Modelling Count Variables with R

PART 1: Poisson Regression

- Poisson regression is used to model count variables.
- Poisson regression has a number of extensions useful for count models.

Examples of Poisson regression

- The number of awards earned by students at a secondary or high school.
- Predictors of the number of awards earned include the type of program in which the student was enrolled (e.g., vocational, general or academic) and the score on their final exam in math.

Conventional OLS regression

- Count outcome variables are sometimes log-transformed and analyzed using OLS regression.
- Many issues arise with this approach, including loss of data due to undefined values generated by taking the log of zero (which is undefined) and biased estimates.

Description of the data

- For the purpose of illustration, we have simulated a data set for the last example.
- The data set is called poisreg.csv
- In this example, num_awards is the outcome variable and indicates the number of awards earned by students at a high school in a year.

Predictor Variables

- math is a continuous predictor variable and represents students' scores on their math final exam,
- prog is a categorical predictor variable with three levels indicating the type of program in which the students were enrolled.
- prog is coded as 1 = "General", 2 = "Academic" and 3 = "Vocational".

```
id
                num_awards
                                                 math
                                    prog
           Min. :0.00
                         General
                                  : 45
                                        Min. :33.0
           1st Qu.:0.00 Academic :105
                                         1st Qu.:45.0
          Median: 0.00 Vocational: 50
                                        Median:52.0
4
          Mean :0.63
                                         Mean :52.6
5
           3rd Qu.:1.00
                                         3rd Qu.:59.0
6
           Max. :6.00
                                         Max. :75.0
  (Other):194
```

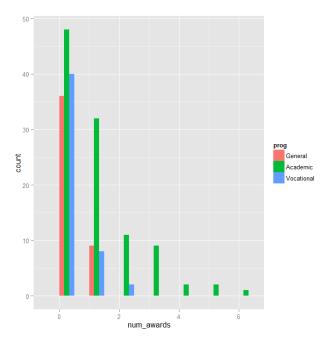


Figure:

- ► Each variable has 200 valid observations and their distributions seem quite reasonable.
- ► The mean and variance of our outcome variable are more or less the same.
- Our model assumes that these values, conditioned on the predictor variables, will be equal (or at least roughly so).

Poisson regression

- ► At this point, we are ready to perform our Poisson regression model analysis using the glm() function.
- We fit the model and save it in the object model1 and get a summary of the model.

```
model1 <- glm(num_awards ~ prog + math,
family="poisson", data=poisreg)
summary(model1)</pre>
```

```
Call:
glm(formula = num_awards ~ prog + math,
     family = "poisson",
     data = poisreg)
Deviance Residuals:
Min 1Q Median 3Q Max
-2.204 -0.844 -0.511 0.256 2.680
```

Signif. codes:

```
Coefficients:
Estimate Std. Error z value Pr(>|z|)
(Intercept) -5.2471 0.6585 -7.97 1.6e-15 ***
progAcademic 1.0839 0.3583 3.03 0.0025 **
progVocational 0.3698 0.4411 0.84 0.4018
math 0.0702 0.0106 6.62 3.6e-11 ***
```

0 '*** 0.001 '** 0.01 '* 0.05 '. ' 0.1 '

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 287.67 on 199 degrees of freedom Residual deviance: 189.45 on 196 degrees of freedom ATC: 373.5

Number of Fisher Scoring iterations: 6

- The output begins with echoing the function call. Then the information on deviance residuals is displayed.
- Deviance residuals are approximately normally distributed if the model is specified correctly.
- Here it shows a little bit of skeweness since median is not quite zero.

- ► The Poisson regression coefficients for each of the variables along with the standard errors, z-scores, p-values and 95% confidence intervals for the coefficients.
- The coefficient for math is 0.07.
- ► This means that the expected log count for a one-unit increase in math is 0.07.

Signif. codes:

```
Coefficients:
Estimate Std. Error z value Pr(>|z|)
(Intercept) -5.2471 0.6585 -7.97 1.6e-15 ***
progAcademic 1.0839 0.3583 3.03 0.0025 **
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math 0.0702 0.0106 6.62 3.6e-11 ***
```

0 '*** 0.001 '** 0.01 '* 0.05 '. ' 0.1 '

- The indicator variable progAcademic compares between prog = Academic and prog =
 "General", the expected log count for prog = Academic increases by about 1.1.
- The indicator variable prog.Vocational is the expected difference in log count (≈ 0.37) between prog = "Vocational" and the reference group (prog = "General").

- ► The output above indicates that the incident rate for prog = "Academic" is 2.96 times the incident rate for the reference group (prog = "General").
- Likewise, the incident rate for prog = "Vocational" is 1.45 times the incident rate for the reference group holding the other variables at constant.

► The percent change in the incident rate of num_awards is by 7% for every unit increase in math.

Deviance

- In statistics, deviance is a quality of fit statistic for a model that is often used for statistical hypothesis testing.
- ► It is a generalization of the idea of using the sum of squares of residuals in ordinary least squares to cases where model-fitting is achieved by maximum likelihood.

- The information on deviance is also provided.
- We can use the residual deviance to perform a goodness of fit test for the overall model.
- The residual deviance is the difference between the deviance of the current model and the maximum deviance of the ideal model where the predicted values are identical to the observed.

- Therefore, if the residual difference is small enough, the goodness of fit test will not be significant, indicating that the model fits the data.
- REMARK: Model Appraisal for GLMs subject of future talk.

- If the test had been statistically significant, it would indicate that the data do not fit the model well.
- We could try to determine if there are omitted predictor variables, if our linearity assumption holds and/or if there is an issue of over-dispersion.

Comparing Candidate Models

- We can also test the overall effect of prog by comparing the deviance of the full model with the deviance of the model excluding prog.
- The two degree-of-freedom chi-square test indicates that prog, taken together, is a statistically significant predictor of num_awards.

Comparing Models

```
# update m1 model dropping prog
m2 <- update(m1, . ~ . - prog)</pre>
```

test model differences with chi square test
anova(m2, m1, test="Chisq")

```
Analysis of Deviance Table
```

```
Model 1: num_awards ~ math

Model 2: num_awards ~ prog + math

Resid. Df Resid. Dev Df Deviance Pr(>Chi)

1    198    204

2    196    189    2    14.6    0.00069 ***
---

Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1
```

Incident Rate Ratios

- Sometimes, we might want to present the regression results as incident rate ratios (IRRs) and their standard errors, together with the confidence interval.
- To compute the standard error for the incident rate ratios, we will use the **Delta method** (Numerical Computation Method).
- ➤ To this end, we make use the function deltamethod implemented in R package msm.

Incident Rate Ratios

A rate ratio (sometimes called an incidence density ratio) in epidemiology, is a relative difference measure used to compare the incidence rates of events occurring at any given point in time. A common application for this measure in analytic epidemiologic studies is in the search for a causal association between a certain risk factor and an outcome.

Incidence Rate Ratio = $\frac{\text{Incidence Rate 1}}{\text{Incidence Rate 2}}$

Incident Rate Ratios

Incidence rate is the occurrence of an event over person-time, for example person-years.

Incidence Rate =
$$\frac{\text{events}}{\text{Person Time}}$$

Note: the same time intervals must be used for both incidence rates.

Delta Method

```
s <- deltamethod(list(~ exp(x1), ~ exp(x2), ~ exp(x3), ~ exp(
```

```
rexp.est

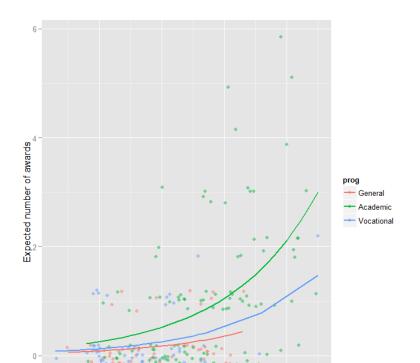
Estimate Robust SE LL UL
(Intercept) 0.005263 0.00340 0.001484 0.01867
progAcademic 2.956065 0.94904 1.575551 5.54620
progVocational 1.447458 0.57959 0.660335 3.17284
math 1.072672 0.01119 1.050955 1.09484
```

- Sometimes, we might want to look at the expected marginal means.
- For example, what are the expected counts for each program type holding math score at its overall mean?
- ➤ To answer this question, we can make use of the predict function.
- First off, we will make a small data set to apply the predict function to it.

```
(s1 <- data.frame(math = mean(p$math),</pre>
 prog = factor(1:3, levels = 1:3,
 labels = levels(p$prog))))
   math
               prog
1 52.65 General
2 52.65 Academic
3 52.65 Vocational
```

```
predict(m1, s1, type="response", se.fit=TRUE)
 $fit
 0.2114 0.6249 0.3060
 $se.fit
 0.07050 0.08628 0.08834
 $residual.scale
 [1] 1
```

- ▶ In the output above, we see that the predicted number of events for level 1 of prog is about 0.21, holding math at its mean.
- ► The predicted number of events for level 2 of prog is higher at 0.62, and the predicted number of events for level 3 of prog is about .31.
- ▶ The ratios of these predicted counts $(\frac{0.625}{0.211} = 2.96, \frac{0.306}{0.211} = 1.45)$ match what we saw looking at the IRR.



- We can also graph the predicted number of events with the commands below.
- ► The graph indicates that the most awards are predicted for those in the academic program (prog = 2), especially if the student has a high math score.
- The lowest number of predicted awards is for those students in the general program (prog = 1).
- ➤ The graph overlays the lines of expected values onto the actual points, although a small amount of random noise was added vertically to lessen overplotting.

Over-Dispersion

- Overdispersion is the presence of greater variability in a data set than would be expected based on a given simple statistical model.
- Poisson Distribution:

Zero-Inflation

- One common cause of over-dispersion is excess zeros, which in turn are generated by an additional data generating process.
- In this situation, zero-inflated model should be considered.
- If the data generating process does not allow for any 0s (such as the number of days spent in the hospital), then a zero-truncated model may be more appropriate.

Over-Dispersion

- When there seems to be an issue of dispersion, we should first check if our model is appropriately specified, such as omitted variables and functional forms.
- For example, if we omitted the predictor variable prog in the example above, our model would seem to have a problem with over-dispersion.
- ▶ In other words, a misspecified model could present a symptom like an over-dispersion problem.

- Assuming that the model is correctly specified, the assumption that the conditional variance is equal to the conditional mean should be checked.
- There are several tests including the likelihood ratio test of over-dispersion parameter alpha by running the same model using negative binomial distribution.
- ➤ The R package **pscl** (Political Science Computational Laboratory, Stanford University) provides many functions for binomial and count data including odTest for testing over-dispersion.

The odTest() command (pscl package)

- ► The function odTest is a likelihood ratio test for over-dispersion in count data
- odTest() Compares the log-likelihoods of a negative binomial regression model and a Poisson regression model.

```
odTest(glmobj, alpha=.05,
  digits = max(3, getOption("digits") - 3))
```

Exposure Variables - SKIP

- Count data often have an exposure variable, which indicates the number of times the event could have happened.
- This variable should be incorporated into a Poisson model with the use of the offset option.
- ► The outcome variable in a Poisson regression cannot have negative numbers, and the exposure cannot have 0s.

Some Remarks

- Many different measures of pseudo-R-squared exist. They all attempt to provide information similar to that provided by R-squared in OLS regression, even though none of them can be interpreted exactly as R-squared in OLS regression is interpreted.
- Poisson regression is estimated via maximum likelihood estimation. It usually requires a large sample size.

Coursera Course: The crabs data set The crabs data set is derived from Agresti (2007, Table 3.2, pp.76-77). It gives 4 variables for each of 173 female horseshoe crabs.

- Satellites number of male partners in addition to the female's primary partner
- ▶ Width width of the female in centimeters
- Dark a binary factor indicating whether the female has dark coloring (yes or no)
- ► **GoodSpine** a binary factor indicating whether the female has good spine condition (yes or no)

```
require(glm2)
data(crabs)
head(crabs)
summary(crabs[,1:4])
```

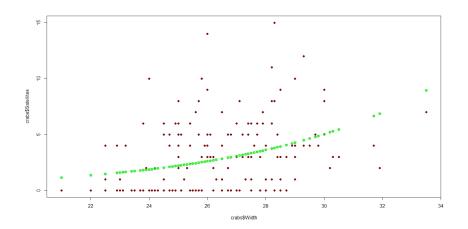
```
> head(crabs)
Satellites Width Dark GoodSpine Rep1 Rep2
              28.3
1
                                      2
                     no
                                nο
                                           5
             22.5
                   yes
                                      4
                                no
3
           9 26.0
                                      5
                                           6
                     no
                               yes
           0 24.8 yes
4
                                           6
                                      6
                                no
5
             26.0
                    yes
                                      6
                                           8
                                no
```

```
> summary(crabs[,1:4])
Satellites
          Width
                          Dark GoodSpine
Min. : 0.000
              Min. :21.0 no:107 no:121
1st Qu.: 0.000
              1st Qu.:24.9 yes: 66 yes: 52
Median : 2.000
              Median: 26.1
Mean : 2.919
              Mean :26.3
3rd Qu.: 5.000
              3rd Qu.:27.7
Max. :15.000
              Max. :33.5
```

- ► Fit a Poisson regression model with the number of Satellites as the outcome and the width of the female as the covariate.
- What is the multiplicative change in the expected number of crabs for each additional centimeter of width?

```
crabs.pois <- glm2(Satellites ~ Width,
data=crabs, family="poisson")
summary(crabs.pois)
exp(0.164)</pre>
```

```
> summary(crabs.pois)
Call:
glm2(formula = Satellites ~ Width,
family = "poisson", data = crabs)
Coefficients:
Estimate Std. Error z value Pr(>|z|)
Width 0.16405
                  0.01997 8.216 < 2e-16 ***
```



Code for Crabs Data Plot

```
plot(crabs$Width, crabs$Satellites,
pch=16, col="darkred")
points(crabs$Width, crabs.pois$fitted.values,
col="green", lwd=3)
```

Poisson Regression "Exposure" and offset

- Poisson regression may also be appropriate for rate data, where the rate is a count of events occurring to a particular unit of observation, divided by some measure of that unit's exposure.
- For example, biologists may count the number of tree species in a forest, and the rate would be the number of species per square kilometre.
- Demographers may model death rates in geographic areas as the count of deaths divided by personyears.
- More generally, event rates can be calculated as events per unit time, which allows the observation window to vary for each unit.

Poisson Regression: Exposure and Offset

In these examples, exposure is respectively unit area, personyears and unit time. In Poisson regression this is handled as an offset, where the exposure variable enters on the right-hand side of the equation, but with a parameter estimate (for log(exposure)) constrained to 1.

$$\log (\mathsf{E}(Y\mid x)) = \log (\mathsf{exposure}) + \theta' x$$

which implies

$$\log (\mathsf{E}(Y\mid x)) - \log (\mathsf{exposure}) = \log \left(\frac{\mathsf{E}(Y\mid x)}{\mathsf{exposure}}\right) = \theta' x$$

Poisson Regression: Exposure and Offset

Offset in the case of a GLM in R can be achieved using the offset() function:

```
glm(y ~ offset(log(exposure)) + x, family=po
```