S02 - Poisson Regression

STAT 401 (Engineering) - Iowa State University

April 23, 2018

Linear regression

For continuous Y_i, we have linear regression

$$\begin{aligned} &Y_i \stackrel{ind}{\sim} N(\mu_i, \sigma^2) \\ &\mu_i = \beta_0 + \beta_1 X_{i,1} + \cdots + \beta_p X_{i,p} \end{aligned}$$

For binary or count with an upper maximum Y_i, we have logistic regression

$$\begin{gathered} Y_i \stackrel{ind}{\sim} Bin(n_i, \theta_i) \\ \log\left(\frac{\theta_i}{1-\theta_i}\right) = \beta_0 + \beta_1 X_{i,1} + \cdots + \beta_p X_{i,p} \end{gathered}$$

What if Y_i is a count without a maximum?

Poisson regression

Let $Y_i \in \{0, 1, 2, \ldots\}$ be a count (typically over some amount of time or some amount of space) with associated explanatory variables $X_{i,1}, \ldots, X_{i,p}$.

Then a Poisson regression model is

$$Y_i \stackrel{ind}{\sim} Po(\lambda_i)$$

and

$$\log(\lambda_i) = \beta_0 + \beta_1 X_{i,1} + \beta_2 X_{i,2} + \cdots + \beta_p X_{i,p}$$

Interpretation

When all explanatory variables are zero, then

$$E[Y_i|X_{i,1} = 0, \ldots, X_{i,p} = 0] = \lambda_i = e^{\beta_0}$$

thus β_0 determines the expected response when all explanatory variables are zero.

More generally,

$$E[Y_i|X_{i,1} = x_1, \ldots, X_{i,p} = x_p] = e^{\beta_0 + \beta_1 x_1 + \cdots + \beta_p x_p}.$$

If $X_{i,1}$ increases by one unit, we have

$$E[Y_i|X_{i,1} = x_1 + 1, \ldots, X_{i,p} = x_p] = e^{\beta_0 + \beta_1 (x_1+1) + \cdots + \beta_p x_p} = e^{\beta_0 + \beta_1 x_1 + \cdots + \beta_p x_p} e^{\beta_1}$$

Thus

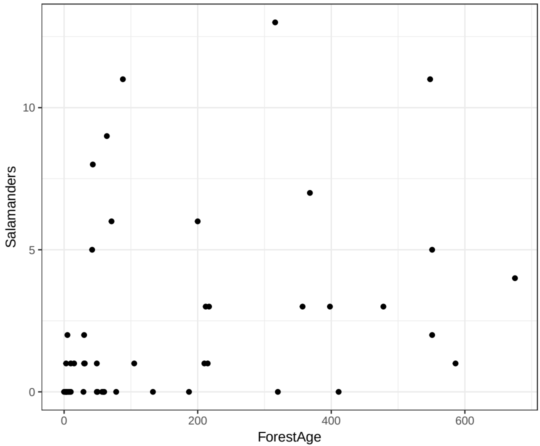
$$\frac{E[Y_i|X_{i,1} = x_1 + 1, \ldots, X_{i,p} = x_p]}{E[Y_i|X_{i,1} = x_1 \quad, \ldots, X_{i,p} = x_p]} = e^{\beta_1}.$$

Thus e^{β_p} is the multiplicative effect on the mean response for a one unit increase in the associated explanatory variable when holding all other explanatory variables constant.

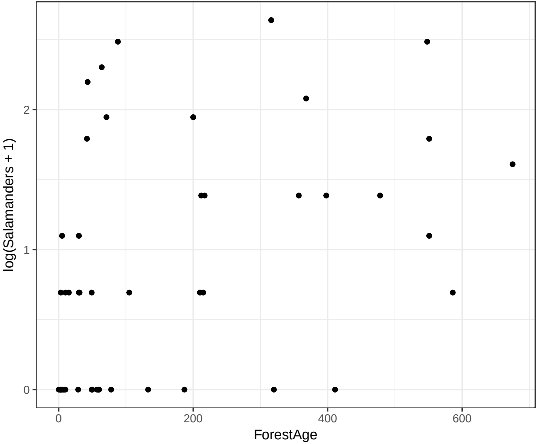
Salamander habitat

The Del Norte Salamander (plethodon elongates) is a small (57 cm) salamander found among rock rubble, rock outcrops and moss-covered talus in a narrow range of northwest California. To study the habitat characteristics of the species and particularly the tendency of these salamanders to reside in dwindling old-growth forests, researchers selected 47 sites from plausible salamander habitat in national forest and parkland. Randomly chosen grid points were searched for the presence of a site with suitable rocky habitat. At each suitable site, a 7 metre by 7 metre search are was examined for the number of salamanders it contained.

```
ggplot(Sleuth3::case2202, aes(ForestAge, Salamanders)) +
  geom_point() +
  theme_bw()
```



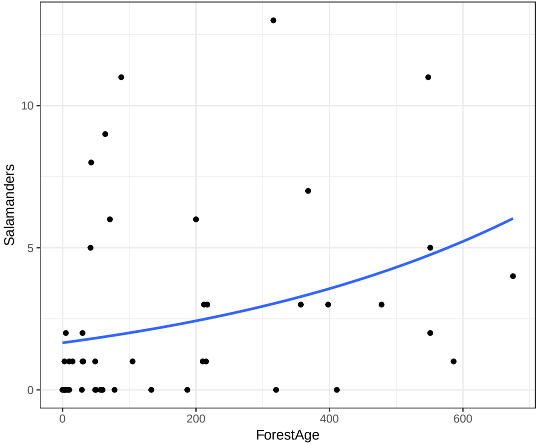
```
ggplot(Sleuth3::case2202, aes(ForestAge, log(Salamanders+1))) +
  geom_point() +
  theme_bw()
```



Analysis

```
m <- glm(Salamanders ~ ForestAge,
         data = Sleuth3::case2202,
         family = "poisson")

summary(m)


Call:
glm(formula = Salamanders ~ ForestAge, family = "poisson", data = Sleuth3::case2202)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.6970  -1.8539  -0.7987   0.2144   4.4582

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) 0.5040207  0.1401385   3.597 0.000322 ***
ForestAge   0.0019151  0.0004155   4.609 4.05e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 190.22  on 46  degrees of freedom
Residual deviance: 170.65  on 45  degrees of freedom
AIC: 259.7

Number of Fisher Scoring iterations: 6
```

```
ggplot(Sleuth3::case2202, aes(ForestAge, Salamanders)) +
  geom_point() +
  stat_smooth(method="glm",
              se=FALSE,
              method.args = list(family="poisson"))  +
  theme_bw()
```



Salamander habitat (cont.)

```
m <- glm(Salamanders ~ ForestAge * PctCover,
         data = Sleuth3::case2202,
         family = "poisson")

summary(m)


Call:
glm(formula = Salamanders ~ ForestAge * PctCover, family = "poisson",
    data = Sleuth3::case2202)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.9710  -1.3237  -0.7378   0.6114   3.9136

Coefficients:
                     Estimate Std. Error z value Pr(>|z|)
(Intercept)        -1.388e+00  5.038e-01  -2.754  0.00588 **
ForestAge          -2.812e-03  6.799e-03  -0.414  0.67918
PctCover            3.147e-02  6.145e-03   5.121 3.04e-07 ***
ForestAge:PctCover  3.141e-05  7.625e-05   0.412  0.68033
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 190.22  on 46  degrees of freedom
Residual deviance: 121.13  on 43  degrees of freedom
AIC: 214.19

Number of Fisher Scoring iterations: 6
```

Offset

If not all counts are based on the same amount of time or space, we need to account for the amount of time or space used. To do this, we can include an offset.

Let T_i represent the amount of time or space, then a Poisson regression model with an offset is

$$Y_i \stackrel{ind}{\sim} Po(\lambda_i)$$

and

$$\log(\lambda_i) = \log(T_i) + \beta_0 + \beta_1 X_{i,1} + \beta_2 X_{i,2} + \cdots + \beta_p X_{i,p}.$$

The offset is $\log(T_i)$ and can be thought of as an explanatory variable with a known coefficient of 1. Note that

$$\log E[Y_i/T_i] = \beta_0 + \beta_1 X_{i,1} + \beta_2 X_{i,2} + \cdots + \beta_p X_{i,p}$$

so we are effectively modeling the rate.

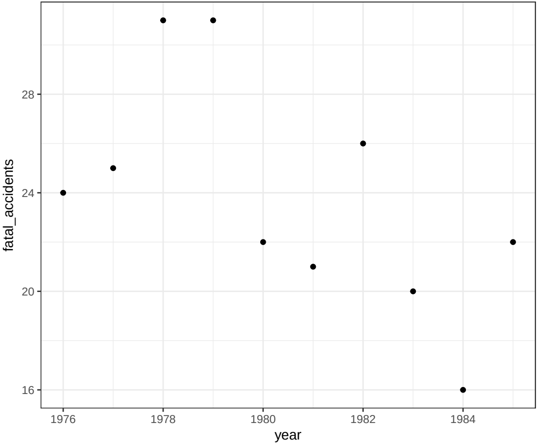
Airline crash data

When considering airline crash data, we need to account for the fact that airlines are (typically) flying more miles year over year.

```
airline = data.frame(year=1976:1985,
                     fatal_accidents = c(24,25,31,31,22,21,26,20,16,22),
                     passenger_deaths = c(734,516,754,877,814,362,764,809,223,1066),
                     death_rate = c(0.19,0.12,0.15,0.16,0.14,0.06,0.13,0.13,0.03,0.15)) %>%
  mutate(miles_flown = passenger_deaths / death_rate)

airline


   year fatal_accidents passenger_deaths death_rate miles_flown
1  1976              24              734       0.19    3863.158
2  1977              25              516       0.12    4300.000
3  1978              31              754       0.15    5026.667
4  1979              31              877       0.16    5481.250
5  1980              22              814       0.14    5814.286
6  1981              21              362       0.06    6033.333
7  1982              26              764       0.13    5876.923
8  1983              20              809       0.13    6223.077
9  1984              16              223       0.03    7433.333
10 1985              22             1066       0.15    7106.667
```

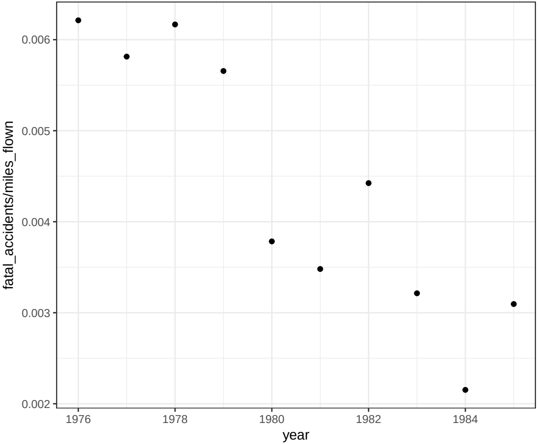
Visualize airline crash data

```
ggplot(airline, aes(year, fatal_accidents)) +
  geom_point() +
  scale_x_continuous(breaks= scales::pretty_breaks()) +
  theme_bw()
```



Visualize airline crash data

```
ggplot(airline, aes(year, fatal_accidents/miles_flown)) +
  geom_point() +
  scale_x_continuous(breaks= scales::pretty_breaks()) +
  theme_bw()
```



Offset in R

```
m <- glm(fatal_accidents ~ year + offset(log(miles_flown)),
         data = airline,
         family = "poisson")

summary(m)


Call:
glm(formula = fatal_accidents ~ year + offset(log(miles_flown)),
    family = "poisson", data = airline)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.2829  -0.5813  -0.1230   0.7254   1.0211

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) 201.32854   45.62354   4.413 1.02e-05 ***
year         -0.10442    0.02304  -4.532 5.84e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 26.133  on 9  degrees of freedom
Residual deviance:  5.457  on 8  degrees of freedom
AIC: 59.426

Number of Fisher Scoring iterations: 4
```

Offset in R

```
m <- glm(fatal_accidents ~ year + log(miles_flown),
         data = airline,
         family = "poisson")

confint(m) # No evidence coefficient for log(miles_flown) is incompatible with 1


                         2.5 %       97.5 %
(Intercept)      -134.5369352 415.57465599
year               -0.2192575   0.07628503
log(miles_flown)   -1.6508503   2.64154996
```

Likelihood ratio tests

To compare nested generalized linear models, we use likelihood ratio tests.

Suppose we have a model $p(y|\theta)$ for our data and two hypotheses

- $H_0 : \theta = \theta_0$ and
- $H_A : \theta \neq \theta_0$.

Then the likelihood is $L(\theta) = p(y|\theta)$ and the likelihood ratio statistics is

$$\lambda = \frac{L(\theta_0)}{L\left(\hat{\theta}_{MLE}\right)} = \frac{p(y|\theta_0)}{p\left(y\middle|\hat{\theta}_{MLE}\right)}.$$

Asymptotically (as we have more data) under H_0,

$$\text{deviance} = -2\log(\lambda) \stackrel{d}{\to} \chi^2_v$$

where χ^2_v is a chi-squared distribution with v degrees of freedom and v is the number of parameters in θ, i.e. the number of parameters set to a known value. The pvalue is

$$pvalue = P\left(\chi^2_v > -2\log(\lambda)\right).$$

χ^2-distributions

If $X \sim \chi^2_v$, then X has a chi-squared distribution with v degrees of freedom.

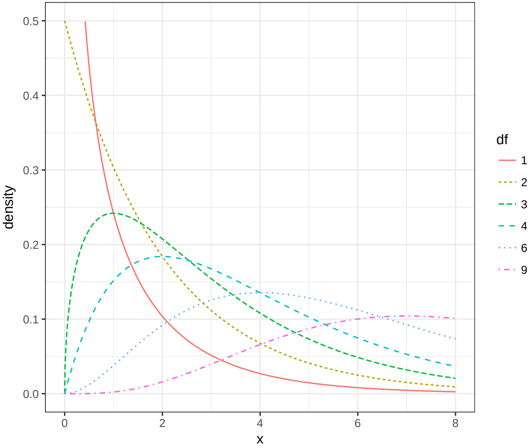
The probability density function is

$$p(x) = \frac{1}{2^{\frac{v}{2}}\Gamma\left(\frac{v}{2}\right)} x^{\frac{v}{2}-1} e^{-\frac{x}{2}}$$

with support $x \in [0, \infty)$. We have

$$\begin{aligned} E[X] &= v \\ Var[X] &= 2v. \end{aligned}$$

χ^2-distribution visualization



Likelihood ratio tests in R

```
m <- glm(Salamanders ~ ForestAge * PctCover,
         data = Sleuth3::case2202,
         family = "poisson")

anova(m, test="Chi")
```

```
Analysis of Deviance Table

Model: poisson, link: log

Response: Salamanders

Terms added sequentially (first to last)


                   Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
NULL                                  46     190.22
ForestAge           1   19.573        45     170.65 9.681e-06 ***
PctCover            1   49.342        44     121.30 2.150e-12 ***
ForestAge:PctCover  1    0.170        43     121.13    0.6797
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```