Solution of assignment 6, ST2304

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

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

in this case

$$\eta = \beta_0 + \beta_{\text{ageage}} + \beta_{\log_{10} \text{ab}} \log_{10} \text{ab}$$
 (2)

which means that we get

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

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

$$p = \frac{1}{1 + e^{-(2.57234 + (-0.06546*15) + (-1.57118*\log 10(1000)))}}$$
(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:
```

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

- - -

(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:

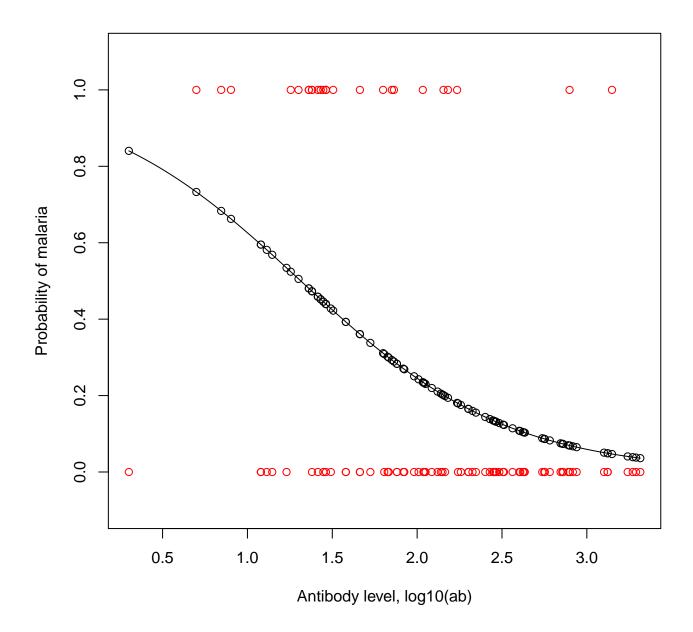


Figure 1: Probablity of malaria against antibody level (on log10 scale) in black and observed data of antibody level againts malaria in red

```
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(ab)",
    ylim=c(-0.1,1.1)
#adding a curve
curve(1/(1+exp(-(2.1552+(-1.6399*x)))),
     ylab="Probability of malaria",
    xlab="Antibody level, log10(ab)",
    ylim=c(-0.1,1.1),add=T,
    from=min(log10(ab)),
     to=max(log10(ab)))
##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:

We see that the confidence interval contains the estimate.