

# MATH552 Group Project

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```
neomod <- read.table("../data/neomod_isam12.dat", header = T)
```

```
#plot(neomod)
```

```
summary(neomod)
```

```
##      cns      size      gest      bwt
## Min.   :0.0000 Min.   :0.0000 Min.   :1.000 Min.   :0.482
## 1st Qu.:0.0000 1st Qu.:0.0000 1st Qu.:2.000 1st Qu.:1.159
## Median :0.0000 Median :1.0000 Median :3.000 Median :1.460
## Mean   :0.4718 Mean   :0.7103 Mean   :3.197 Mean   :1.699
## 3rd Qu.:1.0000 3rd Qu.:1.0000 3rd Qu.:4.000 3rd Qu.:2.041
## Max.   :1.0000 Max.   :1.0000 Max.   :5.000 Max.   :5.443
##      emp.f      emp.m      edu      re.ad
## Min.   :0.0000 Min.   :0.0000 Min.   :1.000 Min.   :0.0000
## 1st Qu.:1.0000 1st Qu.:0.0000 1st Qu.:2.000 1st Qu.:0.0000
## Median :1.0000 Median :0.0000 Median :2.000 Median :0.0000
## Mean   :0.8905 Mean   :0.4832 Mean   :2.421 Mean   :0.4274
## 3rd Qu.:1.0000 3rd Qu.:1.0000 3rd Qu.:3.000 3rd Qu.:1.0000
## Max.   :1.0000 Max.   :1.0000 Max.   :4.000 Max.   :1.0000
##      los      sex      accom
## Min.   :1.386 Min.   :0.0000 Min.   :0.0000
## 1st Qu.:3.045 1st Qu.:0.0000 1st Qu.:0.0000
## Median :3.555 Median :1.0000 Median :1.0000
## Mean   :3.548 Mean   :0.5242 Mean   :0.7298
## 3rd Qu.:4.111 3rd Qu.:1.0000 3rd Qu.:1.0000
## Max.   :5.613 Max.   :1.0000 Max.   :1.0000
```

```
# Attach to allow for better addressing
```

```
attach(neomod)
```

## Factorisation

Modify variables that are int or str to factor.

```
neomod$cns      = factor(cns)
neomod$size     = factor(size)
neomod$gest     = factor(gest)
neomod$emp.f    = factor(emp.f)
neomod$emp.m    = factor(emp.m)
neomod$edu      = factor(edu)
```

```
neomod$re.ad = factor(re.ad)
neomod$sex    = factor(sex)
neomod$accom  = factor(accom)
```

```
summary(neomod)
```

```
##   cns      size    gest      bwt      emp.f    emp.m    edu      re.ad
## 0:786    0: 431    1: 44   Min.   :0.482    0: 163    0:769    1: 77    0:852
## 1:702    1:1057   2:384   1st Qu.:1.159   1:1325    1:719    2:871    1:636
##                               3:500   Median :1.460                               3:376
##                               4:355   Mean  :1.699                               4:164
##                               5:205   3rd Qu.:2.041
##                               Max.   :5.443
##      los      sex    accom
## Min.   :1.386    0:708    0: 402
## 1st Qu.:3.045    1:780    1:1086
## Median :3.555
## Mean    :3.548
## 3rd Qu.:4.111
## Max.    :5.613
```

```
head(neomod)
```

```
##   cns size gest    bwt emp.f emp.m edu re.ad      los sex accom
## 1  0   1   2 1.040     1     0   4     1 4.510860  1     1
## 2  0   1   3 2.353     1     1   4     0 4.234107  1     1
## 3  1   1   5 3.204     1     1   2     0 1.945910  1     1
## 4  1   1   3 1.389     1     1   2     0 3.332205  1     1
## 5  1   0   3 0.970     1     0   3     0 3.367296  0     1
## 6  1   0   5 3.033     1     1   4     0 2.833213  1     1
```

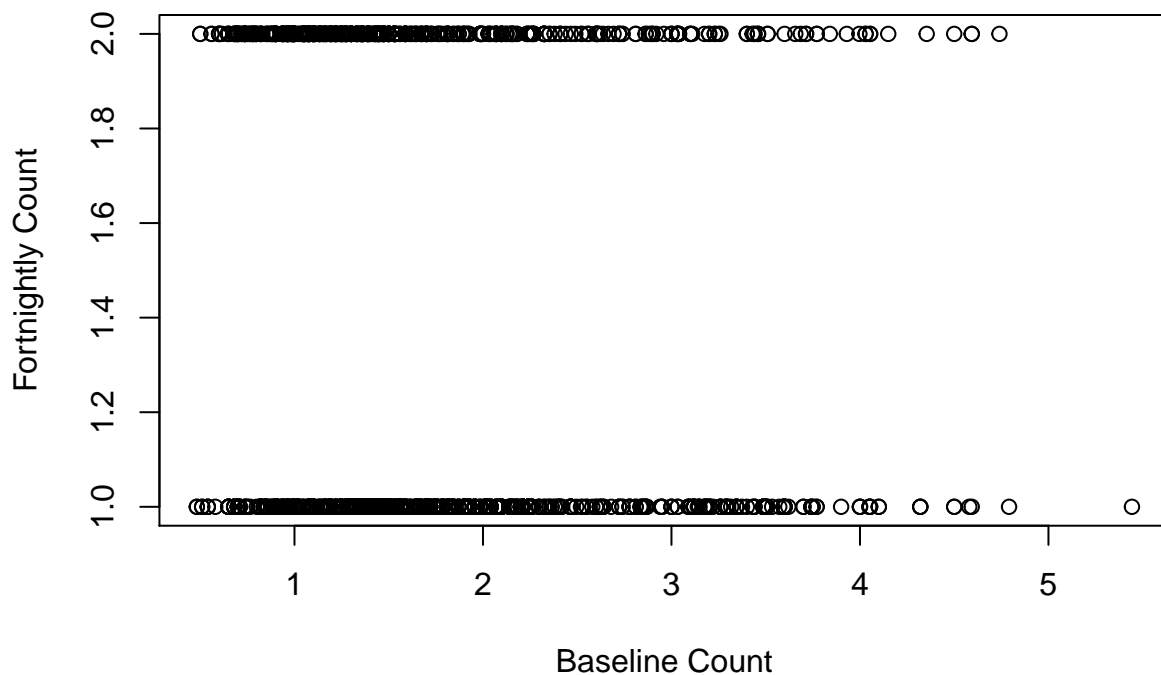
```
# Representative Model
mod1 = glm(re.ad ~ bwt,
           data=neomod,
           family=binomial)
```

```
summary(mod1)
```

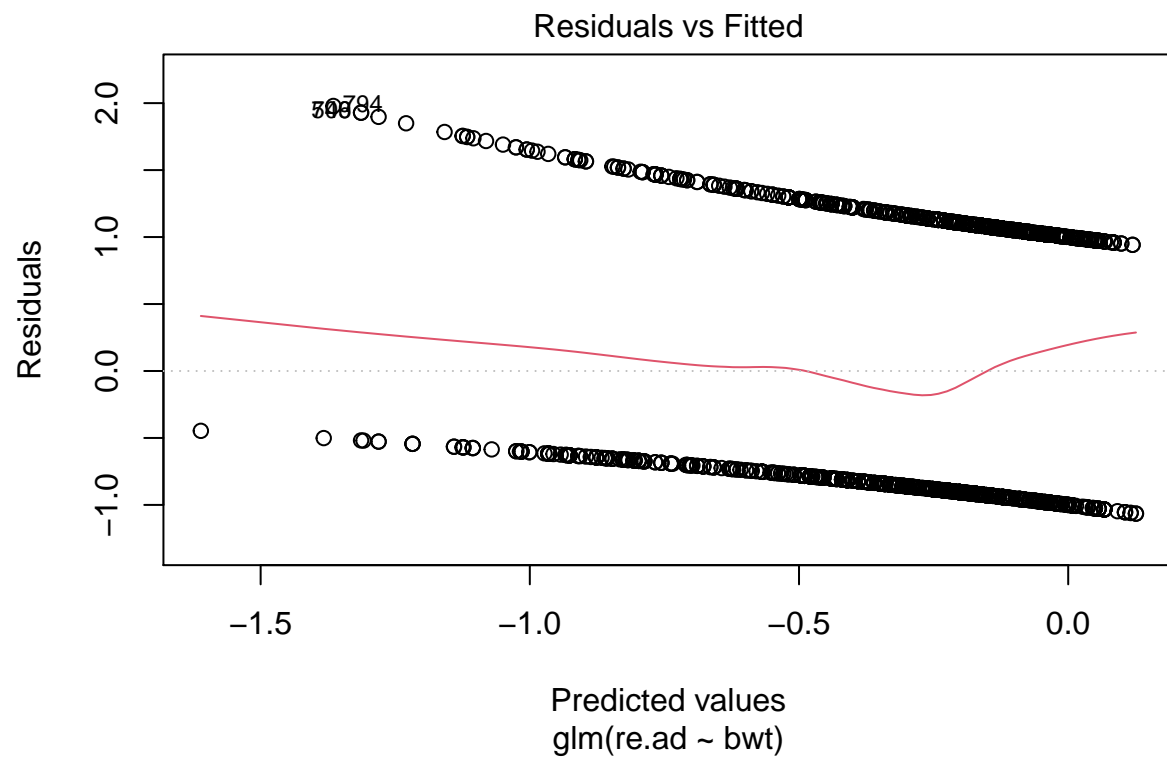
```
##
## Call:
## glm(formula = re.ad ~ bwt, family = binomial, data = neomod)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.2313  -1.0849  -0.8947   1.2369   1.7846
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.29460    0.12571   2.343  0.0191 *
```

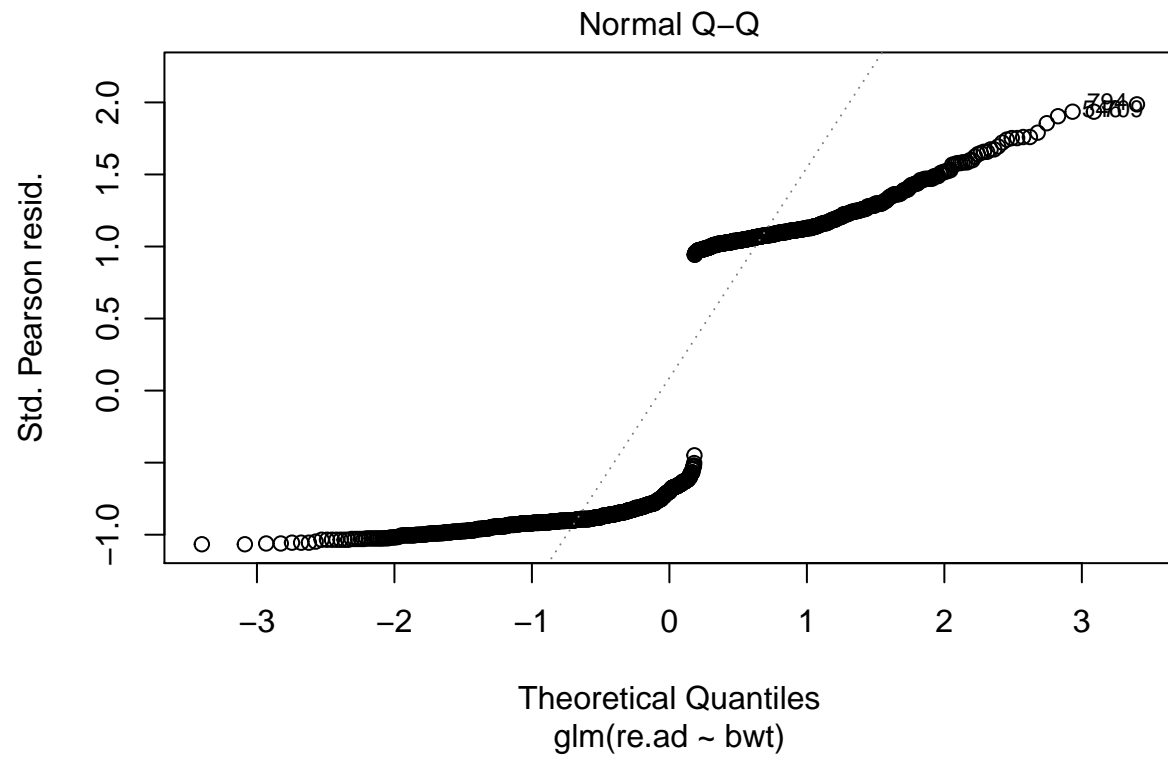
```
## bwt          -0.35011    0.06914   -5.064   4.1e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 2031.3  on 1487  degrees of freedom
## Residual deviance: 2004.2  on 1486  degrees of freedom
## AIC: 2008.2
##
## Number of Fisher Scoring iterations: 4
```

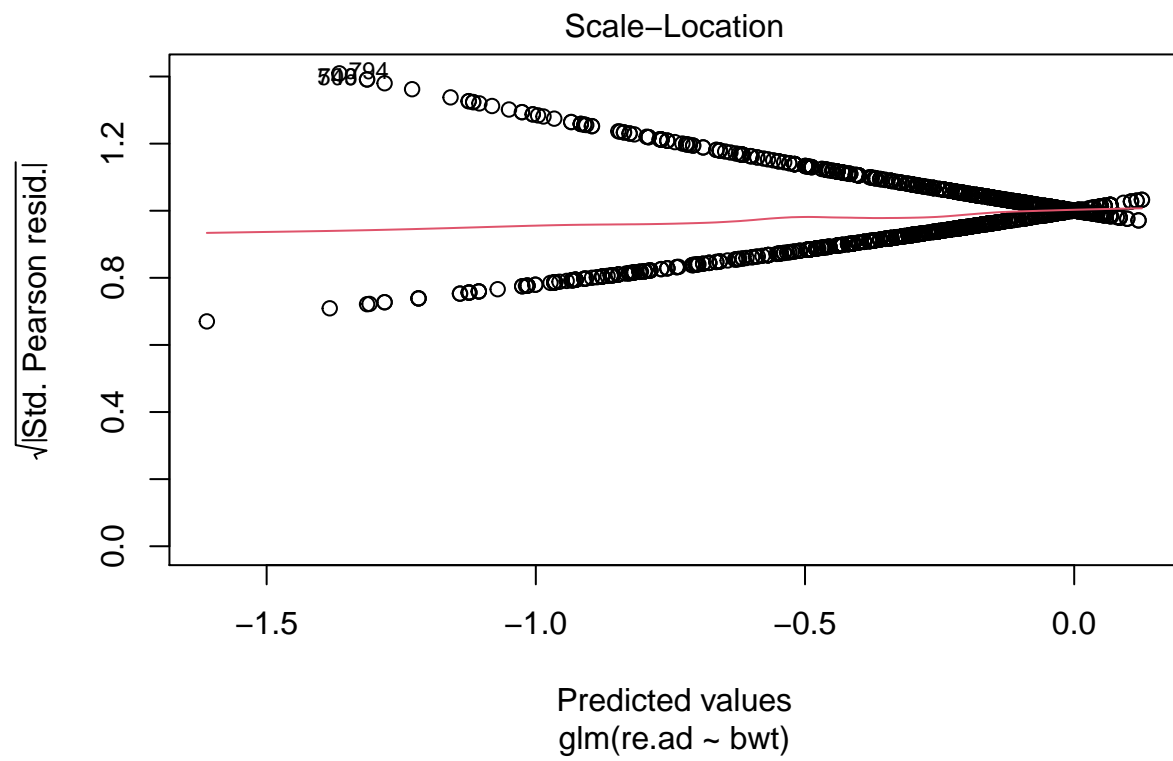
```
# Representative plot
par(mfrow=c(1,1))
plot(neomod$bwt,
      neomod$re.ad,
      xlab="Baseline Count",
      ylab="Fortnightly Count")
abline(mod1, col=2)
```

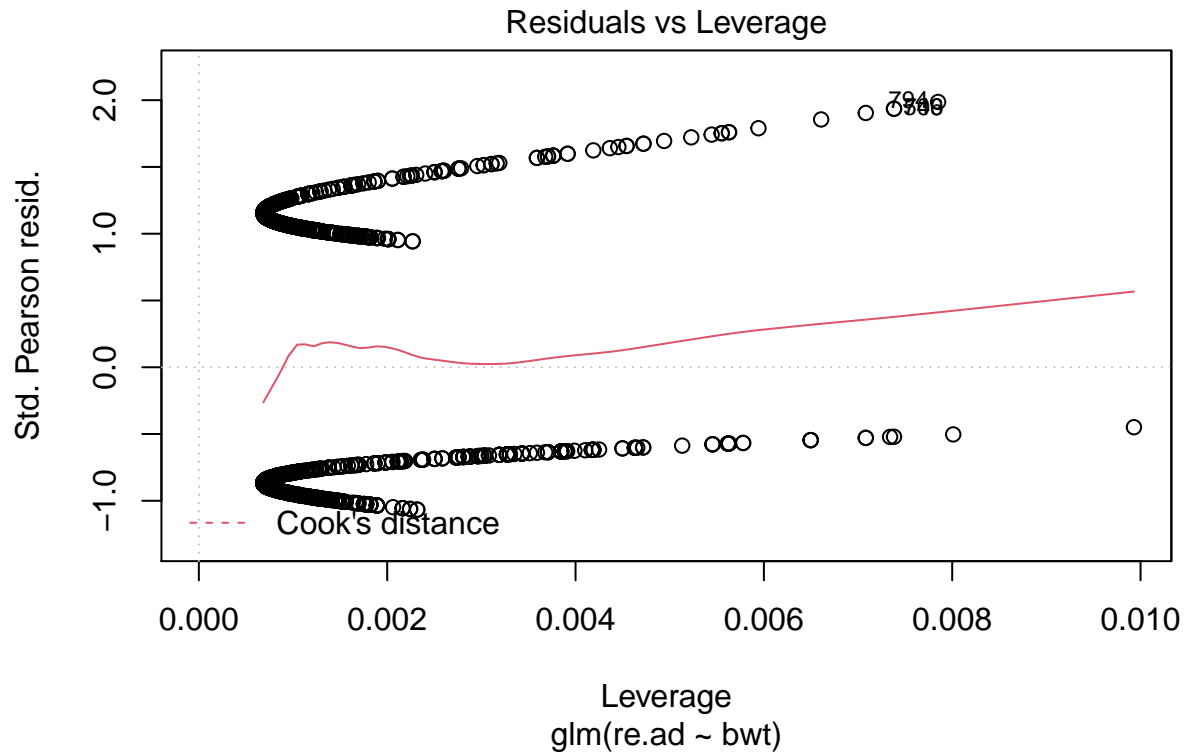


```
# Representative plot
plot(mod1)
```









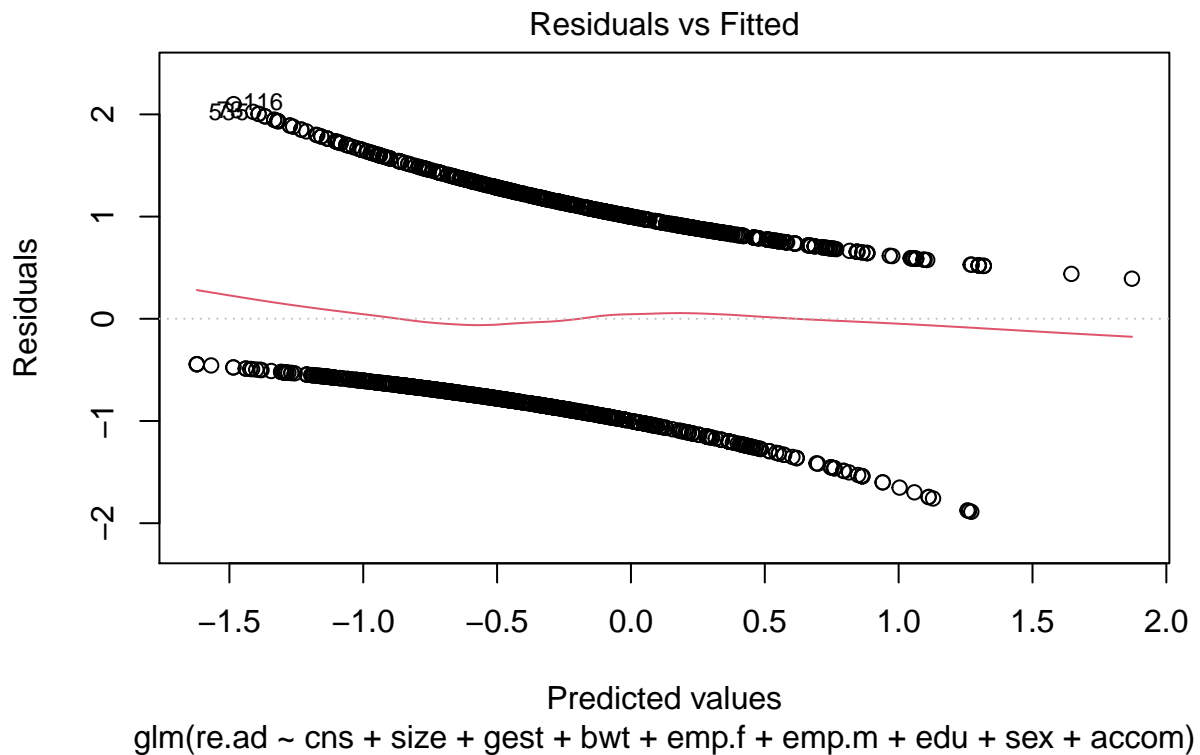
```
# Random model - probably wrong
mod2.re.ad = glm(re.ad ~ cns + size + gest + bwt + emp.f + emp.m + edu + sex + accom,
  data= neomod,
  family=binomial)
```

```
summary(mod2.re.ad)
```

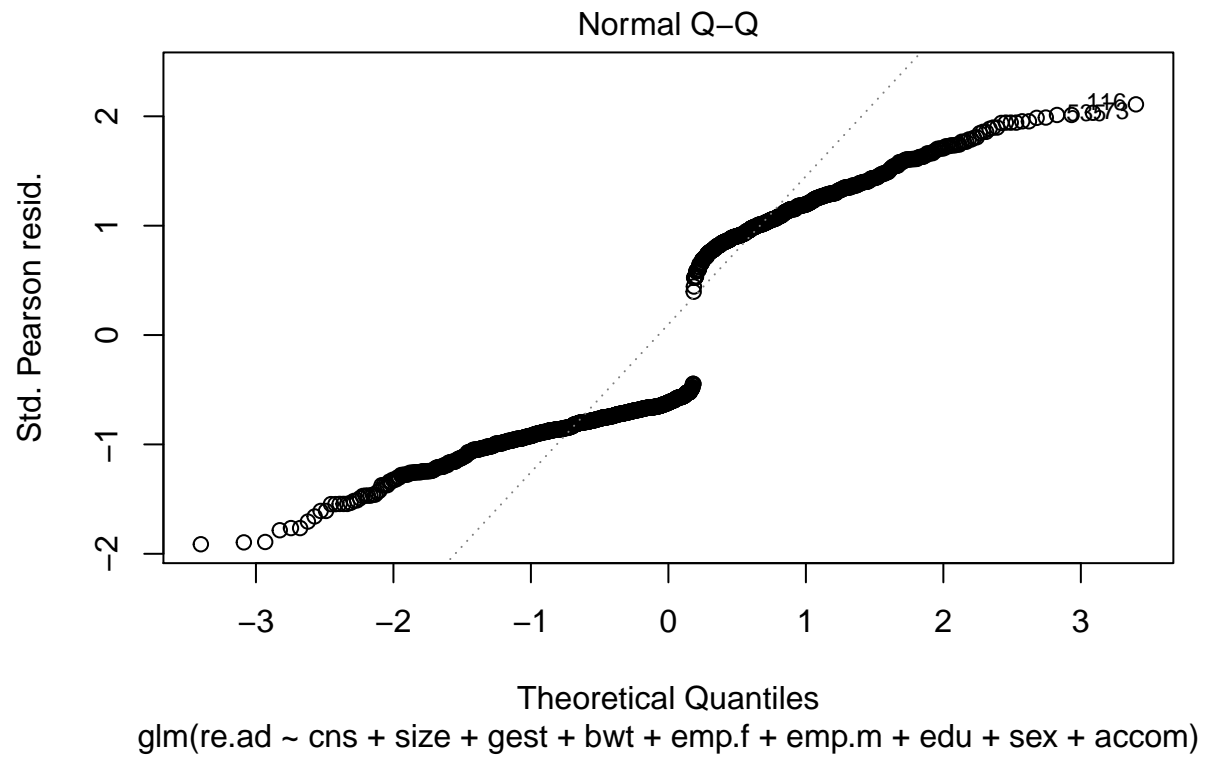
```
##
## Call:
## glm(formula = re.ad ~ cns + size + gest + bwt + emp.f + emp.m +
##      edu + sex + accom, family = binomial, data = neomod)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7427  -1.0038  -0.7997   1.1824   1.8377
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.42839    0.45780   3.120 0.001808 **
## cns1          -0.01603    0.11128  -0.144 0.885433
## size1          0.11750    0.12115   0.970 0.332117
## gest2         -0.76823    0.35558  -2.160 0.030735 *
## gest3         -1.31581    0.36022  -3.653 0.000259 ***
## gest4         -1.44663    0.38183  -3.789 0.000151 ***
## gest5         -1.20174    0.45826  -2.622 0.008731 **
## bwt           -0.21167    0.11790  -1.795 0.072601 .
```

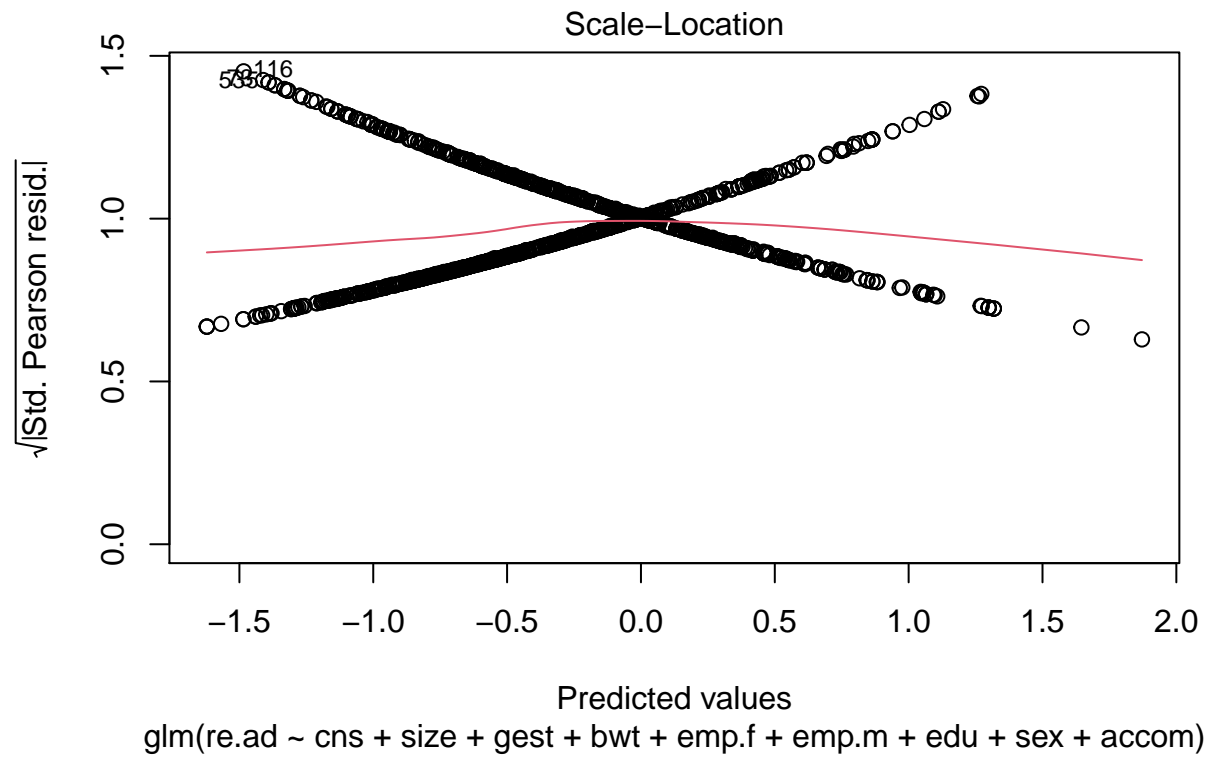
```
## emp.f1      -0.21245    0.18752   -1.133  0.257238
## emp.m1      -0.30657    0.11281   -2.717  0.006578 **
## edu2        -0.06275    0.25075   -0.250  0.802405
## edu3         0.07672    0.26961    0.285  0.775986
## edu4         0.17870    0.29607    0.604  0.546116
## sex1         0.55258    0.11275    4.901  9.54e-07 ***
## accom1      -0.35208    0.13795   -2.552  0.010704 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 2031.3  on 1487  degrees of freedom
## Residual deviance: 1926.1  on 1473  degrees of freedom
## AIC: 1956.1
##
## Number of Fisher Scoring iterations: 4
```

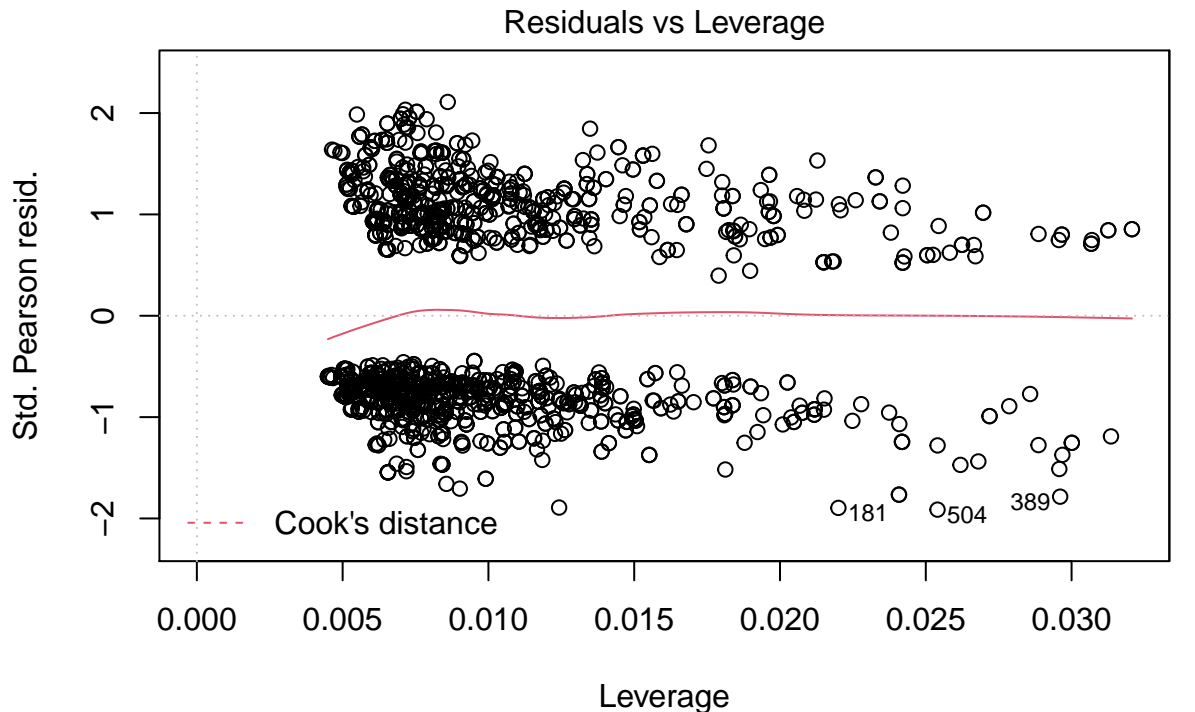
```
plot(mod2.re.ad)
```











glm(re.ad ~ cns + size + gest + bwt + emp.f + emp.m + edu + sex + accom)

```
# Random model - probably wrong
mod2.los = glm(los ~ cns + size + gest + bwt + emp.f + emp.m + edu + sex + accom,
  data= neomod,
  family=Gamma(link=inverse))

summary(mod2.los)
```

```
##
## Call:
## glm(formula = los ~ cns + size + gest + bwt + emp.f + emp.m +
##     edu + sex + accom, family = Gamma(link = inverse), data = neomod)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.62858 -0.07900 -0.00551  0.07554  0.61557
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.167692   0.007882  21.276 < 2e-16 ***
## cns1         0.012280   0.002216   5.540 3.57e-08 ***
## size1        0.003584   0.002393   1.498 0.134469
## gest2        0.019846   0.005224   3.799 0.000151 ***
## gest3        0.050687   0.005485   9.241 < 2e-16 ***
## gest4        0.080400   0.006195  12.978 < 2e-16 ***
## gest5        0.082450   0.008470   9.734 < 2e-16 ***
## bwt          0.032725   0.002614  12.519 < 2e-16 ***
```

```
## emp.f1      0.006436   0.003642   1.767 0.077369 .
## emp.m1      0.004156   0.002248   1.848 0.064734 .
## edu2        0.009237   0.005032   1.836 0.066624 .
## edu3        0.001732   0.005381   0.322 0.747680
## edu4       -0.003761   0.005877  -0.640 0.522338
## sex1       -0.011305   0.002212  -5.111 3.62e-07 ***
## accom1     -0.002905   0.002726  -1.065 0.286849
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.02225456)
##
## Null deviance: 72.645  on 1487  degrees of freedom
## Residual deviance: 33.360  on 1473  degrees of freedom
## AIC: 2305.1
##
## Number of Fisher Scoring iterations: 4
```

```
plot(mod2.los)
```

