bliss

Heejung Shim

IWLS

An experiment measuring death rates for insects, with 30 insects at each of five treatment levels.

We model this with a binomial regression model.

```
library(faraway)
data(bliss)
str(bliss)
```

```
## 'data.frame':    5 obs. of  3 variables:
##  $ dead : num  2 8 15 23 27
##  $ alive: num  28 22 15 7 3
##  $ conc : int  0 1 2 3 4
```

```
bliss
```

```
##   dead alive conc
## 1    2    28    0
## 2    8    22    1
## 3   15    15    2
## 4   23     7    3
## 5   27     3    4
```

```
model <- glm(cbind(dead, alive) ~ conc, family=binomial, bliss)
summary(model)
```

```
##
## Call:
## glm(formula = cbind(dead, alive) ~ conc, family = binomial, data = bliss)
##
## Deviance Residuals:
##       1        2        3        4        5
## -0.4510   0.3597   0.0000   0.0643  -0.2045
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.3238     0.4179  -5.561 2.69e-08 ***
## conc          1.1619     0.1814   6.405 1.51e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 64.76327  on 4  degrees of freedom
## Residual deviance:  0.37875  on 3  degrees of freedom
## AIC: 20.854
##
## Number of Fisher Scoring iterations: 4
```

```
coef(model)
```

```
## (Intercept)        conc
##   -2.323790    1.161895
```

let's implement IWLS.

```
y <- bliss$dead
m <- bliss$dead + bliss$alive

mu <- y
eta <- logit(mu/m)
z <- eta + (y - mu)*m/mu/(m - mu)
w <- mu*(m - mu)/m
lmod <- lm(z ~ conc, weights=w, bliss)
coef(lmod)
```

```
## (Intercept)        conc
##   -2.302462    1.153587
```

```
for (i in 1:5) {
  eta <- lmod$fit
  mu <- m*ilogit(eta)
  z <- eta + (y - mu)*m/mu/(m - mu)
  w <- mu*(m - mu)/m
  lmod <- lm(z ~ conc, weights=w, bliss)
  cat(i, coef(lmod), "\n")
}
```

```
## 1 -2.323672 1.161847
## 2 -2.32379 1.161895
## 3 -2.32379 1.161895
## 4 -2.32379 1.161895
## 5 -2.32379 1.161895
```

LR test using deviance

```
model0 <- glm(cbind(dead, alive) ~ 1, family=binomial, bliss)
pchisq(deviance(model0) - deviance(model), 1, lower.tail=FALSE)
```

```
## [1] 1.023593e-15
```

```
anova(model0, model, test="Chi") # using built in function
```

```
## Analysis of Deviance Table
##
## Model 1: cbind(dead, alive) ~ 1
## Model 2: cbind(dead, alive) ~ conc
```

```
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1         4     64.763
## 2         3      0.379  1   64.385 1.024e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```