# Assignment 2 MATH 523

## YUNHEUM DAN SEOL 2018-02-19

### **A5**

Given a Gamma GLM, we deal with response that has a conditional distribution

$$f(y|\alpha, \beta_i) = \begin{cases} \frac{\beta^{\alpha}}{\Gamma(\alpha)} y^{\alpha - 1} e^{(-\beta y)}; \ y > 0\\ 0 & y \le 0 \end{cases}$$

then we know

$$\mathbb{E}[Y_i] = \frac{\alpha}{\beta} \quad \mathbb{VAR}[Y_i] = \frac{\alpha}{\beta^2}$$

and from class we know

$$I(\beta) = \mathbb{X}^{\mathsf{T}} W \mathbb{X} = [I_{jk}]$$

where

$$I_{jk} = \sum_{i=1}^{n} \left(x_{ij} \left(\frac{\left(\frac{\partial \mu_i}{\partial \eta_i}\right)^2 x_{ik}}{\operatorname{Var}[Y_i]}\right)\right)$$

$$\left(\frac{\partial \mu_i}{\partial \eta_i}\right)^2 \qquad \beta^2$$

$$W = \operatorname{diag}[W_1, ..., W_n]; \quad W_i = \frac{\left(\frac{\partial \mu_i}{\partial \eta_i}\right)^2}{\operatorname{Var}[Y_i]} = \frac{\beta^2}{\alpha(g'(\mu_i))^2}$$

$$I(\beta) = \begin{bmatrix} 1 & \cdots & \cdots & 1 \\ x_1 & \cdots & \cdots & x_n \end{bmatrix} \begin{bmatrix} W_1 & 0 & \cdots & 0 \\ 0 & W_2 & \cdots & 0 \\ 0 & \cdots & \cdots & 0 \\ 0 & \cdots & \cdots & W_n \end{bmatrix} \begin{bmatrix} 1 & x_1 \\ 1 & x_2 \\ \cdots & \cdots \\ 1 & x_n \end{bmatrix}$$

$$= \begin{bmatrix} \frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} & \frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i} \\ \frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i} & \frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i}^{2} \end{bmatrix}$$

for an arbitrary link

when the canonical link is used, i.e.

$$g(\mu_i) = \frac{1}{\mu_i}; g'(\mu_i) = -\frac{1}{\mu_i^2} \implies (\frac{1}{g'(\mu_i)})^2 = \mu_i^4 = \frac{\alpha^4}{\beta_i^4}$$

Our expected information matrix gets to be simplified as

$$\begin{bmatrix} \alpha^3 \sum_{i=1}^n \frac{1}{\beta_i^2} & \alpha^3 \sum_{i=1}^n \frac{x_i}{\beta_i^2} \\ \alpha^3 \sum_{i=1}^n \frac{x_i}{\beta^2} & \alpha^3 \sum_{i=1}^n \frac{x_i^2}{\beta_i^2} \end{bmatrix} = \begin{bmatrix} \alpha \sum_{i=1}^n \mu_i^2 & \alpha \sum_{i=1}^n \mu_i^2 x_i \\ \alpha \sum_{i=1}^n \mu_i^2 x_i & \alpha \sum_{i=1}^n \mu_i^2 x_i^2 \end{bmatrix}$$

##(b) From class, we know

$$\widehat{\beta} \sim_{app} N(\beta, I(\beta)^{-1})$$

as

$$n \to \infty$$

Therefore once we find the variance-covariance matrix  $I(\beta)^{-1}$  The asymptotic variances will be its diagonal entries.

$$\begin{bmatrix} \frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} & \frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i} \\ \frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i} & \frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i}^{2} \end{bmatrix}^{-1}$$

$$= \frac{1}{(\frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}})(\frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i}^{2}) - (\frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i})^{2}} \begin{bmatrix} \frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i}^{2} & -\frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i} \\ -\frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i} & \frac{1}{\alpha} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i} \end{bmatrix}$$

$$= \frac{\alpha^{2}}{(\sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}})(\sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i}^{2}) - (\sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i})^{2}} \frac{1}{\alpha} \begin{bmatrix} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i}^{2} & -\sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i} \\ -\sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i} & \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i} \end{bmatrix}$$

$$= \frac{\alpha}{(\sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}})(\sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i}^{2}) - (\sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i})^{2}} \begin{bmatrix} \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i}^{2} & -\sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i} \\ -\sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i} & \sum_{i=1}^{n} \frac{\beta_{i}^{2}}{g'(\mu_{i})^{2}} x_{i} \end{bmatrix}$$

Since we have acquired the variance-covariance matrix, thus

$$\mathbb{Vol}[\widehat{\beta_0}] = \frac{\alpha \sum_{i=1}^n \frac{\beta_i^2}{g'(\mu_i)^2} x_i^2}{(\sum_{i=1}^n \frac{\beta_i^2}{g'(\mu_i)^2})(\sum_{i=1}^n \frac{\beta_i^2}{g'(\mu_i)^2} x_i^2) - (\sum_{i=1}^n \frac{\beta_i^2}{g'(\mu_i)^2} x_i)^2}$$

$$\mathbb{Vol}[\widehat{\beta_1}] = \frac{\alpha \sum_{i=1}^n \frac{\beta_i^2}{g'(\mu_i)^2}}{(\sum_{i=1}^n \frac{\beta_i^2}{g'(\mu_i)^2})(\sum_{i=1}^n \frac{\beta_i^2}{g'(\mu_i)^2} x_i^2) - (\sum_{i=1}^n \frac{\beta_i^2}{g'(\mu_i)^2} x_i)^2}$$

If you use canonical link,

$$\begin{split} \left[ \frac{\alpha \sum_{i=1}^{n} \mu_{i}^{2}}{\alpha \sum_{i=1}^{n} \mu_{i}^{2} x_{i}} \right]^{-1} &= \frac{\alpha}{(\alpha \sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2})} = \frac{\alpha}{(\alpha \sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2}) - (\alpha \sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2})} \left[ \frac{\sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2}}{-\sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2}} \right]^{-1} \\ &= \frac{\alpha}{\alpha^{2} [(\sum_{i=1}^{n} \mu_{i}^{2})(\sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2}) - (\sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2}) - (\alpha \sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2})^{-1} \left[ \sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2} \right] \\ &= \frac{\alpha}{\alpha^{2} [(\sum_{i=1}^{n} \mu_{i}^{2})(\sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2}) - (\sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2})^{-1} \left[ \sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2} \right] \\ &= \frac{1}{\alpha [(\sum_{i=1}^{n} \mu_{i}^{2})(\sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2}) - (\sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2})} \left[ \sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2} - \sum_{i=1}^{n} \mu_{i}^{2} x_{i} \right] \\ &= \frac{1}{\alpha [(\sum_{i=1}^{n} \mu_{i}^{2})(\sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2}) - (\sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2}) - (\sum_{i=1}^{n} \mu_{i}^{2} x_{i}^{2})^{-1} \right]} \end{split}$$
 and

and

(c)

It is analogous to the setting of A2, thus we can classify our data into two groups such that

$$x_i = \begin{cases} 1 \text{ if } i = 1, ..., n_A \\ 0 \text{ if } i = n_A + 1, ..., n_A + n_B = n \end{cases}$$

 $VAR[\widehat{\beta_1}] = \frac{\sum_{i=1}^{n} \mu_i^2}{\alpha[(\sum_{i=1}^{n} \mu_i^2)(\sum_{i=1}^{n} \mu_i^2 x_i^2) - (\sum_{i=1}^{n} \mu_i^2 x_i)^2]}$ 

From class, we know

$$\widehat{\beta} = (\mathbb{X}^{\mathsf{T}} W \mathbb{X})^{-1} \mathbb{X}^{\mathsf{T}} W \mathbf{Y}$$

where

$$\begin{split} \mathbb{X}^{\mathsf{T}}WY &= \begin{bmatrix} 1 & \dots & 1 \\ x_1 & \dots & x_n \end{bmatrix} \begin{bmatrix} W_1 & 0 & \dots & 0 \\ 0 & W_2 & \dots & 0 \\ 0 & \dots & \dots & 0 \\ 0 & \dots & \dots & W_n \end{bmatrix} \begin{bmatrix} y_1 \\ y_2 \\ \dots \\ y_n \end{bmatrix} = \begin{bmatrix} \alpha \sum_{i=1}^n \mu_i^2 y_i \\ \alpha \sum_{i=1}^n \mu_i^2 x_i y_i \end{bmatrix} \\ &= \alpha \begin{bmatrix} \sum_{i=1}^n \mu_i^2 x_i \\ \sum_{i=1}^n \mu_i^2 x_i y_i \end{bmatrix} \\ &\Rightarrow (\mathbb{X}^{\mathsf{T}}W\mathbb{X})^{-1} \mathbb{X}^{\mathsf{T}}WY = \\ &= \frac{1}{\alpha[(\sum_{i=1}^n \mu_i^2)(\sum_{i=1}^n \mu_i^2 x_i^2) - (\sum_{i=1}^n \mu_i^2 x_i)^2]} \begin{bmatrix} \sum_{i=1}^n \mu_i^2 x_i^2 & -\sum_{i=1}^n \mu_i^2 x_i \\ -\sum_{i=1}^n \mu_i^2 x_i & -\sum_{i=1}^n \mu_i^2 x_i \end{bmatrix} \alpha \begin{bmatrix} \sum_{i=1}^n \mu_i^2 y_i \\ \sum_{i=1}^n \mu_i^2 x_i y_i \end{bmatrix} \\ &= \frac{\alpha}{\alpha[(\sum_{i=1}^n \mu_i^2)(\sum_{i=1}^n \mu_i^2 x_i^2) - (\sum_{i=1}^n \mu_i^2 x_i)^2]} \begin{bmatrix} \sum_{i=1}^n \mu_i^2 x_i^2 & -\sum_{i=1}^n \mu_i^2 x_i \\ -\sum_{i=1}^n \mu_i^2 x_i & -\sum_{i=1}^n \mu_i^2 x_i \end{bmatrix} \begin{bmatrix} \sum_{i=1}^n \mu_i^2 y_i \\ \sum_{i=1}^n \mu_i^2 x_i y_i \end{bmatrix} \\ &= \frac{1}{[(\sum_{i=1}^n \mu_i^2)(\sum_{i=1}^n \mu_i^2 x_i^2) - (\sum_{i=1}^n \mu_i^2 x_i)^2]} \begin{bmatrix} \sum_{i=1}^n \mu_i^2 x_i^2 & -\sum_{i=1}^n \mu_i^2 x_i \\ -\sum_{i=1}^n \mu_i^2 x_i & -\sum_{i=1}^n \mu_i^2 x_i \end{bmatrix} \begin{bmatrix} \sum_{i=1}^n \mu_i^2 y_i \\ \sum_{i=1}^n \mu_i^2 x_i y_i \end{bmatrix} \end{aligned}$$

under our setting, this is equivalent to

$$\begin{split} \frac{1}{[(\sum_{i=1}^{n}\mu_{i}^{2})(\sum_{i=1}^{n_{A}}\mu_{i}^{2}) - (\sum_{i=1}^{n_{A}}\mu_{i}^{2})^{2}]} \begin{bmatrix} \sum_{i=1}^{n_{A}}\mu_{i}^{2} & -\sum_{i=1}^{n_{A}}\mu_{i}^{2} \\ -\sum_{i=1}^{n_{A}}\mu_{i}^{2} & \sum_{i=1}^{n_{A}}\mu_{i}^{2} \end{bmatrix} \begin{bmatrix} \sum_{i=1}^{n}\mu_{i}^{2}y_{i} \\ \sum_{i=1}^{n_{A}}\mu_{i}^{2} & \sum_{i=1}^{n_{A}}\mu_{i}^{2} \end{bmatrix} \\ = \frac{1}{[(\sum_{i=1}^{n_{A}}\mu_{i}^{2} + \sum_{i=n_{A}+1}^{n_{A}+n_{B}}\mu_{i}^{2})(\sum_{i=1}^{n_{A}}\mu_{i}^{2}) - (\sum_{i=1}^{n_{A}}\mu_{i}^{2})^{2}]} \begin{bmatrix} \sum_{i=1}^{n_{A}}\mu_{i}^{2} & -\sum_{i=1}^{n_{A}}\mu_{i}^{2} \\ -\sum_{i=1}^{n_{A}}\mu_{i}^{2} & \sum_{i=1}^{n_{A}}\mu_{i}^{2} \end{bmatrix} \begin{bmatrix} \sum_{i=1}^{n_{A}}\mu_{i}^{2} \\ \sum_{i=1}^{n_{A}}\mu_{i}^{2} & \sum_{i=1}^{n_{A}}\mu_{i}^{2} \end{bmatrix} \begin{bmatrix} \sum_{i=1}^{n_$$

$$\begin{split} \frac{1}{[(\sum_{i=n_A+1}^{n_A+n_B}\mu_i^2)(\sum_{i=1}^{n_A}\mu_i^2)]} & \left[ (\sum_{i=1}^{n_A}\mu_i^2)$$

from A2 we know that we can estimate group means as below

$$\widehat{\mu_A} = \bar{y_A} = \frac{1}{n_A} \sum_{i=1}^{n_A} y_i$$

$$\widehat{\mu_B} = \bar{y_B} = \frac{1}{n_B} \sum_{i=n_A+1}^{n_A+n_B} y_i$$

so our  $\beta$  can be estimated as

$$\begin{bmatrix} \frac{(\sum_{i=n_A+1}^{n_A+n_B} \bar{y_B}^2 y_i)}{[(\sum_{i=n_A+1}^{n_A} \bar{y_B}^2)]} \\ \frac{(\sum_{i=1}^{n_A} \bar{y_A}^2 y_i)}{[(\sum_{i=1}^{n_A} \bar{y_A}^2)]} - \frac{(\sum_{i=n_A}^{n_A+n_B} \bar{y_B}^2 y_i)}{[(\sum_{i=n_A+1}^{n_A+n_B} \bar{y_B}^2)]} \end{bmatrix} = \begin{bmatrix} (\sum_{i=n_A+1}^{n_A+n_B} y_i) \\ (\sum_{i=1}^{n_A} y_i) - (\sum_{i=n_A+1}^{n_A+n_B} y_i) \end{bmatrix}$$

And they will have variance

$$\mathbb{VAR}[\widehat{\beta_0}] = \frac{\sum_{i=1}^{n_A} \mu_i^2}{\alpha[(\sum_{i=1}^n \mu_i^2)(\sum_{i=1}^{n_A} \mu_i^2) - (\sum_{i=1}^{n_A+n_B} \mu_i^2)]} = \frac{\sum_{i=1}^{n_A} \mu_i^2}{\alpha(\sum_{i=1}^{n_A} \mu_i^2)(\sum_{i=n_A+1}^{n_A+n_B} \mu_i^2)} = \frac{1}{\alpha(\sum_{i=n_A+1}^{n_A+n_B} \mu_i^2)}$$

$$\mathbb{VAR}[\widehat{\beta_1}] = \frac{\sum_{i=1}^n \mu_i^2}{\alpha[(\sum_{i=1}^n \mu_i^2)(\sum_{i=1}^n \mu_i^2 x_i^2) - (\sum_{i=1}^n \mu_i^2 x_i)^2]} = \frac{\sum_{i=1}^n \mu_i^2}{\alpha(\sum_{i=1}^{n_A} \mu_i^2)(\sum_{i=n_A+1}^{n_A+n_B} \mu_i^2)}$$

##(d) if you use the log link

$$g(\mu_i) = \ln(\mu_i) \implies g'(\mu_i) = \frac{1}{\mu_i} \implies \frac{1}{g'(\mu_i)} = \mu_i$$

$$W_i = \frac{\beta^2}{\alpha(g'(\mu_i))^2} = \frac{\beta^2}{\alpha} * \mu_i^2 = \frac{\beta^2}{\alpha} * \frac{\alpha^2}{\beta^2} = \alpha$$

Thus

$$W = \alpha I$$

where I is the n\*n identity matrix. so our  $\widehat{\beta}$  would be

$$\widehat{\beta} = (\mathbb{X}^{\mathsf{T}} W \mathbb{X})^{-1} \mathbb{X}^{\mathsf{T}} W \mathbf{Y}$$

where

$$(\mathbb{X}^\intercal W \mathbb{X})^{-1} = [\alpha(\mathbb{X}^\intercal I \mathbb{X})]^{-1} = [\alpha(\mathbb{X}^\intercal \mathbb{X})]^{-1} = \frac{1}{\alpha} \begin{bmatrix} n & n_A \\ n_A & n_A \end{bmatrix}^{-1} = \frac{1}{\alpha} \begin{bmatrix} n_A & -n_A \\ -n_A & n \end{bmatrix}$$

and

$$\mathbb{X}^\intercal W \mathbf{Y} = \alpha \mathbb{X}^\intercal \mathbf{Y} = \alpha \begin{bmatrix} \sum_{i=1}^n y_i \\ \sum_{i=1}^{n} y_i \end{bmatrix}$$

then

$$\widehat{\beta} = \begin{bmatrix} n_A & -n_A \\ -n_A & n \end{bmatrix} \begin{bmatrix} \sum_{i=1}^n y_i \\ \sum_{i=1}^n y_i \end{bmatrix} = \begin{bmatrix} n_A \sum_{i=1}^n y_i - n_A \sum_{i=1}^{n_A} y_i \\ -n_A \sum_{i=1}^n y_i + n \sum_{i=1}^{n_A} y_i \end{bmatrix} = \begin{bmatrix} n_A \sum_{i=n_A+1}^n y_i \\ n_B \sum_{i=1}^{n_A} y_i - n_A \sum_{i=n_A+1}^n y_i \end{bmatrix}$$

##(e) Deviance for

$$Y_i \sim \Gamma(\alpha, \beta)$$

with  $Y_i$  independent We know the formula for deviance for GLM of data distributed according to a pdf in exponential dispersion family (without weight) is

$$D(y, \bar{\mu}) = 2\sum_{i=1}^{n} \{y_i \tilde{\theta}_i - y_i \hat{\theta}_i - b(\tilde{\theta}_i) + b(\hat{\theta}_i)\}$$

where

$$\theta = -\frac{1}{\mu}, \ b(\theta) = ln(\mu)$$

At saturated model  $\tilde{\theta}_i = -\frac{1}{y_i}$  whereas in the model with p parameters we have  $\hat{\theta}_i = -\frac{1}{\widehat{\mu}_i}$  so the deviance would be

$$D(y,\bar{\mu}) = 2\sum_{i=1}^n \{-(y_i)\frac{1}{y_i} + \frac{y_i}{\widehat{\mu_i}} - \ln(\frac{1}{y_i}) + \ln(\frac{1}{\widehat{\mu_i}})\} = 2\sum_{i=1}^n \{\frac{y_i}{\widehat{\mu_i}} - 1 + \ln(\frac{y_i}{\widehat{\mu_i}})\}$$

##(f) Pearson residual:

$$r_{pi} = \frac{r_i}{\sqrt{v(\mu_i)}} = \frac{y_i - \widehat{\mu_i}}{\sqrt{v(\mu_i)}}$$

. For a Gamma GLM, we have

$$\mu_i = \frac{\alpha}{\beta_i}, \mathbb{VAR}[Y_i] = \frac{\alpha}{\beta_i^2}, a(\phi) = \frac{1}{\alpha}$$

Since

$$\mathbb{VAR}[Y_i] = a(\phi)v(\mu_i) = \frac{1}{\alpha}v(\mu_i) \implies v(\mu_i) = \alpha \mathbb{VAR}[Y_i] = \frac{\alpha^2}{\beta_i^2} = \mu_i^2$$

So our pearson residual would be of the form

$$\frac{y_i - \widehat{\mu}_i}{\sqrt{v(\mu_i)}} = \frac{y_i - \widehat{\mu}_i}{\sqrt{\widehat{\mu}_i^2}} = \frac{y_i - \widehat{\mu}_i}{\widehat{\mu}_i}$$

Anscombe residual:

$$r_{Ai} = \frac{A(y_i) - A(\widehat{\mu_i})}{\sqrt{\{A'(\mu_i)\}^2 \ v(\mu_i)}}$$

where

$$A(y) = \int_0^y \frac{1}{(v(\mu))^{\frac{1}{3}}} d\mu = \int_0^y \frac{1}{(\mu^2)^{\frac{1}{3}}} d\mu = \int_0^y \mu^{\frac{-2}{3}} d\mu = 3\mu^{\frac{1}{3}}|_0^y = 3y^{\frac{1}{3}}$$

So our residual would be

$$\begin{split} \frac{A(y_i) - A(\widehat{\mu_i})}{\sqrt{\{A'(\mu_i)\}^2 \ v(\mu_i)}} &= \frac{3y_i^{\frac{1}{3}} - 3\widehat{\mu_i}^{\frac{1}{3}}}{\sqrt{(\frac{d}{d\mu_i} 3\mu_i^{\frac{1}{3})^2} \widehat{\mu_i}^2}} = \frac{3y_i^{\frac{1}{3}} - 3\widehat{\mu_i}^{\frac{1}{3}}}{\sqrt{(\widehat{\mu_i}^{\frac{-2}{3}})^2 \widehat{\mu_i}^2}} &= \frac{3y_i^{\frac{1}{3}} - 3\widehat{\mu_i}^{\frac{1}{3}}}{\sqrt{\widehat{\mu_i}^{\frac{2}{3}}}} \\ &= \frac{3y_i^{\frac{1}{3}} - 3\widehat{\mu_i}^{\frac{1}{3}}}{\widehat{\mu_i}^{\frac{1}{3}}} \end{split}$$

Deviance Residual

$$r_{di} = \sqrt{2\omega_i(y_i(\tilde{\theta}_i - \widehat{\theta}_i) - b(\tilde{\theta}_i) + b(\widehat{\theta}_i))} = \sqrt{2(\frac{y_i}{\widehat{\mu}_i} - 1 + ln(\frac{y_i}{\widehat{\mu}_i}))} sgn(y_i - \widehat{\mu}_i)$$

#A6 (canonical link assumed) Since for normal GLM,

$$\theta = \mu; \ b(\theta) = \frac{\mu^2}{2}$$

The deviance for the normal GLM would be

$$D(y,\widehat{\mu}) = 2\sum_{i=1}^{n} (y_i(y_i - \widehat{\mu}_i) - \frac{y_i^2}{2} + \frac{\widehat{\mu}_i^2}{2}) = \sum_{i=1}^{n} (y_i^2 - 2y_i\widehat{\mu}_i + \widehat{\mu}_i^2)$$
$$= \sum_{i=1}^{n} (y_i - \widehat{\mu}_i)^2$$

So if we take the difference of deviances, it would be of the form

$$D(y, \tilde{\mu}) - D(y, \hat{\mu}) = \sum_{i=1}^{n} (y_i - \tilde{\mu}_i)^2 - \sum_{i=1}^{n} (y_i - \hat{\mu}_i)^2 = SS_{res}(\beta_0) - SS_{res}(\beta_1)$$

This is analogous to the difference between residual sum-of-squares used for model selection that we used in Classical Linear Regression. It helps us to choose a better model by using F test, using the statistics

$$\frac{[SS_{res}(\beta_0) - SS_{res}(\beta_1)]/(p_1 - p_0)}{SS_{res}/(n - p_1)} \sim Fisher - F_{p_1 - p_0, n - p_1}$$

```
\#A7
```

```
library(glmbb)
## Warning: package 'glmbb' was built under R version 3.3.2
data(crabs)
##the response is satell
head(crabs)
##
      color spine width satell weight y
## 1 medium
               bad
                    28.3
                                   3050 1
## 2
                    22.5
                               0
                                   1550 0
       dark
               bad
              good
## 3
      light
                    26.0
                               9
                                   2300 1
                               0
## 4
       dark
                    24.8
                                   2100 0
              bad
## 5
       dark
               bad
                    26.0
                                   2600 1
## 6 medium
               bad
                    23.8
                                   2100 0
summary(crabs)
##
                    spine
                                   width
                                                   satell
       color
                                                                      weight
##
    dark:44
                 bad
                       :121
                               Min.
                                      :21.0
                                               Min.
                                                       : 0.000
                                                                         :1200
                               1st Qu.:24.9
    darker:22
                                               1st Qu.: 0.000
                                                                 1st Qu.:2000
##
                 good: 37
##
    light:12
                 middle: 15
                               Median:26.1
                                               Median : 2.000
                                                                 Median:2350
    medium:95
##
                               Mean
                                      :26.3
                                               Mean
                                                       : 2.919
                                                                 Mean
                                                                         :2437
##
                               3rd Qu.:27.7
                                               3rd Qu.: 5.000
                                                                 3rd Qu.:2850
##
                               Max.
                                      :33.5
                                               Max.
                                                       :15.000
                                                                         :5200
                                                                 Max.
##
          у
            :0.0000
##
    Min.
    1st Qu.:0.0000
    Median :1.0000
##
##
    Mean
            :0.6416
    3rd Qu.:1.0000
##
##
    Max.
            :1.0000
dim(crabs)
## [1] 173
             6
#figure out what the data consists of
attach(crabs)
pairs(cbind(satell, weight, color))
```

```
2000
                                    3000 4000 5000
                                                                            15
                                 o
                                                                            10
                                                           0
                                                                  8
           satell
                                                                            2
                                                                  0
                                  weight
                        0
                       0
   000000000000
                       00
                            00000 00
                                o തരത്താ ത
                                                            color
                                                                            2.0
       000
              0 0 0
                            0
          5
                 10
                        15
                                                    1.0 1.5 2.0 2.5 3.0 3.5 4.0
                                                                              \#\#(a)
#linear model for comparison
lmfit_1 <- lm(satell~(weight+color)^2)</pre>
summary(lmfit_1)
##
## Call:
## lm(formula = satell ~ (weight + color)^2)
##
## Residuals:
               10 Median
                               3Q
## -4.5248 -2.1020 -0.6264 1.4040 11.1470
## Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
##
## (Intercept)
                     -2.685e+00 1.943e+00 -1.382
                                                    0.1688
## weight
                      2.137e-03 8.225e-04
                                            2.598
                                                    0.0102 *
## colordarker
                      2.881e-02 3.704e+00
                                            0.008
                                                    0.9938
## colorlight
                      8.961e+00 6.397e+00
                                            1.401
                                                    0.1631
## colormedium
                      1.266e+00 2.342e+00
                                            0.540
                                                    0.5897
## weight:colordarker 2.634e-05 1.642e-03
                                            0.016
                                                    0.9872
## weight:colorlight -2.971e-03 2.438e-03 -1.218
                                                    0.2249
## weight:colormedium -2.789e-04 9.633e-04 -0.290
                                                    0.7725
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 2.952 on 165 degrees of freedom
## Multiple R-squared: 0.1567, Adjusted R-squared: 0.121
## F-statistic: 4.382 on 7 and 165 DF, p-value: 0.0001748
#The responses are in discrete integers, so let's try poisson
mod1 <- glm(satell~(weight+factor(color))^2, family = poisson(link="log"))</pre>
```

```
summary(mod1)
##
## Call:
## glm(formula = satell ~ (weight + factor(color))^2, family = poisson(link = "log"))
## Deviance Residuals:
##
      Min
                1Q
                    Median
                                  3Q
                                          Max
## -2.9412 -1.8457 -0.6278 0.8346
                                       4.7689
##
## Coefficients:
                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                             -1.463e+00 4.851e-01 -3.016 0.00256 **
                              9.283e-04 1.839e-04
## weight
                                                    5.048 4.47e-07 ***
## factor(color)darker
                             -5.214e-02 9.050e-01 -0.058 0.95406
## factor(color)light
                              3.408e+00 1.127e+00 3.023 0.00250 **
## factor(color)medium
                              1.386e+00 5.345e-01
                                                     2.594 0.00949 **
## weight:factor(color)darker 5.232e-05 3.645e-04 0.144 0.88587
## weight:factor(color)light -1.134e-03 4.287e-04 -2.645 0.00818 **
## weight:factor(color)medium -4.466e-04 2.002e-04 -2.231 0.02570 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for poisson family taken to be 1)
##
      Null deviance: 632.79 on 172 degrees of freedom
## Residual deviance: 541.08 on 165 degrees of freedom
## AIC: 912.38
## Number of Fisher Scoring iterations: 6
(b)
# Fisher information at the last iteration
I <- (t(model.matrix(mod1))%*%diag(mod1$weights))%*%model.matrix(mod1)</pre>
# Inverse Fisher information matrix (i.e. as. covariance matrix of the MLEs)
I.inv <- solve(I)</pre>
dim(I.inv)
## [1] 8 8
# standard errors of the MLEs
sd <- sqrt(diag(I.inv))</pre>
beta <- coefficients(mod1)</pre>
```

```
p.val <- pchisq((beta/sd)^2,df=1,lower.tail=FALSE)
round(p.val,7)</pre>
```

```
##
                   (Intercept)
                                                    weight
##
                     0.0025591
                                                 0.000004
##
          factor(color)darker
                                        factor(color)light
##
                     0.9540605
                                                 0.0025003
##
          factor(color)medium weight:factor(color)darker
##
                     0.0094905
                                                 0.8858701
##
    weight:factor(color)light weight:factor(color)medium
                     0.0081774
##
                                                 0.0256999
```

Against the null hypothesis that the interaction of colorlyl and weight is not significant, we reject the null at  $\alpha = 0.05$  and conclude that we have sufficient evidence to conclude that the interaction factor is significant, except for the color level "darker." It seems that the interaction between weight and color is significant.

(c)

## [1] 0.00105761

```
# Checking the fit of the model using the deviance statistic
# Fitting other models
modb <- glm(satell~weight+factor(color), family=poisson(link=log))</pre>
modc <- glm(satell~weight, family=poisson(link=log))</pre>
modd <- glm(satell~factor(color), family=poisson(link=log))</pre>
anova (mod1)
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: satell
##
## Terms added sequentially (first to last)
##
##
##
                         Df Deviance Resid. Df Resid. Dev
## NULL
                                            172
                                                    632.79
                                                    560.87
## weight
                          1
                              71.925
                                            171
## factor(color)
                          3
                               9.061
                                            168
                                                    551.80
## weight:factor(color)
                          3
                              10.724
                                            165
                                                    541.08
deviance(modb)
## [1] 551.8049
deviance(modc)
## [1] 560.8664
# The saturated model v. our model
pchisq(deviance(mod1), df=169, lower.tail=FALSE)
## [1] 1.580598e-40
# The model with interaction v. the model without interaction
pchisq((deviance(modb)-deviance(mod1)),df=1,lower.tail=FALSE)
```

```
# The saturated model v. the model without interaction
pchisq(deviance(modb), df=170, lower.tail=FALSE)
## [1] 6.868553e-42
# The model with one predictor only
## weight only v. proposed model
pchisq((deviance(modc)-deviance(mod1)), df=2, lower.tail = FALSE)
## [1] 5.054307e-05
## color level only v. proposed model
pchisq((deviance(modd)-deviance(mod1)), df=2, lower.tail = FALSE)
```

## [1] 1.664875e-15

Under our null hypothesis that the nested model is an adequate simplification of the full model with more predictors, we get different results:

#### Model without the interaction v. model with interaction

We fail to reject the null hypothesis at  $\alpha = 0.05$ , and we conclude that we have failed to have sufficient evidence that the model with interaction explains the variation in response better. ###Other cases We can reject our null hypothesis at  $\alpha = 0.05$ , and we conclude that the saturated model might be a better fit.

(d)

```
We can try the "darker" factor level to the "dark" level (the base model) -
```

```
color_mod <- color</pre>
for(i in 1:length(color_mod)){
  if(color_mod[i] == "darker")
    color_mod[i] = "dark"
mod2 <- glm(satell~(weight+factor(color_mod))^2, family=poisson(link=log))</pre>
summary(mod2)
```

```
##
## Call:
## glm(formula = satell ~ (weight + factor(color_mod))^2, family = poisson(link = log))
##
## Deviance Residuals:
##
       Min
                 1Q
                     Median
                                   3Q
                                          Max
## -2.9412 -1.8470 -0.6278
                              0.8346
                                        4.7574
##
## Coefficients:
##
                                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                                 -1.4451144 0.4013956 -3.600 0.000318 ***
## weight
                                  0.0009299
                                             0.0001559
                                                         5.963 2.48e-09 ***
## factor(color mod)light
                                                         3.099 0.001941 **
                                  3.3893600 1.0936607
## factor(color mod)medium
                                  1.3682995 0.4598657
                                                         2.975 0.002926 **
## weight:factor(color_mod)light -0.0011354 0.0004175
                                                        -2.720 0.006536 **
## weight:factor(color_mod)medium -0.0004482 0.0001749 -2.563 0.010380 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

```
##
   (Dispersion parameter for poisson family taken to be 1)
##
##
       Null deviance: 632.79 on 172
##
                                         degrees of freedom
## Residual deviance: 541.27
                                on 167 degrees of freedom
   AIC: 908.57
##
## Number of Fisher Scoring iterations: 6
From the visual inspection of the table we can conclude that all of the predictors are significant. \#\#(e)
# Next, compute the Pearson residuals (these are NOT the standardized residuals)
r.pearson <- residuals(mod2, "pearson")</pre>
# Next, compute the deviance residuals
r.deviance <- residuals(mod2, "deviance")</pre>
par(mfrow=c(1,2))
plot(r.pearson~predict(mod2,type='link'), xlab=expression(hat(eta)), ylab="Pearson residuals", pch=19,
plot(r.deviance~predict(mod2, type="link"), xlab=expression(hat(eta)), ylab="Deviance residuals", pch=19,
       9
                                                  Deviance residuals
Pearson residuals
       4
                                                        \sim
       ^{\circ}
       0
                                                       7
      7
               0.0
                         1.0
                                   2.0
                                                                0.0
                                                                          1.0
                                                                                    2.0
                                                                           ή
# The saturated model v. the model without interaction
deviance (mod2)
## [1] 541.2675
deviance(mod1)
## [1] 541.081
pchisq(deviance(mod2), df=167, lower.tail=FALSE)
## [1] 4.547482e-41
```

#### pchisq(deviance(mod2)-deviance(mod1), df=1, lower.tail=FALSE)

#### ## [1] 0.6658662

The residual plot gets closer to a null plot if the approximate normality is assumed for the response. Even if the other pieces of evidence suggest that the model is a good fit, it is really hard to make a correct judgment based on the residual plot and deviance only since Poisson-distributed random variables do not necessarily behave normally when the mean is not large. That explains some evident "pattern" in our residual plot.

For the deviance test, against the null hypothesis that the simpler model is a better model compared to the saturated model, we reject the null at  $\alpha=0.05$  and claim to have gathered sufficient evidence against the null and say the saturated model might fit the model better. However, among the test between models mod1 and mod2, mod2 can explain the variation in response certainly better.