Assignment 1 - MATH 523 Generalized Linear Models

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The inverse Gaussian distribution has density of the form

$$f(y; \mu, \lambda) = (\frac{\lambda}{2\pi y^3})^{1/2} \exp(-\frac{\lambda(y-\mu)^2}{2\mu^2 y})$$

for

y > 0

and

 $\lambda > 0$

##(a)A random variable

$$Y \sim f(y; \theta, \lambda)$$

belongs to the exponential dispersion family if

$$f(y) = \exp(\frac{y\theta - b(\theta)}{a(\phi)} + c(y, \phi))$$

for some function

 $a(\cdot), b(\cdot)$

and

 $c(\cdot)$

We know if

$$Y \sim inv.Gaussian(y; \mu, \lambda)$$

then the density function of interest would be

$$f(y; \mu, \lambda) = (\frac{\lambda}{2\pi y^3})^{1/2} \exp(-\frac{\lambda(y-\mu)^2}{2\mu^2 y})$$

We use the property

$$x = e^{\ln(x)} \quad \forall x \in \mathbb{R}$$

then we obtain

$$(\frac{\lambda}{2\pi y^3})^{1/2} \exp(-\frac{\lambda (y-\mu)^2}{2\mu^2 y}) = \exp(\ln(\frac{\lambda}{2\pi y^3}^{1/2}) * \exp(-\frac{\lambda (y-\mu)^2}{2\mu^2 y}) = \exp(-\frac{\lambda (y-\mu)^2}{2\mu^2 y} + \frac{1}{2} \ln(\frac{\lambda}{2\pi y^3}))$$

and

$$\begin{split} &\exp(-\frac{\lambda(y-\mu)^2}{2\mu^2y} + \frac{1}{2}ln(\frac{\lambda}{2\pi y^3})) = \exp(-\frac{\lambda(y^2-2y\mu+\mu^2)}{2\mu^2y} + \frac{1}{2}ln(\frac{\lambda}{2\pi y^3})) \\ &= \exp(\lambda[\frac{-y^2}{2\mu^2y} + \frac{2y\mu}{2\mu^2y} + \frac{-\mu^2}{2\mu^2y}] + \frac{1}{2}ln(\frac{\lambda}{2\pi y^3})) = \exp(\lambda[\frac{-y}{2\mu^2} + \frac{1}{\mu} + \frac{-1}{2y}] + \frac{1}{2}ln(\frac{\lambda}{2\pi y^3})) \end{split}$$

and then we have

$$\exp(\lambda[\frac{-y}{2\mu^2} + \frac{1}{\mu} + \frac{-1}{2y}] + \frac{1}{2}ln(\frac{\lambda}{2\pi y^3})) = \exp(\frac{-\lambda y}{2\mu^2} + \frac{\lambda}{\mu} - \frac{\lambda}{2y} + \frac{1}{2}ln(\frac{\lambda}{2\pi y^3})) =$$

$$\begin{split} &\exp(\frac{-\lambda y}{2\mu^2} + \frac{\lambda}{\mu} + [-\frac{\lambda}{2y} + \frac{1}{2}ln(\frac{\lambda}{2\pi y^3})]) = \exp(\frac{\lambda}{2}[\frac{-y}{\mu^2} + \frac{2}{\mu}] + [-\frac{1}{2y} + \frac{1}{2}ln(\frac{\lambda}{2\pi y^3})]) = \\ &\exp(\frac{[\frac{-y}{\mu^2} + \frac{2}{\mu}]}{\frac{2}{\lambda}} + [-\frac{1}{2y} + \frac{1}{2}ln(\frac{\lambda}{2\pi y^3})]) = \exp(\frac{[y*(-\frac{1}{\mu^2}) + \frac{2}{\mu}]}{\frac{2}{\lambda}} + [-\frac{1}{2y} + \frac{1}{2}ln(\frac{\lambda}{2\pi y^3})]) \end{split}$$

then we have the canonical parameter λ and the dispersion parameter ϕ as below:

$$\theta = \frac{-1}{\mu^2}, \phi = \lambda$$

and we have obtained

$$a(\phi) = \frac{2}{\lambda}, b(\theta) = -2\sqrt{-\theta}, \ c(y, \phi) = \left[-\frac{1}{2y} + \frac{1}{2}ln(\frac{\lambda}{2\pi y^3})\right]$$

Since

φ

is unknown inverse Gaussian distribution belongs to the exponential dispersion family.

(b) from lectures we know

$$\mathbb{E}[Y] = b'(\theta) = \frac{d}{d\theta}[b(\theta)]$$

and

$$Var[Y] = a(\phi)b''(\theta) = a(\phi)v(\mu)$$

; for Inverse Gaussian we have obtained from part (a) that

$$a(\phi) = \frac{2}{\lambda}$$

,

$$b(\theta) = -\sqrt{-2\theta}$$

, and

$$\theta = \frac{-1}{\mu^2}$$

so

$$\begin{split} \frac{d}{d\theta}[b(\theta)] &= \frac{d}{d\theta}[-2\sqrt{-\theta}] = -2\frac{d}{d\theta}[\sqrt{-\theta}] = -2(\frac{1}{\sqrt{-\theta}})*(\frac{1}{2})*(-1) = \\ \frac{1}{\sqrt{-\theta}} &= (-\theta)^{-1/2} = (-(\frac{-1}{\mu^2}))^{-1/2} = (\frac{1}{\mu^2})^{-1/2} = (\mu^{-2})^{-1/2} = \mu \end{split}$$

and

$$b''(\theta) = \frac{d}{d\theta}[b'(\theta)] = \frac{d}{d\theta}[(-\theta)^{-1/2}] = \frac{-1}{2} * (-\theta)^{-3/2} * (-1) = \frac{1}{2} * (-\theta)^{-3/2} = \frac{1}{2} * (-\theta)^{-3/2} = \frac{1}{2} * (\mu^{-2})^{-3/2} = \frac{\mu^3}{2}$$

so we have

$$\mathbb{E}[Y] = \mu$$

,

$$v(\mu) = \frac{\mu^3}{2}$$

,

$$Var[Y] = a(\phi) * v\mu = \frac{2}{\lambda} * \frac{\mu^3}{2} = \frac{\mu^3}{\lambda}$$

.

(c) We have our

$$\theta = -\frac{1}{\mu^2}$$

. Since we can omit the negative sign by multiplying

 β_j

's by negative sign, we can take the canonical link function

as

$$\theta = g(\mu_i) = \frac{1}{\mu_i^2}$$

(Square-reciprocal) So our modeling assumption for inverse Gaussian distribtuion GLM using the canonical link would be

$$g(\mu_i) = \frac{1}{\mu_i^2} = \mathbb{X}\beta$$

This link function might not be as sensible as we think because $\frac{1}{x^2}$ is always positive if defined if $\mu \in \mathbb{R}^+$ but our estimators β_j 's can have negative components.

Therefore,

$$g(\mu) = \ln(\mu)$$

might be a much more reasonable choice.

(d) from class, we know that the score equations (likelihood equations) for any GLM using its canonical link would be of the form

$$\frac{\partial l(\theta)}{\partial \beta_j} = \sum_{i=1}^n \left[\frac{y_i - \mu_i}{\text{Var}[y_i]} \right] * \frac{1}{g'(\mu_i)} * x_{ij} = 0$$

$$\implies \frac{\partial l(\theta)}{\partial \beta_j} = \sum_{i=1}^n \left[\frac{y_i - \mu_i}{a(\phi)} x_{ij} \right] = 0$$

Since $a(\phi) = \frac{2}{\lambda}$ for Y ~ $inv.Gaussian(\mu, \lambda)$, our score equations would be of the form

$$\implies \frac{\partial l(\theta)}{\partial \beta_j} = \sum_{i=1}^n \frac{2}{\lambda} [y_i - \mu_i] x_{ij} = 0$$

##(e) (a GLM with inverse Gaussian responses and the canonical link assumed, since the generalization will be made in A2) We get

$$\frac{\partial l(\theta)}{\partial \beta_j} = \sum_{i=1}^n \frac{2}{\lambda} [y_i - \mu_i] x_{ij} = 0$$

$$\implies \frac{\partial l(\theta)}{\partial \beta_0} = \sum_{i=1}^n \frac{2}{\lambda} [y_i - \mu_i]$$

and

$$\frac{\partial l(\theta)}{\partial \beta_1} = \sum_{i=1}^n \frac{2}{\lambda} [y_i - \mu_i] x_i = \sum_{i=1}^{n_A} \frac{2}{\lambda} [y_i - \mu_i] + \sum_{i=n_A+1}^{n_A+n_B} \frac{2}{\lambda} [y_i - \mu_i] * 0 = 0$$

we have

$$g(\mu_i) = \beta_0 + \beta_1 x_i \implies \mu_i = g^{-1}(\beta_0 + \beta_1 x_i)$$

with our canonical link

$$g(x) = \frac{1}{x^2} \implies g^{-1}(x) = \frac{1}{\sqrt{x}}$$

so we will have

$$\mu_i = \frac{1}{\sqrt{\beta_0 + \beta_1 x_i}}$$

. For group A, $x_i = 1, i = 1, ..., n_A$ so we would have

$$\mu_i = \frac{1}{\sqrt{\beta_0 + \beta_1}}$$

For group B, $x_i = 0$, $i = n_A + 1, ..., n_A + n_B$, so we would have

$$\mu_i = \frac{1}{\sqrt{\beta_0}}$$

We know that with canonical link function

$$\sum_{i=1}^{n} y_i = \sum_{i=1}^{n} \mu_i = \sum_{i=1}^{n_A} y_i + \sum_{j=n_A+1}^{n_A+n_B} y_j = \sum_{i=1}^{n_A} \mu_i + \sum_{j=n_A+1}^{n_A+n_B} \mu_j = \frac{n_A}{\sqrt{\beta_0 + \beta_1}} + \frac{n_B}{\sqrt{\beta_0}}$$

then

our fitted group means would be

$$\widehat{\mu_{n_A}} = \frac{1}{n_A} \sum_{i=1}^{n_A} y_i = \frac{1}{n_A} \frac{n_A}{\sqrt{\beta_0 + \beta_1}} = \frac{1}{\sqrt{\beta_0 + \beta_1}}$$

$$\widehat{\mu_{n_A}} = \frac{1}{n_A} \sum_{i=1}^{n_A} y_i = \frac{1}{n_A} \frac{n_A}{\sqrt{\beta_0 + \beta_1}} = \frac{1}{\sqrt{\beta_0 + \beta_1}}$$

$$\widehat{\mu_{n_B}} = \frac{1}{n_B} \sum_{j=n_A+1}^{n_A+n_B} y_j = \frac{1}{n_B} \frac{n_B}{\sqrt{\beta_0}} = \frac{1}{\sqrt{\beta_0}}$$

.

2.

$$\frac{\partial l(\theta)}{\partial \beta_j} = \sum_{i=1}^n \left[\frac{y_i - \mu_i}{\text{Var}[y_i]} \right] * \frac{1}{g'(\mu_i)} * x_{ij} = 0$$

$$\implies \frac{\partial l(\theta)}{\partial \beta_0} = \sum_{i=1}^n \left[\frac{y_i - \mu_i}{\text{Var}[y_i]} \right] * \frac{1}{g'(\mu_i)} = 0$$

$$\implies \frac{\partial l(\theta)}{\partial \beta_1} = \sum_{i=1}^n \left[\frac{y_i - \mu_i}{\text{Var}[y_i]} \right] * \frac{1}{g'(\mu_i)} * x_i = 0 = \sum_{i=1}^{n_A} \frac{y_i - \mu_i}{\text{Var}[y_i]} * \frac{1}{g'(\mu_i)}$$

We know that $\frac{1}{g'(\mu_i)}$, $Var[Y_i]$ are nonzero, we know

$$\sum_{i=1}^{n} y_i = \sum_{i=1}^{n} \mu_i = \sum_{i=1}^{n_A} y_i + \sum_{j=n_A+1}^{n_A+n_B} y_j = \sum_{i=1}^{n_A} \mu_i + \sum_{j=n_A+1}^{n_A+n_B} \mu_j$$

and we have for $i = 1, ..., n_A$

$$\mu_i = g^{-1}(\beta_0 + \beta_1)$$

while for $j = n_A + 1, ..., n_A + n_B$ we have

$$\mu_j = g^{-1}(\beta_0)$$

It follows that

$$\sum_{i=1}^{n_A} y_i = \sum_{i=1}^{n_A} \mu_i = n_A g^{-1} (\beta_0 + \beta_1)$$

and

$$\sum_{j=n_A+1}^{n_A+n_B} y_j = \sum_{j=n_A+1}^{n_A+n_B} \mu_j = n_B g^{-1}(\beta_0)$$

thus our fitted group means should be

$$\frac{1}{n_A} \sum_{i=1}^{n_A} y_i = \frac{n_A}{n_A} g^{-1} (\beta_0 + \beta_1) = g^{-1} (\beta_0 + \beta_1)$$

and

$$\frac{1}{n_B} \sum_{j=n_A+1}^{n_A+n_B} y_j = \frac{n_B}{n_B} g^{-1}(\beta_0) = g^{-1}(\beta_0)$$

.

3.

$$\frac{\partial l(\theta)}{\partial \beta_j} = \sum_{i=1}^n \left[\frac{y_i - \mu_i}{\text{Var}[y_i]} \right] * \frac{1}{g'(\mu_i)} * x_{ij} = 0$$

and we have

$$\frac{1}{g'(\mu_i)} = \frac{\partial \mu_i}{\partial \eta_i}, \ x_{ij} = \frac{\partial \eta_i}{\partial \beta_j}$$

$$\sum_{i=1}^n \left[\frac{y_i - \mu_i}{\text{Var}[Y_i]} \right] * \frac{1}{g'(\mu_i)} x_{ij} = \sum_{i=1}^n \left[\frac{y_i - \mu_i}{\text{Var}[y_i]} \right] \frac{\partial \mu_i}{\partial \eta_i} \frac{\partial \eta_i}{\partial \beta_j} =$$

$$\sum_{i=1}^n \left[\frac{y_i - \mu_i}{\text{Var}[y_i]} \right] \frac{\partial \mu_i}{\partial \beta_j} = 0$$

We can show that this comes from the generalized least squares linear model, if we set the link to be the identity link

$$\mu_i = X_i \beta$$

where X_i would be the ith row of the design matrix X, and β the vector parameter to estimate. We set partials to zero in order to minimize our expression

$$\frac{\partial}{\partial \beta_j} \sum_{i=1}^n \frac{(y_i - \mu_i)^2}{\text{Var}[y_i]} = 0$$

. But

$$0 = \frac{\partial}{\partial \beta_j} \sum_{i=1}^n \frac{(y_i - \mu_i)^2}{\text{Var}[y_i]} = -2 \sum_{i=1}^n \frac{(y_i - \mu_i)}{\text{Var}[y_i]} * x_{ij}$$

 $\forall j = 1, ..., p$ but we have

$$x_{ij} = \frac{\partial \mu_i}{\partial \beta_i}$$

for our linear model!

So we recover the expression

$$\sum_{i=1}^{n} \left[\frac{y_i - \mu_i}{\text{Var}[y_i]} \right] \frac{\partial \mu_i}{\partial \beta_j} = 0$$

(b)

For any GLM with the canonical link with independent $a(\phi)$, we have

$$\frac{\partial l(\theta)}{\partial \beta_j} = \sum_{i=1}^n \frac{[y_i - \mu_i]}{a(\phi)} x_{ij} = 0$$

We obtain

$$a(\phi) \sum_{i=1}^{n} \frac{[y_i - \mu_i]}{a(\phi)} x_{ij} = 0 * a(\phi) = 0$$

but

$$a(\phi) \sum_{i=1}^{n} \frac{[y_i - \mu_i]}{a(\phi)} x_{ij} = \sum_{i=1}^{n} [y_i - \mu_i] x_{ij} = 0$$

 $\forall j = 1, ..., p$ then it follows that

$$\implies \mathbb{X}(\vec{y} - \vec{\mu}) = \vec{0}$$

So we obtain why the residual vector should be orthogonal to the colsp(X).

4.

(a)

```
beetles <- read.table("Beetles2.dat", header=TRUE)
attach(beetles)
head(beetles)</pre>
```

```
## 1 logdose n dead
## 1 1.691 59 6
## 2 1.724 60 13
## 3 1.755 62 18
## 4 1.784 56 28
## 5 1.811 63 52
## 6 1.837 59 53
```

summary(beetles)

```
##
       logdose
                                            dead
            :1.691
                             :56.00
                                              : 6.00
                     Min.
                                      Min.
                     1st Qu.:59.00
##
    1st Qu.:1.747
                                      1st Qu.:16.75
##
    Median :1.798
                     Median :60.00
                                      Median :40.00
##
    Mean
            :1.793
                     Mean
                             :60.12
                                      Mean
                                              :36.38
    3rd Qu.:1.843
                     3rd Qu.:62.00
                                      3rd Qu.:54.75
                                              :61.00
##
    Max.
            :1.884
                     Max.
                             :63.00
                                      Max.
```

```
x <- beetles$logdose
y <- beetles$dead/beetles$n
#fit1 <- glm(y~x, family = binomial(link = "logit"))
#summary(fit1)
plot(y~x,xlim=c(1.6,1.9),ylim=c(0,1),xlab="log of dosage",ylab="Proportion of dead beetles")
                                                                                 0
                                                                           0
                                                                      0
Proportion of dead beetles
                                                                0
      o.
      9.0
                                                         0
      0.4
                                                  0
      0.2
                                           0
                                   0
      0.0
            1.60
                        1.65
                                    1.70
                                                1.75
                                                           1.80
                                                                       1.85
                                                                                   1.90
                                           log of dosage
y_a <- cbind(beetles$dead, beetles$n-beetles$dead)</pre>
logitfit <- glm(y_a~x, family = binomial(link = "logit"))</pre>
summary(logitfit)
##
## Call:
## glm(formula = y_a ~ x, family = binomial(link = "logit"))
##
## Deviance Residuals:
       Min
                  1Q
                       Median
                                     3Q
                                             Max
## -1.5878 -0.4085
                       0.8442
                                          1.5860
                                 1.2455
##
## Coefficients:
##
               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -60.740
                              5.182 -11.72
                                               <2e-16 ***
                  34.286
                              2.913
                                       11.77
                                               <2e-16 ***
## x
##
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
       Null deviance: 284.202 on 7 degrees of freedom
##
## Residual deviance: 11.116 on 6 degrees of freedom
## AIC: 41.314
##
```

```
## Number of Fisher Scoring iterations: 4
```

(b)

The fitted value slope coefficient

$$\widehat{\beta_1} = 34.286$$

would the effect of 1 unit increase in log dosage of carbon disulphide increasing the odds of proportion of dead beetles.

(c)

```
#Next, explore the same GLM model with the probit link
probitfit <- glm(y_a~x,family=binomial(link=probit))</pre>
summary(probitfit)
##
## Call:
## glm(formula = y_a ~ x, family = binomial(link = probit))
##
## Deviance Residuals:
                      Median
##
       Min
                 10
                                    30
                                            Max
                      0.7647
## -1.5627 -0.4848
                                1.0530
                                         1.3149
##
## Coefficients:
##
               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -34.956
                             2.649
                                   -13.20
                                              <2e-16 ***
                 19.741
                             1.488
                                      13.27
                                              <2e-16 ***
## x
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
                               on 7 degrees of freedom
##
       Null deviance: 284.202
## Residual deviance:
                        9.987
                               on 6 degrees of freedom
## AIC: 40.185
## Number of Fisher Scoring iterations: 4
# Finally, explore the complementary log-log link
loglogfit <- glm(y_a~x,family=binomial(link="cloglog"))</pre>
summary(loglogfit)
##
## glm(formula = y_a ~ x, family = binomial(link = "cloglog"))
## Deviance Residuals:
        Min
                   1Q
                         Median
                                        3Q
                                                 Max
## -0.80002 -0.56588
                        0.01475
                                  0.38096
                                             1.31591
```

```
##
## Coefficients:
              Estimate Std. Error z value Pr(>|z|)
##
## (Intercept) -39.522
                        3.236 -12.21
                                             <2e-16 ***
## x
                 22.015
                            1.797
                                    12.25
                                            <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
##
       Null deviance: 284.2024 on 7 degrees of freedom
## Residual deviance: 3.5143 on 6 degrees of freedom
## AIC: 33.712
##
## Number of Fisher Scoring iterations: 4
(d)
library(faraway)
logitfit <- glm(y_a~x, family = binomial(link = "logit"))</pre>
summary(logitfit)
##
## Call:
## glm(formula = y_a ~ x, family = binomial(link = "logit"))
## Deviance Residuals:
##
       Min
                10
                     Median
                                   30
                                           Max
## -1.5878 -0.4085 0.8442 1.2455
                                        1.5860
##
## Coefficients:
              Estimate Std. Error z value Pr(>|z|)
##
## (Intercept) -60.740
                            5.182 -11.72 <2e-16 ***
## x
                 34.286
                             2.913
                                   11.77
                                             <2e-16 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
##
       Null deviance: 284.202 on 7 degrees of freedom
## Residual deviance: 11.116 on 6 degrees of freedom
## AIC: 41.314
##
## Number of Fisher Scoring iterations: 4
probitfit <- glm(y_a~x,family=binomial(link="probit"))</pre>
loglogfit <- glm(y_a~x,family=binomial(link="cloglog"))</pre>
plot(y~x,xlim=c(1.6,1.9),ylim=c(0,1),xlab="log of dosage",ylab="Proportion of dead beetles")
x1 \leftarrow seq(from=1.6, to=1.9, by=0.01)
lines(x1,ilogit(coef(logitfit)[1]+coef(logitfit)[2]*x1),col="darkblue")
```

```
lines(x1,pnorm(coef(probitfit)[1]+coef(probitfit)[2]*x1),col="red")
lines(x1,1-exp(-exp(coef(loglogfit)[1]+coef(loglogfit)[2]*x1)),col="darkgreen")
Proportion of dead beetles
       o.
      9.0
      0.4
      0.2
      0.0
             1.60
                         1.65
                                     1.70
                                                  1.75
                                                              1.80
                                                                          1.85
                                                                                       1.90
                                            log of dosage
\#\#(e)
v1 \leftarrow rep(0, 8)
v2 < - rep(0,8)
v3 \leftarrow rep(0,8)
for(i in 1:8){
v1[i] <- ilogit(coef(logitfit)[1]+coef(logitfit)[2]*logdose[i])</pre>
v2[i] <- pnorm(coef(probitfit)[1]+coef(probitfit)[2]*logdose[i])</pre>
v3[i] <- 1-exp(-exp(coef(loglogfit)[1]+coef(loglogfit)[2]*logdose[i]))</pre>
}
#fitted values for logit link
## [1] 0.05937747 0.16366723 0.36162283 0.60490961 0.79440490 0.90405532
## [7] 0.95546748 0.97925643
#fitted values for probit link
## [1] 0.0577367 0.1781060 0.3780390 0.6032833 0.7866532 0.9045852 0.9626183
## [8] 0.9873227
#fitted values for complementary log-log link
```

[1] 0.09582195 0.18802653 0.33777217 0.54177644 0.75683967 0.91843509

[7] 0.98575181 0.99913561

(f)

model selection with AIC

logitfit\$aic

[1] 41.31361

probitfit\$aic

[1] 40.18499

loglogfit\$aic

[1] 33.71237

Having compared the AIC's for each mode, we can conclude that our model with complementary log-log link seems to be the best fit!