Beetle Example: Logistic Regression with Grouped Data

(Simple) logistic regression is used to model the relationship between a binary response variable and a single numerical predictor. In this example, beetle death is considered an "event" and logdose is the predictor. Note that this data is grouped, meaning that for each of 8 doses we have approximately 60 beetles (either dead or alive) and the data is summarized in only 8 rows (corresponding to 8 doses). The glm function can be used to run logistic regression whether or not the data is grouped, just be careful about the formatting!

```
library(car)
## Loading required package: carData
library(MASS)
Beetle <- read.csv("~/Dropbox/STAT512/Lectures/MultReg5/MR5_Beetles.csv")</pre>
Beetle
##
     lgdose nrtest nrdead
## 1
        1.69
                  59
        1.72
## 2
                  60
                          13
## 3
        1.75
                  62
                          18
## 4
        1.78
                  56
                          28
        1.81
                  63
                          52
## 6
        1.84
                  59
                          53
## 7
        1.86
                  62
                          61
## 8
       1.88
                          60
Beetle$rate <- Beetle$nrdead/Beetle$nrtest</pre>
plot(rate ~ lgdose, data = Beetle)
                                                                    \overline{\circ}
                                                              0
                                                        0
                                                0
                                       0
                              0
                      0
              1.70
                             1.75
                                           1.80
                                                         1.85
                                     Igdose
```

Logistic Regression model

With different N at each dose level, we provide a 2-column matrix of #successes and failures as the response "variable".

```
Model1 <- glm(cbind(nrdead, nrtest-nrdead) ~ lgdose, family = binomial(link = "logit"), data = Beetle)
summary(Model1)</pre>
```

```
## Call:
## glm(formula = cbind(nrdead, nrtest - nrdead) ~ lgdose, family = binomial(link = "logit"),
      data = Beetle)
##
## Deviance Residuals:
                1Q Median
                                  3Q
      Min
                                          Max
## -1.4242 -0.6084 0.7535 1.1080
                                      1.6837
##
## Coefficients:
##
              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -59.282
                         4.995 -11.87 <2e-16 ***
                            2.814 11.91
                33.519
                                           <2e-16 ***
## lgdose
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
##
      Null deviance: 284.2024 on 7 degrees of freedom
## Residual deviance: 9.9971 on 6 degrees of freedom
## AIC: 40.195
## Number of Fisher Scoring iterations: 4
Anova(Model1, type = 3)
## Analysis of Deviance Table (Type III tests)
## Response: cbind(nrdead, nrtest - nrdead)
         LR Chisq Df Pr(>Chisq)
## lgdose
            274.2 1 < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#Odds ratio estimates and CIs
#To compute odds ratio estimates: exponentiate estimates and CI endpoints.
exp(Model1$coef)
## (Intercept)
                     lgdose
## 1.794846e-26 3.607265e+14
confint(Model1)
## Waiting for profiling to be done...
                  2.5 %
                           97.5 %
## (Intercept) -69.61409 -49.97808
## lgdose
               28.27950 39.34206
exp(confint(Model1))
## Waiting for profiling to be done...
                     2.5 %
                                 97.5 %
##
## (Intercept) 5.847726e-31 1.971502e-22
## lgdose
             1.912621e+12 1.219095e+17
```

Examine Fit

Here we calculate (McFadden's) psuedo R2 and graph the data with the fitted logistic curve overlaid. For the predict function, note that the type = "response" option returns the response on the proportion (or probability) scale instead of the default logit scale.

```
#Calculate McFadden's Pseudo R2 "by hand"
NullModel <- glm(cbind(nrdead, nrtest-nrdead) ~ 1, family = binomial(link = "logit"), data = Beetle)
1-logLik(Model1)/logLik(NullModel)
## 'log Lik.' 0.883392 (df=2)
#Plot the fitted curve
plot(rate ~ lgdose, data = Beetle)
lgdosenew \leftarrow seq(1.66, 1.9, 0.01)
phat <- predict(Model1, list(lgdose = lgdosenew), type = "response")</pre>
lines(phat ~ lgdosenew)
                                                               0
     9.0
rate
             1.70
                           1.75
                                        1.80
                                                     1.85
                                   Igdose
```

Estimate LD(p)

dose.p() from MASS package computes LD's for various probs. cf=1:2 tells it that coef[1] is the intercept and coef[2] is the slope.

```
probs <- seq(0.1, 0.9, 0.05)
ld <- dose.p(Model1, cf = 1:2, p = probs)
ld</pre>
```

```
## p = 0.10: 1.703059 0.007155075
## p = 0.15: 1.716861 0.006217407
## p = 0.20: 1.727252 0.005566667
## p = 0.25: 1.735834 0.005079572
## p = 0.30: 1.743332 0.004703378
## p = 0.35: 1.750142 0.004412019
## p = 0.40: 1.756514 0.004192013
## p = 0.45: 1.762623 0.004036757
## p = 0.50: 1.768610 0.003943864
## p = 0.55: 1.774597 0.003913824
```

```
## p = 0.60: 1.780707 0.003949443

## p = 0.65: 1.787078 0.004055959

## p = 0.70: 1.793888 0.004242038

## p = 0.75: 1.801386 0.004522291

## p = 0.80: 1.809968 0.004922971

## p = 0.85: 1.820360 0.005496139

## p = 0.90: 1.834161 0.006363428
```