

Session 5: loglinear regression part 2

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CUNY SPH Biostatistics 2

Learning objectives and outline

Learning objectives

- 1 Define and identify over-dispersion in count data
- 2 Define the negative binomial (NB) distribution and identify applications for it
- 3 Define zero-inflated count models
- 4 Fit and interpret Poisson and NB, with and without zero inflation

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Learning
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Review

Over-
dispersion

Zero Inflation

- ① Review of log-linear Poisson glm
- ② Review of diagnostics and interpretation of coefficients
- ③ Over-dispersion
 - Negative Binomial distribution
- ④ Zero-inflated models
 - Vittinghoff section 8.1-8.3

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Components of GLM

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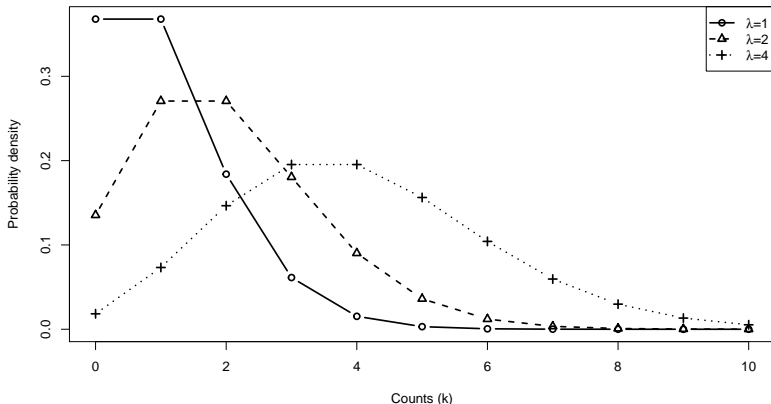
Over-
dispersion

Zero Inflation

- **Random component** specifies the conditional distribution for the response variable - it doesn't have to be normal but can be any distribution that belongs to the "exponential" family of distributions
- **Systematic component** specifies linear function of predictors (linear predictor)
- **Link** [denoted by $g(\cdot)$] specifies the relationship between the expected value of the random component and the systematic component, can be linear or nonlinear

Motivating example: Choice of Distribution

- Count data are often modeled as Poisson distributed:
 - mean λ is greater than 0
 - variance is also λ
 - Probability density $P(k, \lambda) = \frac{\lambda^k}{k!} e^{-\lambda}$



Poisson model: the GLM

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The **systematic part** of the GLM is:

$$\log(\lambda_i) = \beta_0 + \beta_1 \text{RACE}_i + \beta_2 \text{TRT}_i + \beta_3 \text{ALCH}_i + \beta_4 \text{DRUG}_i$$

Or alternatively:

$$\lambda_i = \exp(\beta_0 + \beta_1 \text{RACE}_i + \beta_2 \text{TRT}_i + \beta_3 \text{ALCH}_i + \beta_4 \text{DRUG}_i)$$

The **random part** is (Recall the λ_i is both the mean and variance of a Poisson distribution):

$$y_i \sim \text{Poisson}(\lambda_i)$$

Example: Risky Drug Use Behavior

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- Load the “needle_sharing” dataset
- Outcome is # times the drug user shared a syringe in the past month (shared_syr)
- Predictors: sex, ethn, homeless
 - filtered to only sex “M” or “F”, ethn “White”, “AA”, “Hispanic”

```
summary(needledat2$shared_syr)
```

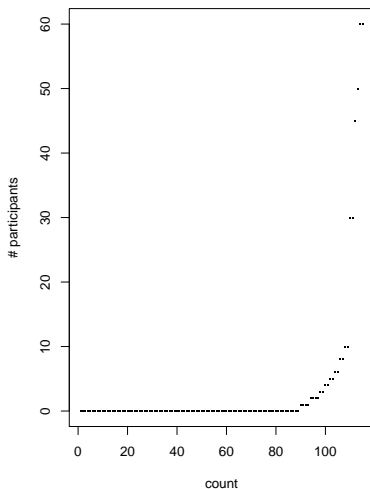
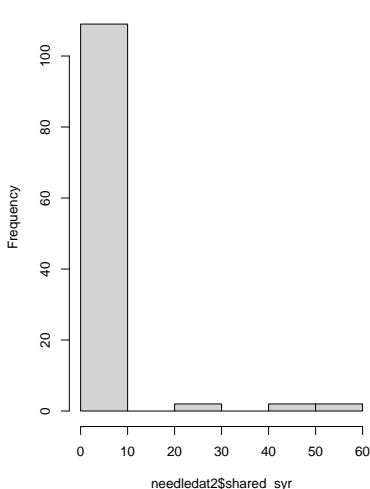
```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.      NA's  
##    0.000   0.000   0.000   3.122   0.000   60.000         2
```

```
var(needledat2$shared_syr, na.rm = TRUE)
```

```
## [1] 113.371
```

Example: Risky Drug Use Behavior

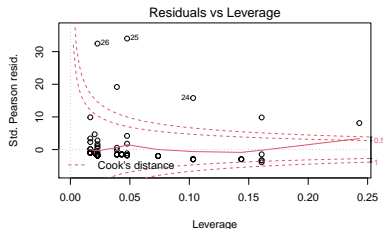
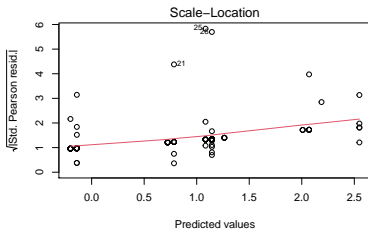
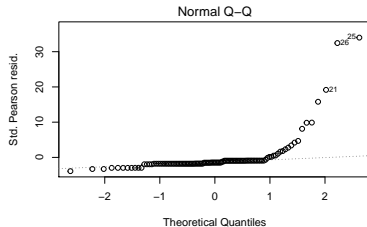
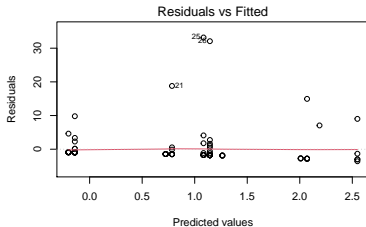
Exploratory plots



Risky Drug Use Behavior: fitting a Poisson model

```
fit.pois <- glm(shared_syr ~ sex + ethn + homeless,  
                data = needledat2,  
                family = poisson(link = "log"))
```

Risky Drug Use Behavior: residuals plots



* Poisson model is definitely not a good fit.

Over-dispersion

When the Poisson model doesn't fit

- inference from log-linear models is sensitive to assumptions on the distribution of residuals (e.g. Poisson)
- In the Poisson distribution, the variance is equal to the mean.
- *i.e.* if subjects with a particular pattern of covariates have a mean of 4 visits/yr, then variance is also 4 and the standard deviation is 2 visits / yr.
- The Poisson distribution often fails when the variance exceeds the mean
 - You can *check* this assumption
- Can use alternative random distributions:
 - Negative binomial distribution
- Can introduce zero-inflation

Negative binomial distribution

- The binomial distribution is the number of successes in n trials:
 - Roll a die ten times, how many times do you see a 6?
- The negative binomial distribution is the number of successes it takes to observe r failures:
 - How many times do you have to roll the die to see a 6 ten times?
 - Note that the number of rolls is no longer fixed.
 - In this example, $p=5/6$ and a 6 is a “failure”

Negative binomial GLM

One way to parametrize a NB model is with a **systematic part** equivalent to the Poisson model:

$$\log(\lambda_i) = \beta_0 + \beta_1 \text{RACE}_i + \beta_2 \text{TRT}_i + \beta_3 \text{ALCH}_i + \beta_4 \text{DRUG}_i$$

Or:

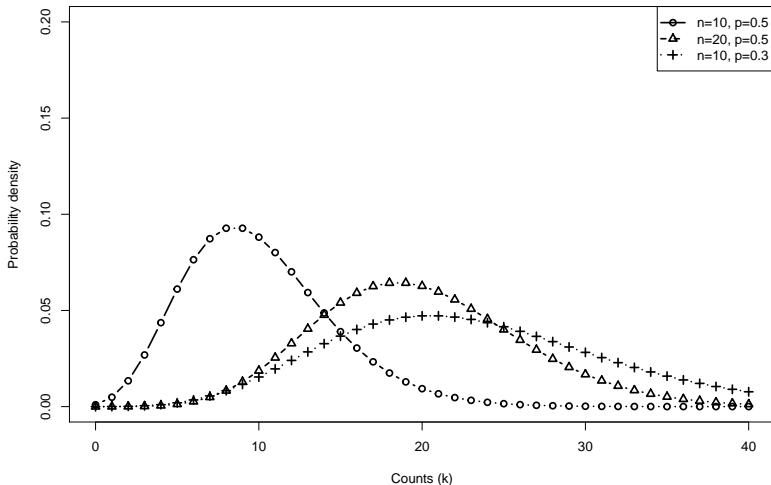
$$\lambda_i = \exp(\beta_0 + \beta_1 \text{RACE}_i + \beta_2 \text{TRT}_i + \beta_3 \text{ALCH}_i + \beta_4 \text{DRUG}_i)$$

And a **random part**:

$$y_i \sim NB(\lambda_i, \theta)$$

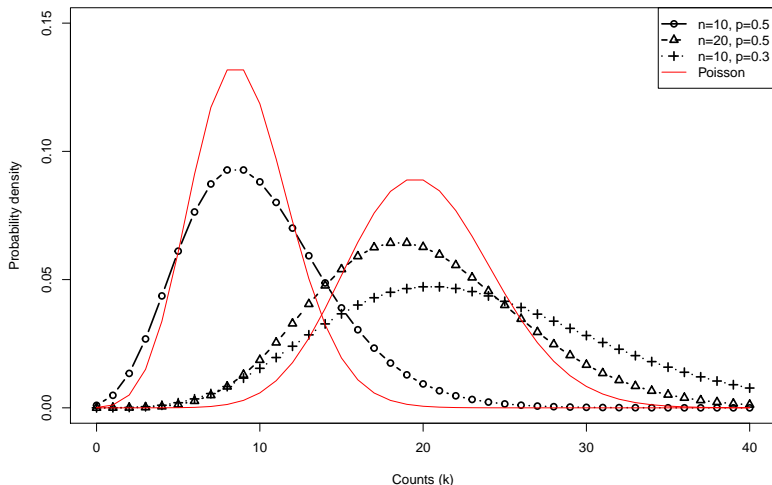
- θ is a **dispersion parameter** that is estimated
- When $\theta = 0$ it is equivalent to Poisson model
- `MASS::glm.nb()` uses this parametrization, `dnbinom()` does not
- The Poisson model can be considered **nested** within the Negative Binomial model

Negative Binomial Random Distribution



Compare Poisson vs. Negative Binomial

Negative Binomial Distribution has two parameters: # of trials n , and probability of success p



Risky drug behavior: Negative Binomial Regression

```
library(MASS)
fit.negbin <- MASS::glm.nb(shared_syr ~ sex +
                           ethn + homeless,
                           data = needledat2)
```

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```
summary(fit.negbin)
```

```
##
## Call:
## MASS::glm.nb(formula = shared_syr ~ sex + ethn + homeless, data = needledat2,
##   init.theta = 0.07743871374, link = log)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.8801  -0.7787  -0.6895  -0.5748   1.5675
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.4641     0.8559   0.542   0.5876
## sexM          -1.0148     0.8294  -1.224   0.2211
## ethnHispanic   1.3424     1.3201   1.017   0.3092
## ethnWhite      0.2429     0.7765   0.313   0.7544
## homelessyes    1.6445     0.7073   2.325   0.0201 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(0.0774) family taken to be 1)
##
##      Null deviance: 62.365  on 114  degrees of freedom
## Residual deviance: 56.232  on 110  degrees of freedom
## (2 observations deleted due to missingness)
## AIC: 306.26
##
## Number of Fisher Scoring iterations: 1
##
##
##              Theta:  0.0774
##              Std. Err.: 0.0184
##
## 2 x log-likelihood: -294.2550
```

Likelihood ratio test

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Basis: Under H_0 : no improvement in fit by more complex model, difference in model residual deviances is χ^2 -distributed.

Deviance: $\Delta(D) = -2 * \Delta(\log \text{likelihood})$

```
(ll.negbin <- logLik(fit.negbin))
```

```
## 'log Lik.' -147.1277 (df=6)
```

```
(ll.pois <- logLik(fit.pois))
```

```
## 'log Lik.' -730.0133 (df=5)
```

```
pchisq(2 * (ll.negbin - ll.pois), df=1,  
       lower.tail=FALSE)
```

```
## 'log Lik.' 1.675949e-255 (df=6)
```

NB regression residuals plots

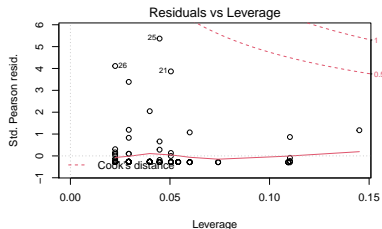
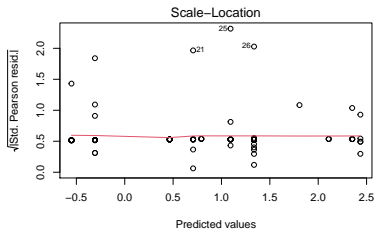
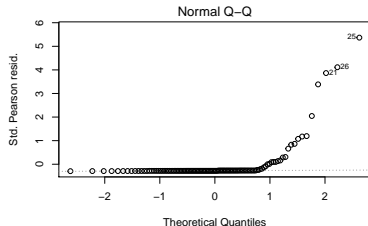
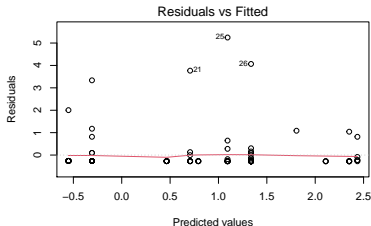
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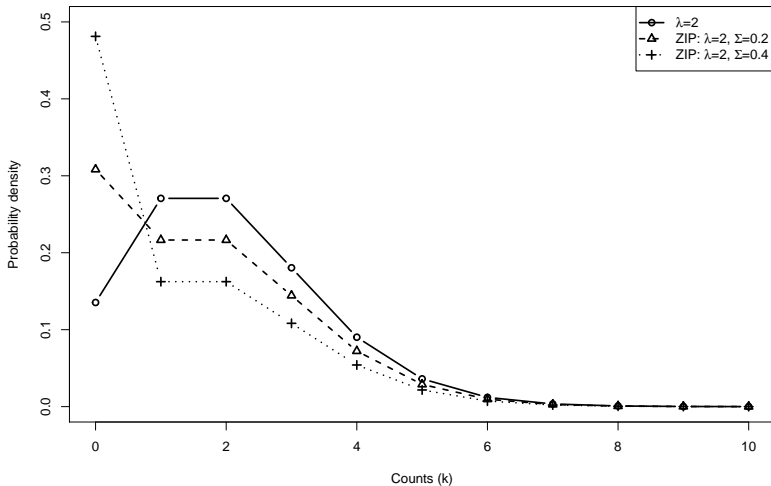
Zero Inflation

Zero inflated “two-step” models

Step 1: logistic model to determine whether count is zero or Poisson/NB

Step 2: Poisson or NB regression distribution for y_i not set to zero by 1.

Poisson Distribution with Zero Inflation



Risky drug behavior: Zero-inflated Poisson regression

```
library(pscl)
fit.ZIpois <- zeroinfl(shared_syr ~ sex + ethn + home
                        dist = "poisson",
                        data = needledat2)
```

Zero-inflated Poisson regression - the model

```
summary(fit.ZIpois)
```

```
##
```

```
## Call:
```

```
## zeroinfl(formula = shared_syr ~ sex + ethn + homel
```

```
##       dist = "poisson")
```

```
##
```

```
## Pearson residuals:
```

```
##      Min      1Q  Median      3Q      Max
```

```
## -1.0761 -0.5784 -0.4030 -0.3341 10.6835
```

```
##
```

```
## Count model coefficients (poisson with log link):
```

```
##              Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept)    3.2168    0.1796  17.908 < 2e-16
```

```
## sexM           -1.4725    0.1442 -10.212 < 2e-16
```

```
## ethnHispanic  -0.1524    0.1576  -0.968 0.333244
```

```
## ethnWhite      0.5826    0.1464   3.977 0.000249
```

Risky drug behavior: Zero-inflated Negative Binomial regression

```
fit.ZInegbin <- zeroinfl(shared_syr ~ sex + ethn + ho  
                        dist = "negbin",  
                        data = needledat2)
```

- *NOTE*: zero-inflation model can include any of your variables as predictors
- *WARNING* Default in `zeroinfl()` function is to use *all* variables as predictors in logistic model

Zero-inflated Negative

Binomial distribution

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```
summary(fit.ZInegbin)
```

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```
##
## Call:
## zeroinfl(formula = shared_syr ~ sex + ethn + homeless, data = needledat2,
##   dist = "negbin")
##
## Pearson residuals:
##      Min      1Q  Median      3Q      Max
## -0.5402 -0.3255 -0.2714 -0.1926  5.1496
##
## Count model coefficients (negbin with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.8410     1.1845   2.399  0.01646 *
## sexM          -2.2282     0.9351  -2.383  0.01718 *
## ethnHispanic  -0.4123     0.9831  -0.419  0.67492
## ethnWhite     -0.4299     0.8648  -0.497  0.61908
## homelessyes    1.9460     0.7103   2.740  0.00615 **
## Log(theta)    -1.1971     0.5159  -2.320  0.02032 *
##
## Zero-inflation model coefficients (binomial with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.6867     0.8465   1.993  0.0463 *
## sexM          -0.9920     0.8016  -1.238  0.2159
## ethnHispanic -13.1868    281.9134  -0.047  0.9627
## ethnWhite     -0.7455     0.7304  -1.021  0.3074
## homelessyes    0.3554     0.7397   0.480  0.6309
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 0.3021
## Number of iterations in BFGS optimization: 24
```

Zero-inflated Negative Binomial regression - simplified ZI model

- Model is much more interpretable if the exposure of interest is *not* included in the zero-inflation model.
- E.g. with HIV status as the only predictor in zero-inflation model:

```
fit.ZInb2 <- zeroinfl(shared_syr ~ sex + ethn + homel  
                      dist = "negbin",  
                      data = needledat2)
```

Zero-inflated Negative

Binomial distribution

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```
summary(fit.ZInb2)
```

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```
##
## Call:
## zeroinfl(formula = shared_syr ~ sex + ethn + homeless + hiv | hiv, data = needledat2,
##   dist = "negbin")
##
## Pearson residuals:
##      Min      1Q  Median      3Q      Max
## -0.4299 -0.3646 -0.3559 -0.3299  6.3053
##
## Count model coefficients (negbin with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   3.6685     0.9470   3.874 0.000107 ***
## sexM          -1.7648     0.6205  -2.844 0.004454 **
## ethnHispanic  -1.5807     0.7446  -2.123 0.033769 *
## ethnWhite     -1.1267     0.6924  -1.627 0.103687
## homelessyes    1.0313     0.5693   1.812 0.070028 .
## hivpositive   -1.0820     1.0167  -1.064 0.287235
## hivyes        2.3724     0.7829   3.030 0.002444 **
## Log(theta)    0.1395     0.4647   0.300 0.764009
##
## Zero-inflation model coefficients (binomial with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    1.2163     0.2851   4.265 2e-05 ***
## hivpositive    -0.3493     0.9389  -0.372 0.710
## hivyes        -17.9654  3065.6271 -0.006 0.995
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 1.1497
## Number of iterations in BFGS optimization: 12
```

Intercept-only zero-inflation

model

```
fit.ZInb3 <- zeroinfl(shared_syr~sex+ethn+homeless|1,  
                      dist="negbin", data=needledat2)  
summary(fit.ZInb3)
```

```
##  
## Call:  
## zeroinfl(formula = shared_syr ~ sex + ethn + homeless | 1, data = needledat2,  
##         dist = "negbin")  
##  
## Pearson residuals:  
##      Min      1Q  Median      3Q      Max  
## -0.3159 -0.3123 -0.3040 -0.2953  5.2940  
##  
## Count model coefficients (negbin with log link):  
##              Estimate Std. Error z value Pr(>|z|)  
## (Intercept)   2.08542    1.42671   1.462  0.1438  
## sexM         -1.43809    0.89189  -1.612  0.1069  
## ethnHispanic  0.48130    1.16642   0.413  0.6799  
## ethnWhite    -0.07418    0.81066  -0.092  0.9271  
## homelessyes   1.62076    0.67706   2.394  0.0167 *  
## Log(theta)   -1.12538    0.89372  -1.259  0.2080  
##  
## Zero-inflation model coefficients (binomial with logit link):  
##              Estimate Std. Error z value Pr(>|z|)  
## (Intercept)   0.5211     0.7600   0.686  0.493  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Theta = 0.3245  
## Number of iterations in BFGS optimization: 13  
## Log-likelihood: -146.8 on 7 Df
```

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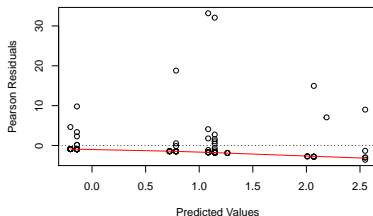
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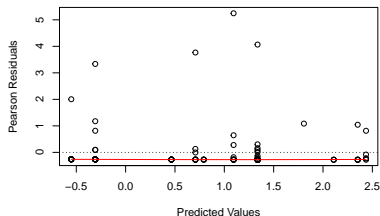
Residuals vs. fitted values

I invisibly define functions `plotpanel1` and `plotpanel2` that will work for all types of models (see lab). These use Pearson residuals.

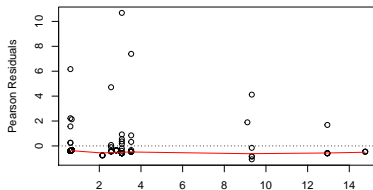
Residuals vs. Fitted
Poisson



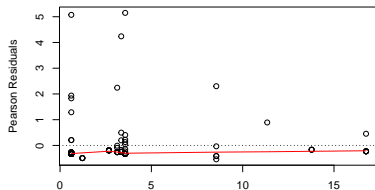
Residuals vs. Fitted
Negative Binomial



Residuals vs. Fitted
Zero-inflated Poisson



Residuals vs. Fitted
Zero-inflated Negative Binomial



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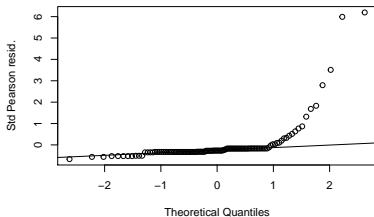
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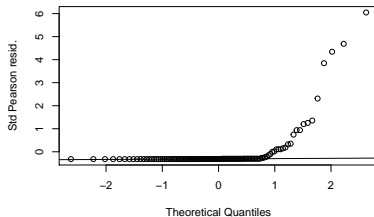
Zero Inflation

Quantile-quantile plots for residuals

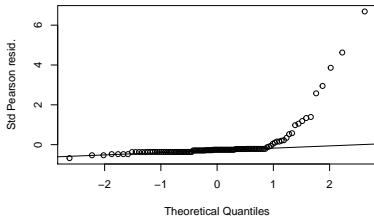
Normal Q-Q Plot
Poisson



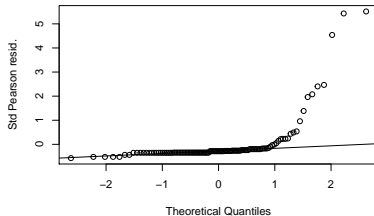
Normal Q-Q Plot
Negative Binomial



Normal Q-Q Plot
Zero-inflated Poisson



Normal Q-Q Plot
Zero-inflated Negative Binomial

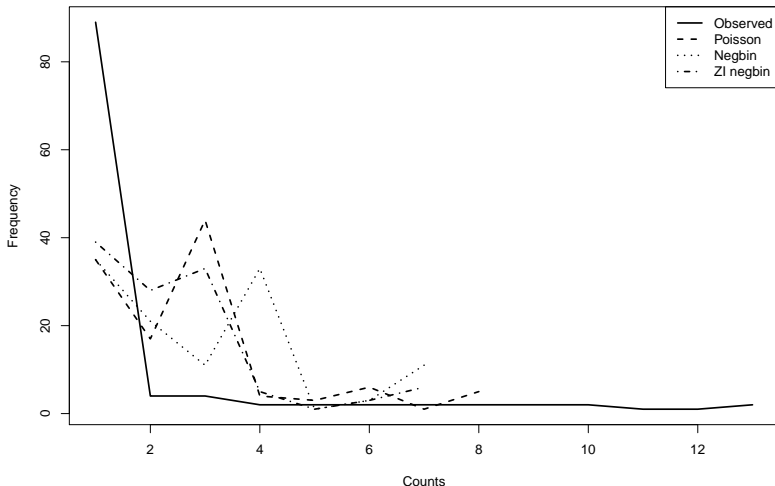


still over-dispersed - ideas?

Inference from the different models

% Error: Unrecognized object type. Zero-inflated models are 3) Poisson, 4) Negative Binomial, and 5) Negative Binomial with intercept-only zero inflation model.

Example of plotting observed and predicted counts



Resources for R (and SAS)

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- Short, practical tutorials on regression in R and SAS from UCLA at <http://www.ats.ucla.edu/stat/>:
 - Poisson Regression:
<http://www.ats.ucla.edu/stat/r/dae/poissonreg.htm>
 - Negative Binomial:
<http://www.ats.ucla.edu/stat/r/dae/nbreg.htm>
 - Zero-inflated Poisson:
<http://www.ats.ucla.edu/stat/r/dae/zipoisson.htm>
 - Zero-inflated Negative Binomial:
<http://www.ats.ucla.edu/stat/r/dae/zinbreg.htm>