432 Class 16 Slides

github.com/THOMASELOVE/2019-432

2019-03-28

Setup

```r
library(skimr)
library(arm)
library(rms)
library(boot)
library(MASS)
library(HSAUR)
library(pscl)
library(lmtest)
library(VGAM)
library(sandwich)
library(broom)
library(tidyverse)
```

Today's Materials

Regression Models for Count Outcomes

- Poisson Regression model
- Negative Binomial Regression model
- Zero-inflated models
  - ZIP (Zero-inflated Poisson)
  - ZINB (Zero-inflated Neg. Binomial)
- Hurdle models
- Tobit (censored) regression models

The `medicare` data

The `medicare` example

The data we will use come from the `NMES1988` data set in R's `AER` package, although I have built a cleaner version for you in the `medicare.csv` file on our web site. These are essentially the same data as are used in my main resource from the University of Virginia for hurdle models.

These data are a cross-section originating from the US National Medical Expenditure Survey (NMES) conducted in 1987 and 1988. The NMES is based upon a representative, national probability sample of the civilian non-institutionalized population and individuals admitted to long-term care facilities during 1987. The data are a subsample of individuals ages 66 and over all of whom are covered by Medicare (a public insurance program providing substantial protection against health-care costs), and some of whom also have private supplemental insurance.

```
medicare <- read.csv("data/medicare.csv") %>% tbl_df
```

The `medicare` code book

Variable	Description
`subject`	subject number
`visits`	outcome of interest: number of physician office visits
`hospital`	number of hospital stays
`health`	self-perceived health status (poor, average, excellent)
`chronic`	number of chronic conditions
`sex`	male or female
`school`	number of years of education
`insurance`	is the subject (also) covered by private insurance? (yes or no)

Today's Goal

Predict `visits` using some combination of these 6 predictors...

Predictor	Description
`hospital`	number of hospital stays
`health`	self-perceived health status (poor, average, excellent)
`chronic`	number of chronic conditions
`sex`	male or female
`school`	number of years of education
`insurance`	is the subject (also) covered by private insurance? (yes or no)

The `medicare` tibble

```
# A tibble: 4,406 x 8
   subject visits hospital health chronic sex   school
     <int>  <int>    <int> <fct>    <int> <fct>  <int>
 1       1      5        1 avera~       2 male       6
 2       2      1        0 avera~       2 fema~     10
 3       3     13        3 poor         4 fema~     10
 4       4     16        1 poor         2 male       3
 5       5      3        0 avera~       2 fema~      6
 6       6     17        0 poor         5 fema~      7
 7       7      9        0 avera~       0 fema~      8
 8       8      3        0 avera~       0 fema~      8
 9       9      1        0 avera~       0 fema~      8
10      10      0        0 avera~       0 fema~      8
# ... with 4,396 more rows, and 1 more variable:
#   insurance <fct>
```

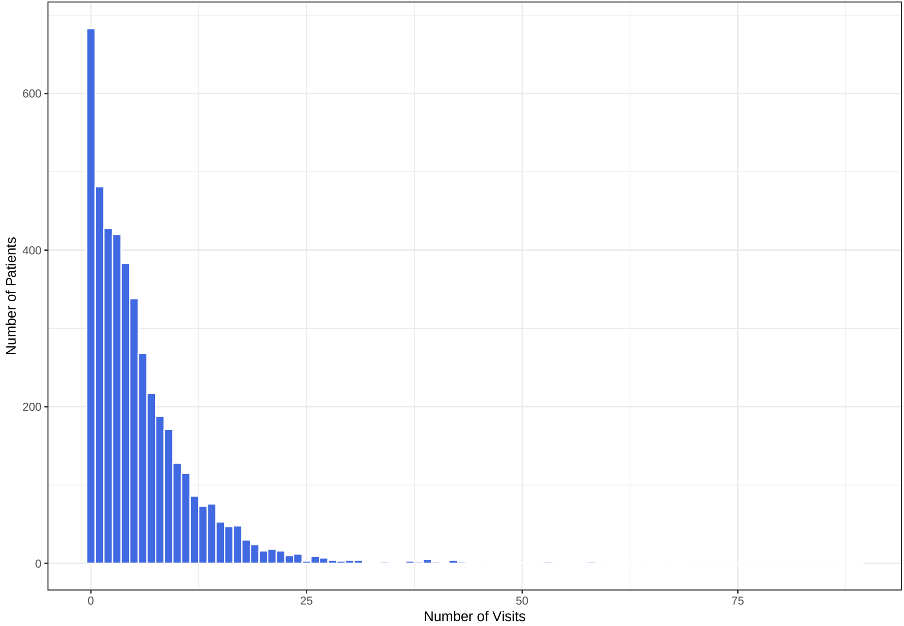
A skim of medicare

```
> skim(medicare)
Skim summary statistics
 n obs: 4406
 n variables: 8

Variable type: factor
  variable missing complete    n n_unique                           top_counts ordered
    health       0     4406 4406        3 ave: 3509, poo: 554, exc: 343, NA: 0   FALSE
 insurance       0     4406 4406        2           yes: 3421, no: 985, NA: 0    FALSE
       sex       0     4406 4406        2         fem: 2628, mal: 1778, NA: 0    FALSE

Variable type: integer
 variable missing complete    n    mean      sd p0     p25 median     p75 p100     hist
  chronic       0     4406 4406    1.54    1.35  0       1      1       2    8
 hospital       0     4406 4406     0.3    0.75  0       0      0       0    8
   school       0     4406 4406   10.29    3.74  0       8     11      12   18
  subject       0     4406 4406  2203.5 1272.05  1 1102.25 2203.5 3304.75 4406
   visits       0     4406 4406    5.77    6.76  0       1      4       8   89
```

Our outcome, `visits`



Counting the visits

```
medicare %>% count(visits)
```

```
# A tibble: 60 x 2
   visits     n
    <int> <int>
 1      0   683
 2      1   481
 3      2   428
 4      3   420
 5      4   383
 6      5   338
 7      6   268
 8      7   217
 9      8   188
10      9   171
# ... with 50 more rows
```

visits summary

```r
describe(medicare$visits)
```

```
medicare$visits
       n  missing distinct     Info     Mean      Gmd
    4406        0       60    0.992    5.774    6.227
     .05      .10      .25      .50      .75      .90
       0        0        1        4        8       13
     .95
      17

lowest :  0  1  2  3  4, highest: 63 65 66 68 89
```

Reiterating the Goal

Predict `visits` using some combination of these 6 predictors...

Predictor	Description
`hospital`	number of hospital stays
`health`	self-perceived health status (poor, average, excellent)
`chronic`	number of chronic conditions
`sex`	male or female
`school`	number of years of education
`insurance`	is the subject (also) covered by private insurance? (yes or no)

Model 1: A Poisson Regression

Poisson Regression

Assume our count data (`visits`) follows a Poisson distribution with a mean conditional on our predictors.

```
mod_1 <- glm(visits ~ hospital + health + chronic +
                  sex + school + insurance,
              data = medicare, family = "poisson")
```

Store Predictions

```r
mod_1_aug <- augment(mod_1, medicare,
                     type.predict = "response",
                     type.residuals = "response")

mod_1_aug %>% select(visits, .fitted, .resid) %>% head(2)
```

```
# A tibble: 2 x 3
  visits .fitted .resid
   <int>   <dbl>  <dbl>
1      5    5.66 -0.659
2      1    5.96 -4.96
```

Calculating a Pseudo-R^2 for mod_1

```
(mod_1_r <- with(mod_1_aug, cor(visits, .fitted)))
```

```
[1] 0.3144637
```

```
(mod_1_r^2)
```

```
[1] 0.09888744
```

Summarizing the Model's Fit

```
glance(mod_1)
```

```
# A tibble: 1 x 7
  null.deviance df.null  logLik    AIC    BIC deviance
          <dbl>   <int>   <dbl>  <dbl>  <dbl>    <dbl>
1        26943.    4405 -17972. 35959. 36010.   23168.
# ... with 1 more variable: df.residual <int>
```

Building a Rootogram

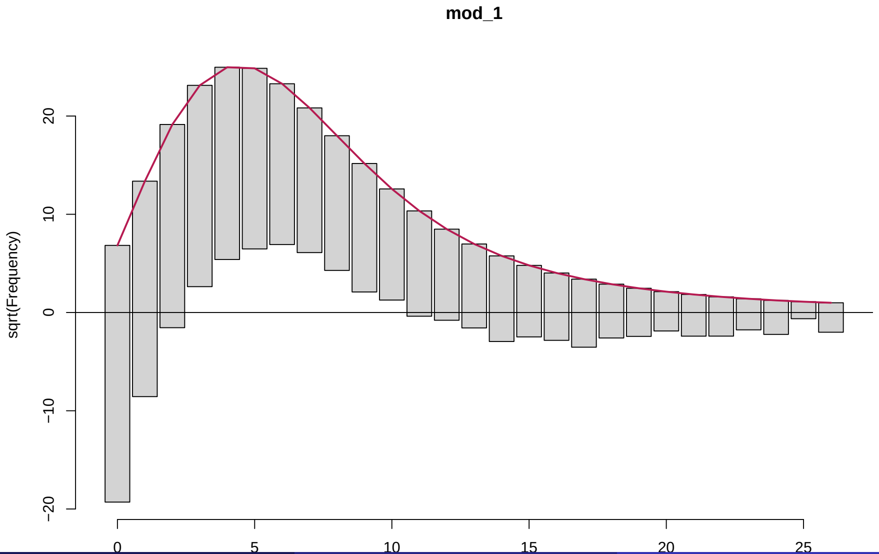
To build a rootogram, you need to load the `countreg` package. This package is housed on R-Forge, rather than CRAN, so you need to install it with ...

```
install.packages("countreg",
                 repos="http://R-Forge.R-project.org")
```

in order to use it.

Rootogram: See the Fit (using default choices)

```
countreg::rootogram(mod_1)
```



Interpreting the Hanging Rootogram

- The red curved line is the theoretical Poisson fit.
- "Hanging" from each point on the red line is a bar, the height of which represents the observed counts.
  - A bar hanging below 0 indicates that the model under-predicts that value. (Model predicts fewer values than the data show.)
  - A bar hanging above 0 indicates over-prediction of that value. (Model predicts more values than the data show.)
- The counts have been transformed with a square root transformation to prevent smaller counts from getting obscured and overwhelmed by larger counts.

For more information on rootograms, check out https://arxiv.org/pdf/1605.01311

How many zero counts does Model 1 predict?

```
lam <- predict(mod_1, type = "response") # exp. mean count
exp <- sum(dpois(x = 0, lambda = lam)) # sum the prob(0)
round(exp)
```

```
[1] 47
```

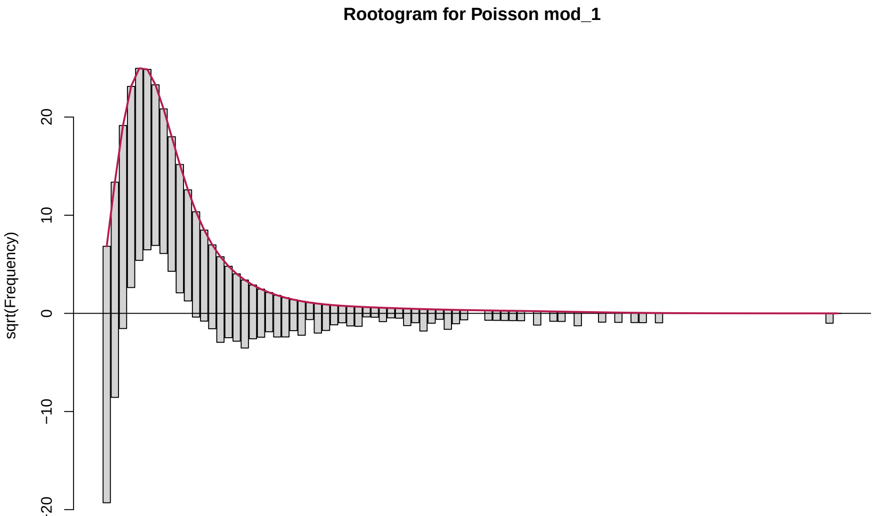
How many subjects with zero visits did we see?

```
medicare %>% count(visits == 0)
```

```
# A tibble: 2 x 2
  `visits == 0`     n
  <lgl>         <int>
1 FALSE          3723
2 TRUE            683
```

The Complete Hanging Rootogram for Model 1

```
countreg::rootogram(mod_1, max = 90,
                    main = "Rootogram for Poisson mod_1")
```



Interpreting the Rootogram for Model 1

In `mod_1`, we see a great deal of underfitting for counts of 0 and 1, then overfitting for visit counts in the 3-10 range, with some underfitting again at more than a dozen or so visits.

- Our Poisson model (`mod_1`) doesn't fit enough zeros or ones, and fits too many 3-12 values, then not enough of the higher values.

Do we have an overdispersion problem?

```
overdispersion ratio is  6.706136

p value of overdispersion test:  0
```

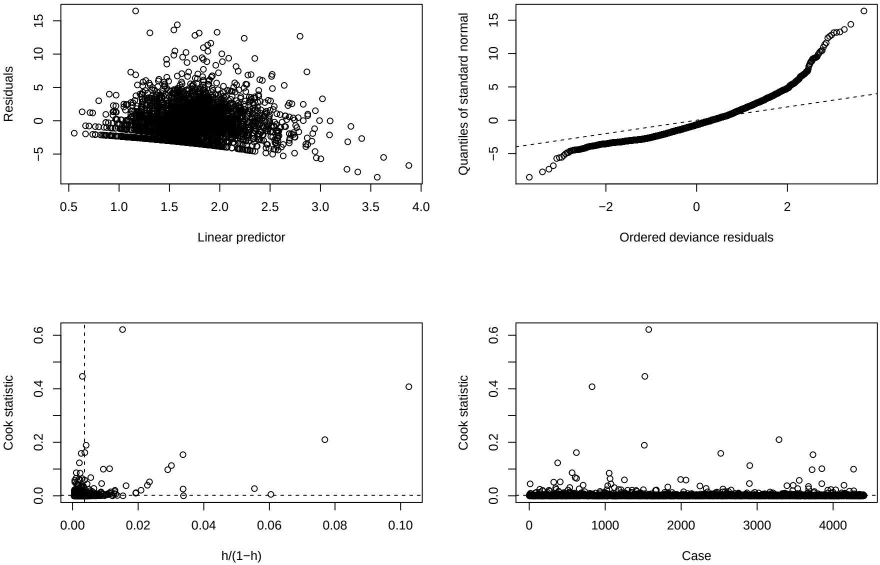
Dealing with Overdispersion?

To address the overdispersion, we'll adopt a negative binomial approach, in part because the rootogram tool we're using doesn't handle the quasipoisson model.

Code used on previous slide

```
yhat <- predict(mod_1, type = "response")
n <- 4406; k <- 8 # use display(mod_1) to see these
z <- (mod_1_aug$visits - mod_1_aug$.fitted) /
    sqrt(mod_1_aug$.fitted)
cat("overdispersion ratio is ", sum(z^2)/ (n - k), "\n")
cat("p value of overdispersion test: ",
    pchisq(sum(z^2)/(n-k), n-k), "\n")
```

glm.diag.plots from boot for Model 1



Model 2: A Negative Binomial Model

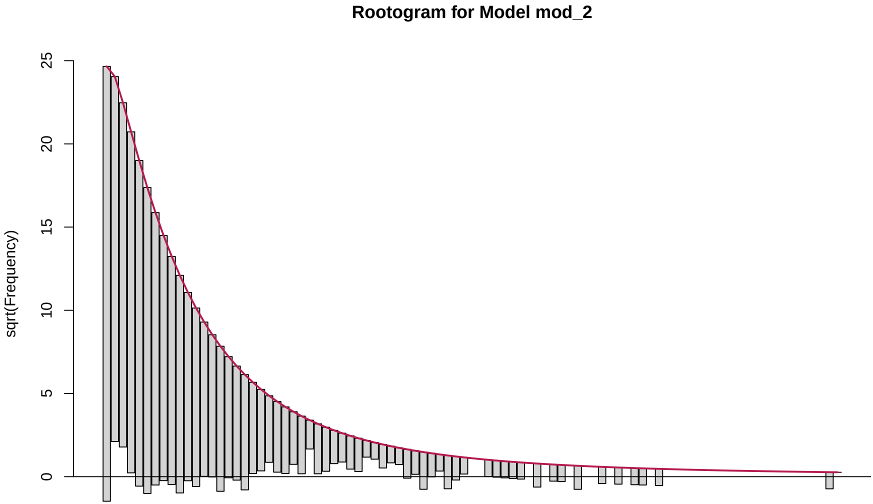
Fitting the Negative Binomial Model

Looks like our data are overdispersed compared to what a Poisson model expects.

```
mod_2 <- MASS::glm.nb(visits ~ hospital + health + chronic +
                      sex + school + insurance,
                  data = medicare)
```

Rootogram for Negative Binomial Model

```
countreg::rootogram(mod_2, max = 90,
                    main = "Rootogram for Model mod_2")
```



Save predicted values and residuals

```
mod_2_aug <- medicare %>%
    mutate(fitted = fitted(mod_2, type = "response"),
           resid = resid(mod_2, type = "response"))

mod_2_aug %>%
    dplyr::select(visits, fitted, resid) %>%
    head(2)
```

```
# A tibble: 2 x 3
  visits fitted  resid
   <int>  <dbl>  <dbl>
1      5   5.79 -0.787
2      1   5.88 -4.88
```

Pseudo-R^2 for Neg. Bin. model (`mod_2`)

We can calculate a proxy for R^2 as the squared correlation of the fitted values and the observed values.

```
mod2_r <- with(mod_2_aug, cor(visits, fitted))
mod2_r^2
```

```
[1] 0.08271151
```

So Far . . .

Model	Pseudo-R^2	Rootogram?	Comments
Poisson	0.099	Many problems.	Data appear overdispersed.
Neg. Bin.	0.083	Better.	Still not enough zeros.

Model 3: Zero-Inflated Poisson (ZIP) Model

Zero-Inflated Poisson (ZIP) model

The zero-inflated Poisson or (ZIP) model is used to describe count data with an excess of zero counts.

The model posits that there are two processes involved:

- a logit model is used to predict excess zeros
- while a Poisson model is used to predict the counts

The `pscl` package is used to fit these zero-inflated models.

```
mod_3 <- pscl::zeroinfl(visits ~ hospital + health +
                    chronic + sex + school + insurance,
                    data = medicare)
```

`summary(mod_3)` (and see next 2 slides)

```
> summary(mod_3)

Call:
zeroinfl(formula = visits ~ hospital + health + chronic + sex + school + insurance, data = medicare)

Pearson residuals:
    Min      1Q  Median      3Q     Max 
-5.4092 -1.1579 -0.4769  0.5435 25.0380 

Count model coefficients (poisson with log link):
                 Estimate Std. Error z value Pr(>|z|)    
(Intercept)      1.405812   0.024175  58.152  < 2e-16 ***
hospital         0.159011   0.006060  26.239  < 2e-16 ***
healthexcellent -0.304134   0.031151  -9.763  < 2e-16 ***
healthpoor       0.253454   0.017705  14.315  < 2e-16 ***
chronic          0.101836   0.004721  21.571  < 2e-16 ***
sexmale         -0.062332   0.013054  -4.775 1.80e-06 ***
school           0.019144   0.001873  10.221  < 2e-16 ***
insuranceyes     0.080557   0.017145   4.699 2.62e-06 ***

Zero-inflation model coefficients (binomial with logit link):
                Estimate Std. Error z value Pr(>|z|)    
(Intercept)     -0.08102    0.14233  -0.569 0.569219    
hospital        -0.30330    0.09158  -3.312 0.000927 ***
healthexcellent  0.23786    0.14990   1.587 0.112550    
healthpoor       0.02166    0.16170   0.134 0.893431    
chronic         -0.53117    0.04601 -11.545  < 2e-16 ***
sexmale          0.41527    0.08919   4.656 3.22e-06 ***
school          -0.05677    0.01223  -4.640 3.49e-06 ***
insuranceyes    -0.75294    0.10257  -7.341 2.12e-13 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 

Number of iterations in BFGS optimization: 24 
Log-likelihood: -1.613e+04 on 16 Df
```

The Fitted Equation (part 1 of 2)

The form of the model equation for a zero-inflated Poisson regression requires us to take two separate models into account.

First, we have a logistic regression model to predict the log odds of zero visits. . .

```
logit(visits = 0) = -0.08 - 0.30 hospital +
             0.24 health = excellent + 0.21 health = poor -
             0.53 chronic + 0.42 sex = male - 0.06 school -
             0.75 insurance = yes
```

That takes care of the *extra* zeros.

Zero-inflation model coefficients in `mod_3`

```
Zero-inflation model coefficients (binomial with logit link):
                 Estimate Std. Error z value Pr(>|z|)    
(Intercept)      -0.08102    0.14233  -0.569 0.569219    
hospital         -0.30330    0.09158  -3.312 0.000927 ***
healthexcellent   0.23786    0.14990   1.587 0.112550    
healthpoor        0.02166    0.16170   0.134 0.893431    
chronic          -0.53117    0.04601 -11.545  < 2e-16 ***
sexmale           0.41527    0.08919   4.656 3.22e-06 ***
school           -0.05677    0.01223  -4.640 3.49e-06 ***
insuranceyes     -0.75294    0.10257  -7.341 2.12e-13 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The Fitted Equation (part 2 of 2)

The form of the model equation for a zero-inflated Poisson regression requires us to take two separate models into account.

Second, we have a Poisson regression model to predict log(visits)...

```
log(visits) = 1.41 + 0.16 hospital -
             0.30 health = excellent + 0.25 health = poor +
             0.10 chronic - 0.06 sex = male + 0.02 school +
             0.08 insurance = yes
```

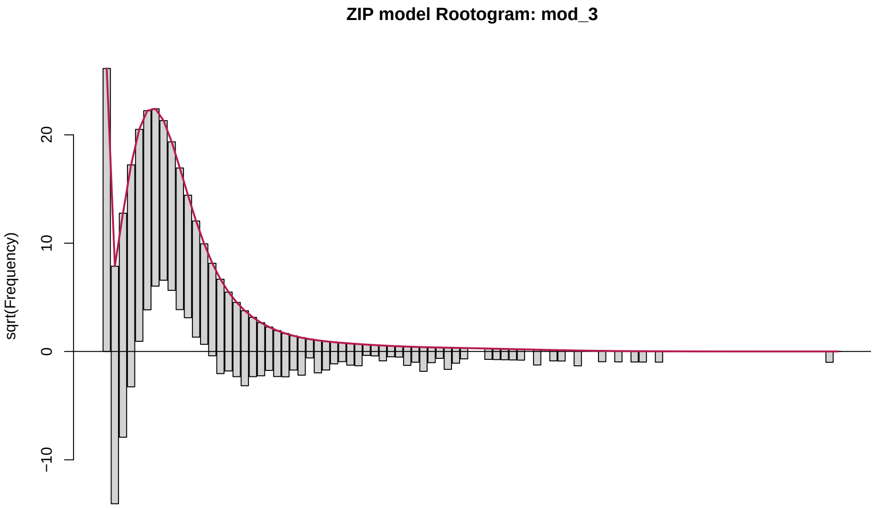
This may produce some additional zero count estimates.

Count model coefficients in `mod_3`

```
Count model coefficients (poisson with log link):
                  Estimate Std. Error z value Pr(>|z|)    
(Intercept)       1.405812   0.024175  58.152  < 2e-16 ***
hospital          0.159011   0.006060  26.239  < 2e-16 ***
healthexcellent -0.304134   0.031151  -9.763  < 2e-16 ***
healthpoor        0.253454   0.017705  14.315  < 2e-16 ***
chronic           0.101836   0.004721  21.571  < 2e-16 ***
sexmale          -0.062332   0.013054  -4.775 1.80e-06 ***
school            0.019144   0.001873  10.221  < 2e-16 ***
insuranceyes      0.080557   0.017145   4.699 2.62e-06 ***
```

Rootogram for ZIP model

```
countreg::rootogram(mod_3, max = 90,
                    main = "ZIP model Rootogram: mod_3")
```



Save predicted values and residuals

```
mod_3_aug <- medicare %>%
    mutate(fitted = predict(mod_3, type = "response"),
           resid = resid(mod_3, type = "response"))

mod_3_aug %>%
    dplyr::select(visits, fitted, resid) %>%
    head(2)
```

```
# A tibble: 2 x 3
  visits fitted  resid
   <int>  <dbl>  <dbl>
1      5   5.98 -0.982
2      1   6.05 -5.05
```

Is ZIP significantly better than Poisson (Vuong test)

```r
vuong(mod_3, mod_1)
```

```
Vuong Non-Nested Hypothesis Test-Statistic:
(test-statistic is asymptotically distributed N(0,1) under the
 null that the models are indistinguishible)
-------------------------------------------------------------
              Vuong z-statistic             H_A    p-value
Raw                    17.13459 model1 > model2 < 2.22e-16
AIC-corrected          17.05999 model1 > model2 < 2.22e-16
BIC-corrected          16.82163 model1 > model2 < 2.22e-16
```

- Conclusion: ZIP model shows evidence of superiority over Poisson.
- Vuong QH (1989) Likelihood ratio tests for model selection and non-nested hypotheses. *Econometrica* 57:307-333.

Pseudo-R^2 for ZIP model (mod_3)

We can calculate a proxy for R^2 as the squared correlation of the fitted values and the observed values.

```
mod3_r <- with(mod_3_aug, cor(visits, fitted))
mod3_r^2
```

```
[1] 0.1073657
```

Model 4: Zero-Inflated Negative Binomial Model

Fitting the Zero-Inflated Negative Binomial (mod_4)

```
mod_4 <- zeroinfl(visits ~ hospital + health + chronic +
                      sex + school + insurance,
                  dist = "negbin", data = medicare)
```

summary(mod_4) (and see next 2 slides)

```
> summary(mod_4)

Call:
zeroinfl(formula = visits ~ hospital + health + chronic + sex + school + insurance, data = medicare, dist = "negbin")

Pearson residuals:
    Min      1Q  Median      3Q     Max 
-1.1966 -0.7097 -0.2784  0.3256 17.7661 

Count model coefficients (negbin with log link):
                 Estimate Std. Error z value Pr(>|z|)    
(Intercept)      1.193466   0.056737  21.035  < 2e-16 ***
hospital         0.201214   0.020392   9.867  < 2e-16 ***
healthexcellent -0.313540   0.062977  -4.979 6.40e-07 ***
healthpoor       0.287190   0.045940   6.251 4.07e-10 ***
chronic          0.128955   0.011938  10.802  < 2e-16 ***
sexmale         -0.080093   0.031035  -2.581  0.00986 ** 
school           0.021338   0.004368   4.886 1.03e-06 ***
insuranceyes     0.126815   0.041687   3.042  0.00235 ** 
Log(theta)       0.394731   0.035145  11.231  < 2e-16 ***

Zero-inflation model coefficients (binomial with logit link):
                Estimate Std. Error z value Pr(>|z|)    
(Intercept)     -0.06354    0.27668  -0.230  0.81837    
hospital        -0.81760    0.43875  -1.863  0.06240 .  
healthexcellent  0.10488    0.30965   0.339  0.73484    
healthpoor       0.10178    0.44071   0.231  0.81735    
chronic         -1.24630    0.17918  -6.956 3.51e-12 ***
sexmale          0.64937    0.20046   3.239  0.00120 ** 
school          -0.08481    0.02676  -3.169  0.00153 ** 
insuranceyes    -1.15808    0.22436  -5.162 2.45e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 

Theta = 1.484 
Number of iterations in BFGS optimization: 31 
Log-likelihood: -1.209e+04 on 17 Df
```

Zero-inflation model coefficients in `mod_4`

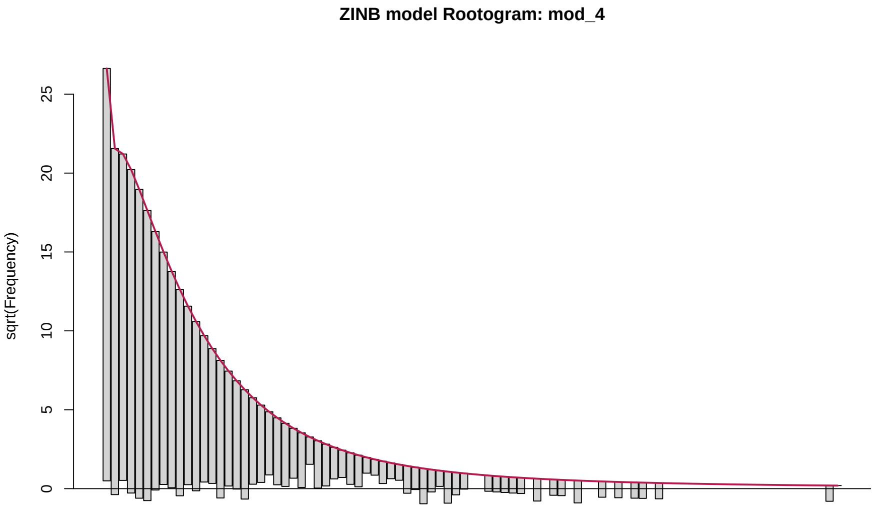
```
Zero-inflation model coefficients (binomial with logit link):
                Estimate Std. Error z value Pr(>|z|)
(Intercept)     -0.06354    0.27668  -0.230  0.81837
hospital        -0.81760    0.43875  -1.863  0.06240 .
healthexcellent  0.10488    0.30965   0.339  0.73484
healthpoor       0.10178    0.44071   0.231  0.81735
chronic         -1.24630    0.17918  -6.956 3.51e-12 ***
sexmale          0.64937    0.20046   3.239  0.00120 **
school          -0.08481    0.02676  -3.169  0.00153 **
insuranceyes    -1.15808    0.22436  -5.162 2.45e-07 ***
```

Count model coefficients in `mod_4`

```
Count model coefficients (negbin with log link):
                 Estimate Std. Error z value Pr(>|z|)    
(Intercept)      1.193466   0.056737  21.035  < 2e-16 ***
hospital         0.201214   0.020392   9.867  < 2e-16 ***
healthexcellent -0.313540   0.062977  -4.979 6.40e-07 ***
healthpoor       0.287190   0.045940   6.251 4.07e-10 ***
chronic          0.128955   0.011938  10.802  < 2e-16 ***
sexmale         -0.080093   0.031035  -2.581  0.00986 ** 
school           0.021338   0.004368   4.886 1.03e-06 ***
insuranceyes     0.126815   0.041687   3.042  0.00235 ** 
Log(theta)       0.394731   0.035145  11.231  < 2e-16 ***
```

Rootogram for ZINB model

```
countreg::rootogram(mod_4, max = 90,
                    main = "ZINB model Rootogram: mod_4")
```



Save predicted values and residuals

```
mod_4_aug <- medicare %>%
    mutate(fitted = fitted(mod_4, type = "response"),
           resid = resid(mod_4, type = "response"))

mod_4_aug %>%
    dplyr::select(visits, fitted, resid) %>%
    head(2)
```

```
# A tibble: 2 x 3
  visits fitted resid
   <int>  <dbl> <dbl>
1      5   6.14 -1.14
2      1   5.94 -4.94
```

Is ZINB significantly better than Negative Binomial?

```r
vuong(mod_4, mod_2)
```

```
Vuong Non-Nested Hypothesis Test-Statistic:
(test-statistic is asymptotically distributed N(0,1) under the
 null that the models are indistinguishible)
-------------------------------------------------------------
              Vuong z-statistic             H_A    p-value
Raw                    5.917202 model1 > model2 1.6373e-09
AIC-corrected          5.324799 model1 > model2 5.0532e-08
BIC-corrected          3.431859 model1 > model2 0.00029973
```

Pseudo-R^2 for ZINB model (`mod_4`)

We can calculate a proxy for R^2 as the squared correlation of the fitted values and the observed values.

```
mod4_r <- with(mod_4_aug, cor(visits, fitted))
mod4_r^2
```

```
[1] 0.09620424
```

So Far . . .

Model	Pseudo-R^2	Rootogram?	Comments
Poisson	0.099	Many problems.	Data appear overdispersed.
Neg. Bin.	0.083	Better.	Still not enough zeros.
ZIP	0.107	All but 0 a problem.	Not enough 1-3.
ZINB	0.096	Better.	Zeros not a perfect fit.

Model 5: The Hurdle Model (Poisson)

The Hurdle Model

The hurdle model is a two-part model that specifies one process for zero counts and another process for positive counts. The idea is that positive counts occur once a threshold is crossed, or put another way, a hurdle is cleared. If the hurdle is not cleared, then we have a count of 0.

- The first part of the model is typically a **binary logistic regression** model. This models whether an observation takes a positive count or not.
- The second part of the model is usually a truncated Poisson or Negative Binomial model. Truncated means we're only fitting positive counts, and not zeros.

In fitting a hurdle model to our [medicare] data, the interpretation would be that one process governs whether a patient visits a doctor or not, and another process governs how many visits are made.

Fitting a Hurdle Model / Poisson-Logistic

```r
mod_5 <- hurdle(visits ~ hospital + health + chronic +
                  sex + school + insurance,
              dist = "poisson", zero.dist = "binomial",
              data = medicare)
```

Summary of Hurdle Model / Poisson-Logistic

```
> summary(mod_5)

Call:
hurdle(formula = visits ~ hospital + health + chronic + sex + school +
    insurance, data = medicare, dist = "poisson", zero.dist = "binomial")

Pearson residuals:
    Min      1Q  Median      3Q     Max 
-5.4144 -1.1565 -0.4770  0.5432 25.0228 

Count model coefficients (truncated poisson with log link):
                 Estimate Std. Error z value Pr(>|z|)    
(Intercept)      1.406459   0.024180  58.167  < 2e-16 ***
hospital         0.158967   0.006061  26.228  < 2e-16 ***
healthexcellent -0.303677   0.031150  -9.749  < 2e-16 ***
healthpoor       0.253521   0.017708  14.317  < 2e-16 ***
chronic          0.101720   0.004719  21.557  < 2e-16 ***
sexmale         -0.062247   0.013055  -4.768 1.86e-06 ***
school           0.019078   0.001872  10.194  < 2e-16 ***
insuranceyes     0.080879   0.017139   4.719 2.37e-06 ***
Zero hurdle model coefficients (binomial with logit link):
                 Estimate Std. Error z value Pr(>|z|)    
(Intercept)      0.043147   0.139852   0.309 0.757688    
hospital         0.312449   0.091437   3.417 0.000633 ***
healthexcellent -0.289570   0.142682  -2.029 0.042409 *  
healthpoor      -0.008716   0.161024  -0.054 0.956833    
chronic          0.535213   0.045378  11.794  < 2e-16 ***
sexmale         -0.415658   0.087608  -4.745 2.09e-06 ***
school           0.058541   0.011989   4.883 1.05e-06 ***
insuranceyes     0.747120   0.100880   7.406 1.30e-13 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Logistic Regression Model to predict zeros

```
Zero hurdle model coefficients (binomial with logit link):
                   Estimate Std. Error z value Pr(>|z|)
(Intercept)        0.043147   0.139852   0.309 0.757688
hospital           0.312449   0.091437   3.417 0.000633 ***
healthexcellent -0.289570   0.142682  -2.029 0.042409 *
healthpoor        -0.008716   0.161024  -0.054 0.956833
chronic            0.535213   0.045378  11.794  < 2e-16 ***
sexmale           -0.415658   0.087608  -4.745 2.09e-06 ***
school             0.058541   0.011989   4.883 1.05e-06 ***
insuranceyes       0.747120   0.100880   7.406 1.30e-13 ***
```

Truncated Poisson to predict non-zero counts

```
Count model coefficients (truncated poisson with log link):
                 Estimate Std. Error z value Pr(>|z|)
(Intercept)      1.406459   0.024180  58.167  < 2e-16 ***
hospital         0.158967   0.006061  26.228  < 2e-16 ***
healthexcellent -0.303677   0.031150  -9.749  < 2e-16 ***
healthpoor       0.253521   0.017708  14.317  < 2e-16 ***
chronic          0.101720   0.004719  21.557  < 2e-16 ***
sexmale         -0.062247   0.013055  -4.768 1.86e-06 ***
school           0.019078   0.001872  10.194  < 2e-16 ***
insuranceyes     0.080879   0.017139   4.719 2.37e-06 ***
```

The Fitted Equation

Logistic Regression to predict log odds of zero visits…

```
logit(visits = 0) = .04 + .31 hospital - .29 health = Exc
        - .01 health = Poor + .54 chronic - .42 sex = male
        + .06 school + .75 insurance = yes
```

Truncated[1] Poisson model to predict log(visits)

```
log(visits) = max( 0, -1.4 + .15 hospital - .30 health = Exc
   + .25 health = Poor + .10 chronic - .06 sex = male
   + .02 school + .08 insurance = yes )
```

[1] to produce only estimates greater than 0

Confidence Intervals around coefficients

```
> confint(mod_5)
                            2.5 %       97.5 %
count_(Intercept)      1.35906781  1.453849989
count_hospital         0.14708813  0.170846838
count_healthexcellent -0.36473054 -0.242623743
count_healthpoor       0.21881501  0.288227575
count_chronic          0.09247176  0.110968673
count_sexmale         -0.08783320 -0.036660471
count_school           0.01541018  0.022746684
count_insuranceyes     0.04728775  0.114470242
zero_(Intercept)      -0.23095748  0.317251001
zero_hospital          0.13323624  0.491660923
zero_healthexcellent  -0.56922139 -0.009919046
zero_healthpoor       -0.32431694  0.306885255
zero_chronic           0.44627272  0.624152555
zero_sexmale          -0.58736685 -0.243949220
zero_school            0.03504270  0.082039766
zero_insuranceyes      0.54939962  0.944840005
```

Exponentiated Coefficients

```
> exp(coef(mod_5))
     count_(Intercept)         count_hospital
             4.0814769              1.1722998
count_healthexcellent       count_healthpoor
             0.7380991              1.2885548
         count_chronic          count_sexmale
             1.1070737              0.9396509
          count_school    count_insuranceyes
             1.0192616              1.0842397
      zero_(Intercept)          zero_hospital
             1.0440911              1.3667677
 zero_healthexcellent        zero_healthpoor
             0.7485852              0.9913220
          zero_chronic           zero_sexmale
             1.7078113              0.6599059
           zero_school     zero_insuranceyes
             1.0602887              2.1109114
```

Exponentiated Confidence Intervals

```
> exp(confint(mod_5))
                            2.5 %    97.5 %
count_(Intercept)       3.8925630 4.2795591
count_hospital          1.1584561 1.1863090
count_healthexcellent   0.6943837 0.7845667
count_healthpoor        1.2446010 1.3340609
count_chronic           1.0968822 1.1173599
count_sexmale           0.9159136 0.9640034
count_school            1.0155295 1.0230074
count_insuranceyes      1.0484236 1.1212793
zero_(Intercept)        0.7937732 1.3733472
zero_hospital           1.1425199 1.6350296
zero_healthexcellent    0.5659659 0.9901300
zero_healthpoor         0.7230211 1.3591850
zero_chronic            1.5624775 1.8666634
zero_sexmale            0.5557888 0.7835274
zero_school             1.0356639 1.0854990
zero_insuranceyes       1.7322127 2.5724018
```

Two Specific Variables

after exponentiation. . .

Coefficient	Logistic	Truncated Poisson
`chronic`	1.71 (1.56, 1.87)	1.11 (1.10. 1.12)
`sex` = male	0.66 (0.56, 0.78)	0.94 (0.92, 0.96)

Comparison to ZIP model

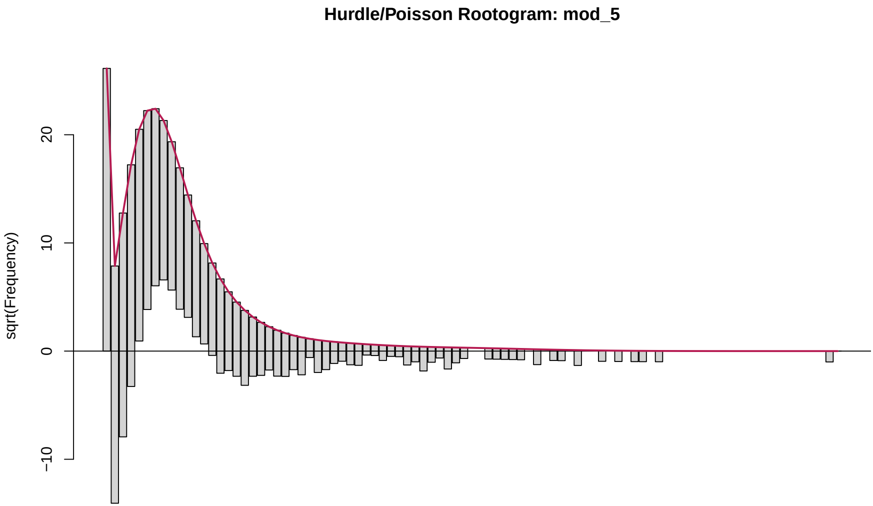
```r
vuong(mod_3, mod_5)
```

```
Vuong Non-Nested Hypothesis Test-Statistic:
(test-statistic is asymptotically distributed N(0,1) under the
 null that the models are indistinguishible)
-------------------------------------------------------------
              Vuong z-statistic             H_A  p-value
Raw                    2.190241 model1 > model2 0.014253
AIC-corrected          2.190241 model1 > model2 0.014253
BIC-corrected          2.190241 model1 > model2 0.014253
```

- Looks like the ZIP model may fit a little better than this Hurdle model.

Rootogram for Hurdle/Poisson

```
countreg::rootogram(mod_5, max = 90,
                    main = "Hurdle/Poisson Rootogram: mod_5")
```



Save Fitted Values and Residuals

```
mod_5_aug <- medicare %>%
    mutate(fitted = fitted(mod_5, type = "response"),
           resid = resid(mod_5, type = "response"))

mod_5_aug %>%
    dplyr::select(visits, fitted, resid) %>%
    head(2)
```

```
# A tibble: 2 x 3
  visits fitted  resid
   <int>  <dbl>  <dbl>
1      5   5.98 -0.981
2      1   6.05 -5.05
```

Pseudo-R^2 for Hurdle/Poisson model (`mod_5`)

Squared correlation of the fitted values and the observed values.

```
mod5_r <- with(mod_5_aug, cor(visits, fitted))
mod5_r^2
```

```
[1] 0.1073668
```

Model 6: The Hurdle Model (Negative Binomial)

Hurdle Model (Negative Binomial-Logistic)

```
mod_6 <- hurdle(visits ~ hospital + health + chronic +
                  sex + school + insurance,
              dist = "negbin", zero.dist = "binomial",
              data = medicare)
```

Comparison to ZINB model

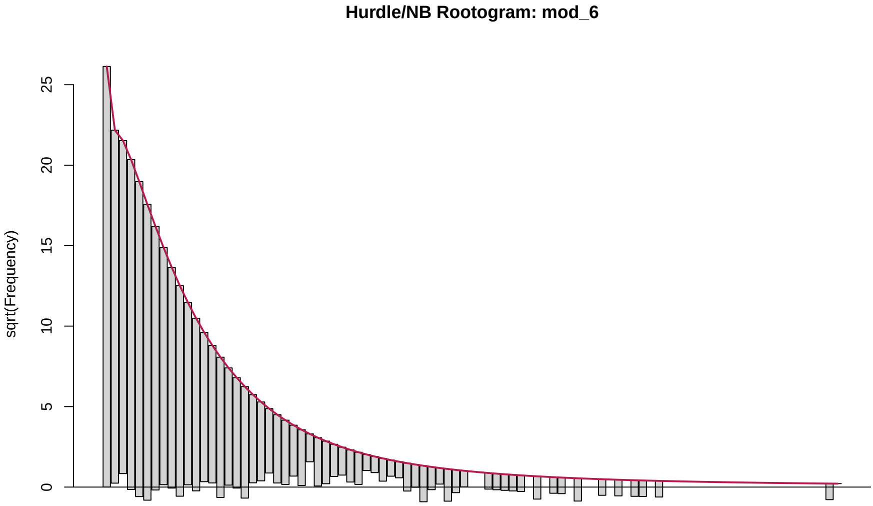
```r
vuong(mod_4, mod_6)
```

```
Vuong Non-Nested Hypothesis Test-Statistic:
(test-statistic is asymptotically distributed N(0,1) under the
 null that the models are indistinguishible)
-------------------------------------------------------------
              Vuong z-statistic             H_A p-value
Raw                   -0.391012 model2 > model1 0.34789
AIC-corrected         -0.391012 model2 > model1 0.34789
BIC-corrected         -0.391012 model2 > model1 0.34789
```

- No significant difference between ZINB and this Hurdle model.

Rootogram for Hurdle/Negative Binomial

```
countreg::rootogram(mod_6, max = 90,
                    main = "Hurdle/NB Rootogram: mod_6")
```



Save Fitted Values and Residuals

```
mod_6_aug <- medicare %>%
    mutate(fitted = fitted(mod_6, type = "response"),
           resid = resid(mod_6, type = "response"))

mod_6_aug %>%
    dplyr::select(visits, fitted, resid) %>%
    head(2)
```

```
# A tibble: 2 x 3
  visits fitted resid
   <int>  <dbl> <dbl>
1      5   6.07 -1.07
2      1   5.94 -4.94
```

Pseudo-R^2 for Hurdle/NB model (`mod_6`)

Squared correlation of the fitted values and the observed values.

```
mod6_r <- with(mod_6_aug, cor(visits, fitted))
mod6_r^2
```

```
[1] 0.09223186
```

So Far ...

Model	Pseudo-R^2	Rootogram?	Comments
Poisson	0.099	Many problems.	Data appear overdispersed.
Neg. Bin.	0.083	Better.	Still not enough zeros.
ZIP	0.107	Not good.	0's fine, not enough 1-3.
ZINB	0.096	Better.	Zeros not a perfect fit.
Hurdle (P)	0.107	Like ZIP	Not enough 1-3.
Hurdle (NB)	0.092	Like ZINB	Exact on 0.

Model 7: The Tobit (Censored Regression) Model

The Tobit (Censored Regression) Model

The idea of the tobit model (sometimes called a censored regression model) is to estimate associations for outcomes where we can see either left-censoring (censoring from below) or right-censoring (censoring from above.)

- Here, we might think of a broader latent (unobserved) variable that describes good health.
- We have censoring from below (at 0) where a person with good health (or better) has value 0.
- All of the people with better-than-good health take the same value (0) for visits.

The tobit model postulates that the value 0 in our model is just the lower limit of the underlying measure of poor physical health that we would actually observe in the population if we had a stronger measure.

Fitting the Tobit Model (uses `VGAM::vglm`)

```
mod_7 <- vglm(visits ~ hospital + health + chronic +
                  sex + school + insurance,
                  tobit(Lower = 0),
                  type.fitted = "censored",
                  data = medicare)
```

Summary of Model 7

```
> summary(mod_7)

Call:
vglm(formula = visits ~ hospital + health + chronic + sex + school +
    insurance, family = tobit(Lower = 0), data = medicare, type.fitted = "censored")


Pearson residuals:
             Min      1Q   Median      3Q    Max
mu       -12.188 -0.4716  0.04917 0.53947  9.892
loge(sd)  -1.013 -0.8205 -0.66567 0.08536 74.700

Coefficients:
                Estimate Std. Error z value Pr(>|z|)
(Intercept):1   -0.33163    0.39892  -0.831    0.406
(Intercept):2    1.96495    0.01306 150.484  < 2e-16 ***
hospital         1.73811    0.15121  11.495  < 2e-16 ***
healthexcellent -1.73968    0.43529  -3.997 6.42e-05 ***
healthpoor       1.91404    0.35897   5.332 9.71e-08 ***
chronic          1.22040    0.08913  13.693  < 2e-16 ***
sexmale         -0.93035    0.22770  -4.086 4.39e-05 ***
school           0.18937    0.03203   5.912 3.38e-09 ***
insuranceyes     1.68072    0.28739   5.848 4.97e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Number of linear predictors:  2

Names of linear predictors: mu, loge(sd)

Log-likelihood: -13198.82 on 8803 degrees of freedom

Number of iterations: 7
```

Detailed Coefficient Summary

```
Coefficients:
                 Estimate Std. Error z value Pr(>|z|)    
(Intercept):1    -0.33163    0.39892  -0.831    0.406    
(Intercept):2     1.96495    0.01306 150.484  < 2e-16 ***
hospital          1.73811    0.15121  11.495  < 2e-16 ***
healthexcellent -1.73968    0.43529  -3.997 6.42e-05 ***
healthpoor        1.91404    0.35897   5.332 9.71e-08 ***
chronic           1.22040    0.08913  13.693  < 2e-16 ***
sexmale          -0.93035    0.22770  -4.086 4.39e-05 ***
school            0.18937    0.03203   5.912 3.38e-09 ***
insuranceyes      1.68072    0.28739   5.848 4.97e-09 ***
---
```

Confidence Intervals for Coefficients

```
> confint(mod_7)
                     2.5 %     97.5 %
(Intercept):1    -1.113509  0.4502458
(Intercept):2     1.939359  1.9905434
hospital          1.441756  2.0344698
healthexcellent  -2.592820 -0.8865337
healthpoor        1.210463  2.6176118
chronic           1.045715  1.3950864
sexmale          -1.376642 -0.4840553
school            0.126586  0.2521463
insuranceyes      1.117443  2.2440013
```

Fitted Equation

Using the `type.fitted = "censored"` approach, we'll get predictions limited to visit counts of 0 and larger. If the model below yields predicted visits < 0, we will fit 0. The model equation is:

```
visits = -0.33 + 1.74 hospital - 1.74 health = Excellent
       + 1.91 health = Poor + 1.22 chronic - 0.93 sex = M
       + 0.19 school + 1.68 insurance = yes
```

Tobit model regression coefficients are interpreted as we would a set of OLS coefficients, except that the linear effect is on the **uncensored latent variable**, rather than on the observed outcome.

Save Fitted Values and Residuals

```
mod_7_aug <- medicare %>%
    mutate(fitted = fitted(mod_7, type.fitted = "censored"),
           resid = visits - fitted)

mod_7_aug %>%
    dplyr::select(visits, fitted, resid) %>%
    head(2)
```

```
# A tibble: 2 x 3
  visits fitted[,1] resid[,1]
   <int>      <dbl>     <dbl>
1      5       5.73    -0.734
2      1       5.68    -4.68
```

Rootogram? Not really. Table?

```
table(mod_7_aug$visits, round(mod_7_aug$fitted,0))
```

	0	1	2	3	4	5	6	7	8	9	10	11	12
0	67	71	104	136	117	88	42	20	15	7	7	4	0
1	21	29	59	85	111	77	42	26	14	3	4	2	2
2	10	20	52	68	113	66	43	30	9	7	4	2	3
3	7	25	40	75	82	66	55	29	14	11	6	5	2
4	7	10	32	57	69	65	55	34	22	19	8	0	2
5	4	3	23	41	63	78	42	40	14	9	7	7	3
6	2	3	15	34	54	48	43	27	15	13	7	4	1
7	3	1	7	16	30	40	46	18	22	15	5	3	6
8	4	6	8	12	26	28	38	22	15	6	4	5	4
9	1	2	4	16	19	32	27	21	18	15	7	7	1
10	0	2	9	9	19	24	19	9	13	11	1	6	2
11	2	1	4	17	14	19	16	15	5	6	6	4	1
12	0	1	5	6	9	14	14	15	9	2	1	4	3
13	0	1	4	2	8	14	13	6	8	7	3	2	2

Tables of Observed and Fitted `visits` from Tobit

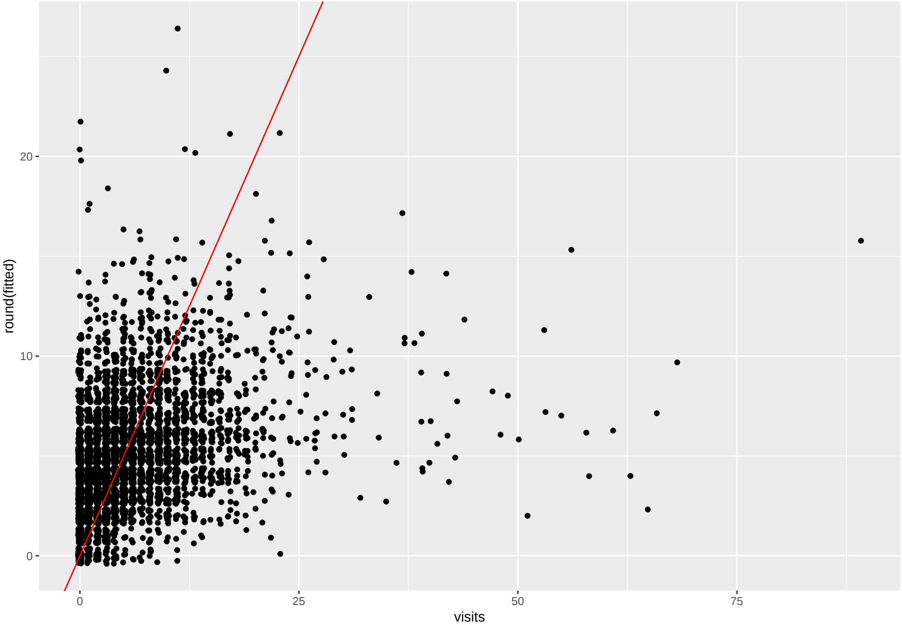
```
addmargins(table(round(mod_7_aug$fitted,0)))
```

```
   0    1    2    3    4    5    6    7    8    9   10   11
 129  179  381  593  784  704  563  368  235  162  101   79
  12   13   14   15   16   17   18   20   21   22   24   26
  44   28   18   15    8    3    3    4    2    1    1    1
 Sum
4406
```

```
addmargins(table(mod_7_aug$visits))
```

```
   0    1    2    3    4    5    6    7    8    9   10   11
 683  481  428  420  383  338  268  217  188  171  128  115
  12   13   14   15   16   17   18   19   20   21   22   23
  86   73   76   53   47   48   30   24   16   18   16   10
  24   25   26   27   28   29   30   31   32   33   34   35
  12    3    9    7    4    3    4    4    1    1    2    1
```

Plot?



Pseudo-R^2 for Tobit model (mod_7)

Squared correlation of the fitted values and the observed values.

```
mod7_r <- with(mod_7_aug, cor(visits, fitted))
mod7_r^2
```

```
          [,1]
[1,] 0.1242918
```

Next Time

Modeling Multi-Categorical Outcomes