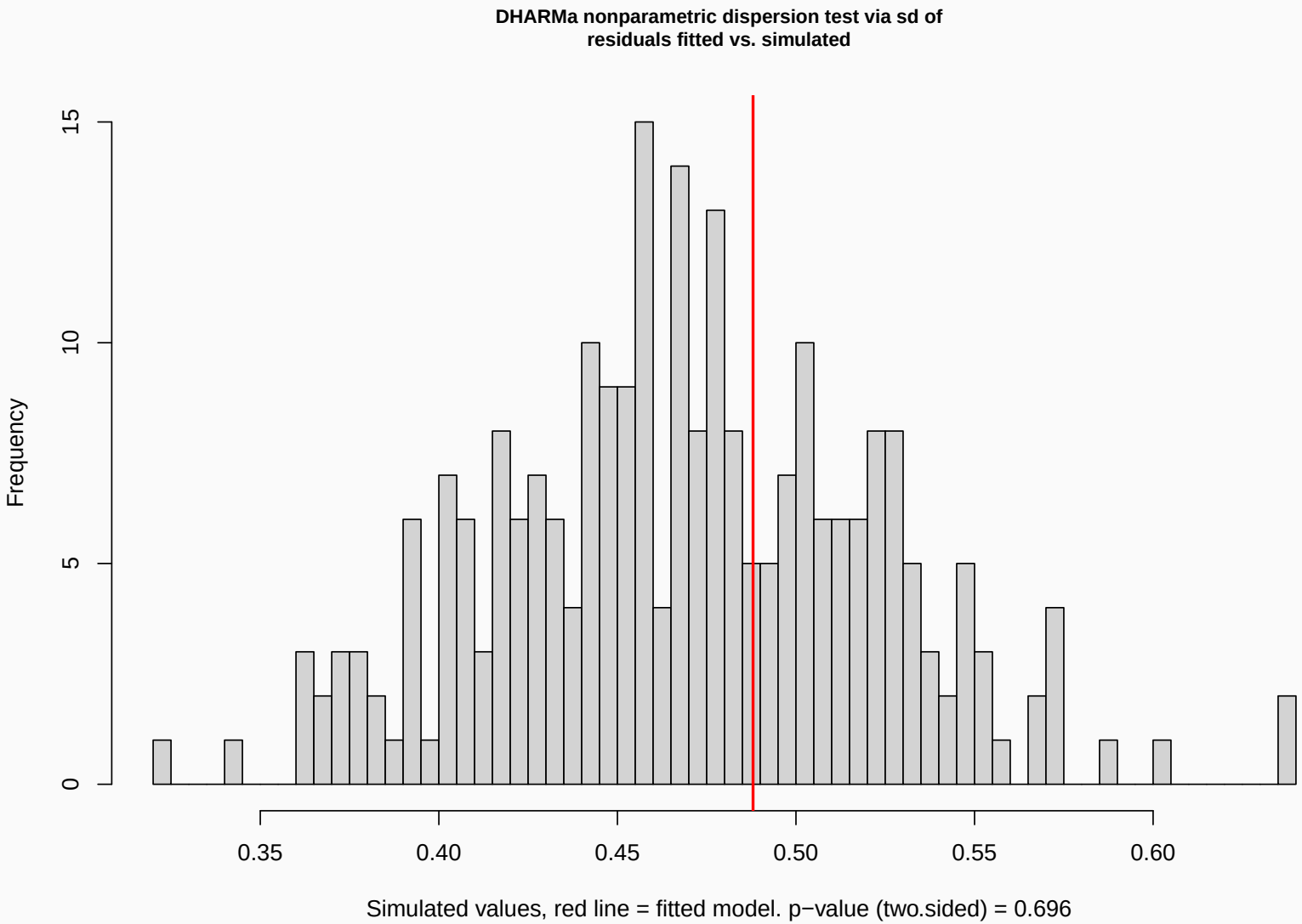
Checking ZIP model with DHARMa

```
testZeroInflation(eggs.zip.res)
```



Checking ZIP model with DHARMa

```
testDispersion(eggs.zip.res)
```



Modelling egg number as Zero-Inflated Negative Binomial (ZINB)

(If there were overdispersion with Poisson)

```
eggs.zinb <- glmmTMB(n.eggs ~ diameter,
                     family = "nbinom2",
                     ziformula = ~ old,
                     data = eggs)
```

Modelling egg number as ZINB

```
 Family: nbinom2  ( log )
Formula:          n.eggs ~ diameter
Zero inflation:          ~old
Data: eggs

     AIC      BIC   logLik deviance df.resid
   995.7   1014.2   -492.8    985.7      295


Dispersion parameter for nbinom2 family ():  143

Conditional model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   0.4118     0.1389   2.964  0.00304 **
diameter      0.1128     0.0118   9.561  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Zero-inflation model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.4160     0.2846  -8.489   <2e-16 ***
oldyes        5.4995     0.5850   9.401   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Comparing models

```
library("parameters")
compare_models(eggs.poi, eggs.zip, eggs.zinb)
```

Parameter	eggs.poi	eggs.zip	eggs.zinb
(Intercept)	0.31 (0.06, 0.56)	0.42 (0.15, 0.68)	0.41 (0.14, 0.68)
diameter	0.11 (0.09, 0.14)	0.11 (0.09, 0.14)	0.11 (0.09, 0.14)
old (yes)	-3.79 (-5.60, -1.98)		
old (yes) * diameter	0.09 (-0.06, 0.23)		
Observations	300	300	300

Comparing models

```
library("performance")
compare_performance(eggs.poi, eggs.zip, eggs.zinb)
```

```
# Comparison of Model Performance Indices

Name      |   Model |      AIC |      BIC |  RMSE |   Sigma | Score_log | Score_sph
-------------------------------------------------------------------------------------
eggs.poi  |     glm | 1176.701 | 1191.516 | 2.324 |   1.334 |    -1.948 |
eggs.zip  | glmmTMB |  993.790 | 1008.605 | 2.324 |   1.000 |    -1.643 |
eggs.zinb | glmmTMB |  995.666 | 1014.185 | 2.324 | 143.279 |           |
```

Accounting for zero-inflation with hurdle models

Tracking measles outbreak

Counting number of hives/person

Many people not sick (0 hives)

Those sick, have many hives (>1)

ZIP/ZINB vs Hurdle models

ZIP/ZINB:

1. Binomial model: probability of zero

Hurdle:

ZIP/ZINB vs Hurdle models

ZIP/ZINB:

1. Binomial model: probability of zero
2. Count model (Poisson/NegBin) includes zero

Hurdle:

ZIP/ZINB vs Hurdle models

ZIP/ZINB:

1. Binomial model: probability of zero
2. Count model (Poisson/NegBin) includes zero

Hurdle:

1. Binomial model: probability of non-zero

ZIP/ZINB vs Hurdle models

ZIP/ZINB:

1. Binomial model: probability of zero
2. Count model (Poisson/NegBin) includes zero

Hurdle:

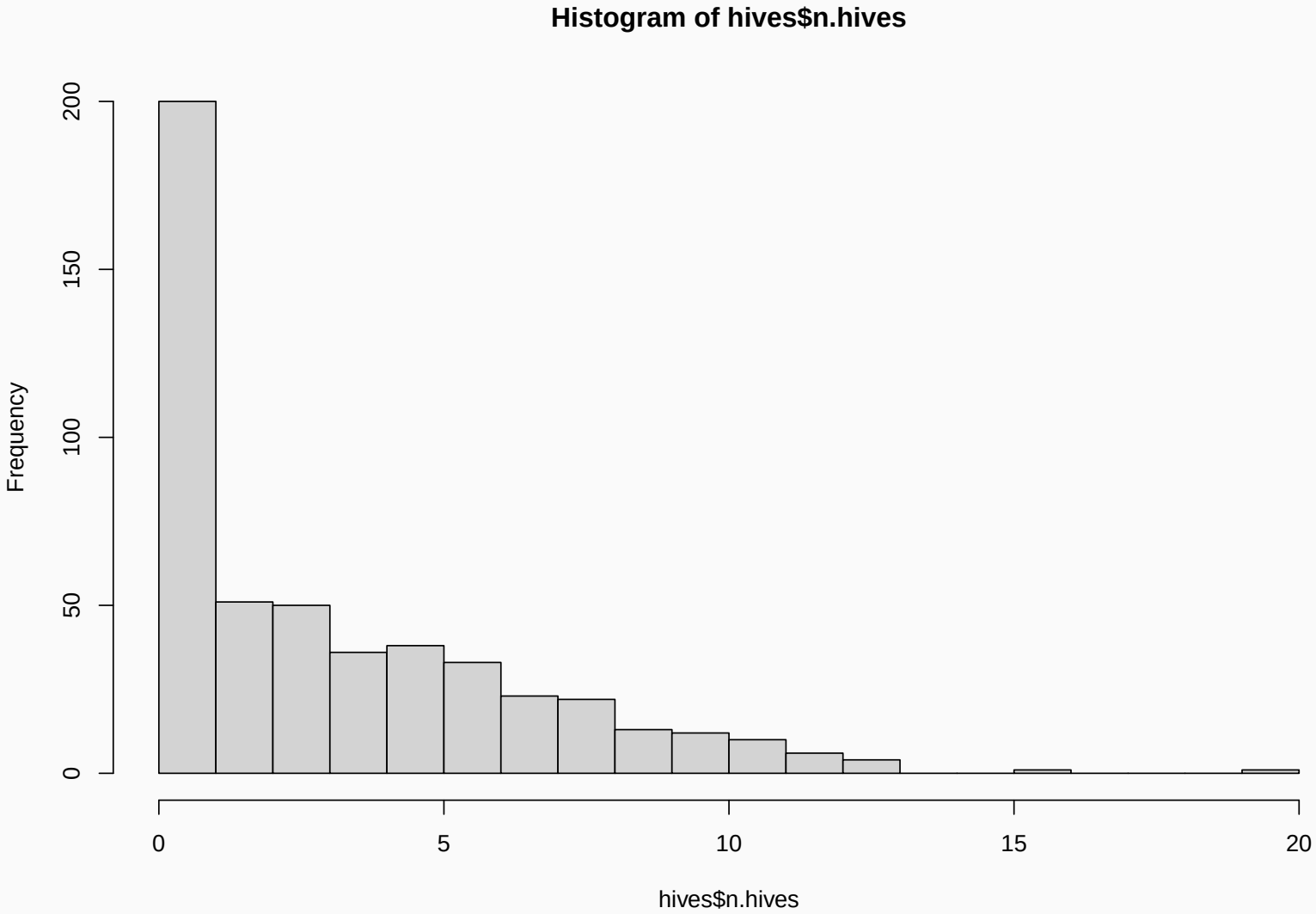
1. Binomial model: probability of non-zero
2. Count model truncated at 1

How many hives per skin area?

```
hives <- read.csv("data/hives.csv")
```

```
      age          vaccinated       area.cm2         n.hives      
 Min.   : 1.0   Min.   :0.000   Min.   : 5.000   Min.   : 0.000  
 1st Qu.:23.0   1st Qu.:0.000   1st Qu.: 6.000   1st Qu.: 0.000  
 Median :45.0   Median :1.000   Median : 8.000   Median : 2.000  
 Mean   :44.7   Mean   :0.648   Mean   : 7.482   Mean   : 3.256  
 3rd Qu.:65.0   3rd Qu.:1.000   3rd Qu.: 9.000   3rd Qu.: 5.250  
 Max.   :90.0   Max.   :1.000   Max.   :10.000   Max.   :20.000  
```

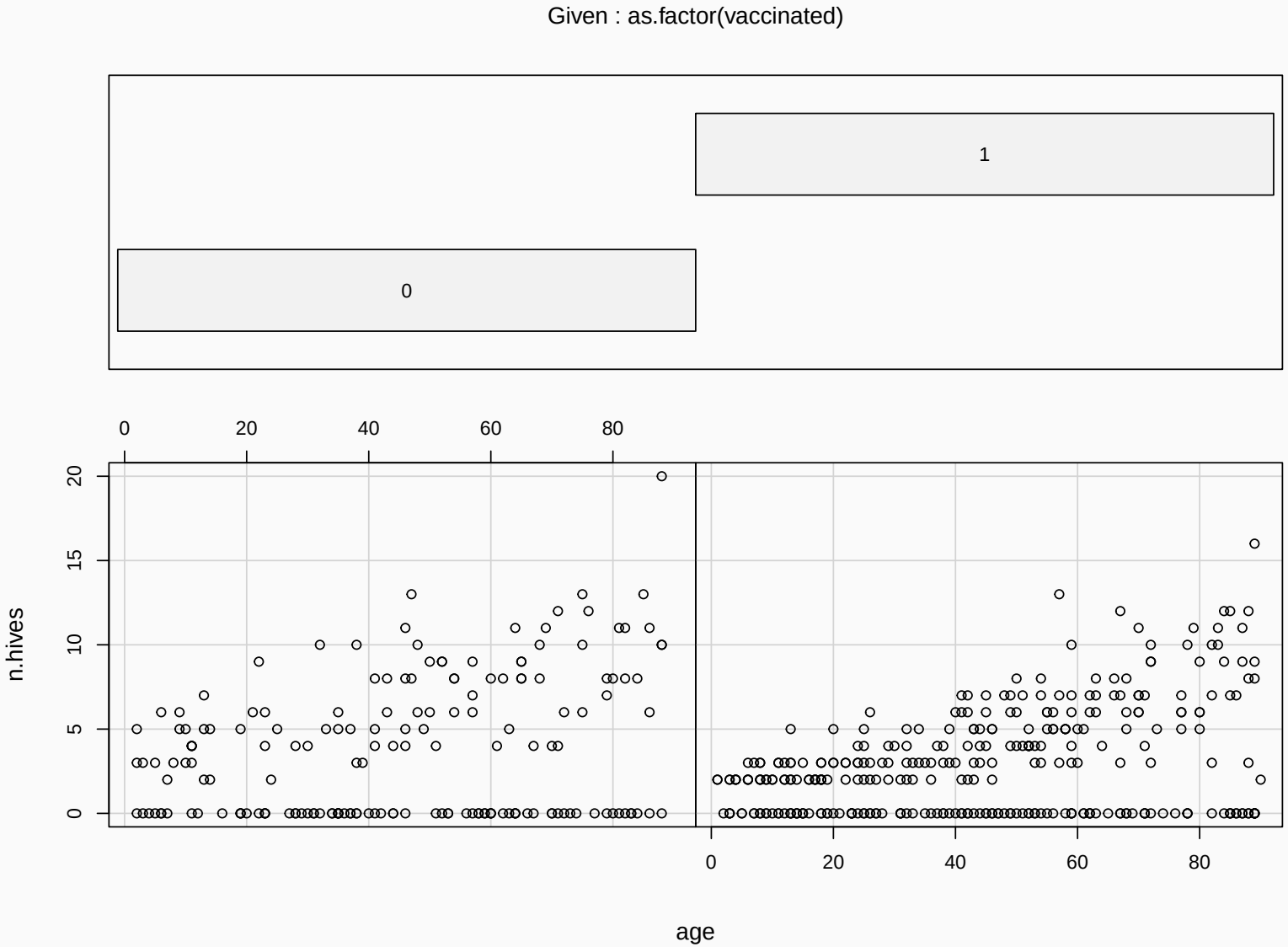
Many people with 0 hives



(that does not mean we need zero-inflated model!)

Number of hives ~ age * vaccinated

```
coplot(n.hives ~ age | as.factor(vaccinated), data = hives)
```



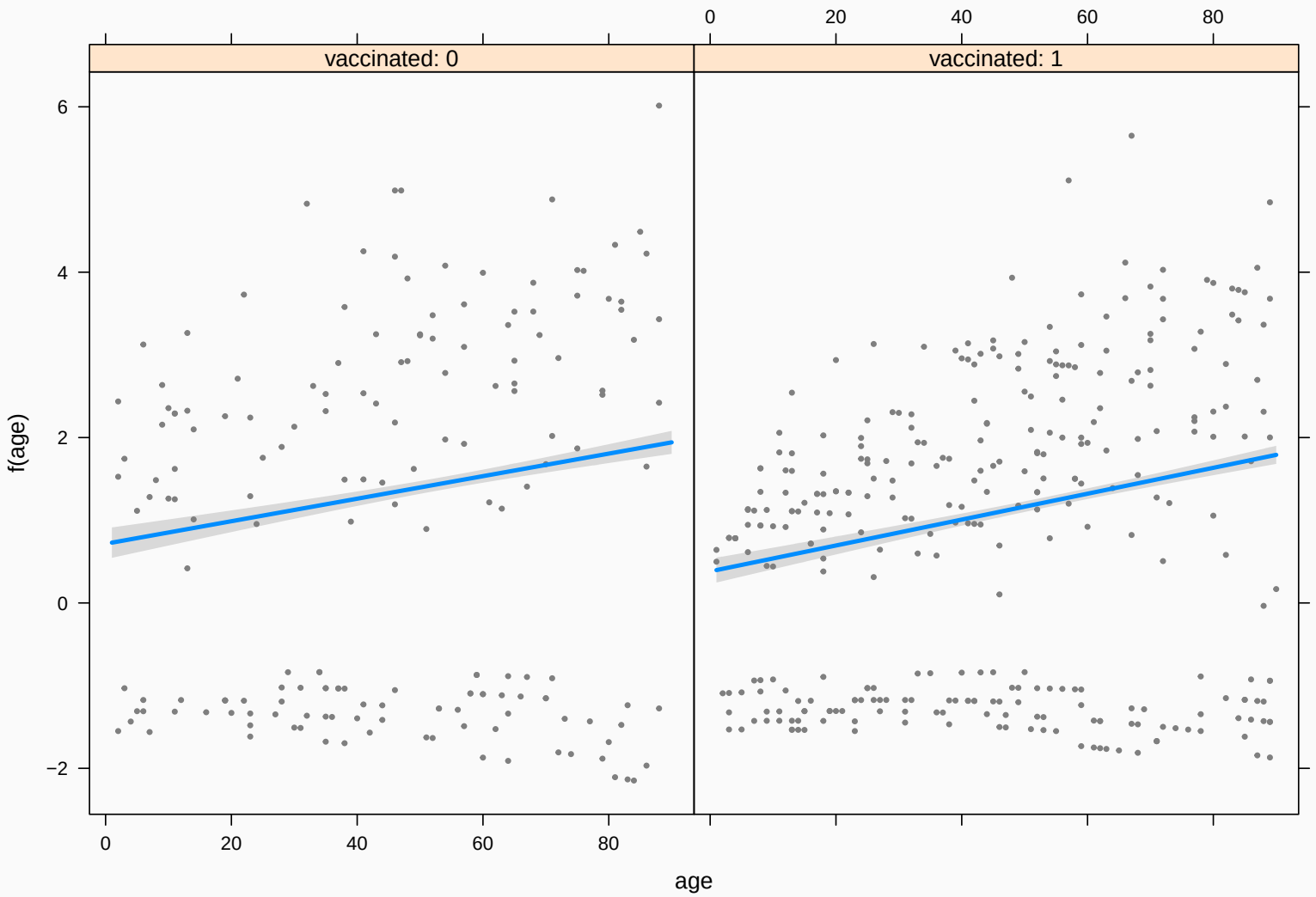
Trying Poisson GLM

```
hives.poi <- glm(n.hives ~ vaccinated * age,
                 offset = log(area.cm2),
                 data = hives,
                 family = poisson)
```

Trying Poisson GLM

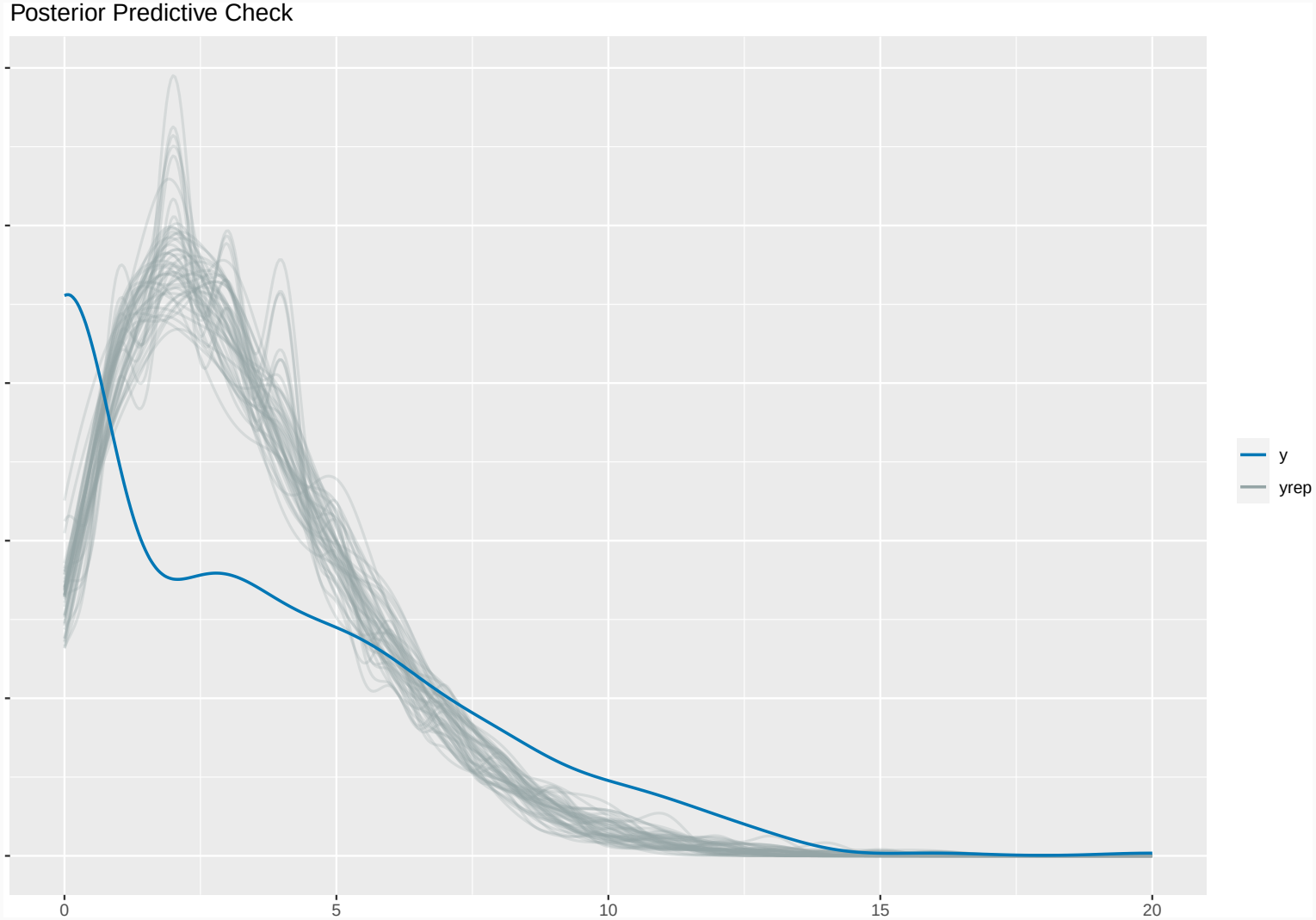
```
Call:
glm(formula = n.hives ~ vaccinated * age, family = poisson, data = hives,
    offset = log(area.cm2))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-4.0081  -2.2235   0.1396   1.2155   4.2198

Coefficients:
                Estimate Std. Error z value Pr(>|z|)
(Intercept)    -1.363696   0.095097 -14.340  < 2e-16 ***
vaccinated     -0.334184   0.122887  -2.719  0.00654 **
age             0.013626   0.001623   8.395  < 2e-16 ***
vaccinated:age  0.002034   0.002075   0.980  0.32708
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 2137.0  on 499  degrees of freedom
Residual deviance: 1891.7  on 496  degrees of freedom
AIC: 2925.6
```

Visualising fitted Poisson GLM



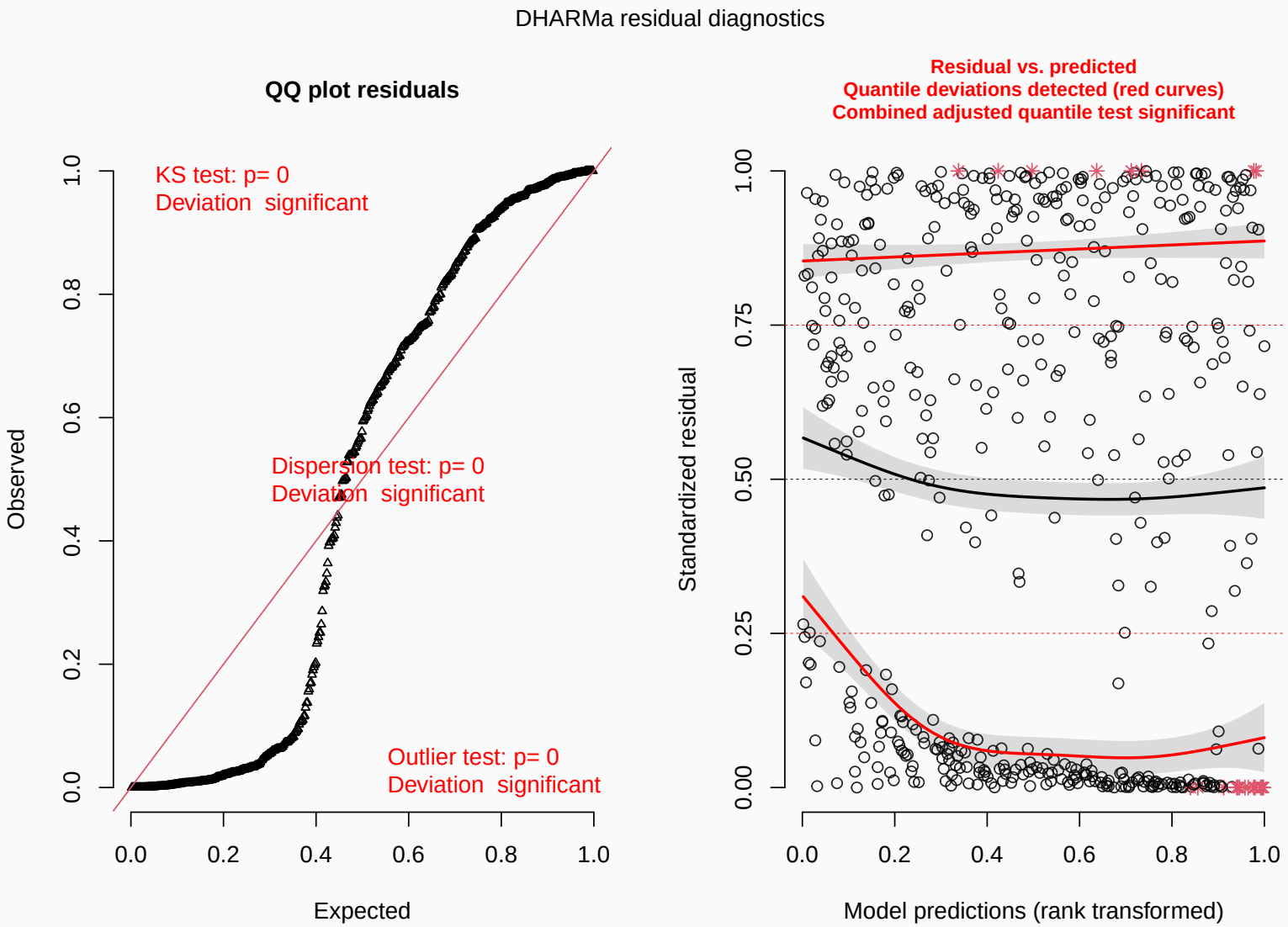
Checking Poisson GLM

```
pp_check(hives.poi)
```



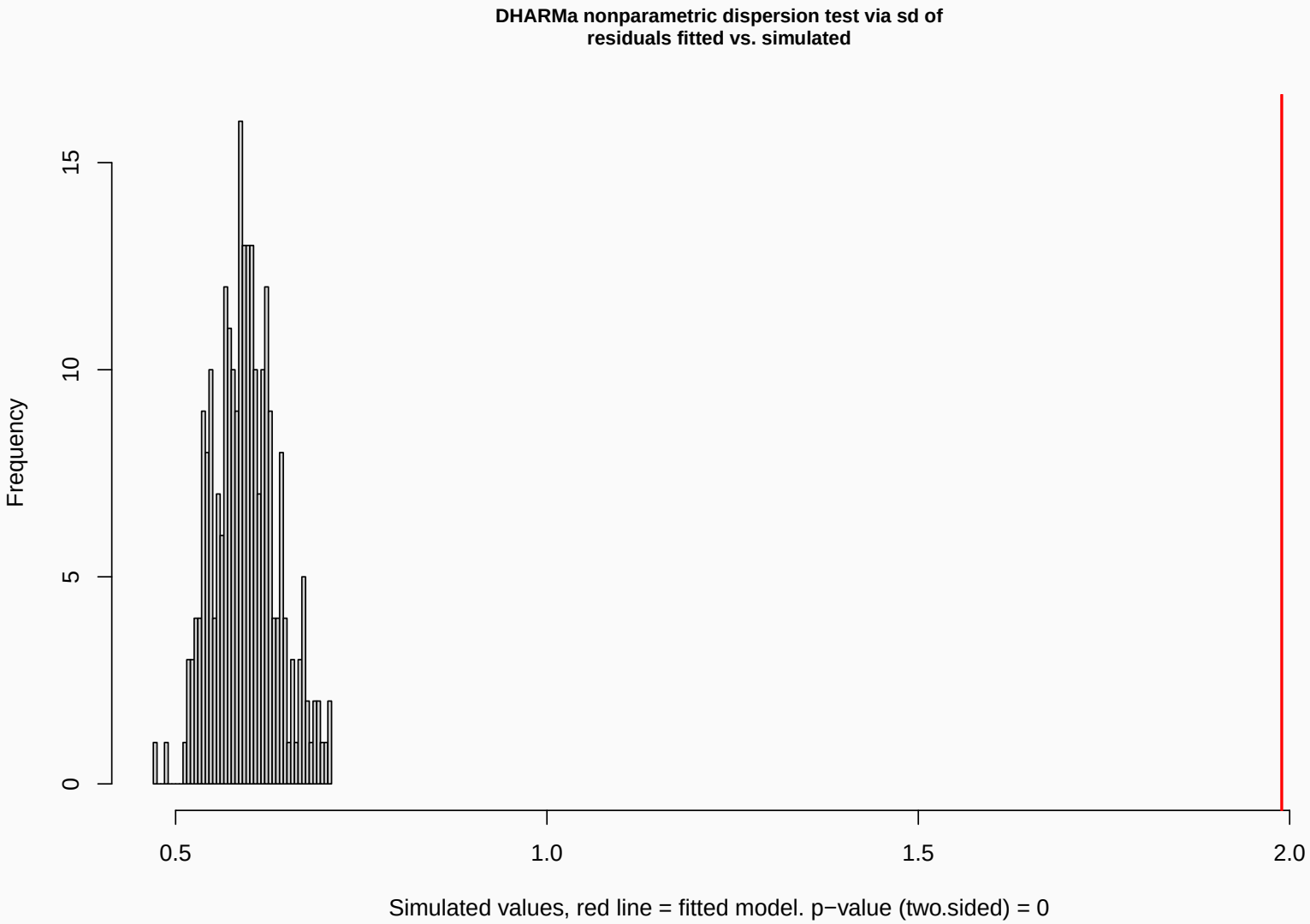
Checking Poisson GLM

```
hives.poi.res <- simulateResiduals(hives.poi, plot = TRUE)
```



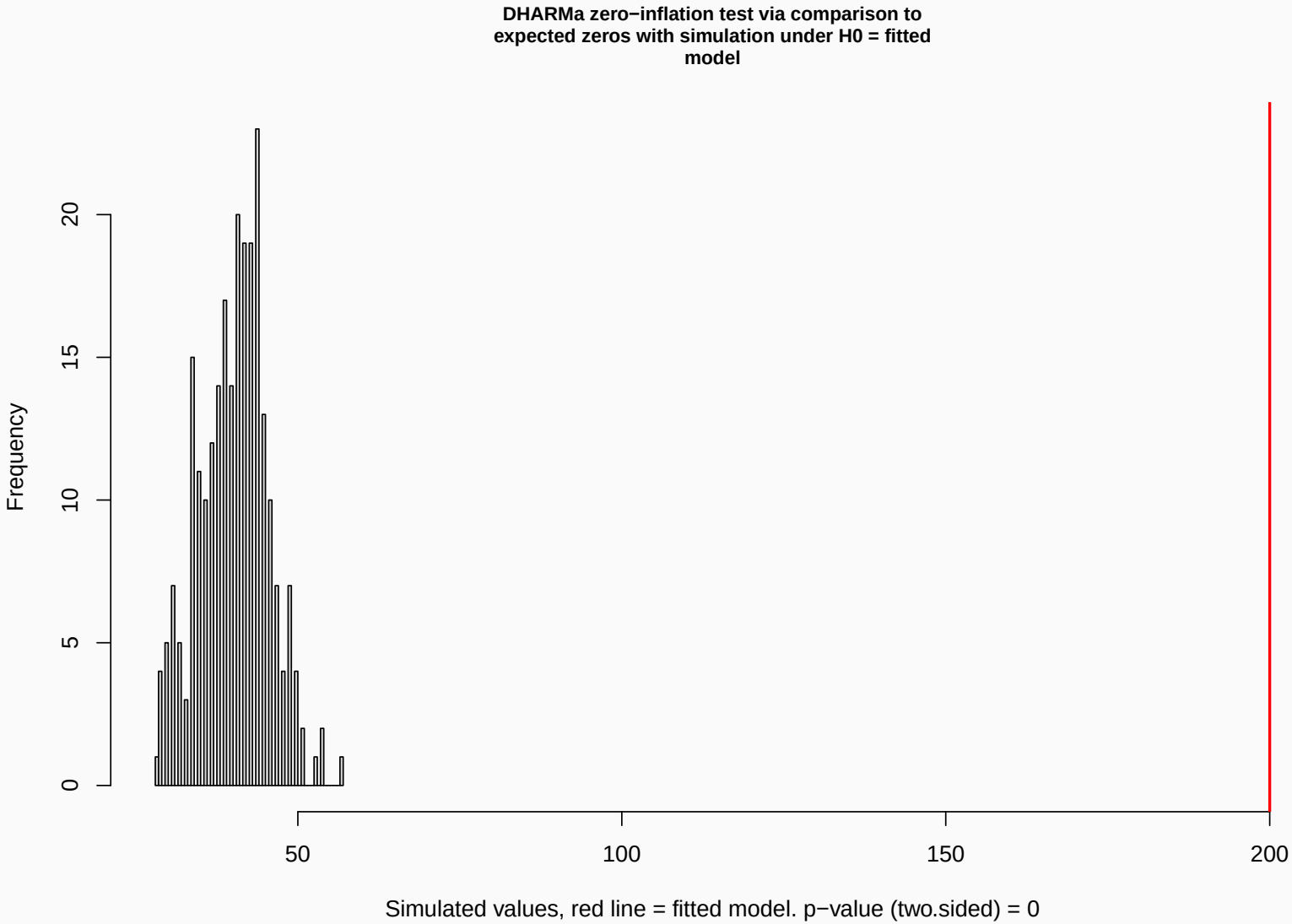
Checking overdispersion

```
testDispersion(hives.poi.res)
```



Checking zero inflation

```
testZeroInflation(hives.poi.res)
```



Accounting for zero-inflation with hurdle model

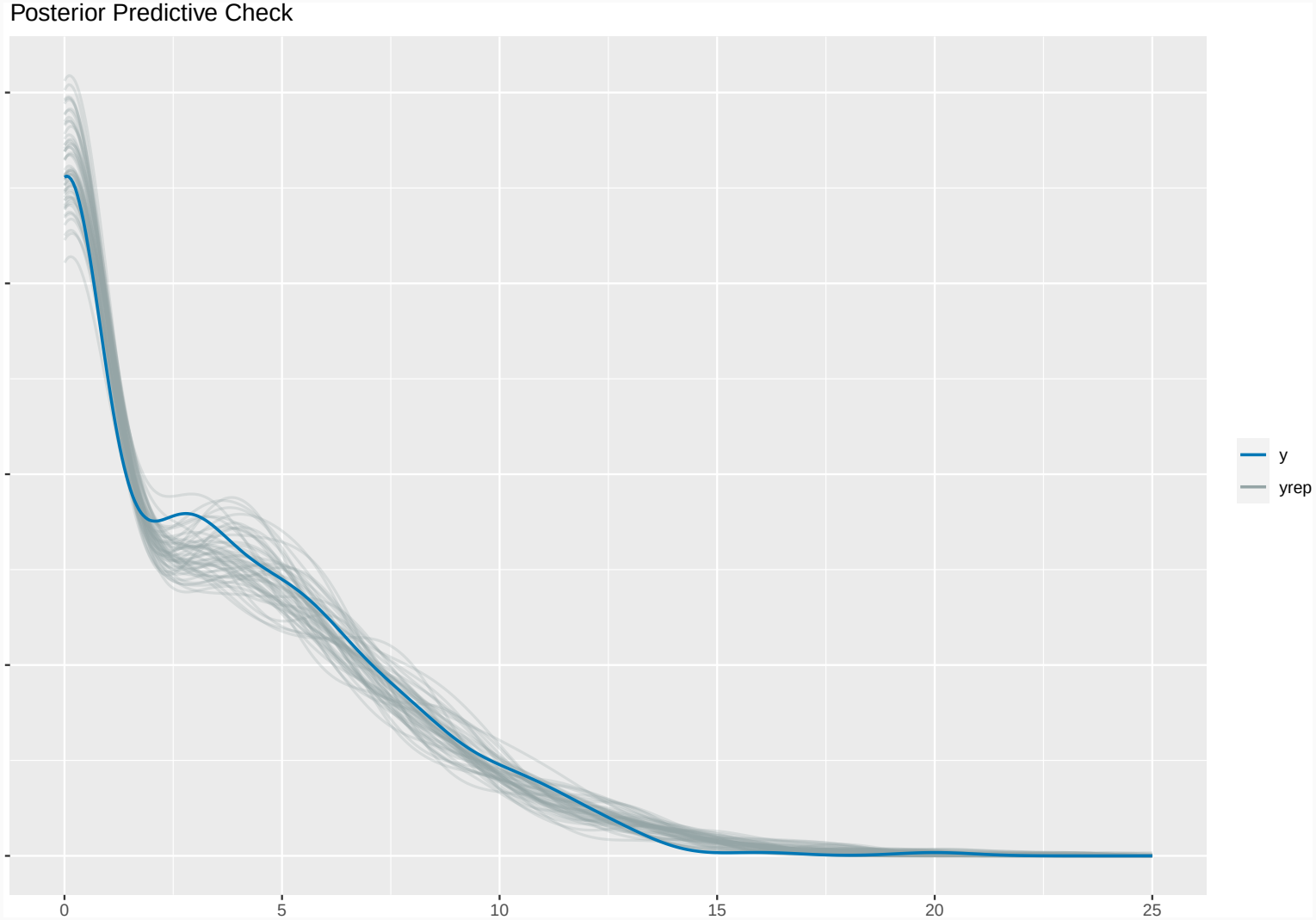
```
hives.hur <- glmmTMB(n.hives ~ vaccinated + age,
                     family = truncated_poisson,
                     ziformula = ~ 1,
                     offset = log(area.cm2),
                     data = hives)
```

Accounting for zero-inflation with hurdle model

```
 Family: truncated_poisson  ( log )
Formula:          n.hives ~ vaccinated + age
Zero inflation:           ~1
Data: hives
 Offset: log(area.cm2)

     AIC      BIC   logLik deviance df.resid
  1932.1   1949.0   -962.1   1924.1      496


Conditional model:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.853885   0.070755 -12.068  < 2e-16 ***
vaccinated  -0.365664   0.051532  -7.096 1.29e-12 ***
age          0.014860   0.001065  13.955  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Zero-inflation model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.40547    0.09129  -4.442 8.93e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

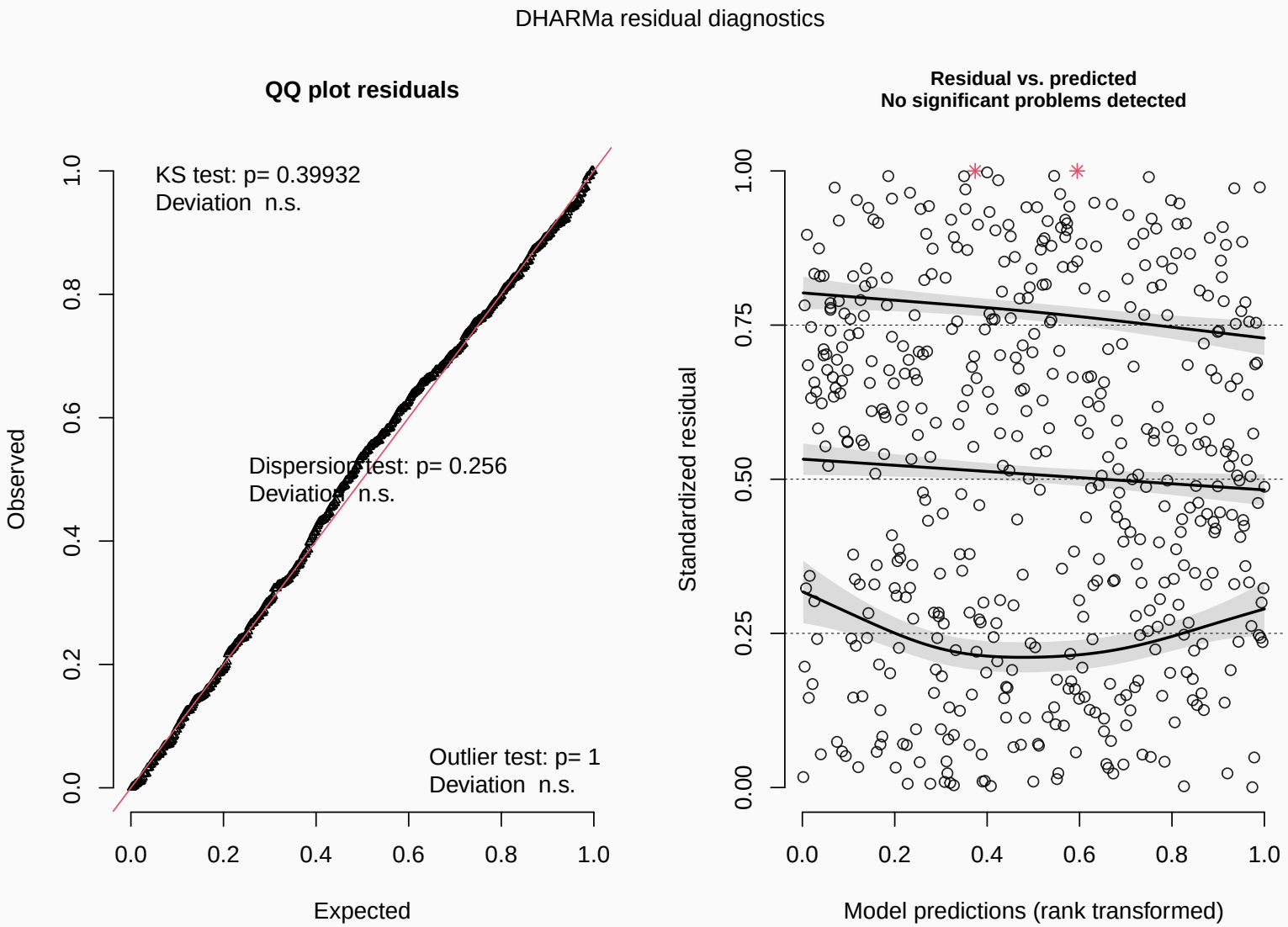
Checking hurdle model

```
pp_check(hives.hur)
```



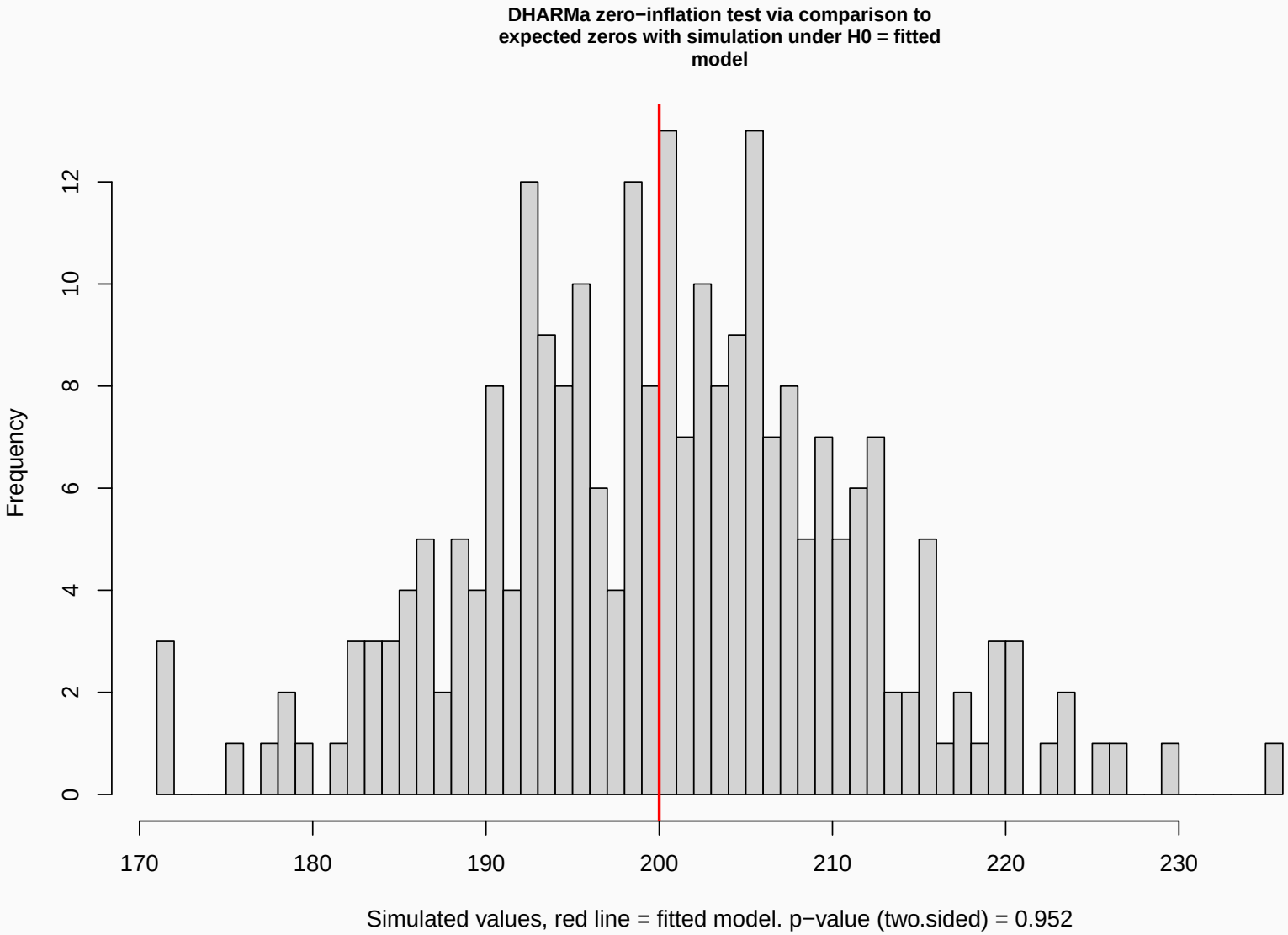
Checking hurdle model with DHARMa

```
hives.hur.res <- simulateResiduals(hives.hur, plot = TRUE)
```



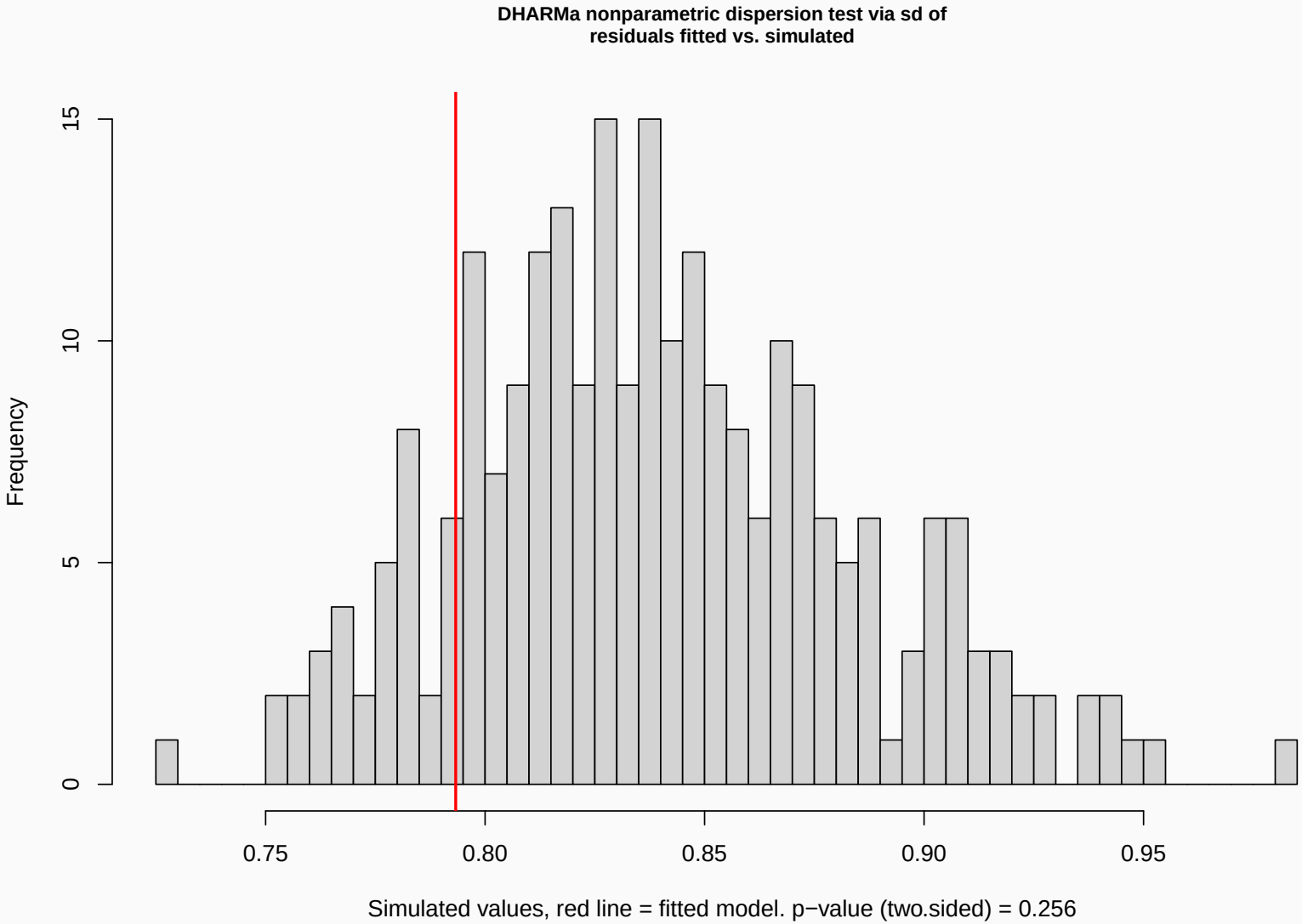
Checking zero inflation

```
testZeroInflation(hives.hur.res)
```



Checking overdispersion

```
testDispersion(hives.hur.res)
```



Comparing models

```
compare_models(hives.poi, hives.hur)
```

Parameter	hives.poi	hives.hur
(Intercept)	-1.36 (-1.55, -1.18)	-0.85 (-0.99, -0.72)
vaccinated	-0.33 (-0.58, -0.09)	-0.37 (-0.47, -0.26)
age	0.01 (0.01, 0.02)	0.01 (0.01, 0.02)
vaccinated * age	2.03e-03 (0.00, 0.01)	
Observations	500	500

Comparing models

```
compare_performance(hives.poi, hives.hur)
```

```
# Comparison of Model Performance Indices

Name      |   Model |      AIC |      BIC |  RMSE | Sigma | Score_log | Score_spher
-------------------------------------------------------------------------------------
hives.poi |     glm | 2925.603 | 2942.462 | 3.299 | 1.953 |    -2.918 |           0
hives.hur | glmmTMB | 1932.124 | 1948.982 | 3.313 | 1.000 |    -2.262 |           0
```