More Checking Models

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Checking the Probability of 0

- The Poisson and binomial distributions both are suitable for count data.
- In some situations, the proportion of observed zeros can be larger than the model predicts.
- One solution is to use a model with overdispersion.
- An alternative is to use logistic regression to model presense/absence and then a different model to model the counts when present.
- Here we will examine the use of simulation to check the goodness of fit of real data to data simulated under a Poisson model.
- We will see if using a model with overdispersion is sufficient when a Poisson model fails.

Case Study:

- The *Dusky Sound* is a large fjord in southwest New Zealand noted for abundant wildlife.
- Biologists conducted a study to examine the relationship between the seaweed *Ecklonia radiata* and the sea urchin *Evechinus chloroticus* in the seas of the fjord.
- The goal is to predict seaweed abundance from urchin abundance and other variables.
- Other predictors include the distance to the mouth of the fjord (in km), the distance to the nearest point of land (in km), and the *fetch*, a sum of distances in km to the nearest land along several radial directions.
- Higher *fetch* values are associated with windier conditions and greater waves.
- There are 103 separate sample locations.
- The number of seaweed and urchins are counted in a 25 m by 1m area.

Data

```
> sw = read.table("seaweed.txt", header = T)
> str(sw)

'data.frame':        103 obs. of  5 variables:
 $ seaweed: int  0 0 0 2 2 1 1 0 0 3 ...
 $ urchin : int  5 9 1 1 0 3 2 5 11 2 ...
 $ fjord  : num  11.5 13 9.7 9.6 7.3 9.1 7 7.5 5.6 10.2 ...
 $ land   : num  0.6 0.7 1 0.7 0.8 1 0.5 1.1 0.8 0.2 ...
 $ fetch  : num  28.1 39.7 39.4 33.5 17.4 29.4 27.5 38.9 33.6 36.2 ...
```

Data Summaries

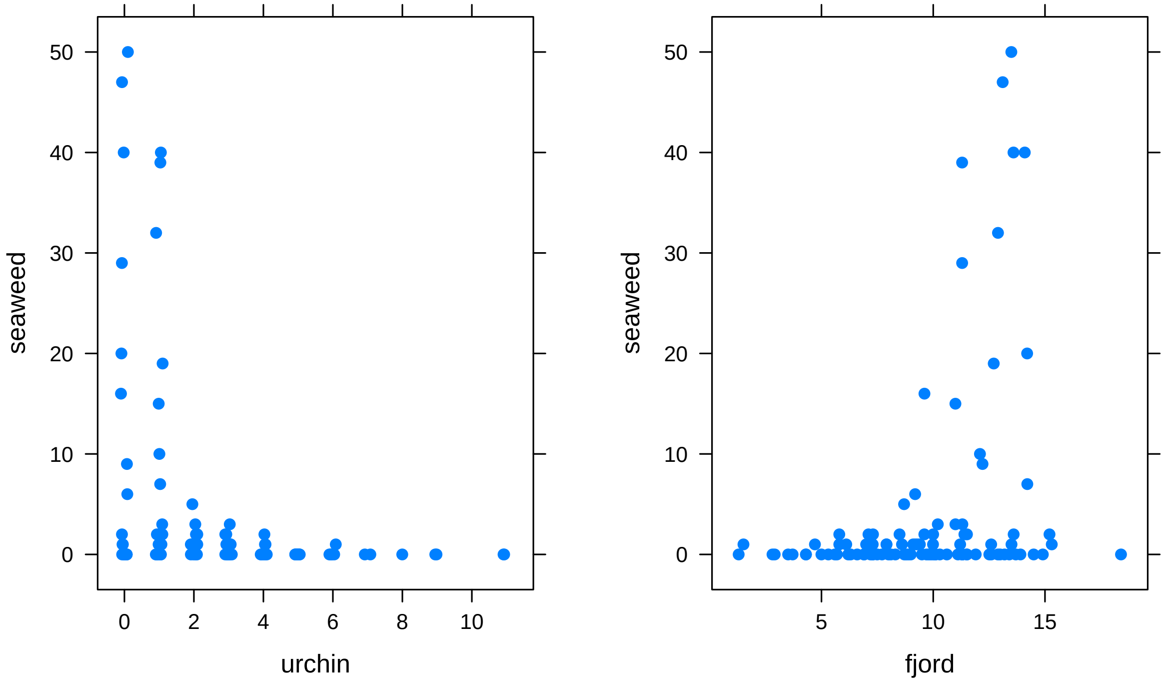
```
> summary(sw)
```

```
    seaweed          urchin           fjord            land       
 Min.   : 0.000   Min.   : 0.000   Min.   : 1.30   Min.   :0.2000  
 1st Qu.: 0.000   1st Qu.: 1.000   1st Qu.: 7.30   1st Qu.:0.6000  
 Median : 0.000   Median : 2.000   Median : 9.70   Median :0.7000  
 Mean   : 4.194   Mean   : 2.748   Mean   : 9.58   Mean   :0.7058  
 3rd Qu.: 2.000   3rd Qu.: 4.000   3rd Qu.:12.00   3rd Qu.:0.8000  
 Max.   :50.000   Max.   :11.000   Max.   :18.40   Max.   :1.2000  
     fetch      
 Min.   :17.40  
 1st Qu.:28.50  
 Median :32.30  
 Mean   :32.30  
 3rd Qu.:36.05  
 Max.   :48.30  
```

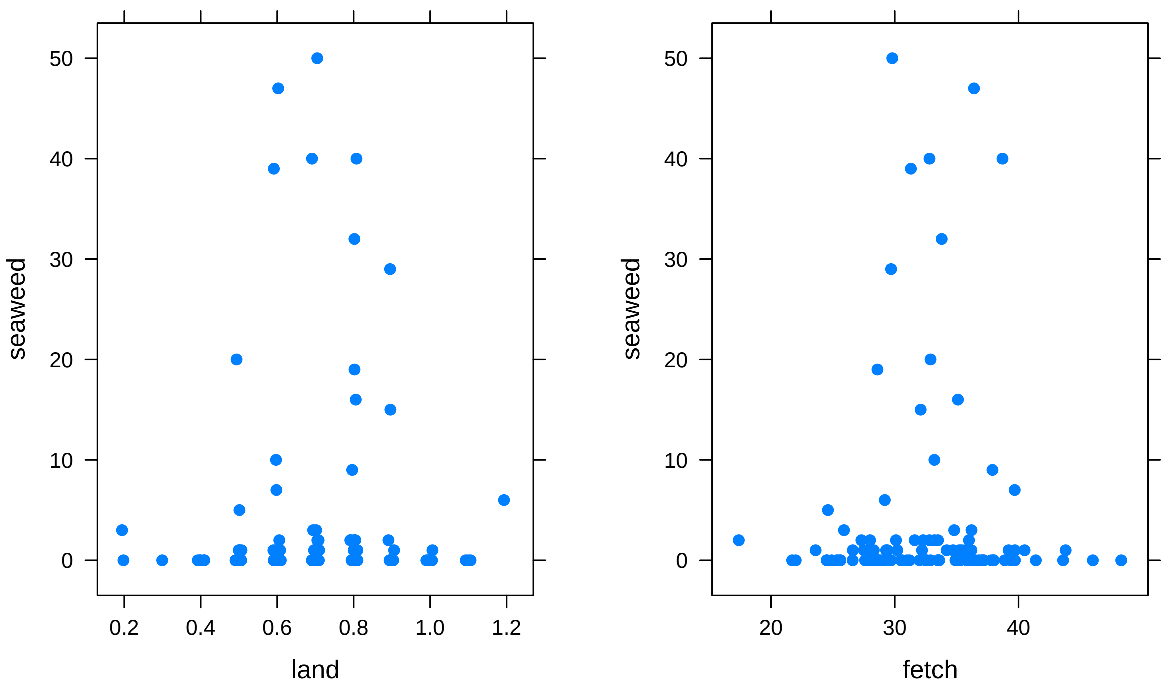

Figure commands

```
> library(lattice)
> fig1 = xyplot(seaweed ~ urchin, data = sw, jitter.x = T,
+     pch = 16)
> fig2 = xyplot(seaweed ~ fjord, data = sw, jitter.x = T,
+     pch = 16)
> fig3 = xyplot(seaweed ~ land, data = sw, jitter.x = T,
+     pch = 16)
> fig4 = xyplot(seaweed ~ fetch, data = sw, jitter.x = T,
+     pch = 16)
> print(fig1, split = c(1, 1, 2, 1))
> print(fig2, split = c(2, 1, 2, 1), new = F)
> print(fig3, split = c(1, 1, 2, 1))
> print(fig4, split = c(2, 1, 2, 1), new = F)
```

Scatter plots



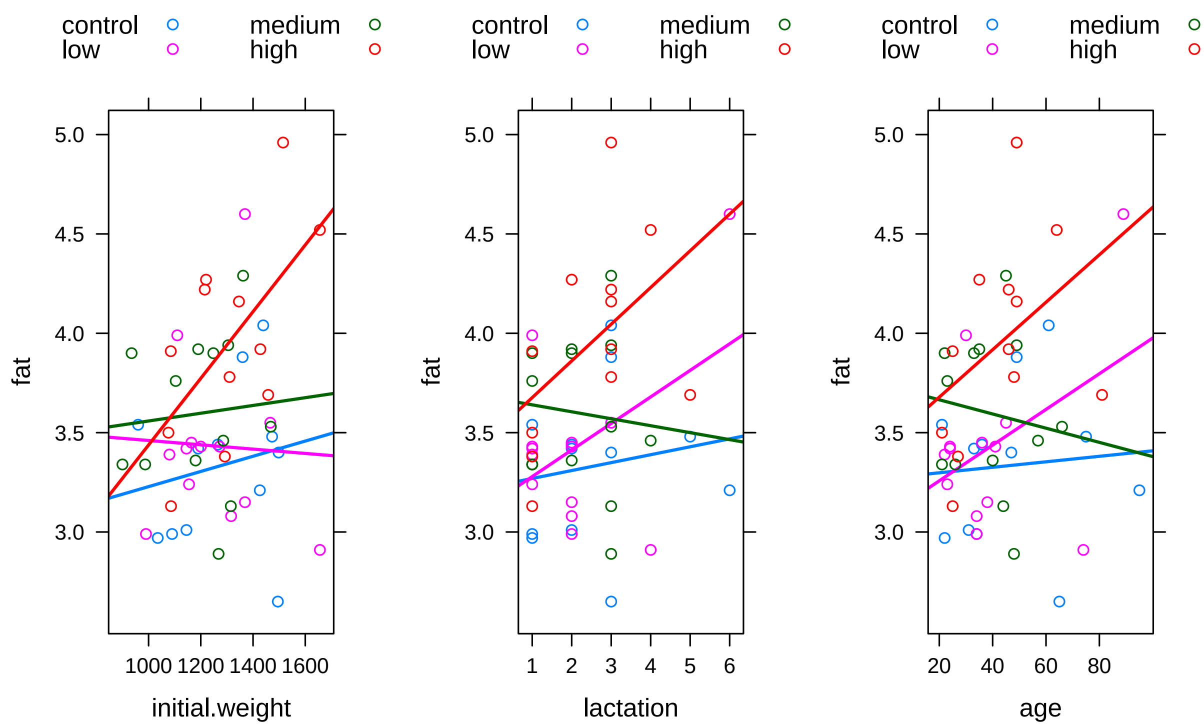
Scatter plots



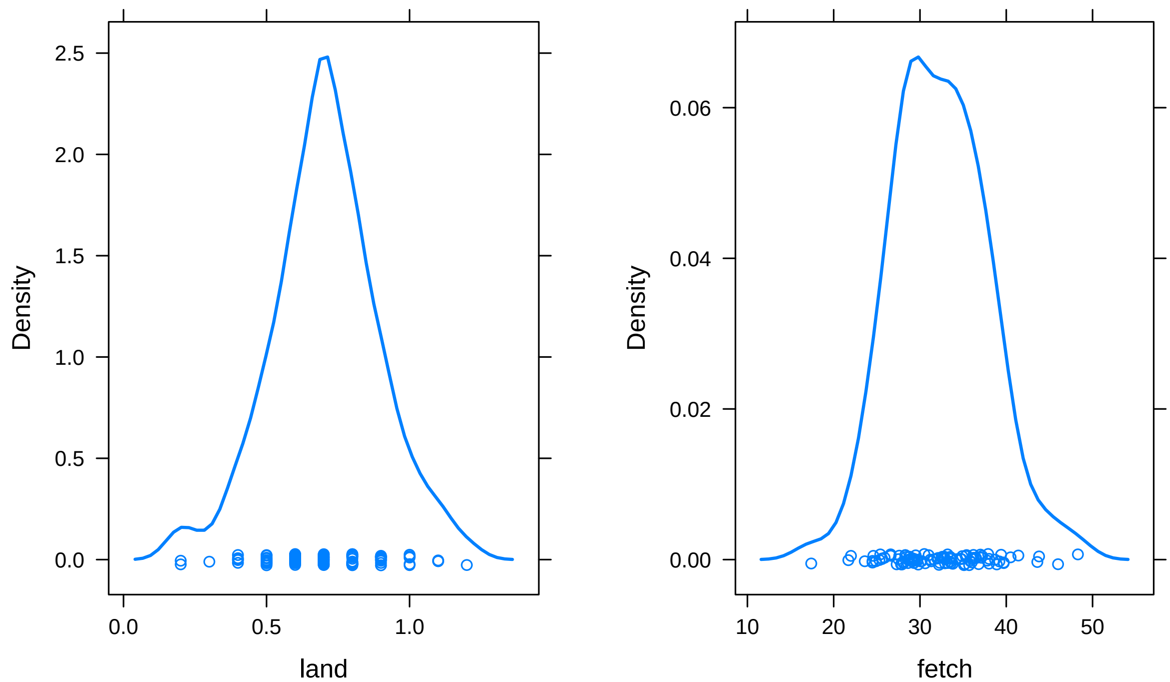
More Figure Commands

```
> fig5 = histogram(~urchin, data = sw)
> fig6 = densityplot(~fjord, data = sw, lwd = 2)
> fig7 = densityplot(~land, , data = sw, lwd = 2)
> fig8 = densityplot(~fetch, data = sw, lwd = 2)
> print(fig5, split = c(1, 1, 2, 1))
> print(fig6, split = c(2, 1, 2, 1), new = F)
> print(fig7, split = c(1, 1, 2, 1))
> print(fig8, split = c(2, 1, 2, 1), new = F)
```


Plots



Plots

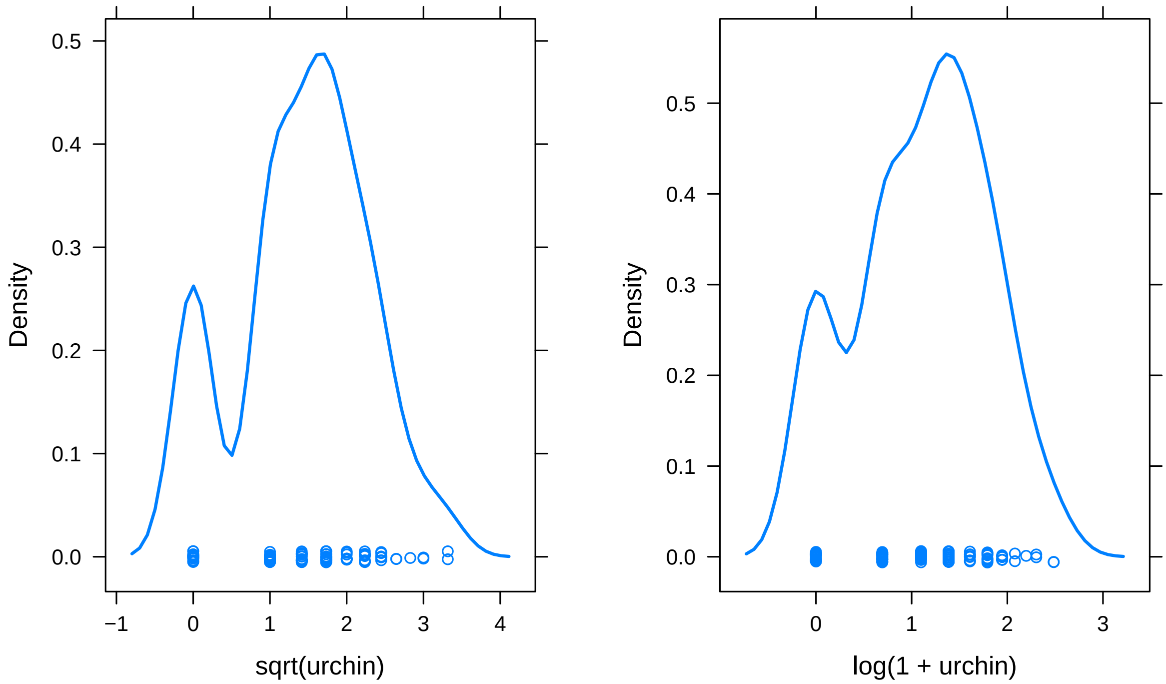


Transformations

- Consider transformations to the urchin variable to decrease the effect of the skewness.
- As there are zeros, we cannot take logarithms directly.
- Square root is a possibility.
- We can also try adding one and then taking logs.
- See the graphs and that both are more symmetric.
- We will use the $\log(1 + x)$ transformation to follow the authors.

```
> fig9 = densityplot(~sqrt(urchin), data = sw, lwd = 2)
> fig10 = densityplot(~log(1 + urchin), data = sw, lwd = 2)
> print(fig9, split = c(1, 1, 2, 1))
> print(fig10, split = c(2, 1, 2, 1), new = F)
```

Plots



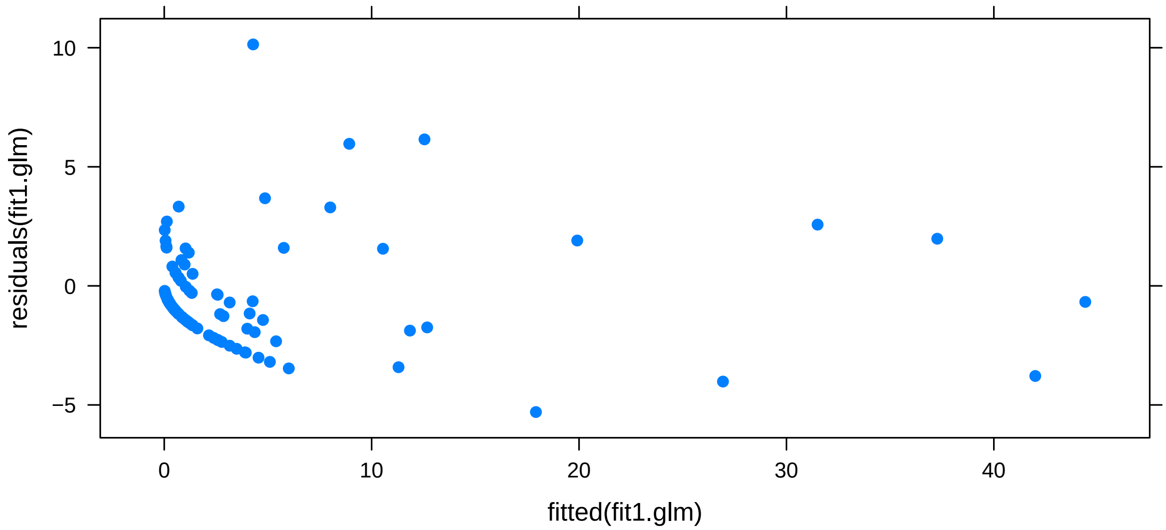
Fitting a Poisson Regression

```
> fit1.glm = glm(seaweed ~ log(1 + urchin) + fjord + land +
+     fetch, data = sw, family = poisson)
> display(fit1.glm)

glm(formula = seaweed ~ log(1 + urchin) + fjord + land + fetch,
    family = poisson, data = sw)
                coef.est coef.se
(Intercept)     -1.89     0.46
log(1 + urchin) -1.91     0.09
fjord            0.35     0.02
land             0.75     0.30
fetch            0.01     0.01
---
  n = 103, k = 5
  residual deviance = 491.8, null deviance = 1407.1 (difference = 915.3)
```

Residual Plot

```
> print(xyplot(residuals(fit1.glm) ~ fitted(fit1.glm),
+     pch = 16))
```



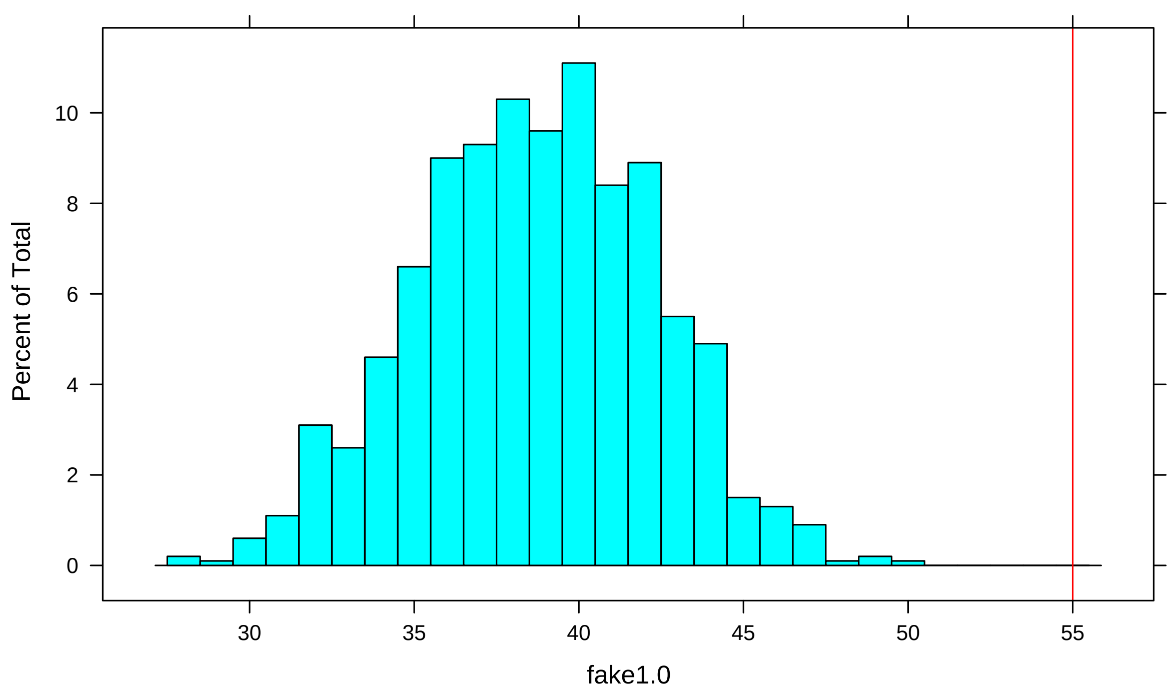
Checking 0 probability

- Biological count data often has an excess of zeros relative to what a standard model predicts.
- We can examine this by simulation and compare the number of zeros in simulated data to the number in the real data.
- We can do this by generating Poisson random variables with means as the fitted values.

Checking 0 probability

```
> count0 = function(x) {
+     return(sum(x == 0))
+ }
> with(sw, count0(seaweed))
[1] 55
> n = nrow(sw)
> mu = fitted(fit1.glm)
> fake1.0 = replicate(1000, count0(rpois(n, mu)))
```


Checking 0 probability



Observations

- Notice that the actual data set has 55 zeros, but the fake simulated data sets never have more than 50 zeros.
- We can try to fit a model with an overdispersion parameter.
- An alternative would be to fit a logistic regression model for the zeros and fit a different model for the positive outcomes.
- We can use simulation to see if the overdispersed-Poisson model produces as many zeros as we observe in the real data.

Negative Binomial Distribution

- An example of the overdispersed-Poisson model is the *negative binomial distribution*.
- We can parameterize this distribution with a parameter μ which is the mean and α which is a shape parameter.
- In R we estimate μ with the fitted values and $\alpha = \mu/(w - 1)$ where w is the overdispersion parameter.
- The function `rnbinom()` generates random variables with arguments `mu` and `size` for α.

Fitting an Over-dispersed Poisson Regression

```
> fit2.glm = glm(seaweed ~ log(1 + urchin) + fjord + land +
+     fetch, data = sw, family = quasipoisson)
> display(fit2.glm)
```

```
glm(formula = seaweed ~ log(1 + urchin) + fjord + land + fetch,
    family = quasipoisson, data = sw)
                coef.est coef.se
(Intercept)     -1.89     1.27
log(1 + urchin) -1.91     0.25
fjord            0.35     0.06
land             0.75     0.81
fetch            0.01     0.03
---
  n = 103, k = 5
  residual deviance = 491.8, null deviance = 1407.1 (difference = 915.3)
  overdispersion parameter = 7.4
```

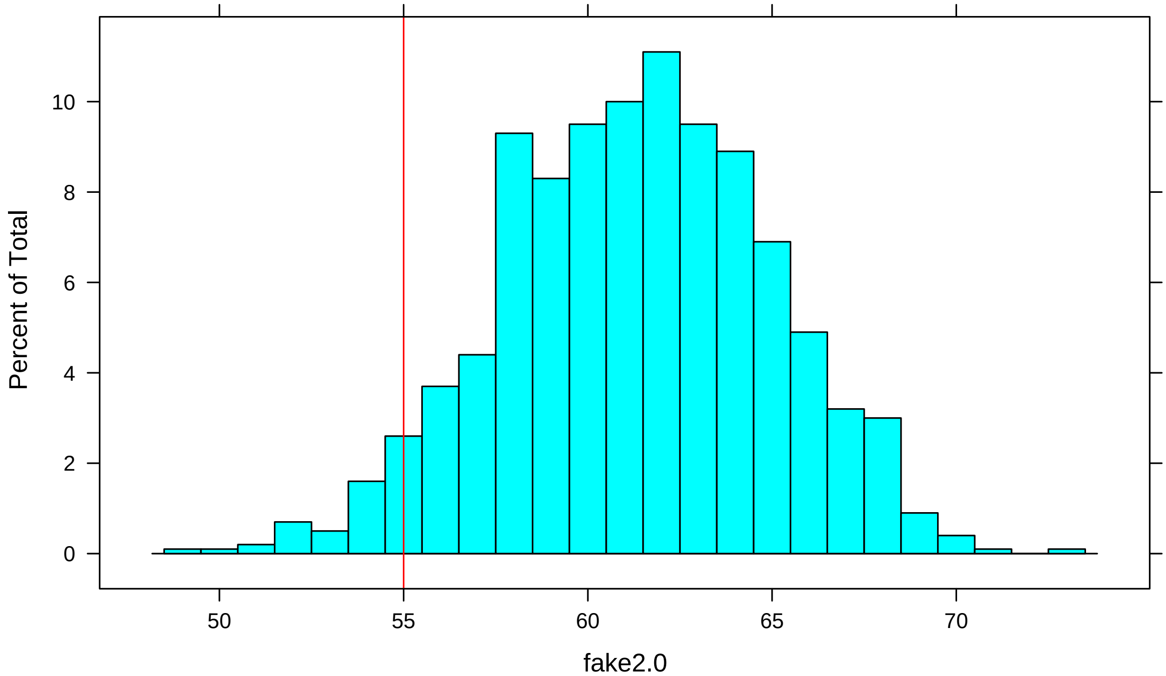

Checking 0 probability

```
> with(sw, count0(seaweed))
```

```
[1] 55
```

```
> n = nrow(sw)
> mu = fitted(fit2.glm)
> alpha = mu/(7.4 - 1)
> fake2.0 = replicate(1000, count0(rnbinom(n, mu = mu,
+     size = alpha)))
```

Checking 0 probability



Observations

- The actual number of zeros, 55, is fairly typical for this distribution.
- We could also test other aspects of the data to see if the simulated data is similar to the actual data.