

R Code Chapter 4

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4.4.1 Model building for the beetle data

```
getwd()
```

```
## [1] "C:/Users/wewol/Google Drive/Courses/Sheffield/MAS6003TaskSolutions"
```

```
load("data/MAS367-GLMs.RData", envir = e <- new.env())  
grep("beetle", names(e))
```

```
## [1] 8
```

Fitting minimal model

```
beetle<-e$beetle  
lapply(beetle, class)
```

```
## $conc  
## [1] "numeric"  
##  
## $number  
## [1] "integer"  
##  
## $dead  
## [1] "integer"  
##  
## $propn.dead  
## [1] "numeric"
```

```
head(beetle)
```

```
##      conc number dead propn.dead  
## 1 1.6907     59   6  0.1016949  
## 2 1.7242     60  13  0.2166667  
## 3 1.7552     62  18  0.2903226  
## 4 1.7842     56  28  0.5000000  
## 5 1.8113     63  52  0.8253968  
## 6 1.8369     59  53  0.8983051
```

```
null.glm <- glm(propn.dead ~ 1, family=binomial(logit), weights=number, data=beetle)  
null.glm
```

```
##
## Call:  glm(formula = propn.dead ~ 1, family = binomial(logit), data = beetle,
##        weights = number)
##
## Coefficients:
## (Intercept)
##      0.4263
##
## Degrees of Freedom: 7 Total (i.e. Null);  7 Residual
## Null Deviance:      284.2
## Residual Deviance: 284.2    AIC: 312.4
```

Adding a log concentration term

```
linear.glm <- glm(propn.dead~1+conc, binomial(logit), weights = number, data=beetle)
summary(linear.glm)
```

```
##
## Call:
## glm(formula = propn.dead ~ 1 + conc, family = binomial(logit),
##      data = beetle, weights = number)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5941  -0.3944   0.8329   1.2592   1.5940
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -60.717      5.181  -11.72  <2e-16 ***
## conc          34.270      2.912   11.77  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 284.202  on 7  degrees of freedom
## Residual deviance:  11.232  on 6  degrees of freedom
## AIC: 41.43
##
## Number of Fisher Scoring iterations: 4
```

Example of computing χ^2 values in R.

```
sum(residuals(linear.glm, type = "pearson")^2)
```

```
## [1] 10.02682
```

Numbers from point 3: Analysis of deviance in nested models

```
null.glm$deviance
```

```
## [1] 284.2024
```

```
linear.glm$deviance
```

```
## [1] 11.23223
```

```
null.glm$deviance - linear.glm$deviance
```

```
## [1] 272.9702
```

```
qchisq(0.95,1)
```

```
## [1] 3.841459
```

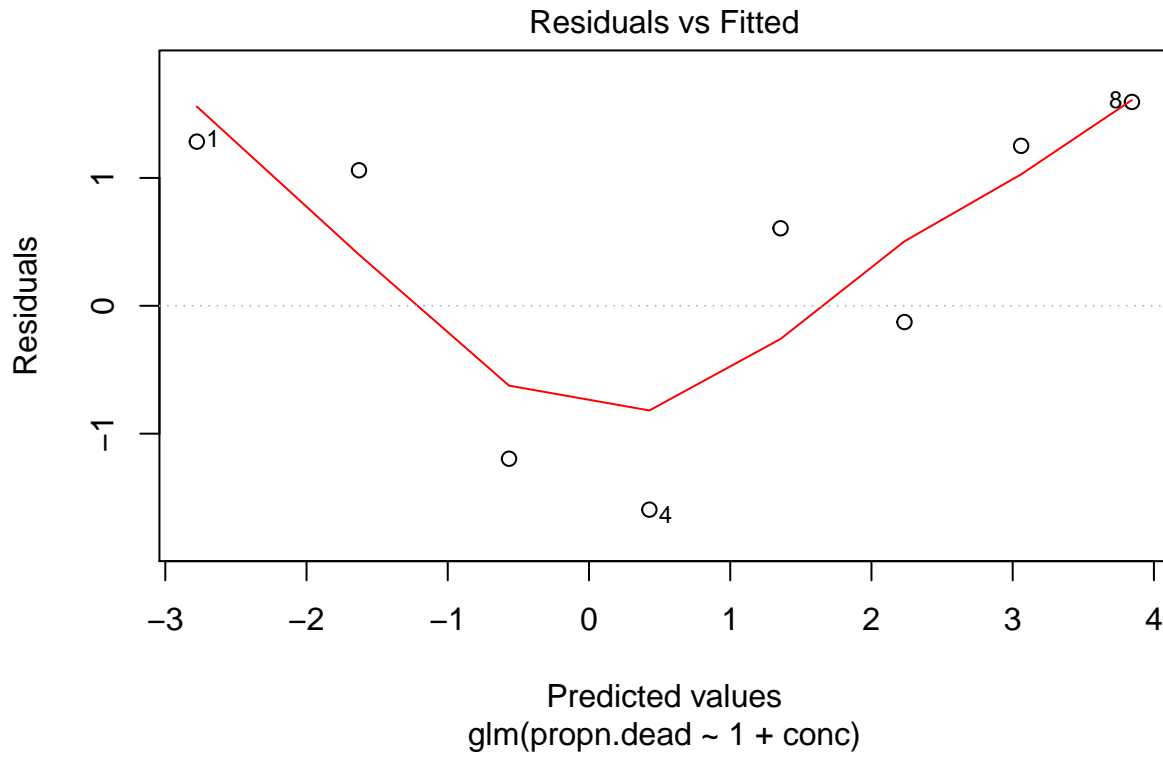
Is fit acceptable ?

```
qchisq(0.95,6)
```

```
## [1] 12.59159
```

Plotting Pearson (?) residuals against predicted values

```
plot(linear.glm,which = 1)
```



Fitting quadratic model

```
quad.glm <- glm(propn.dead ~ 1 + conc + I(conc^2), binomial(logit), weights= number, data= beetle)
quad.glm
```

```
##
## Call:  glm(formula = propn.dead ~ 1 + conc + I(conc^2), family = binomial(logit),
##       data = beetle, weights = number)
##
## Coefficients:
## (Intercept)      conc      I(conc^2)
##      431.1      -520.6       156.4
##
## Degrees of Freedom: 7 Total (i.e. Null);  5 Residual
## Null Deviance:      284.2
## Residual Deviance: 3.195    AIC: 35.39
```

Change in deviance

```
linear.glm$deviance - quad.glm$deviance
```

```
## [1] 8.037326
```

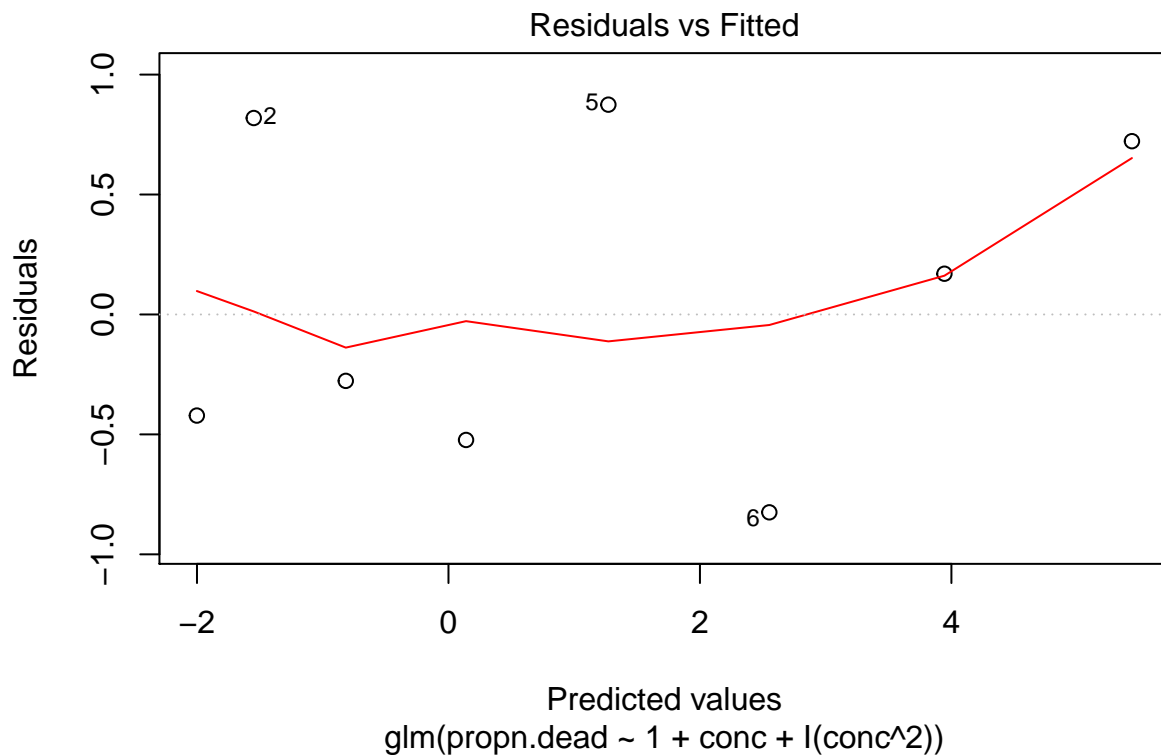
```
qchisq(0.95,1)
```

```
## [1] 3.841459
```

```
qchisq(0.95,5)
```

```
## [1] 11.0705
```

```
plot(quad.glm,which = 1)
```



10 Wald t-test

```
summary(quad.glm)
```

```
##
```

```
## Call:
```

```
## glm(formula = propn.dead ~ 1 + conc + I(conc^2), family = binomial(logit),  
##      data = beetle, weights = number)
```

```
##
```

```
## Deviance Residuals:
```

```
##      1      2      3      4      5      6      7      8
```

```
## -0.4215  0.8189 -0.2769 -0.5232  0.8746 -0.8249  0.1698  0.7224
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   431.11     180.65   2.386  0.01702 *
## conc         -520.62     204.52  -2.546  0.01091 *
## I(conc^2)      156.41      57.86   2.703  0.00687 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 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:  3.1949  on 5  degrees of freedom
## AIC: 35.393
##
## Number of Fisher Scoring iterations: 4
```

```
2*pnorm(-156.41/57.86)
```

```
## [1] 0.006866524
```

4.4.2

```
anova(linear.glm, quad.glm, test="Chi")
```

```
## Analysis of Deviance Table
##
## Model 1: propn.dead ~ 1 + conc
## Model 2: propn.dead ~ 1 + conc + I(conc^2)
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1          6    11.2322
## 2          5     3.1949  1   8.0373 0.004582 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4.4.3

$$AIC = -2l + 2p$$

$$\frac{l_{min} - l_{mod}}{l_{min}}$$

```
quad.glm$aic
```

```
## [1] 35.39294
```

```
l_mod<-length(quad.glm$coefficients) - 0.5*quad.glm$aic
l_min<-length(null.glm$coefficients) - 0.5*null.glm$aic
(l_min-l_mod)/l_min
```

```
## [1] 0.9053064
```

4.4.4 Calculating residuals for the beetle quadratic model

```
residuals(quad.glm,type = "pearson")
```

```
##          1          2          3          4          5          6
## -0.4122545  0.8425072 -0.2754990 -0.5238566  0.8516013 -0.8716078
##          7          8
##  0.1654446  0.5113471
```

```
y=beetle$propn.dead
fitted = quad.glm$fitted
n = beetle$number
```

Lets define function:

```
pearson_resid <- function(y, fitted, n){
  (y-fitted)/sqrt(fitted * (1-fitted)/n)
}
```

and run it:

```
pearson_resid(y, fitted, n)
```

```
##          1          2          3          4          5          6
## -0.4122545  0.8425072 -0.2754990 -0.5238566  0.8516013 -0.8716078
##          7          8
##  0.1654446  0.5113471
```

Other residuals are available:

Def function to compute d_i deviance residuals:

```
d_i_deviance <- function(y, fitted, n){
  sign(y- fitted)*sqrt(-2*n*(y*log(fitted/y)+(1-y)*log((1-fitted)/(1-y+0.000001))))
}
```

```
d_i_deviance(y, fitted, n)
```

```
##          1          2          3          4          5          6
## -0.4215475  0.8189611 -0.2769161 -0.5232272  0.8746384 -0.8249153
##          7          8
##  0.1698457  0.7223680
```

compare with r computed values

```
residuals(quad.glm,type="deviance")
```

```
##          1          2          3          4          5          6
## -0.4215335  0.8189537 -0.2768937 -0.5232165  0.8746312 -0.8249082
##          7          8
##  0.1698092  0.7223680
```

Task 12

```
residuals(linear.glm, "pearson")[1]
```

```
##          1
## 1.409296
```

```
residuals(linear.glm, "deviance")[1]
```

```
##          1
## 1.283678
```

```
linear.glm$fitted.values[1]
```

```
##          1
## 0.05860103
```

```
pearson_resid(linear.glm$y, linear.glm$fitted.values, linear.glm$prior.weights)
```

```
##          1          2          3          4          5          6
## 1.4092960  1.1011003 -1.1762596 -1.6123815  0.5944454 -0.1281090
##          7          8
## 1.0914228  1.1331102
```

```
d_i_deviance(linear.glm$y, linear.glm$fitted.values, linear.glm$prior.weights)
```

```
##          1          2          3          4          5          6
## 1.2836823  1.0596957 -1.1961175 -1.5941279  0.6061509 -0.1272048
##          7          8
## 1.2510760  1.5939850
```

4.4.5 Example 2 of model building : plant anthers

```
anthers <- e$anthers
```


Plot data

```
head(anthers)
```

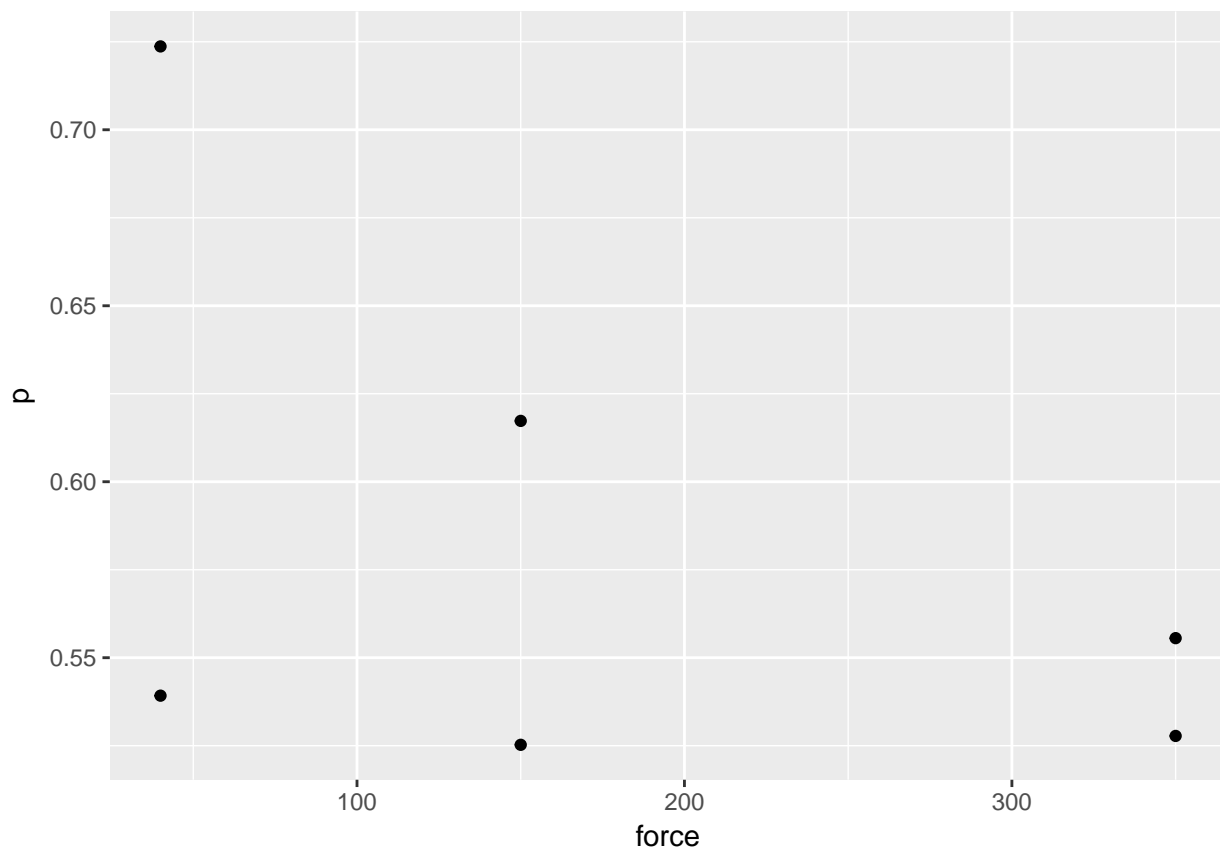
```
##      group force prepared obtained
## 1 control   40     102      55
## 2 control  150      99      52
## 3 control  350     108      57
## 4 treatment  40      76      55
## 5 treatment 150      81      50
## 6 treatment 350      90      50
```

```
anthers$p <- anthers$obtained/anthers$prepared
```

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.3.2
```

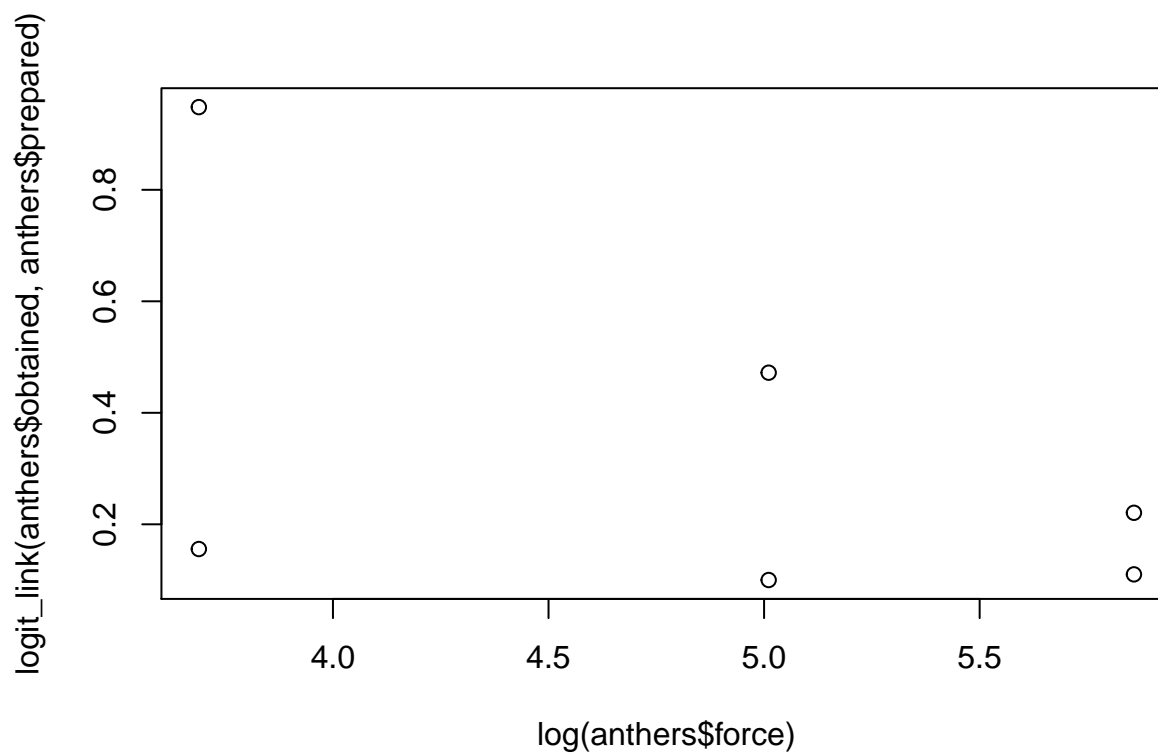
```
ggplot(anthers, aes(force,p), colour= group) + geom_point()
```



2 consider logit link

```
logit_link <- function(s,n){  
  y <- (s + 1/2)/(n+1)  
  log(y/(1-y))  
}
```

```
plot(log(anthers$force),logit_link(anthers$obtained,anthers$prepared))
```



Minimal Model

```
glm.0 <- glm(p ~ 1, weights = prepared, data = anthers, binomial(logit))  
summary(glm.0)
```

```
##  
## Call:  
## glm(formula = p ~ 1, family = binomial(logit), data = anthers,  
##      weights = prepared)  
##  
## Deviance Residuals:  
##      1      2      3      4      5      6  
## -0.7029 -0.9716 -0.9622  2.7078  0.7965 -0.3483
```

```
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.29713    0.08576   3.465 0.000531 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 10.452  on 5  degrees of freedom
## Residual deviance: 10.452  on 5  degrees of freedom
## AIC: 42.02
##
## Number of Fisher Scoring iterations: 3
```

Model 1

$\eta = \alpha$. Dobson is referenced, to make the lecture notes more confusing model 1 in dobson is model 3 in notes.

```
anthers$p <- anthers$obtained/anthers$prepared
anthers$logForce <- log(anthers$force)
glm.1 <- glm(p ~ group, weights = prepared, data = anthers, family = binomial(logit))
summary(glm.1)
```

```
##
## Call:
## glm(formula = p ~ group, family = binomial(logit), data = anthers,
##      weights = prepared)
##
## Deviance Residuals:
##      1      2      3      4      5      6
##  0.17150 -0.10947 -0.06177  1.77208 -0.19040 -1.39686
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.1231     0.1140   1.080  0.2801
## grouptreatment  0.3985     0.1741   2.289  0.0221 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 10.452  on 5  degrees of freedom
## Residual deviance:  5.173  on 4  degrees of freedom
## AIC: 38.741
##
## Number of Fisher Scoring iterations: 3
```

```
summary.lm(glm.1)
```

```
##
## Call:
```

```
## glm(formula = p ~ group, family = binomial(logit), data = anthers,
##      weights = prepared)
##
## Weighted Residuals:
##      1      2      3      4      5      6
## 0.17144 -0.10949 -0.06178  1.73385 -0.19074 -1.41234
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.1231    0.1285   0.958   0.392
## grouptreatment  0.3985    0.1963   2.030   0.112
##
## Residual standard error: 1.127 on 4 degrees of freedom
## Multiple R-squared:  0.05731,    Adjusted R-squared:  -0.1784
## F-statistic: 0.2432 on 1 and 4 DF,  p-value: 0.6478
```

Model 2

```
anthers$p <- anthers$obtained/anthers$prepared
anthers$logForce <- log(anthers$force)
glm.2 <- glm(p ~ group + logForce, weights = prepared, data = anthers, family = binomial(logit))
summary(glm.2)
```

```
##
## Call:
## glm(formula = p ~ group + logForce, family = binomial(logit),
##      data = anthers, weights = prepared)
##
## Deviance Residuals:
##      1      2      3      4      5      6
## -0.74964 -0.00509  0.72746  0.99006 -0.13512 -0.72744
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.87673    0.48701   1.800   0.0718 .
## grouptreatment  0.40684    0.17462   2.330   0.0198 *
## logForce       -0.15459    0.09702  -1.593   0.1111
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 10.4520  on 5  degrees of freedom
## Residual deviance:  2.6188  on 3  degrees of freedom
## AIC: 38.187
##
## Number of Fisher Scoring iterations: 3
```

```
summary.lm(glm.2)
```

```
##
```

```
## Call:
## glm(formula = p ~ group + logForce, family = binomial(logit),
##      data = anthers, weights = prepared)
##
## Weighted Residuals:
##      1      2      3      4      5      6
## -0.752149 -0.005092  0.727404  0.975233 -0.135287 -0.730611
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.87673    0.45321   1.934   0.1485
## grouptreatment  0.40684    0.16250   2.504   0.0874 .
## logForce      -0.15459    0.09029  -1.712   0.1854
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9306 on 3 degrees of freedom
## Multiple R-squared:  0.1477, Adjusted R-squared:  -0.4204
## F-statistic:  0.26 on 2 and 3 DF,  p-value: 0.7868
```

Model 3

```
lapply(anthers, class)
```

```
## $group
## [1] "factor"
##
## $force
## [1] "integer"
##
## $prepared
## [1] "integer"
##
## $obtained
## [1] "integer"
##
## $p
## [1] "numeric"
##
## $logForce
## [1] "numeric"
```

```
glm.3 <-glm(p ~ group * logForce , weights = prepared, data = anthers, family = binomial(logit))
summary(glm.3)
```

```
##
## Call:
## glm(formula = p ~ group * logForce, family = binomial(logit),
##      data = anthers, weights = prepared)
##
## Deviance Residuals:
```

```
##           1           2           3           4           5           6
## 0.03611 -0.09370 0.05466 0.04305 -0.09855 0.05560
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.23389   0.62839   0.372  0.7097
## grouptreatment    1.97711   0.99802   1.981  0.0476 *
## logForce        -0.02274   0.12685  -0.179  0.8577
## grouptreatment:logForce -0.31862   0.19888  -1.602  0.1091
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 10.451974 on 5 degrees of freedom
## Residual deviance: 0.027728 on 2 degrees of freedom
## AIC: 37.596
##
## Number of Fisher Scoring iterations: 3
```

Task 13

```
glm.1 <-glm(p ~ group, weights = prepared, data = anthers, family = binomial(logit))
glm.1
```

```
##
## Call: glm(formula = p ~ group, family = binomial(logit), data = anthers,
## weights = prepared)
##
## Coefficients:
## (Intercept) grouptreatment
##      0.1231      0.3985
##
## Degrees of Freedom: 5 Total (i.e. Null); 4 Residual
## Null Deviance: 10.45
## Residual Deviance: 5.173 AIC: 38.74
```

```
glm.2 <-glm(p ~ group + force, weights = prepared, data = anthers, family = binomial(logit))
glm.2
```

```
##
## Call: glm(formula = p ~ group + force, family = binomial(logit), data = anthers,
## weights = prepared)
##
## Coefficients:
## (Intercept) grouptreatment force
##      0.306643      0.405554 -0.000997
##
## Degrees of Freedom: 5 Total (i.e. Null); 3 Residual
## Null Deviance: 10.45
## Residual Deviance: 2.922 AIC: 38.49
```

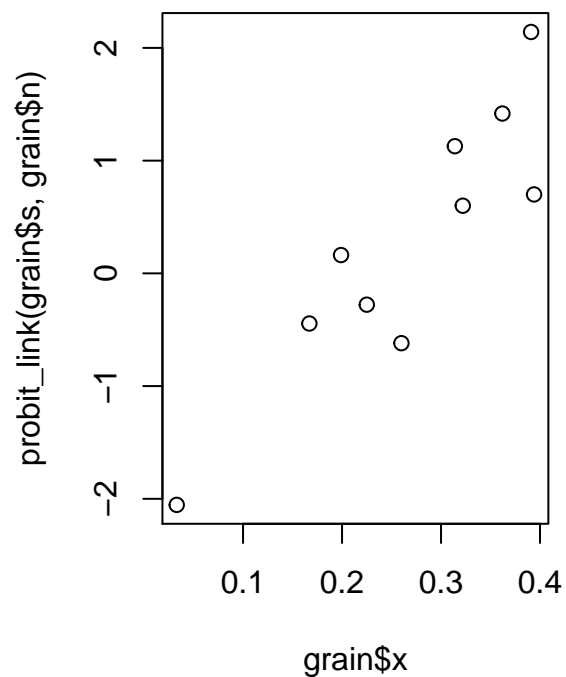
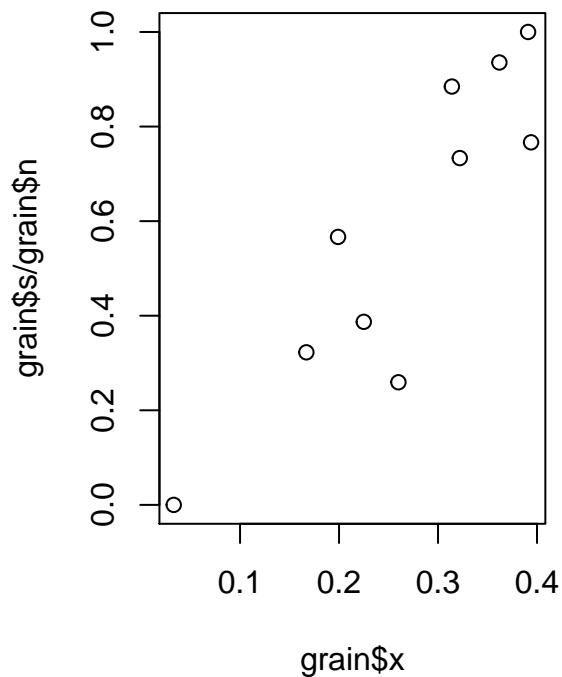
The conclusions do not change at all. The residual deviances for both models are rather similar.

4.5.1 (Task 14)

```
grain <- e$grain

probit_link<- function(s,n){
  y<-(s+0.5)/(n+1)
  (qnorm(y))
}

par(mfrow=c(1,2))
plot(grain$x, grain$s/ grain$n)
plot(grain$x, probit_link(grain$s, grain$n))
```



```
head(grain)
```

```
##      x  n  s
## 1 0.394 30 23
## 2 0.391 30 30
```

```
## 3 0.362 31 29
## 4 0.322 30 22
## 5 0.314 26 23
## 6 0.260 27 7
```

```
grain$p_star <- (grain$s + 0.5)/ (grain$n+1)
grain$p <- (grain$s)/ (grain$n)
```

2 Null deviance

```
glm(p ~ 1 , weights = grain$n, data= grain, family=binomial(link= 'probit'))
```

```
##
## Call: glm(formula = p ~ 1, family = binomial(link = "probit"), data = grain,
## weights = grain$n)
##
## Coefficients:
## (Intercept)
## 0.2444
##
## Degrees of Freedom: 9 Total (i.e. Null); 9 Residual
## Null Deviance: 138
## Residual Deviance: 138 AIC: 167.6
```

Can reproduce results from script only with `p_start`. But so far we only fitted models with $p = s/n$. Using `p_star` also produces a warning

```
#glm(p_star ~ 1 + x , weights = grain$n, data= grain, family=binomial(link= 'probit'))
glin <- glm(p ~ 1 + x , weights = grain$n, data= grain, family=binomial(link= 'probit'))
names(glin)
```

```
## [1] "coefficients" "residuals" "fitted.values"
## [4] "effects" "R" "rank"
## [7] "qr" "family" "linear.predictors"
## [10] "deviance" "aic" "null.deviance"
## [13] "iter" "weights" "prior.weights"
## [16] "df.residual" "df.null" "y"
## [19] "converged" "boundary" "model"
## [22] "call" "formula" "terms"
## [25] "data" "offset" "control"
## [28] "method" "contrasts" "xlevels"
```

```
glin$deviance
```

```
## [1] 35.47649
```

```
glin$null.deviance
```

```
## [1] 138.0006
```



```
glin$null.deviance-glin$deviance
```

```
## [1] 102.5241
```

The change in deviance (94 on 1 df) is clearly very high showing an improvement of the model with a linear term over the null model (overwhelming evidence to reject $H_0: \beta_1 = 0$)

But the actual deviance for the model is high 35.4764889 providing evidence against this Binomial model $\chi^2_{8,0.9995}$:

```
qchisq(0.9995,8 )
```

```
## [1] 27.86805
```

5

Binomial model estimating ϕ as $D(y, \hat{\mu})/(n - p)$.

```
glin$deviance / (glin$df.residual)
```

```
## [1] 4.434561
```

```
glq <- glm(p ~ 1 + x , weights = grain$n, data= grain, family=quasi)
glq$deviance
```

```
## [1] 5.633424
```

6

Standard errors for parameter estimates are then multiplied by:

```
sqrt(glin$deviance / glin$df.residual)
```

```
## [1] 2.10584
```

7

Improvement over the null model on 1 df.

```
(glin$null.deviance-glin$deviance)/ (glin$deviance / glin$df.residual)
```

```
## [1] 23.11934
```

The scaled deviance for this model:

```
glin$deviance/(glin$deviance / glin$df.residual)
```

```
## [1] 8
```

```
qchisq(0.95,7)
```

```
## [1] 14.06714
```

```
sglin <- summary(glin)
```

with $e.s.e(\hat{\beta}_1) =$

```
sglin$coefficients[2,"Std. Error"]
```

```
## [1] 0.9810898
```

```
sglin$coefficients[2,"Std. Error"] * sqrt(glin$deviance / glin$df.residual)
```

```
## [1] 2.066018
```

```
ese_b=sglin$coefficients[2,"Std. Error"] * sqrt(glin$deviance / glin$df.residual)
```

So the wald test statistics

```
coefficients(glin)[2]
```

```
##          x
```

```
## 8.641606
```

```
coefficients(glin)[2] / ese_b
```

```
##          x
```

```
## 4.182735
```

```
t = coefficients(glin)[2] / ese_b
```

The slope is highly significant.

```
1-pt(t, df=7)
```

```
##          x
```

```
## 0.00206159
```

using quasi (same as subsection 5)

```
glq <- glm(p_star ~ 1 + x , weights = grain$n, data= grain, family=quasi())
glq$deviance
```

```
## [1] 5.254139
```

Somehow the numbers obtained are not equal to those in the lecture notes (3.62): Also trying to run the glm with `quasi(link = "probit", variance = "constant")` does fail.

4.6

120 individuals collected as part of a case-control study:

```
CHD <- e$CHD
head(CHD)
```

```
##      status sat.fat gender age
## 1         1         2      1  48
## 2         1         1      1  58
## 3         0         0      0  49
## 4         1         1      0  47
## 5         0         1      0  46
## 6         1         2      0  47
```

```
null.glm<-glm(status~1, family=binomial,data=CHD)

gender.glm<-glm(status~gender,family=binomial,data=CHD)
summary(gender.glm)
```

```
##
## Call:
## glm(formula = status ~ gender, family = binomial, data = CHD)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.515  -1.163   0.874   0.874   1.192
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.03509    0.26495  -0.132   0.8946
## gender       0.80056    0.37875   2.114   0.0345 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 162.30  on 119  degrees of freedom
## Residual deviance: 157.74  on 118  degrees of freedom
## AIC: 161.74
##
## Number of Fisher Scoring iterations: 4
```

```
anova(gender.glm, null.glm, test="Chi")
```

```
## Analysis of Deviance Table
##
## Model 1: status ~ gender
## Model 2: status ~ 1
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      118      157.74
## 2      119      162.30 -1   -4.5554  0.03282 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Odds ratio for being affected by CHD in males compared to females is $e^{\hat{\beta}_1}$:

```
exp(coefficients(gender.glm)[2])
```

```
##   gender
## 2.226786
```

4.6.2 X_i is a factor with 3 levels

```
head(CHD)
```

```
##   status sat.fat gender age
## 1      1      2      1  48
## 2      1      1      1  58
## 3      0      0      0  49
## 4      1      1      0  47
## 5      0      1      0  46
## 6      1      2      0  47
```

```
unique(CHD$sat.fat)
```

```
## [1] 2 1 0
```

```
satfat.glm<- glm(status~sat.fat,family=binomial,data=CHD)
summary(satfat.glm)
```

```
##
## Call:
## glm(formula = status ~ sat.fat, family = binomial, data = CHD)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7439  -1.0279   0.7023   0.9909   1.3346
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept)  -0.3623      0.2970  -1.220  0.22251
## sat.fat      0.8181      0.2644   3.095  0.00197 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 162.30  on 119  degrees of freedom
## Residual deviance: 151.86  on 118  degrees of freedom
## AIC: 155.86
##
## Number of Fisher Scoring iterations: 4
```

```
qchisq(0.995,satfat.glm$df.residual)
```

```
## [1] 161.3141
```

```
anova(satfat.glm, null.glm,test="Chi")
```

```
## Analysis of Deviance Table
##
## Model 1: status ~ sat.fat
## Model 2: status ~ 1
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1         118       151.86
## 2         119       162.30 -1  -10.438 0.001234 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4.6.3 X_i is continous

```
head(CHD)
```

```
##   status sat.fat gender age
## 1      1      2      1  48
## 2      1      1      1  58
## 3      0      0      0  49
## 4      1      1      0  47
## 5      0      1      0  46
## 6      1      2      0  47
```

```
age.glm<- glm(status~age,family=binomial,data=CHD)
summary(age.glm)
```

```
##
## Call:
## glm(formula = status ~ age, family = binomial, data = CHD)
##
## Deviance Residuals:
```

```
##      Min      1Q   Median      3Q      Max
## -1.6543 -1.2462  0.8034   1.0269   1.4730
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.20096    1.11289  -1.978   0.0480 *
## age          0.05459    0.02340   2.333   0.0196 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 162.30  on 119  degrees of freedom
## Residual deviance: 156.42  on 118  degrees of freedom
## AIC: 160.42
##
## Number of Fisher Scoring iterations: 4
```

```
qchisq(0.995,age.glm$df.residual)
```

```
## [1] 161.3141
```

```
qchisq(0.995,1)
```

```
## [1] 7.879439
```

```
anova(age.glm, null.glm,test="Chi")
```

```
## Analysis of Deviance Table
##
## Model 1: status ~ age
## Model 2: status ~ 1
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      118      156.42
## 2      119      162.30 -1   -5.8799  0.01531 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4.6.4 Multiple explanatory variables

```
colnames(CHD)
```

```
## [1] "status" "sat.fat" "gender" "age"
```

```
gender.glm<-glm(status~gender+age ,family=binomial,data=CHD)
summary(gender.glm)
```

```
##
## Call:
## glm(formula = status ~ gender + age, family = binomial, data = CHD)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8323  -1.1603   0.7256   0.9596   1.5802
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.59535     1.13704  -2.283   0.0225 *
## gender       0.80587     0.38835   2.075   0.0380 *
## age         0.05436     0.02347   2.317   0.0205 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 162.30  on 119  degrees of freedom
## Residual deviance: 152.03  on 117  degrees of freedom
## AIC: 158.03
##
## Number of Fisher Scoring iterations: 4
```

```
coefficients(gender.glm)[2]
```

```
##      gender
## 0.8058682
```

Adjusting for age does not change the estimated odds ratio 2.2386393.