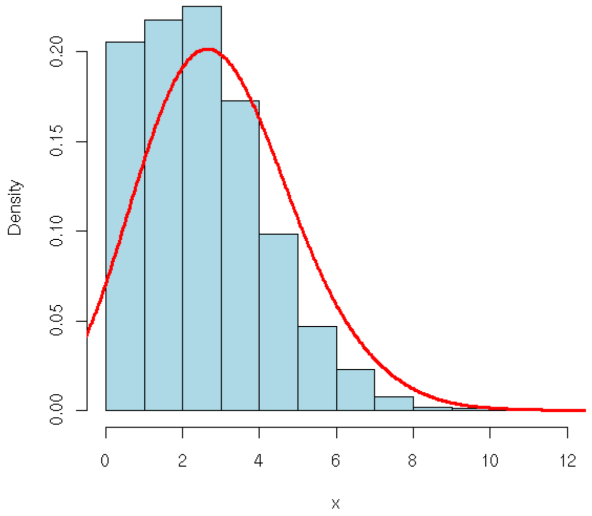
Poisson Regression

Using count data

What if we have count data?

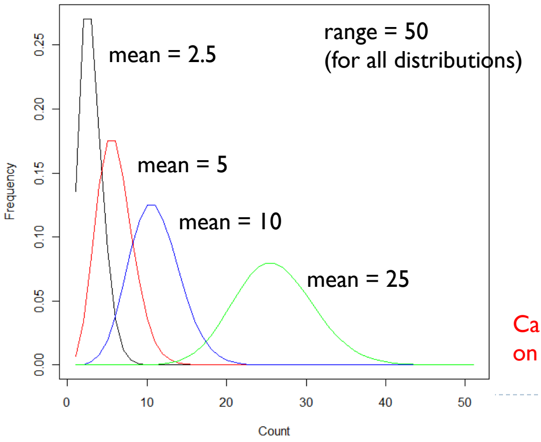
- Suppose we have data that are *aggregate counts* of some event over a given area
  - Area-level vs. individual-level data
- Nature of count data
  - Discrete, skewed distribution
  - High proportion of zero outcomes
  - Always > 0
- Why OLS won't work
  - The relationship between X and Y is nonlinear
  - Counts are heteroskedastic
  - Can't predict non-negative values

What is a Poisson distribution?



"Large" vs. "small" Poissons

- "Large Poissons are like Gaussians, but small Poissons are quite different"
  - As mean increases, Poisson approximates Normal distribution



Can we use OLS regression on "large" Poissons?

Link functions

- Remember, for Generalized Linear Models, we use the link function to transform y:
  - Normal: $G(y) = y$ (identity link)
  - Binomial/logistic: $G(y) = \log\left(\frac{P}{1-P}\right)$
- Poisson: $G(y) = \log(y)$

Interpretation

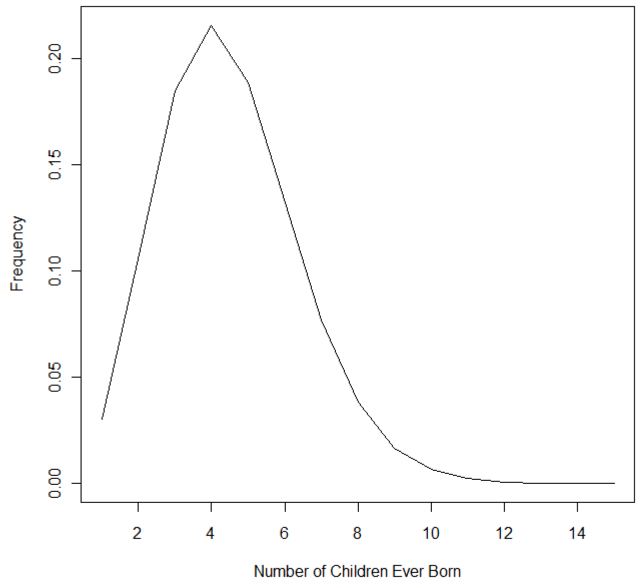
- If we take the transformed y and add a regression equation, we get a Poisson regression:

$$\log(y) = \alpha + \beta x$$

- As in least-squares regression, the relationship between the log(y) and x is assumed to be linear
  - Log(y) changes linearly as a function of explanatory variables
  - Or one unit change in y = exp(x) change in x

Example: children ever born

- The dataset has 70 rows representing group-level data on the number of children ever born to women in Fiji:
  - Number of children ever born
  - Number of women in the group
  - Duration of marriage
    - 1=0-4, 2=5-9, 3=10-14, 4=15-19, 5=20-24, 6=25-29
  - Residence
    - 1=Suva (capital city), 2=Urban, 3=Rural
  - Education
    - 1=none, 2=lower primary, 3=upper primary, 4=secondary+



Poisson regression in R

```
> ceb1<-glm(y ~ educ + res, offset=log(n), family = "poisson",
  data = ceb)
```

Need to account for different population sizes in each area/group unless data are from same-size populations

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.43029    0.01795  79.691   <2e-16 ***
educnone     0.21462    0.02183   9.831   <2e-16 ***
educsec+    -1.00900    0.05217 -19.342   <2e-16 ***
educupper   -0.40485    0.02956 -13.696   <2e-16 ***
resSuva     -0.05997    0.02819  -2.127   0.0334 *
resurban     0.06204    0.02442   2.540   0.0111 *
---

    Null deviance: 3731.5  on 69  degrees of freedom
Residual deviance: 2646.5  on 64  degrees of freedom
AIC: Inf
```

Assessing model fit

1. Examine AIC score – smaller is better

2. Examine the deviance as an approximate goodness of fit test
   - Expect the residual deviance/degrees of freedom to be approximately 1

```
> ceb2$deviance/ceb2$df.residual
[1] 41.35172
```

3. Compare residual deviance to a $\chi 2$ distribution

```
> pchisq(2646.5, 64, lower=F)
[1] 0
```

Interpretation

$$\log(y) = 1.43 + .21x_{edunone} - 1.0x_{eduse+} - 0.41x_{eduup} - 0.06x_{resSuv} + 0.06x_{resurb}$$

- The predicted number of children for a women with no education living in Suva is given by

$$\begin{aligned} \log(y) &= 1.43 + .21(1) - 1.0(0) - 0.41(0) - 0.06(1) + 0.06(0) \\ &= 1.58 \\ \exp(1.58) &= 4.85 \end{aligned}$$

- The predicated number of children for a woman with a secondary education, living in a rural area is:

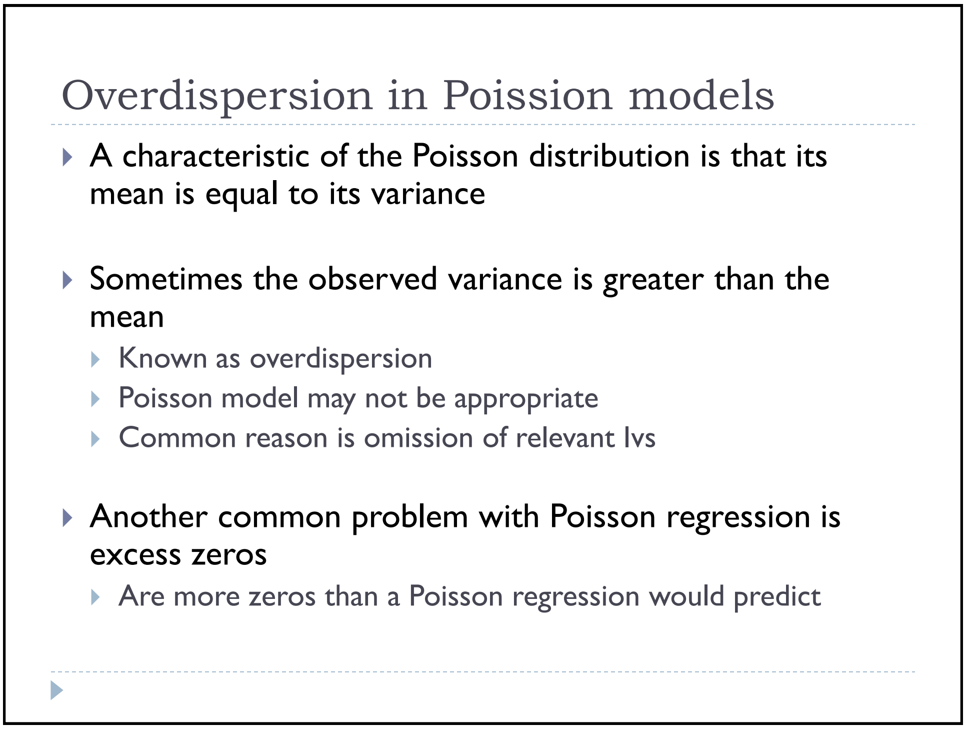
$$\begin{aligned} \log(y) &= 1.43 + .21(0) - 1.0(1) - 0.41(0) - 0.06(0) + 0.06(0) \\ &= .43 \\ \exp(.43) &= 1.53 \end{aligned}$$

Model fitting: analysis of deviance

- Similar to logistic regression, we want to compare the differences in the size of residuals between models

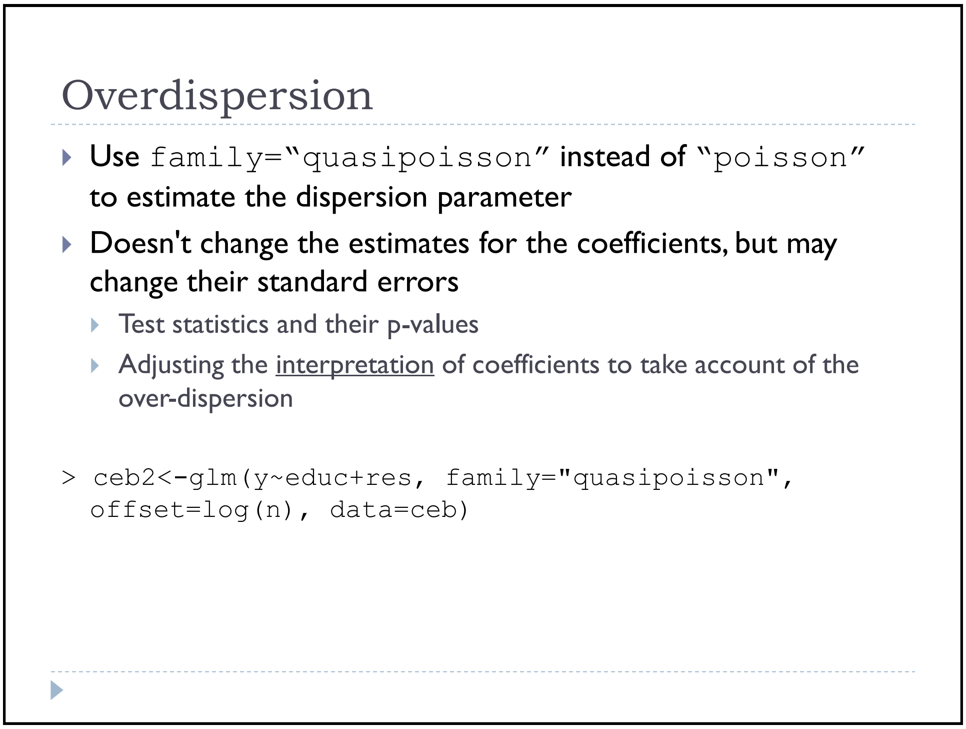
```
> ceb1<-glm(y~educ, family=“poisson", offset=log(n), data=
  ceb)
> ceb2<-glm(y~educ+res, family=“poisson", offset=log(n),
  data= ceb)


> 1-pchisq(deviance(ceb1)-deviance(ceb2),
  df.residual(ceb1)-df.residual(ceb2))
[1] 0.0007124383
```

- Since the p-value is small, there is evidence that the addition of `res` explains a significant amount (more) of the deviance



Overdispersion in Poisson models

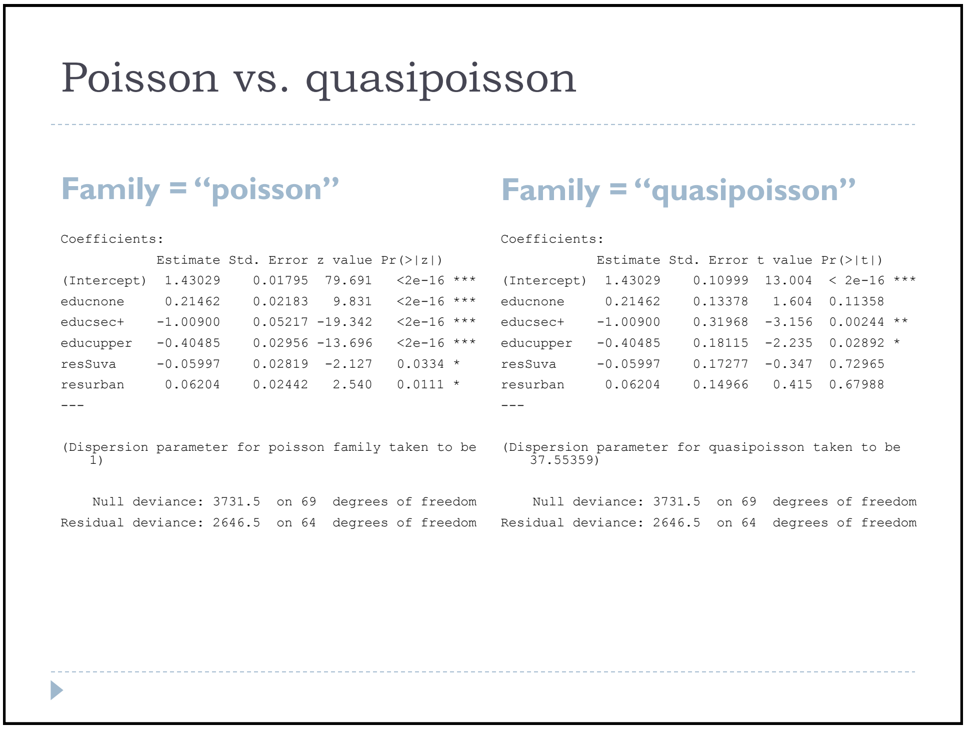
- A characteristic of the Poisson distribution is that its mean is equal to its variance
- Sometimes the observed variance is greater than the mean
  - Known as overdispersion
  - Poisson model may not be appropriate
  - Common reason is omission of relevant Ivs
- Another common problem with Poisson regression is excess zeros
  - Are more zeros than a Poisson regression would predict



Overdispersion

- Use `family="quasipoisson"` instead of `"poisson"` to estimate the dispersion parameter
- Doesn't change the estimates for the coefficients, but may change their standard errors
  - Test statistics and their p-values
  - Adjusting the interpretation of coefficients to take account of the over-dispersion

```
> ceb2<-glm(y~educ+res, family="quasipoisson",
  offset=log(n), data=ceb)
```



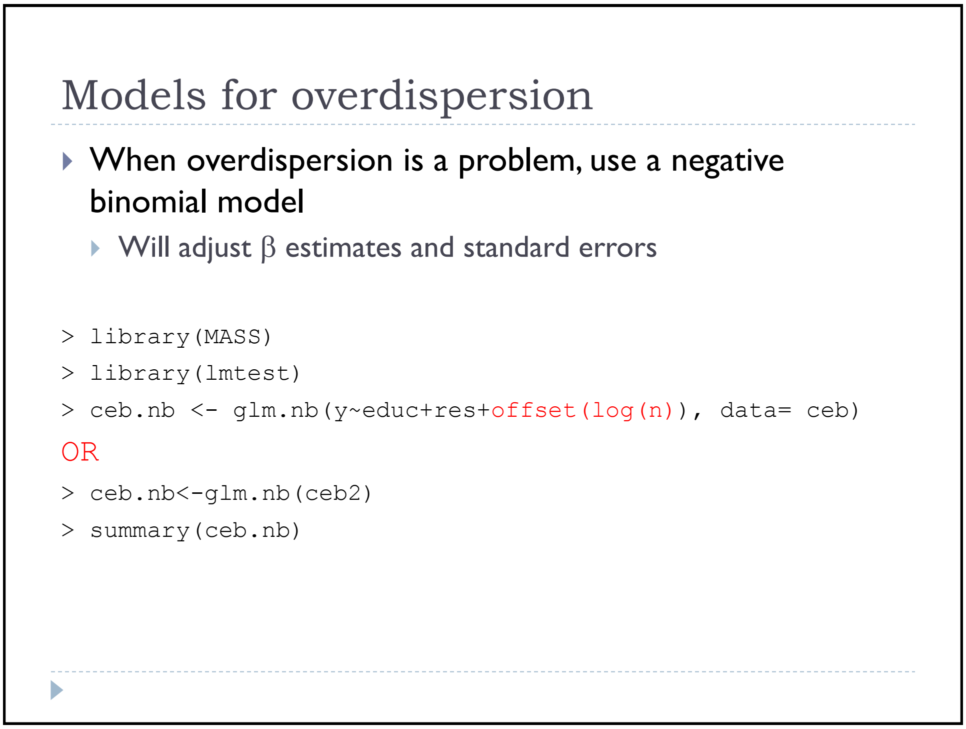
Poisson vs. quasipoisson

Family = “poisson”

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.43029    0.01795  79.691   <2e-16 ***
educnone     0.21462    0.02183   9.831   <2e-16 ***
educsec+    -1.00900    0.05217 -19.342   <2e-16 ***
educupper   -0.40485    0.02956 -13.696   <2e-16 ***
resSuva     -0.05997    0.02819  -2.127   0.0334 *
resurban     0.06204    0.02442   2.540   0.0111 *
---

(Dispersion parameter for poisson family taken to be
    1)

    Null deviance: 3731.5  on 69  degrees of freedom
Residual deviance: 2646.5  on 64  degrees of freedom
```

Family = “quasipoisson”

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.43029    0.10999  13.004  < 2e-16 ***
educnone     0.21462    0.13378   1.604  0.11358
educsec+    -1.00900    0.31968  -3.156  0.00244 **
educupper   -0.40485    0.18115  -2.235  0.02892 *
resSuva     -0.05997    0.17277  -0.347  0.72965
resurban     0.06204    0.14966   0.415  0.67988
---

(Dispersion parameter for quasipoisson taken to be
    37.55359)

    Null deviance: 3731.5  on 69  degrees of freedom
Residual deviance: 2646.5  on 64  degrees of freedom
```



Models for overdispersion

- When overdispersion is a problem, use a negative binomial model
  - Will adjust β estimates and standard errors

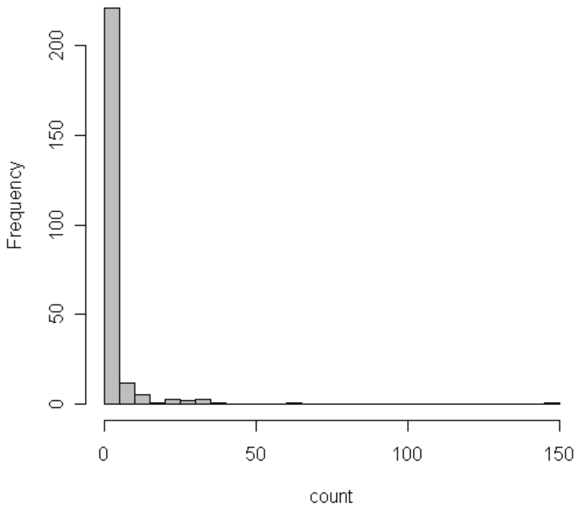
```
> library(MASS)
> library(lmtest)
> ceb.nb <- glm.nb(y~educ+res+offset(log(n)), data= ceb)
OR
> ceb.nb<-glm.nb(ceb2)
> summary(ceb.nb)
```

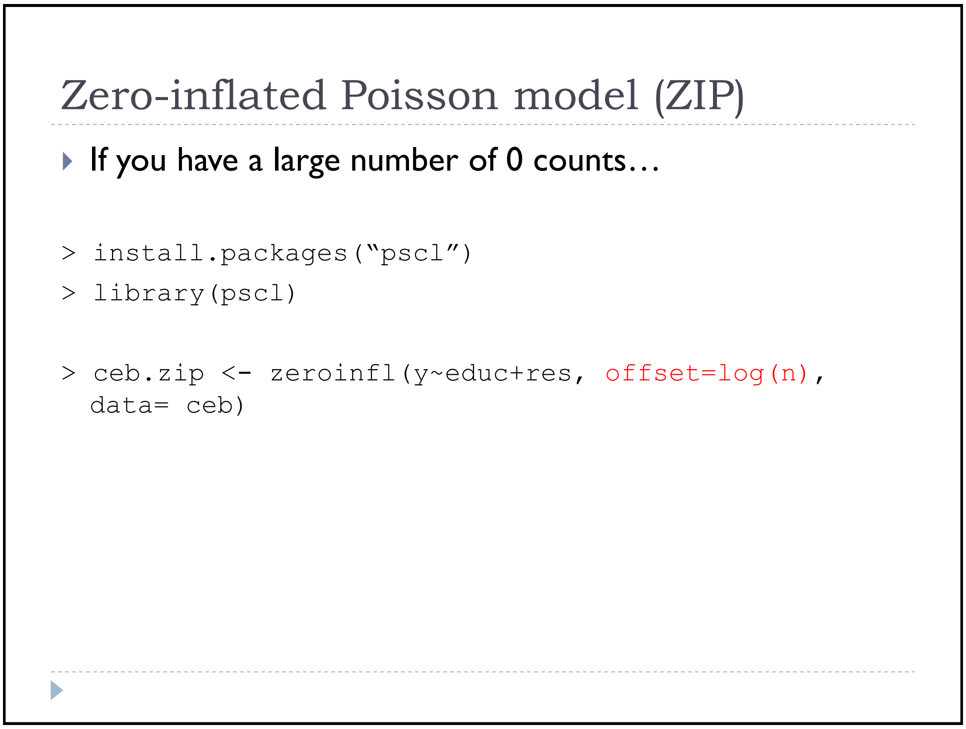
NB model in R

```
glm.nb(formula = ceb2, x = T, init.theta = 3.38722121141125, link = log)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.490043   0.160589   9.279  < 2e-16 ***
educnone     0.002317   0.183754   0.013  0.98994
educsec+    -0.630343   0.200220  -3.148  0.00164 **
educupper   -0.173138   0.184210  -0.940  0.34727
resSuva     -0.149784   0.165622  -0.904  0.36580
resurban     0.055610   0.165391   0.336  0.73670
---

(Dispersion parameter for Negative Binomial(3.3872) family taken to be 1)

    Null deviance: 85.001  on 69  degrees of freedom
Residual deviance: 71.955  on 64  degrees of freedom
AIC: 740.55

              Theta:  3.387
          Std. Err.:  0.583

 2 x log-likelihood:  -726.555
```

```
> ceb.nb$deviance/ceb.nb$df.residual
[1] 1.124297
```

What if your data looked like…





Zero-inflated Poisson model (ZIP)

- If you have a large number of 0 counts…

```
> install.packages(“pscl”)
> library(pscl)

> ceb.zip <- zeroinfl(y~educ+res, offset=log(n),
  data= ceb)
```