10. Introduction to Generalized Linear Models II

We learnt in the last lecture that Poisson regression is not an appropriate model when data shows signs of over-dispersion.

Causes of Over-dispersion

- Subject heterogeneity. If some relevant predictors are not in the model, then the unexplained heterogeneity among the subjects will cause greater variation in the response than the Poisson model predicts.
- Outliers in the data.
- Positive correlation between responses in clustered data. Examples of naturally occurring clusters are families, households, litters, colonies, and neighbourhoods.

Negative Binomial Regression

When there are signs of over-dispersion, alternatively a Negative Binomial pdf can be considered that permits the variance to exceed the mean.

The Binomial distribution counts the number of successes in a fixed number of Bernoulli trials. On the other hand, the Negative Binomial Distribution counts the number of Bernoulli trials required to get a fixed number of successes, *r*. The distribution, mean and variance are:

$$f(y) = \binom{r+y-1}{y} p^r (1-p)^y, \qquad y = 0,1,...$$

$$E(y) = \mu = \frac{r(1-p)}{p},\ Var(y) = \frac{r(1-p)}{p^2}$$

This shows the interesting property of this distribution that

$$Var(y) = \mu + \frac{1}{r}\mu^2$$

That is, the variance is a quadratic function of the mean.

Also, If $r \to \infty$ and $p \to 1$ such that $r(1-p) \to \lambda$, then

$$E(y) = \frac{r(1-p)}{p} \to \lambda \text{ and } Var(y) = \frac{r(1-p)}{p^2} \to \lambda$$

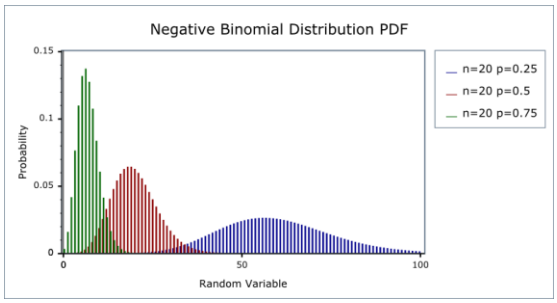
That is, the Negative Binomial distribution includes the Poisson distribution as a limiting case.

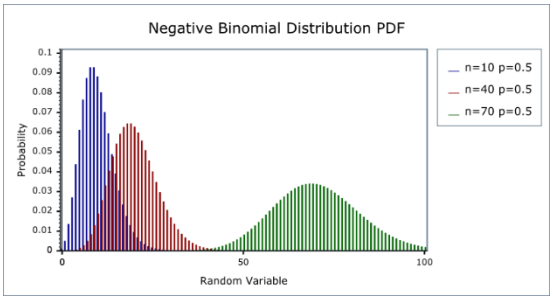
Note: The non-canonical link function for Negative Binomial distribution is natural log.

The density can be re-written as:

$$f(y) = (-1)^y \binom{-r}{y} p^r (1-p)^y$$

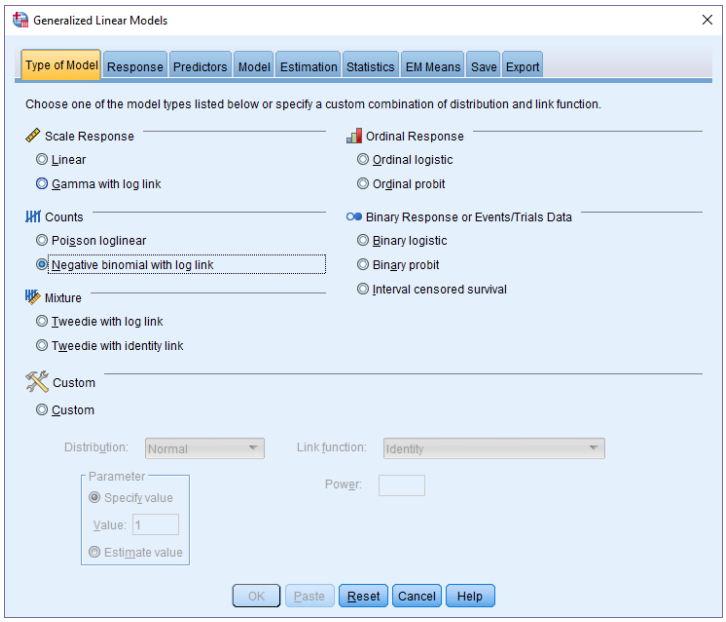
This explains the name Negative Binomial.





Example 10.1

We repeat the GLZ regression analysis this time for a Negative Binomial distribution. Here, only a selection of output is included.



Model Information

Dependent Variable	Infections
Probability Distribution	Negative binomial (1)
Link Function	Log

Goodness of Fit[a]

	Value	df	Value/df
Deviance	350.247	282	**1.242**
Scaled Deviance	350.247	282	
Pearson Chi-Square	403.188	282	**1.430**
Scaled Pearson Chi-Square	403.188	282	
Log Likelihood[b]	-451.969		
Akaike's Information Criterion (AIC)	913.939		
Finite Sample Corrected AIC (AICC)	914.152		
Bayesian Information Criterion (BIC)	932.236		
Consistent AIC (CAIC)	937.236		

Dependent Variable: Infections

Model: (Intercept), Swimmer, Location, Sex, Age

a. Information criteria are in smaller-is-better form.

b. The full log likelihood function is displayed and used in computing information criteria.

Tests of Model Effects

	Type III		
Source	Wald Chi-Square	df	Sig.
(Intercept)	5.947	1	.015
Swimmer	14.736	1	.000
Location	8.792	1	.003
Sex	.198	1	.656
Age	3.213	1	.073

Dependent Variable: Infections

Model: (Intercept), Swimmer, Location, Sex, Age

Parameter Estimates

Parameter	B	Std. Error	95% Wald Confidence Interval		Hypothesis Test			Exp(B)	95% Wald Confidence Interval for Exp(B)	
			Lower	Upper	Wald Chi-Square	df	Sig.		Lower	Upper
(Intercept)	.430	.4155	-.385	1.244	1.070	1	.301	1.537	.681	3.470
[Swimmer=1]	.614	.1600	.301	.928	14.736	1	.000	1.848	1.351	2.529
[Swimmer=2]	0[a]	.	.	.	.	.	.	1	.	.
[Location=1]	.488	.1645	.165	.810	8.792	1	.003	1.629	1.180	2.249
[Location=2]	0[a]	.	.	.	.	.	.	1	.	.
[Sex=1]	-.077	.1732	-.416	.262	.198	1	.656	.926	.659	1.300
[Sex=2]	0[a]	.	.	.	.	.	.	1	.	.
Age	-.033	.0184	-.069	.003	3.213	1	.073	.968	.933	1.003
(Scale)	1[b]									
(Negative binomial)	1[b]									

Dependent Variable: Infections

Model: (Intercept), Swimmer, Location, Sex, Age

a. Set to zero because this parameter is redundant.

b. Fixed at the displayed value.

Notice that now, and compared to the Poisson model, Values/df are closer to one, log Likelihood is larger and Information Criteria are smaller, all indicating a better fit. On the other hand, Age is now marginally insignificant.

Zero-Inflated Poisson Models

In modelling count data, there may be circumstances that the variance is too large because there are many zeros as well as a few very high values. As we just discussed the negative binomial model is an alternative model in such cases.

But sometimes it is just a matter of having too many zeros than a Poisson model would predict. In this case, a better solution is often the Zero-Inflated Poisson (ZIP) model. (And when extra variation occurs too, Zero-Inflated Negative Binomial model).

ZIP models assume that some zeros occurred by a Poisson process, but others were not even eligible to have the event occur. So, there are two processes at work—one that determines if the individual is even eligible for a non-zero response, and the other that determines the count of that response for eligible individuals.

The problem is either process can result in a zero count. Since you cannot tell which zeros were eligible for a non-zero count, you cannot tell which zeros were results of which process. The ZIP model fits, simultaneously, two separate regression models. One is a logistic or probit model that models the probability of being eligible for a non-zero count. The other models the size of that count.

Both models use the same predictor variables, but estimate their coefficients separately. So, the predictors can have vastly different effects on the two processes.

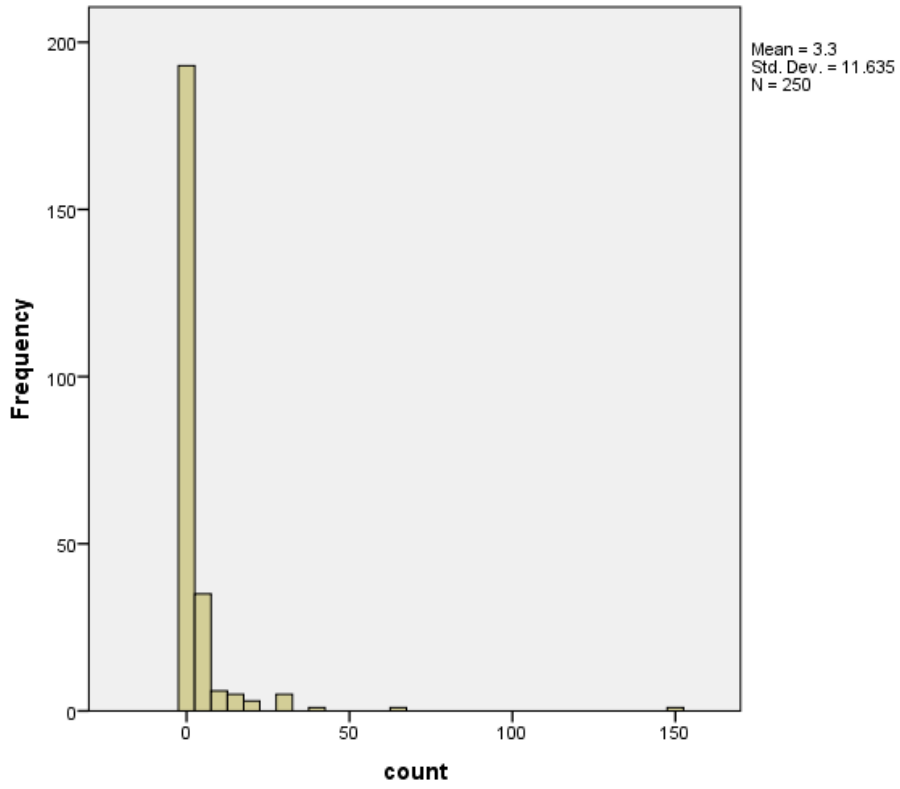
However, ZIP model requires it be theoretically plausible that some individuals are ineligible for a count. For example, consider modelling the number of alcoholic drinks consumed in a day, which could plausibly be fit with a ZIP model. Some participants do drink alcohol, but will have consumed zero that day, by chance. But others just do not drink alcohol, so will never have a non-zero response. The ZIP model can determine which predictors affect the probability of being an alcohol consumer and which predictors affect how many drinks the consumers consume. They may not be the same predictors for the two models, or they could even have opposite effects on the two processes.

Example 10.2

(Partly adopted from https://stats.idre.ucla.edu/r/dae/zip/)

The state wildlife biologists want to model how many fish are being caught by fishermen at a state park. Visitors are asked how long they stayed, how many people were in the group, were there children in the group and how many fish were caught. Some visitors do not fish, but there is no data on whether a person fished or not. Some visitors who did fish did not catch any fish so there are excess zeros in the data because of the people that did not fish.

The data file (https://stats.idre.ucla.edu/stat/data/fish.csv) consists of 250 groups that went to a park. Each group was questioned about how many fish they caught (count), how many children were in the group (child), how many people were in the group (persons), and whether or not they brought a camper to the park (camper).



ZIP Output

```
library(pscl)
model1 = zeroinfl(count ~ child + camper | persons, data = fish)
summary(model1)
```

```
Pearson residuals:
    Min      1Q  Median      3Q     Max
-1.2369 -0.7540 -0.6080 -0.1921 24.0847

Count model coefficients (poisson with log link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.59789    0.08554  18.680   <2e-16 ***
child       -1.04284    0.09999 -10.430   <2e-16 ***
camper       0.83402    0.09363   8.908   <2e-16 ***
```

```
Zero-inflation model coefficients (binomial with logit link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   1.2974     0.3739   3.470 0.000520 ***
persons      -0.5643     0.1630  -3.463 0.000534 ***
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Number of iterations in BFGS optimization: 12
Log-likelihood: -1032 on 5 Df
```

Standard Poisson Model

```
summary(model2 <- glm(count ~ child + camper, family = poisson, data = fish))
```

```
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.7736  -2.2293  -1.2024  -0.3498  24.9492

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.91026    0.08119   11.21   <2e-16 ***
child       -1.23476    0.08029  -15.38   <2e-16 ***
camper       1.05267    0.08871   11.87   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 2958.4  on 249  degrees of freedom
Residual deviance: 2380.1  on 247  degrees of freedom
AIC: 2723.2

Number of Fisher Scoring iterations: 6
```

Comparing Two Models

The Vuong test compares the zero-inflated model with an ordinary Poisson regression model. In this example, we can see that our test statistic is significant, indicating that the zero-inflated model is superior to the standard Poisson model.

```
vuong(model2, model1)
```

```
Vuong Non-Nested Hypothesis Test-Statistic:
(test-statistic is asymptotically distributed N(0,1) under the
 null that the models are indistinguishable)
-------------------------------------------------------------
              Vuong z-statistic             H_A    p-value
Raw                   -3.574254 model2 > model1 0.00017561
AIC-corrected         -3.552392 model2 > model1 0.00019087
BIC-corrected         -3.513900 model2 > model1 0.00022079
```

ZINB Output

```
ibrary(pscl)
model3 = zeroinfl(count ~ child + camper | persons,dist="negbin", data = fish)
summary(model3)
```

```
Pearson residuals:
    Min      1Q  Median      3Q     Max
-0.5861 -0.4617 -0.3886 -0.1974 18.0135

Count model coefficients (negbin with log link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   1.3710     0.2561   5.353 8.64e-08 ***
child        -1.5153     0.1956  -7.747 9.41e-15 ***
camper        0.8791     0.2693   3.265   0.0011 **
Log(theta)   -0.9854     0.1760  -5.600 2.14e-08 ***

Zero-inflation model coefficients (binomial with logit link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   1.6031     0.8365   1.916   0.0553 .
persons      -1.6666     0.6793  -2.453   0.0142 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Theta = 0.3733
Number of iterations in BFGS optimization: 22
Log-likelihood: -432.9 on 6 Df
```

Similarly, this model can be compared with the corresponding standard Negative Binomial model.

Standard Negative Binomial

```
library(MASS)
summary(model4 <- glm.nb (count ~ child + camper, data = fish))
```

```
Call:
glm.nb(formula = count ~ child + camper, data = fish, init.theta = 0.25529
31119,
    link = log)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.3141  -1.0361  -0.7266  -0.1720   4.0163

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   1.0727     0.2425   4.424 9.69e-06 ***
child        -1.3753     0.1958  -7.025 2.14e-12 ***
camper        0.9094     0.2836   3.206  0.00135 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(0.2553) family taken to be 1)

    Null deviance: 258.93  on 249  degrees of freedom
Residual deviance: 201.89  on 247  degrees of freedom
AIC: 887.42

Number of Fisher Scoring iterations: 1


              Theta:  0.2553
          Std. Err.:  0.0329

 2 x log-likelihood:  -879.4210
```

```
vuong(model3, model4)
```

```
Vuong Non-Nested Hypothesis Test-Statistic:
(test-statistic is asymptotically distributed N(0,1) under the
 null that the models are indistinguishable)
-------------------------------------------------------------
              Vuong z-statistic             H_A  p-value
Raw                   1.7017116 model1 > model2 0.044405
AIC-corrected         1.2026316 model1 > model2 0.114559
BIC-corrected         0.3238863 model1 > model2 0.373012
```

The test suggests zero-inflated negative binomial model is a significant improvement over a standard negative binomial model.