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

Outline

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

Resources:

- Vittinghoff section 8.1-8.3
- Short tutorials on regression in R (and Stata, SAS, SPSS, Mplus)
    - https://stats.idre.ucla.edu/other/dae/

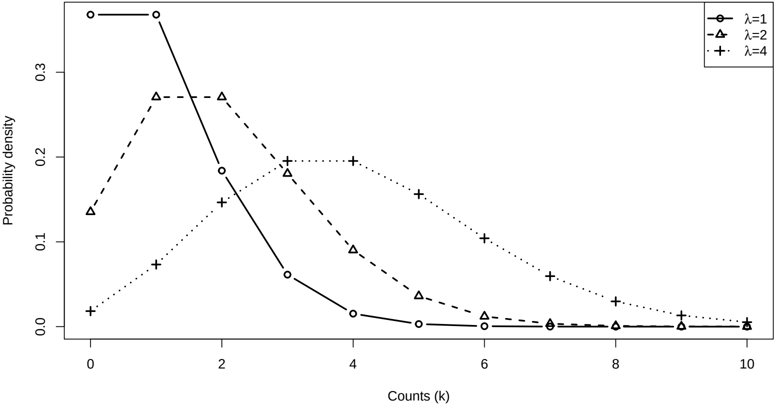
Review

Components of GLM

- **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(.)] 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

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

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

Or alternatively:

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

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

$$y_i \sim Poisson(\lambda_i)$$

Example: Risky Drug Use Behavior

- Outcome is # times the drug user shared a syringe in the past month (`shared_syr`)
- Predictors: `sex`, `ethn`, `homeless`
    - filtered to `sex` "M" or "F", `ethn` "White", "AA", "Hispanic"

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

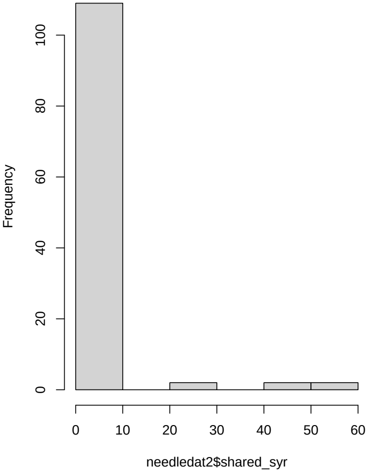
```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##   0.000   0.000   0.000   3.122   0.000  60.000       2
```

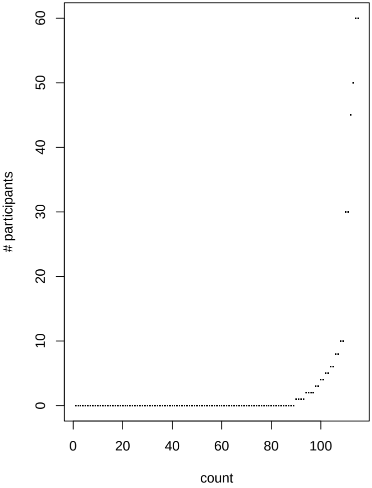
```
var(needledat2$shared_syr, na.rm = TRUE)
```

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

Example: Risky Drug Use Behavior

Exploratory plots



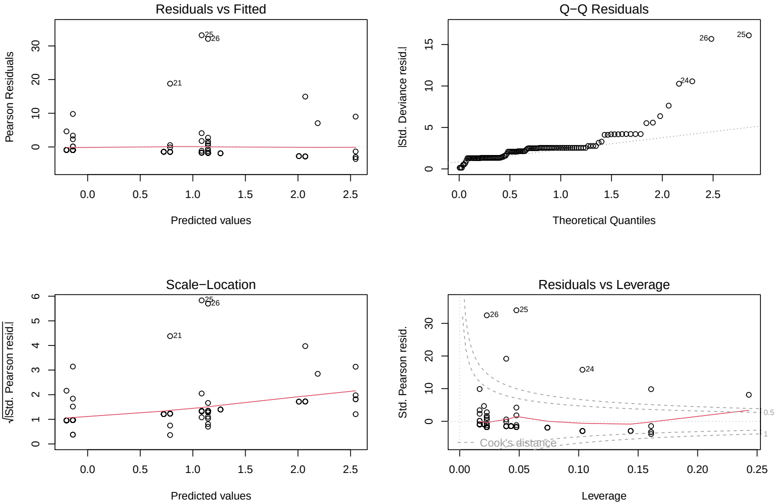


- There are a *lot* of zeros and variance is much greater than

Fitting a Poisson model

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

Residuals plots



* Poisson model is definitely not a good fit.

Over-dispersion

When the Poisson model doesn't fit

1. Variance > mean (over-dispersion)
    - Negative binomial distribution
2. Excess zeros (zero inflation)
    - 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:

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

Or:

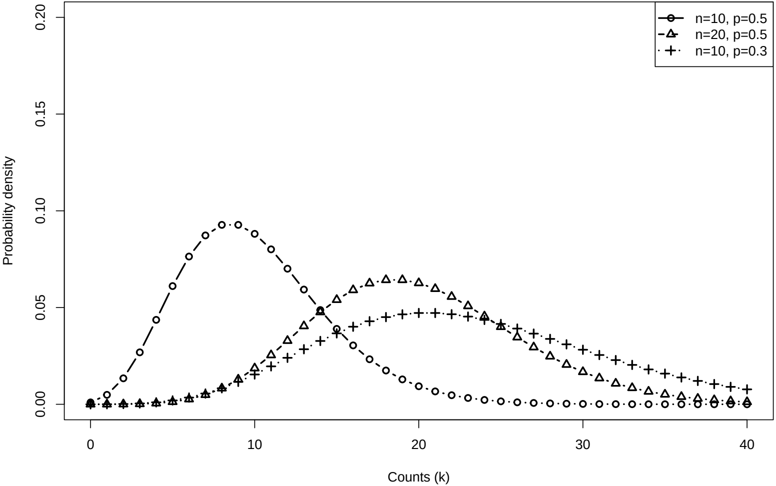
$$\lambda_i = exp\left(\beta_0 + \beta_1 \mathrm{RACE}_i + \beta_2 \mathrm{TRT}_i + \beta_3 \mathrm{ALCH}_i + \beta_4 \mathrm{DRUG}_i\right)$$

And a **random part**:

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

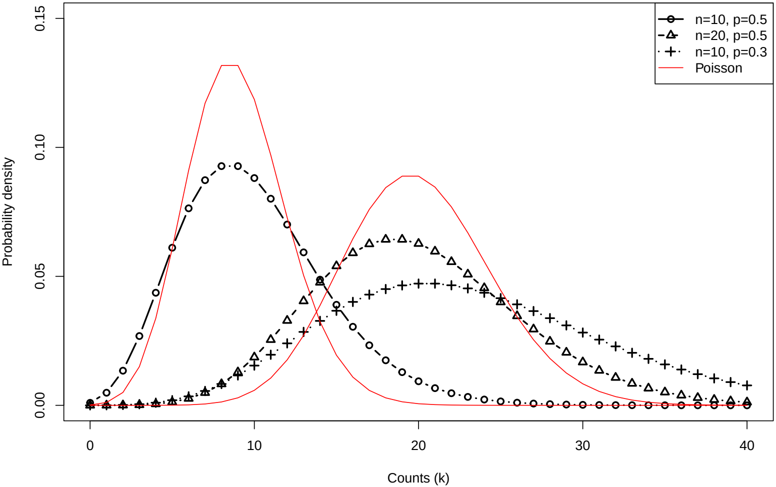
- θ is a **dispersion parameter** that is estimated
- When $\theta = 0$ it is equivalent to Poisson model
- `MASS::glm.nb()` uses this parametrization, `dnbinom()` does not
- The Poisson model can be considered **nested** within the Negative Binomial model

Negative Binomial Random Distribution



Compare Poisson vs. Negative Binomial

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



Negative Binomial Regression

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

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

```
## 
## Call:
## MASS::glm.nb(formula = shared_syr ~ sex + ethn + homeless, data = needledat2, 
##     init.theta = 0.07743871374, link = log)
## 
## 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

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

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

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

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

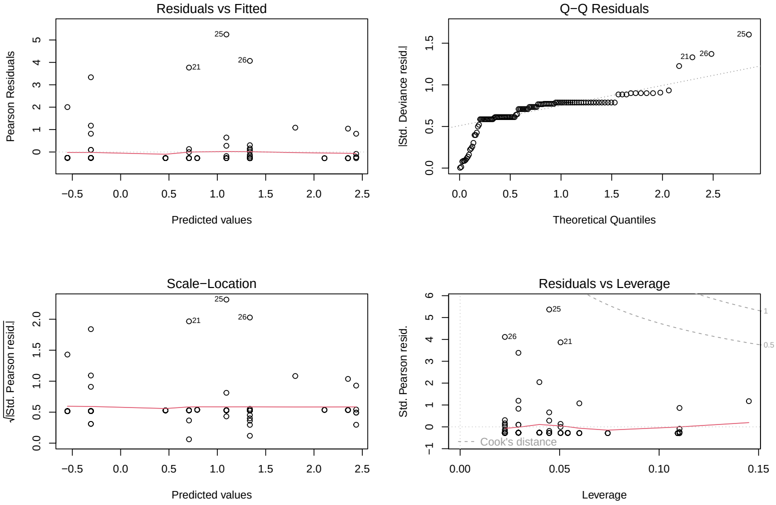
```
(ll.pois <- logLik(fit.pois))
```

```
## '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



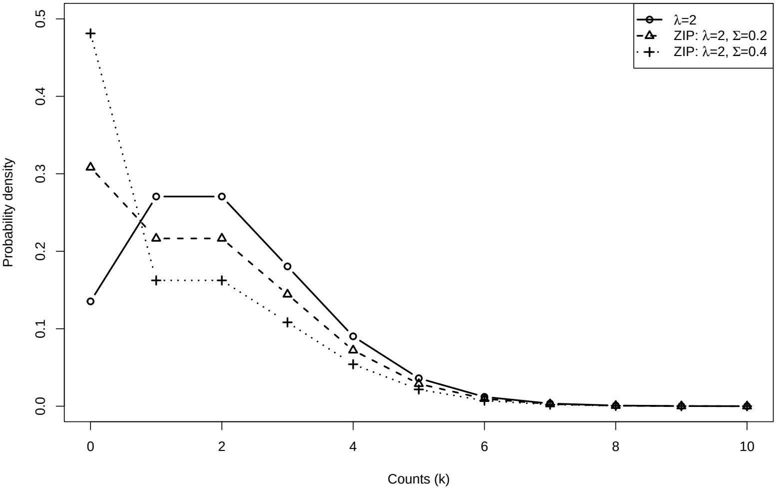
Zero Inflation

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



Zero-inflated Poisson regression

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

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

```
##
## Call:
## pscl::zeroinfl(formula = shared_syr ~ sex + ethn + homeless, data = needledat2,
##     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     -0.5236     0.1464  -3.577 0.000348 ***
## homelessyes    1.2034     0.1455   8.268  < 2e-16 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.06263    0.65227   3.162  0.00157 **
## sexM         -0.05068    0.58252  -0.087  0.93068
## ethnHispanic -1.76122    0.81177  -2.170  0.03004 *
## ethnWhite    -0.50187    0.56919  -0.882  0.37792
## homelessyes  -0.53013    0.48108  -1.102  0.27047
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of iterations in BFGS optimization: 12
## Log-likelihood: -299.8 on 10 Df
```

Zero-inflated Negative Binomial regression

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

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

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

```
##
## Call:
## pscl::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
## Log-likelihood: -142.8 on 11 Df
```

Zero-inflated NB - simplified

- 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 <- pscl::zeroinfl(shared_syr ~ sex + ethn +
                               homeless + hiv | hiv,
                             dist = "negbin",
                             data = needledat2)
```

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

```
##
## Call:
## pscl::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
## Log-likelihood: -122.5 on 11 Df
```

Intercept-only ZI model

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

```r
summary(fit.ZInb3)
```

```
##
## Call:
## pscl::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
```

Confidence intervals

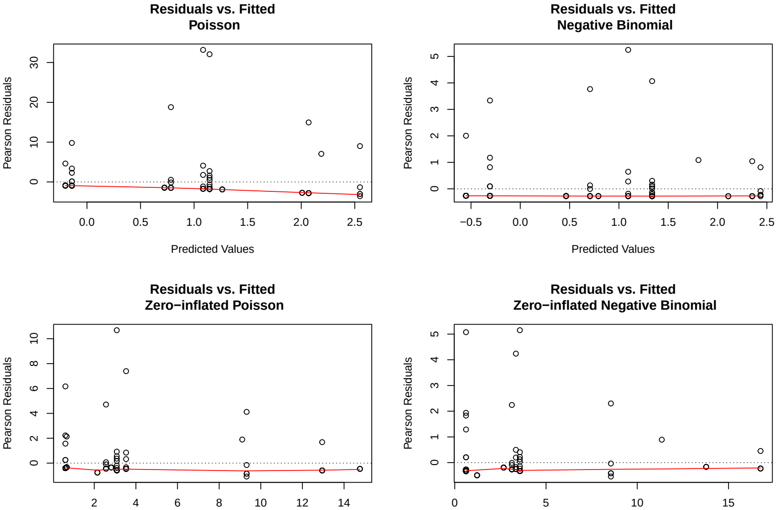
Use the `confint()` function for all these models (don't try to specify which package confint comes from). E.g.:

```
confint(fit.ZInb3)
```

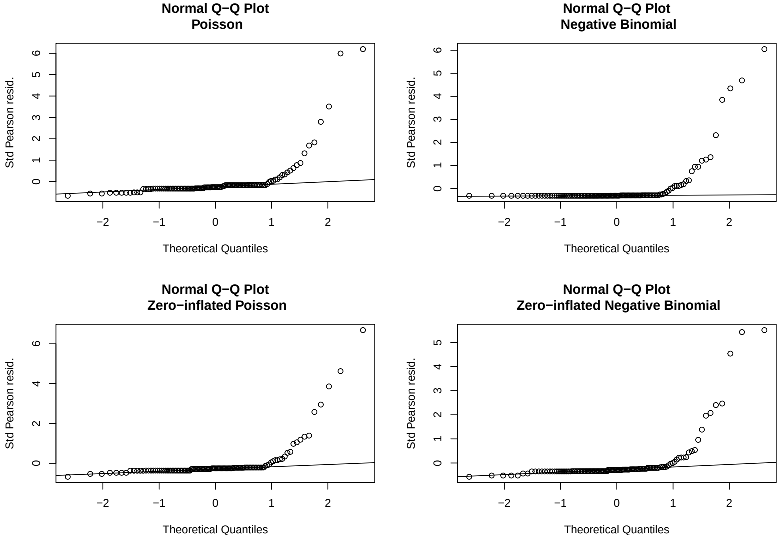
```
##                          2.5 %    97.5 %
## count_(Intercept)   -0.7108906 4.8817285
## count_sexM          -3.1861592 0.3099794
## count_ethnHispanic -1.8048349 2.7674386
## count_ethnWhite     -1.6630517 1.5146931
## count_homelessyes   0.2937565 2.9477701
## zero_(Intercept)   -0.9685313 2.0106906
```

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.



Quantile-quantile plots for residuals



still over-dispersed - ideas?

Summary / Conclusions

- These are multiplicative models
- Fitting zero-inflated models can be problematic (convergence, over-complicated default models), especially for small samples
- Use QQ and residuals plots to assess model fit
- Can use LRT to compare nested models