hw2

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2/3/2021

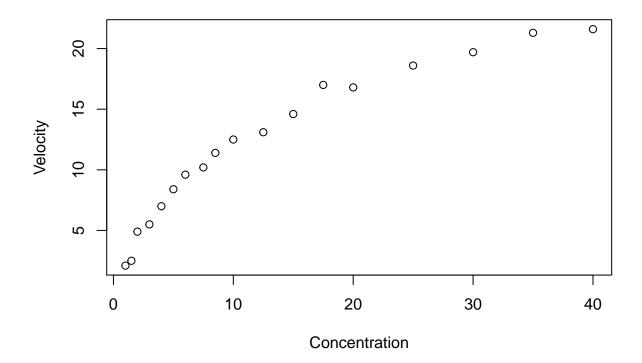
## Homework 2

1.

- (a) The starting points for Gauss-Newton I chose are 25 for gamma0 and 1 for gamma1. From the equation  $\frac{1}{2}$
- $1/E(Y_i) = (1/X_i)\gamma_1/\gamma_0 + 1/\gamma_0$
- $\rightarrow$  As X approaches infinity,  $1/X_i$  approaches 0.
- $\rightarrow$  Then  $1/E(Y_i)$  approaches  $1/\gamma_0$ , or  $Y_i$  approaches  $\gamma_0$ .
- $\rightarrow \gamma_0$  is the horizontal asymptote of this function.

From the plot of the data, the points seem to converge towards near 25, so I picked 25 as the starting point. Also, as X increases, Y also increases, so I expect  $\gamma_1$  to be positive, and the magnitude of it tells us how fast Y increases as X increases, so I picked the starting value 1.

```
#read data
enzyme <- read.delim("/Users/giangvu/Desktop/STAT 2132 - Applied Stat Method 2/HW/HW2/Enzyme.txt")
#plot data
plot(enzyme$X, enzyme$Y, xlab="Concentration", ylab="Velocity")</pre>
```



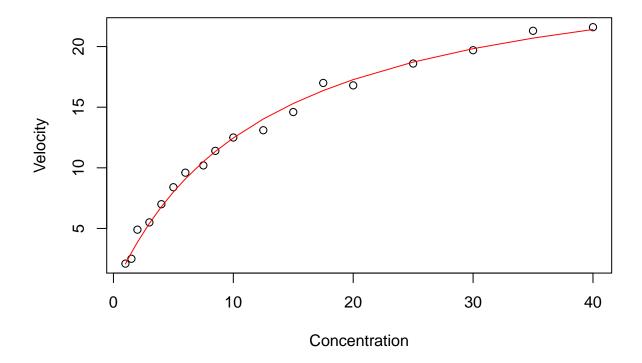
(b) Gamma0 and gamma1 are estimated using the starting points from part (a) below

```
#nls
out.start <- nls(Y ~ (gamma0*X)/(gamma1 + X), data = enzyme, start = list(gamma0=25,gamma1=1))
#estimates for gamma's
gamma.hat <- out.start$m$getAllPars()
gamma.hat
## gamma0 gamma1
## 28.13703 12.57443</pre>
```

2.

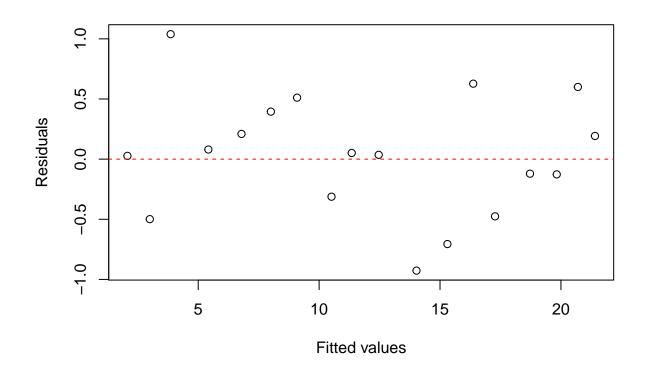
(a) The fit seems to be adequate.

```
#plot data
plot(enzyme$X, enzyme$Y, xlab="Concentration", ylab="Velocity")
#add the nonlinear regression function line
lines(enzyme$X, out.start$m$fitted(), col="red")
```



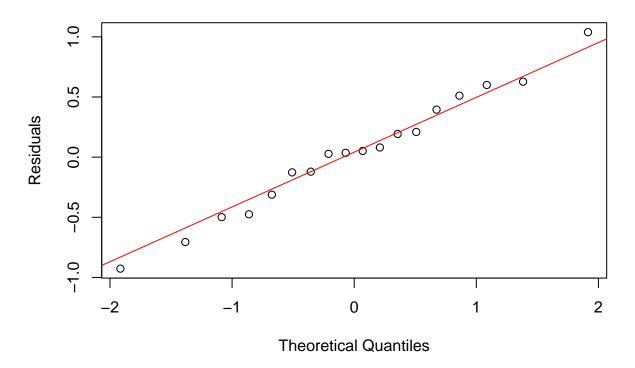
(b) Based on the residual plot and the qq-plot, the assumptions of constant variances and normality are both satisfied. The residual plots show no trend, and the tail of the qq-plot shows no skewness.

```
#residual plot - constant variances - satisfied
plot(out.start$m$fitted(), out.start$m$resid(), xlab="Fitted values", ylab="Residuals"); abline(h=0, co
```



```
#qq plot - normality
qqnorm(out.start$m$resid(), ylab="Residuals")
qqline(out.start$m$resid(), col="red")
```

## Normal Q-Q Plot



## (c) Null hypothesis: Gamma1 = 20

Alternative hypothesis: Gamma1 different from 20

Assumptions: The residuals are not correlated with X, and with each other. They are also normally distributed. The test statistic is -9.73141 with 16 degrees of freedom.

The p-value is basically 0, very small

The 95% CI is (11.23,13.91)

We reject the null hypothesis, we have strong evidence to conclude that gamma1 cannot be equal to 20.

```
#test gamma1 = 20
#Jacobian

J <- out.start$m$gradient()  #The 44 x 2 gradient matrix. This acts as our design matrix.
#MSE
sigma2 <- sum(out.start$m$resid()^2)/(nrow(J)-ncol(J))  #nrow(J) = n, ncol(J) = p
#SE for inference
se.gamma0 <- sqrt(sigma2)*sqrt( solve(t(J)%*%J)[1,1] )
se.gamma1 <- sqrt(sigma2)*sqrt( solve(t(J)%*%J)[2,2] )
#t-stat for test gamma1 = 20, df = n-p = 16
t.gam1 <- (gamma.hat[2]-20)/se.gamma1

#CI
CI.gamma0 <- gamma.hat[1] + c(-1,1)*se.gamma0*qt(p = 0.95, df = nrow(J)-ncol(J))
CI.gamma1 <- gamma.hat[2] + c(-1,1)*se.gamma1*qt(p = 0.95, df = nrow(J)-ncol(J))</pre>
```

## 3.

After running a bootstrap with 1000 samples, the 95% percentile confidence intervals for gamma1 obtained is (11.03, 13.94). This is quite close compared to the interval based on the large sample theory we obtained in problem 2.

```
#bootstrap with 1000 samples
set.seed(200)
enzyme_bootfcn <- function(x,i){</pre>
 d < -x[i,]
  out.boot <- nls(Y ~ (gamma0*X)/(gamma1 + X), data = d, start = list(gamma0=25,gamma1=1))
  gamma.boot <- out.boot$m$getAllPars()</pre>
  return(gamma.boot[2])
enzyme_bootobj <- boot(enzyme,enzyme_bootfcn,R=1000)</pre>
head(enzyme_bootobj$t)
##
            [,1]
## [1,] 12.12552
## [2,] 11.60097
## [3,] 11.79980
## [4,] 11.06739
## [5,] 13.05811
## [6,] 12.56629
#bootstrap 95% percentile CI
enzyme_bootci <- boot.ci(enzyme_bootobj)</pre>
enzyme_bootci
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 1000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = enzyme_bootobj)
##
## Intervals :
              Normal
## Level
                                   Basic
                            (11.21, 14.12)
## 95%
         (11.23, 14.06)
##
## Level
             Percentile
                                    BCa
         (11.03, 13.94)
                            (11.11, 14.09)
## 95%
## Calculations and Intervals on Original Scale
```

4) a) Nsmg Bayes' Theorem for 3 events 
$$y = 1$$
,  $x$ , and  $z = 1$ 

$$P(y=1|x,z=1) = \frac{P(z=1|y=1,x) \cdot P(y=1|x)}{P(z=1|y=0,x) \cdot P(y=0|x)}$$

$$= \frac{Y_1 \cdot P(y=1|x)}{Y_2 \cdot P(y=1|x) + P(y=1|x) + P(z=1|y=0,x) \cdot P(y=0|x)}$$

$$= \log_{12} \left\{ P(y=1|x,z=1) \right\} = \log_{12} \left( \frac{P(y=1|x)}{P(y=0|x)} / (P(y=0|x)) / (P(y=0|x)) \right)$$

$$= \log_{12} \left( \frac{P(y=1|x,z=1)}{P(y=0|x)} \right) + \log_{12} \left( \frac{P(y=1|x)}{P(y=0|x)} \right)$$

$$= \log_{12} \left( \frac{P(y=1|x)}{P(y=0|x)} \right) + \log_{12} \left( \frac{P(y=1|x)}{P(y=0|x)} \right)$$

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$$= \log_{12} \left( \frac{P(y=1|x)}{P(y=1|x)} \right) + \log_{12} \left( \frac{P(y=1|x)}{P(y=0|x)} \right)$$

$$= \log_{12} \left\{ P(y=1|x,z=1) \right\} = \frac{P_0^2 + P_0^2 + P_0^2}{P_0^2 + P_0^2 + P_0^2} + \log_{12} \left( \frac{P_0^2}{P_0^2} \right)$$

- b) Since after the enriched study, Bz does not change in the logit function, we can still use the estimated effect of X to infer the effect in the general population. This effect only depends on Bz.
- E) However, Bo is changed into Bo with enriched study sample, we comnot use estimated probability of Y = 1 given X = xo to infer this for the population. This probability depends on both Bo and B1. And also the probability of Y = 1 given X = xo is only based on one value xo of X, so it cannot be generalized for the population.

5) a) 
$$M(\theta) = E\left\{e^{\theta Y}\right\}$$
 $K(\theta) = \log \left\{M(\theta)\right\}$ 
 $K'(0) = \frac{M'(\theta)}{M(\theta)}\Big|_{\theta=0} = \frac{E(Y)}{1} = E(Y)$ 
 $K''(0) = \left(\frac{M''(\theta)}{M(\theta)} - \frac{M'(\theta)^2}{M(\theta)^2}\right)\Big|_{\theta=0}$ 
 $= E(Y^2) - E(Y)^2 = Var(Y)$ 

b) Call the normalizing constant 
$$\alpha$$
  
=>  $f(y, \theta) = \alpha e^{\theta y} f_0(y)$ ,  $\theta \in \mathbb{R}$   
=>  $f(y, \theta) dy = 1$ 

$$=)$$
  $\alpha \cdot M(\theta) = 1$ 

=) 
$$\alpha = \frac{1}{M(\theta)}$$
 is the normalizing constant

c) 
$$l(y;\theta) = log\{\{\{y;\theta\}\}\} = log\{\frac{1}{M(\theta)}e^{\theta y}\}_{\theta}(y)^{2}$$
  
 $= -log(M(\theta)) + log(e^{\theta y}) + log(\{\{b(y)\}\})$   
 $= -K(\theta) + \theta y + log(\{\{b(y)\}\})$ 

log (40(y)) only depends ony, we can call it h(y)

=) 
$$\ell(y,\theta) = -K(\theta) + \theta y + h(y)$$
,  $\theta \in R$ 

d) 
$$k_{\theta}(t) = \log E\{e^{tY}\}$$
  
 $= \log E\{e^{(\theta+t-\theta)Y}\}$   
 $= \log E\{e^{(\theta+t)Y}\} + \log E\{e^{-\theta Y}\}$   
 $= K(\theta+t) - K(\theta)$ 

5d) (continued)

We have 
$$K_{\theta}(t) = K(\theta + t) - K(\theta)$$

But we adjustedly know  $K_{\theta}'(0) = E(y)$ 

=)  $\left[K'(\theta + t) - K'(\theta)\right]' \Big|_{t=0} = E(y)$ 

(+ake the derivative writt)

=)  $\frac{M'(\theta + t)}{M(\theta + t)} \Big|_{t=0} = E(y)$ 

=)  $\frac{M'(\theta + t)}{M(\theta)} = E(y)$ 

=)  $\frac{M'(\theta)}{M(\theta)} = E(y)$ 

Also  $K_{\theta}''(0) = Var(y)$ 

=)  $\left[K''(\theta + t) - K''(\theta)\right]' \Big|_{t=0} = Var(y)$ 

=)  $\left[K''(\theta + t) - K''(\theta)\right]' \Big|_{t=0} = Var(y)$ 

=)  $\left[K'''(\theta + t) - K'''(\theta)\right]' \Big|_{t=0} = Var(y)$ 

Also 
$$K_{\theta}''(0) = Var(Y)$$

$$= Var(Y)$$

5e) (i) 
$$g(\beta) = \frac{2}{12} l(y_r, x_r^T \beta)$$

$$= \frac{2}{12} \left\{ h(y_r) + x_r^T \beta y_r^T - K(x_r^T \beta) \right\}$$

When we take the second derivative of  $g(\beta)$ , the terms  $(0)$  and  $(0)$  will disappear  $(0)$  with respect to  $(0)$ .

But we know that  $K''(\theta) = Var(Y) > 0$ 

$$= Var(Y) > 0$$

$$= Var(Y) > 0$$