Solution of assignment 6, ST2304

Problem 1 1. The inverse of the logit function is the logistic function. If logit(p) = z, then

$$p = \frac{1}{1 + e^{-\eta}} \tag{1}$$

in this case

$$\eta = \beta_0 + \beta_{\text{ageage}} + \beta_{\text{log}_{10}} \operatorname{ab} \log_{10} \operatorname{ab} \tag{2}$$

which means that we get

$$p = \frac{1}{1 + e^{-(\beta_0 + \beta_{age} age + \beta_{\log_{10}} ab \log_{10} ab)}}$$
(3)

We set in for age =15 and antibody level =1000 and β 's from the summary() of the logistic regression:

$$p = \frac{1}{1 + e^{-(\beta_0 + \beta_a geage + \beta_{\log_{10}} ab \log_{10} ab)}}$$
(4)

The estimated probability of developing malaria is then: 0.04216440

> summary(malreg)

```
Call:
```

glm(formula = mal ~ age + log10(ab), family = binomial("logit"))

Deviance Residuals:

Coefficients:

Estimate Std. Error z value Pr(>|z|)
(Intercept) 2.57234 0.95184 2.702 0.006883 **
age -0.06546 0.06772 -0.967 0.333703
log10(ab) -1.57118 0.45019 -3.490 0.000483 ***

Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 116.652 on 99 degrees of freedom Residual deviance: 98.017 on 97 degrees of freedom

AIC: 104.02

Number of Fisher Scoring iterations: 5

```
Rcode:
```

```
attach(malaria)
malreg=glm(mal~age+log10(ab),family=binomial("logit"))
summary(malreg)
probmal=1/( 1+exp (-( 2.57234+ (-0.06546*15)+(-1.57118*log10(1000)) ) ) )
```

malaria <- read.table("http://www.math.ntnu.no/~jarlet/statmod/malaria.dat")</pre>

2. We see that age is non-significant. We fit a reduced model, and inspect the output

```
malreg2=glm(mal~log10(ab),family=binomial("logit"))
```

> summary(malreg2)

Call:

glm(formula = mal ~ log10(ab), family = binomial("logit"))

Deviance Residuals:

Coefficients:

Estimate Std. Error z value Pr(>|z|)
(Intercept) 2.1552 0.8401 2.565 0.010305 *
log10(ab) -1.6399 0.4449 -3.686 0.000228 ***

Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 116.652 on 99 degrees of freedom Residual deviance: 98.968 on 98 degrees of freedom

AIC: 102.97

Number of Fisher Scoring iterations: 4

3. Probability of malaria (wihtout age):

$$p = \frac{1}{1 + e^{-(2.1552 + (-1.6399 \log_{10} ab))}}$$
 (5)

Plotting p against antibody level (ab):

R code:

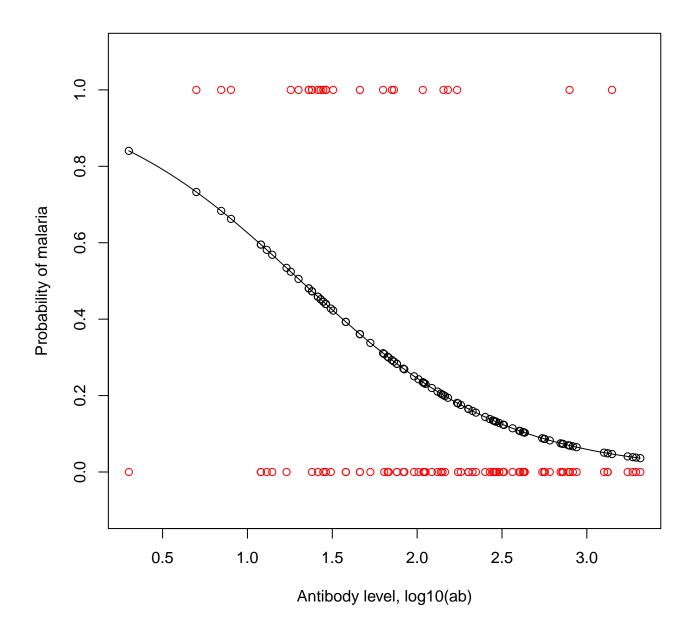


Figure 1: Probablity of malaria against antibody level (on log10 scale) in black and observed data of antibody level againts malaria in red

```
probmal=1/(1+exp(-(2.1552+ (-1.6399*log10(ab))))

#Plotting the probability againts ab
plot(log10(ab),probmal,ylab="Probability of malaria", xlab="Antibody level, log10(a
#adding a curve
curve(1/(1+exp(-(2.1552+ (-1.6399*x)))),ylab="Probability of malaria", xlab="Antibody
##add observed values of ab
points(x=log10(ab),y=mal,col="RED")
#saving the plot (in the current directory)
dev.copy2pdf(file="plot1oving6.pdf")
```

- 4. The regression coefficient β for log antibody level represents the the increase in logit(p) (or log odds) for a unit change in \log_{10} antibody level equivalent to a 10-fold increase in antibody level. The odds thus change by an oddsratio equal to $\exp(\beta)$. Based on the estimate of β , the estimate of the oddsratio becomes $\exp(-1.6399) = 0.1940$.
- 5. Using *confint* on the fitted model:

```
##CI for the regression coefficients of the fitted model
10^(confint(malreg2))
Waiting for profiling to be done...
                  2.5 %
                              97.5 %
(Intercept) 3.797791202 8029.6355942
log10(ab)
            0.002567519
                        0.1483947
##CI for the odds ratio of the fitted model
> exp(confint(malreg2))
Waiting for profiling to be done...
                 2.5 %
                           97.5 %
(Intercept) 1.78520113 49.6349805
log10(ab)
           0.07498356 0.4366682
```

We see that the confidence interval contains the estimate.