

bliss

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IWLS

$$y_i \sim \text{Bin}(n_i=30, p_i) \quad p_i = \frac{e^{\beta_0 + \beta_1 x_i}}{1 + e^{\beta_0 + \beta_1 x_i}}$$

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
```

$$g(\mu) = \log \frac{\mu}{m - \mu}$$

$$= \log \frac{\frac{\mu}{m}}{\frac{\mu}{m} - 1} = \log \text{it} \left(\frac{\mu}{m} \right)$$

$$g'(\mu) = \frac{1}{\mu} + \frac{1}{m - \mu} = \frac{m}{\mu(m - \mu)}$$

$$\text{exercise: } \sum \hat{\eta}_i^2 = g'(\mu_i)^2 v(\mu_i) = \frac{m_i}{\mu_i(m_i - \mu_i)}$$

$$\hat{\mu}^{(0)} = y = \begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ y_4 \\ y_5 \end{bmatrix}$$

$$n=0$$

$$z_i^{(n)} = g(\hat{\mu}_i^{(n)})$$

$$+ (y_i - \hat{\mu}_i^{(n)}) g'(\hat{\mu}_i^{(n)})$$

$$= \log \pi \left(\frac{\mu_i^{(n)}}{m_i} \right)$$

$$+ (y_i - \hat{\mu}_i^{(n)}) \cdot \frac{m_i}{\hat{\mu}_i^{(n)} (m_i - \hat{\mu}_i^{(n)})}$$

$$W_{ii}^{(n)} = \frac{1}{\sum \hat{\eta}_i^{(n)}} = \frac{\hat{\mu}_i^{(n)} (m_i - \hat{\mu}_i^{(n)})}{m_i}$$

$$\hat{\mu}^{(n+1)} = (X^T W^{(n)} X)^{-1} X^T W^{(n)} z^{(n)}$$

$$\hat{\mu}^{(n+1)} = g^{-1}(x_i^T \hat{\beta}^{(n+1)})$$

$$= m \hat{p}^{(n+1)}$$

```
##
## 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
```

Full model.

$$y_i = \mu_0 + \beta_1 x_i$$

reduced model $y_i = \mu_0$

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 < 0.05
```

```
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
```

of parameter