R Notebook

This is an R Markdown Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Ctrl+Shift+Enter*.

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

#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)
```

```r
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
```

```r
head(neomod)
```

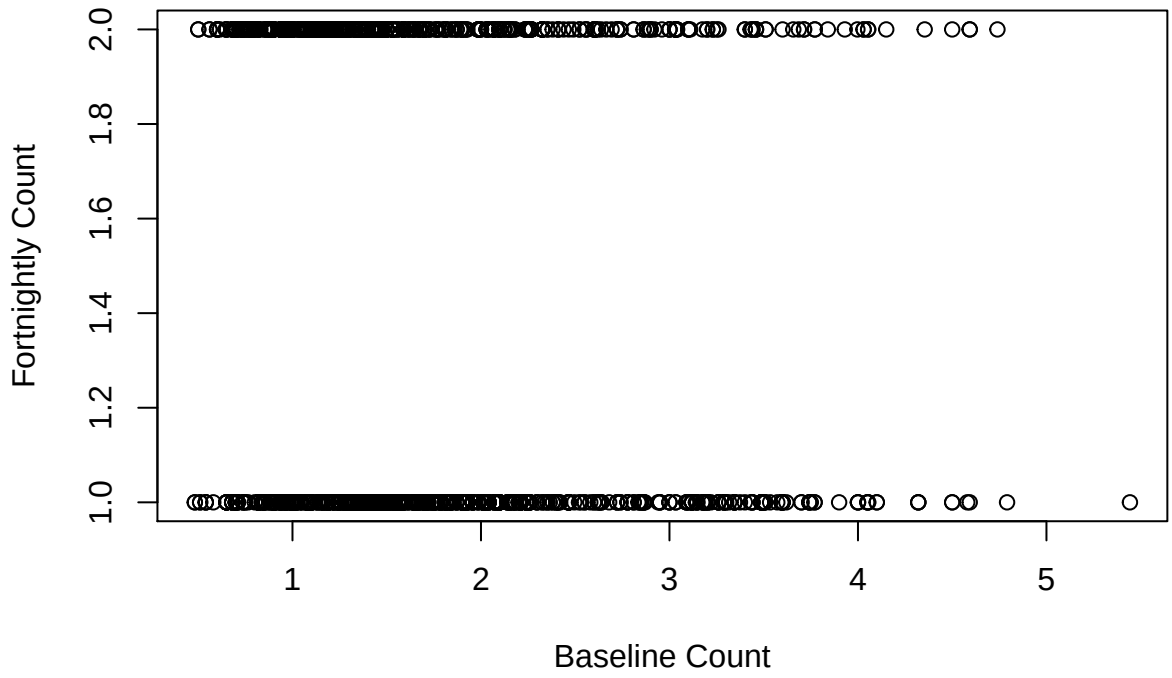
```
##   cns size gest   bwt emp.f emp.m edu re.ad      los sex accom
## 1   0    1    2 1.040     1     0   4     1 4.510860   1     1
## 2   0    1    3 2.353     1     1   4     0 4.234107   1     1
## 3   1    1    5 3.204     1     1   2     0 1.945910   1     1
## 4   1    1    3 1.389     1  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

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


summary(mod1)
```

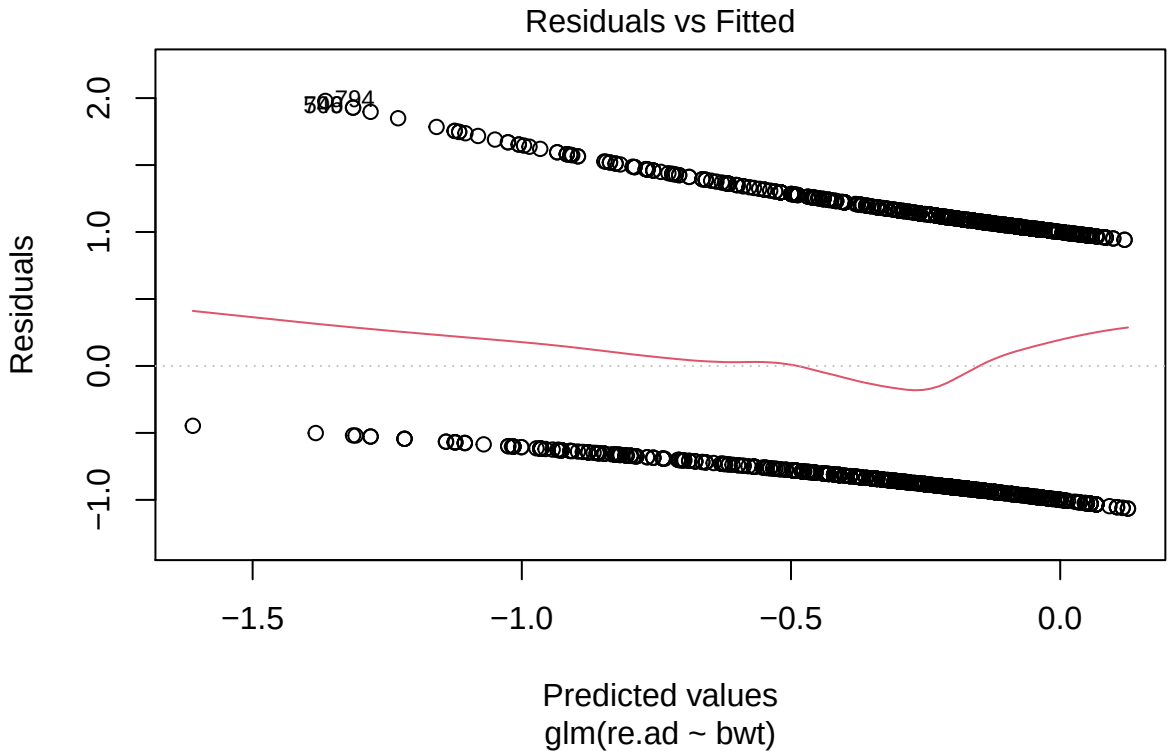
```
##
## Call:
## glm(formula = re.ad ~ bwt, family = binomial, data = neomod)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2313  -1.0849  -0.8947   1.2369   1.7846
```

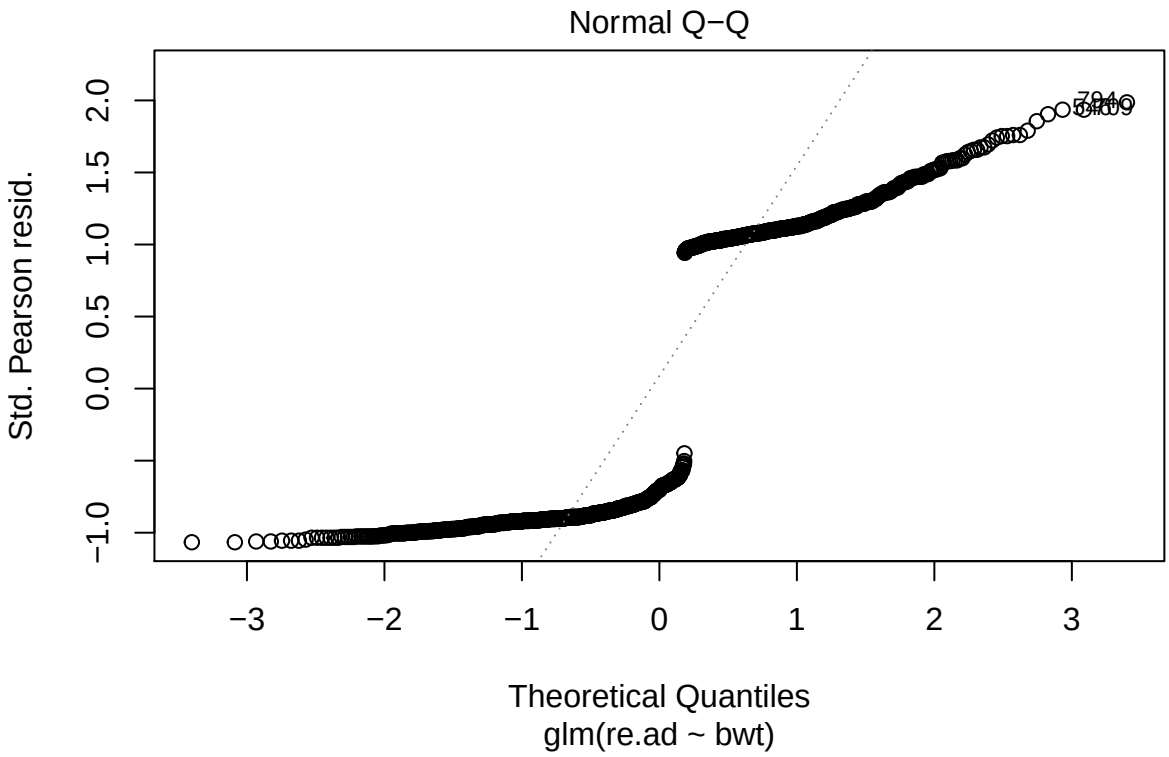
```
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.29460    0.12571   2.343   0.0191 *
## bwt         -0.35011    0.06914  -5.064  4.1e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family 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
```

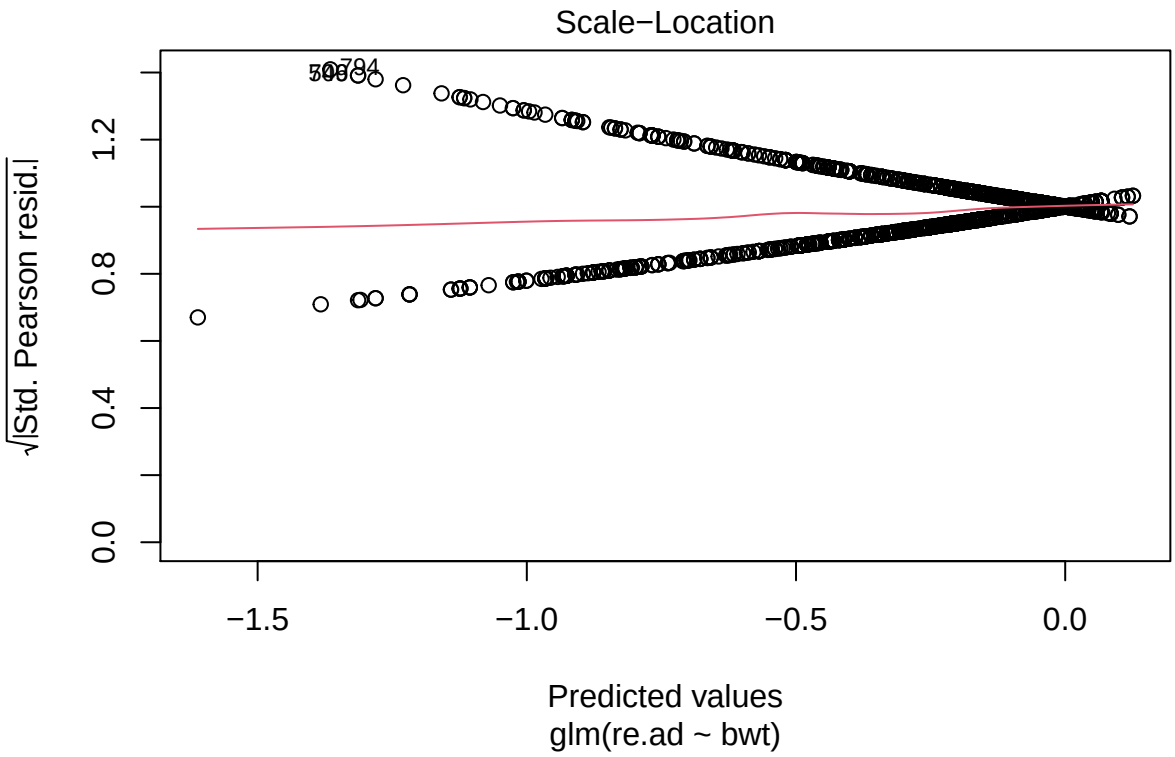
```r
# Representative plot
par(mfrow=c(1,1))
plot(neomod$bwt,
     neomod$re.ad,
     xlab="Baseline Count",
     ylab="Fortnightly Count")
abline(mod1, col=2)
```

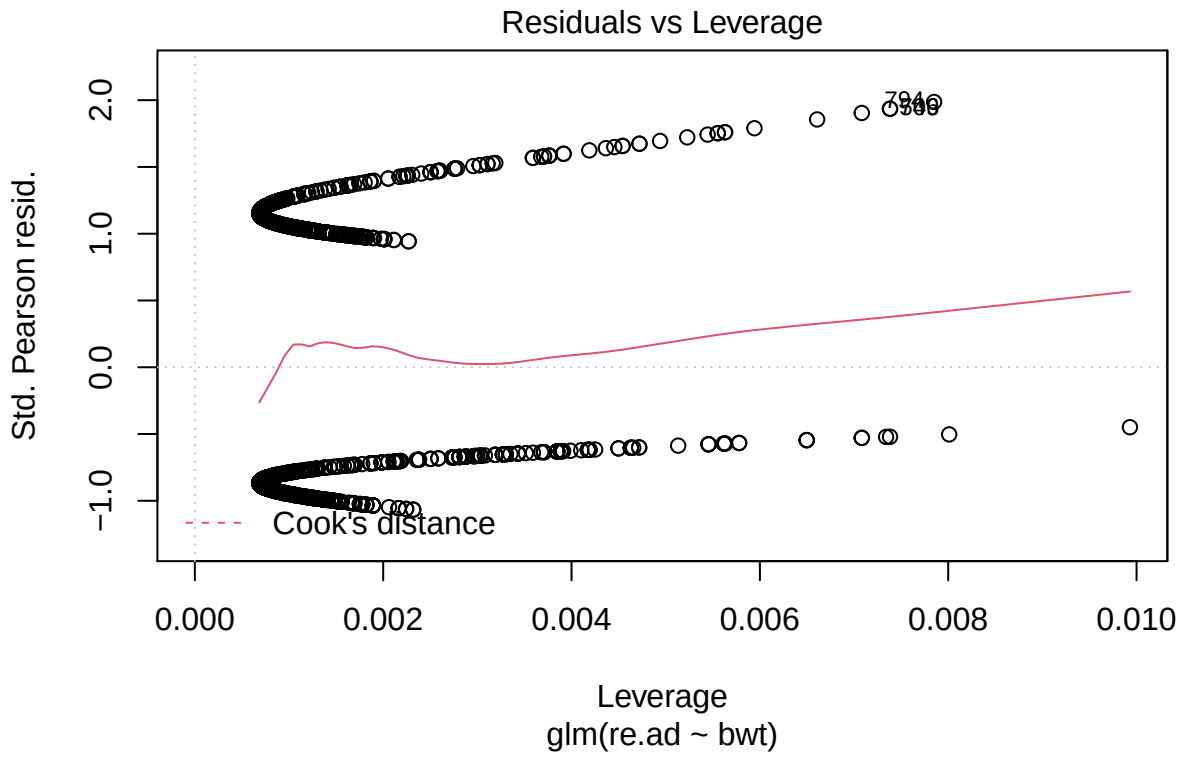


```r
# Representative plot
plot(mod1)
```




Normal Q−Q
Std. Pearson resid.
−1.0
0.0
0.5
1.0
1.5
2.0
−3
−2
−1
0
1
2
3
Theoretical Quantiles
glm(re.ad ~ bwt)


Scale−Location
√|Std. Pearson resid.|
0.0
0.4
0.8
1.2
−1.5
−1.0
−0.5
0.0
Predicted values
glm(re.ad ~ bwt)

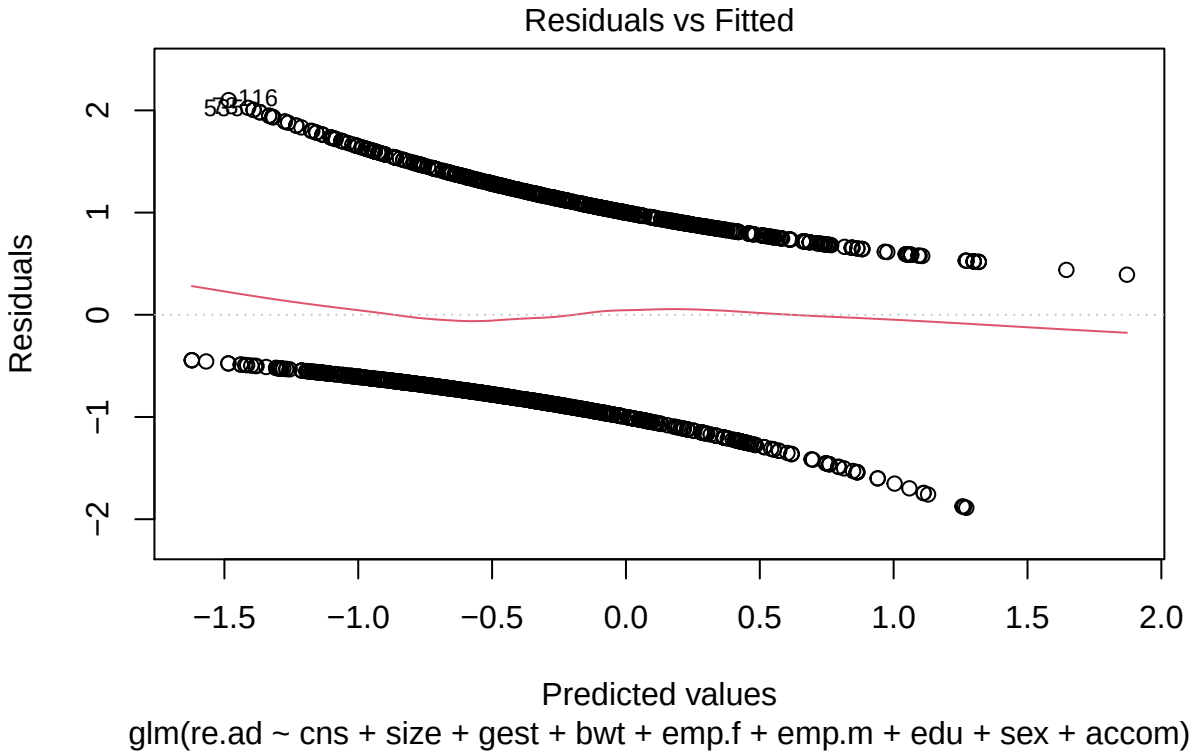


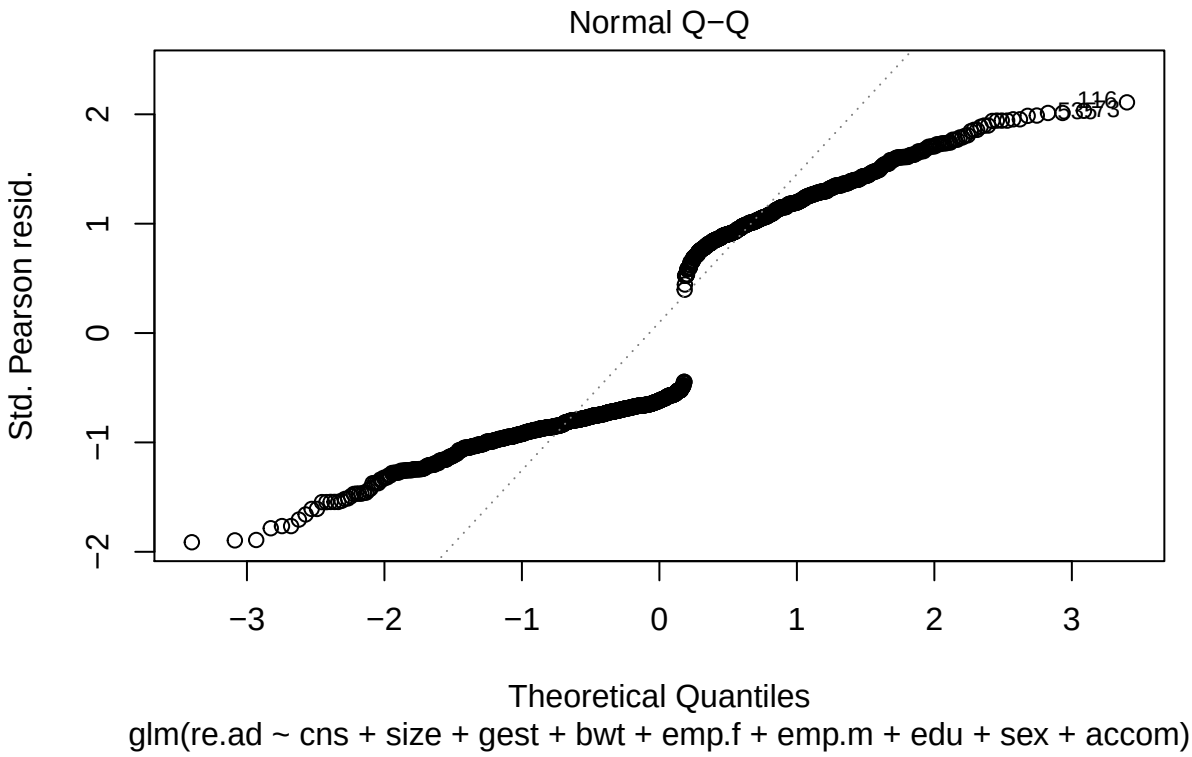

```
# Random model - probably wrong
mod2.re.ad = glm(re.ad ~ cns + size + gest + bwt + emp.f + emp.m + edu + sex + accom,
           data= neomod,
           family=binomial)

summary(mod2.re.ad)
```

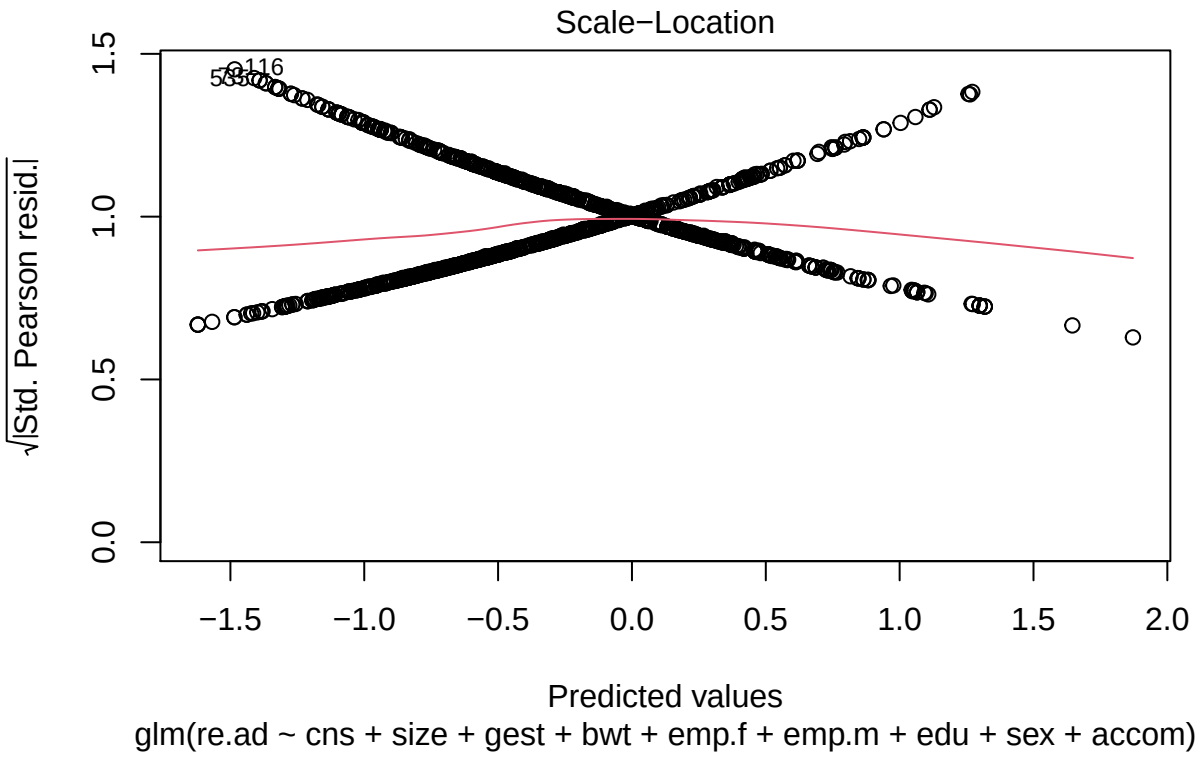
```
##
## Call:
## glm(formula = re.ad ~ cns + size + gest + bwt + emp.f + emp.m +
##     edu + sex + accom, family = binomial, data = neomod)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.7427  -1.0038  -0.7997   1.1824   1.8377
##
## Coefficients:
##             Estimate 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)
```




Normal Q−Q
Std. Pearson resid.
Theoretical Quantiles
glm(re.ad ~ cns + size + gest + bwt + emp.f + emp.m + edu + sex + accom)
116
−3
−2
−1
0
1
2
3

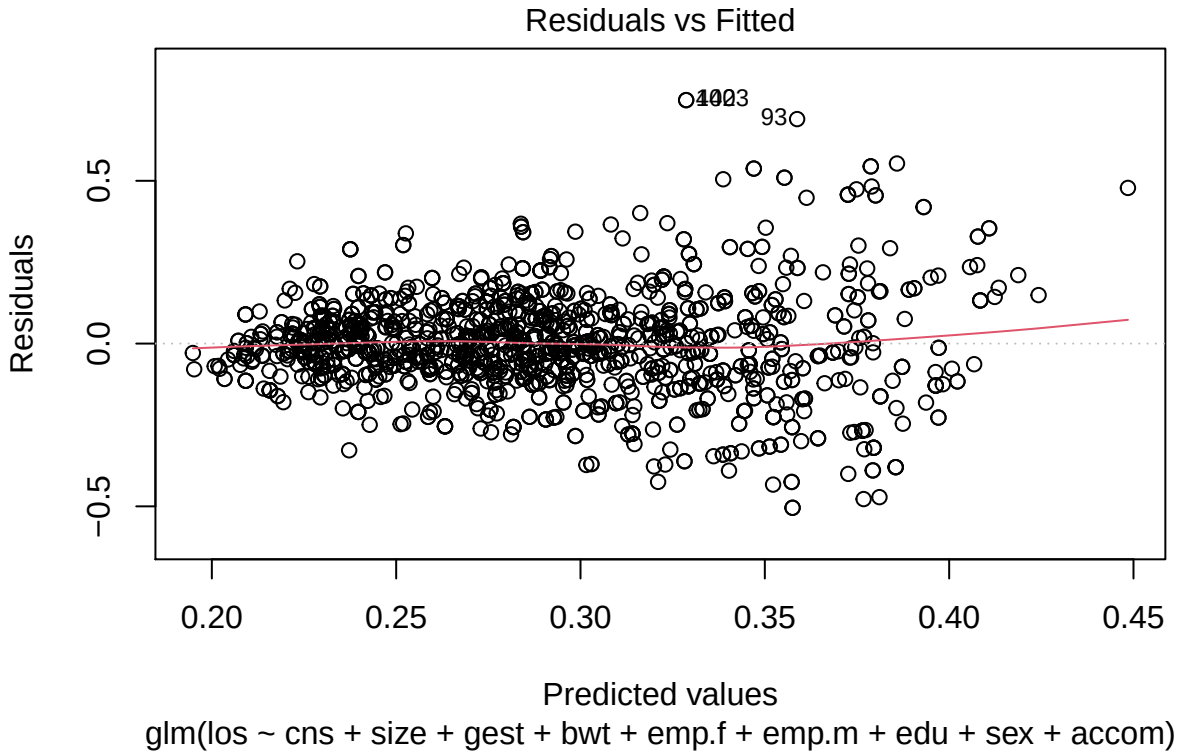

Scale−Location
116
√|Std. Pearson resid.|
0.0
0.5
1.0
1.5
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
Predicted values
glm(re.ad ~ cns + size + gest + bwt + emp.f + emp.m + edu + sex + accom)

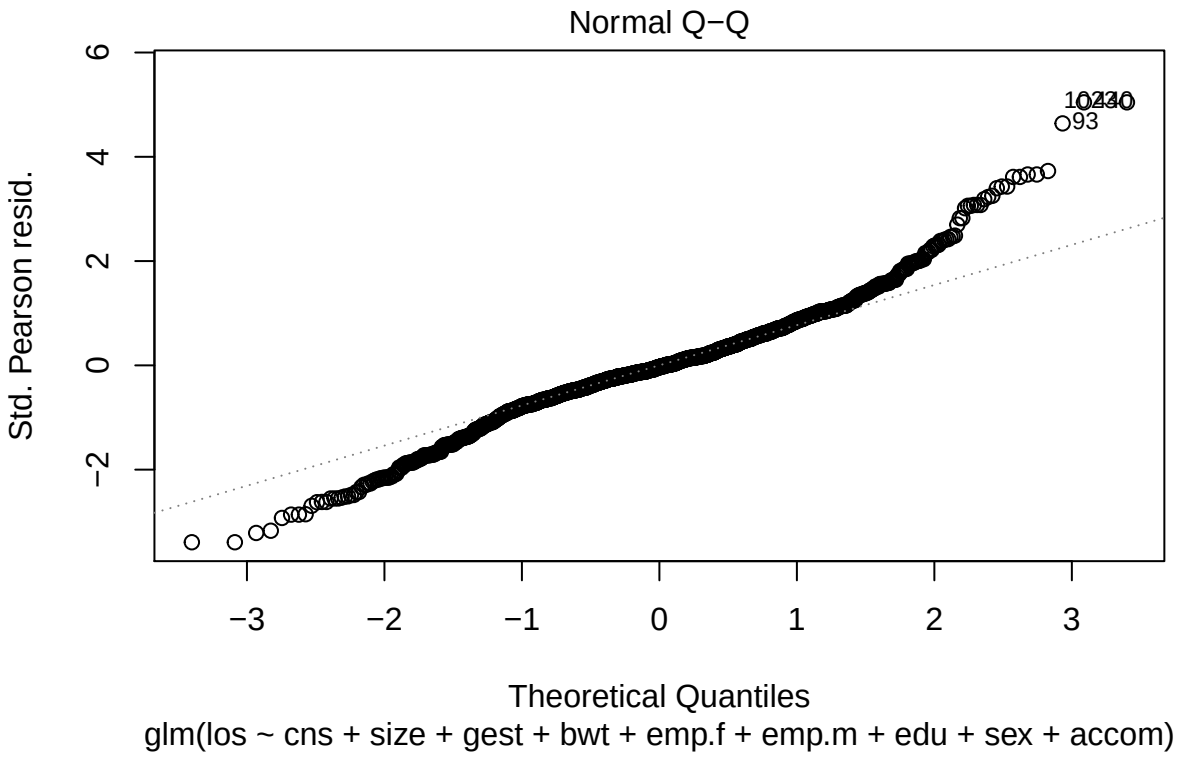

```
# Random model - probably wrong
mod2.los = glm(los ~ cns + size + gest + bwt + emp.f + emp.m + edu + sex + accom,
           data= neomod,
           family=Gamma(link=inverse))

summary(mod2.los)
```

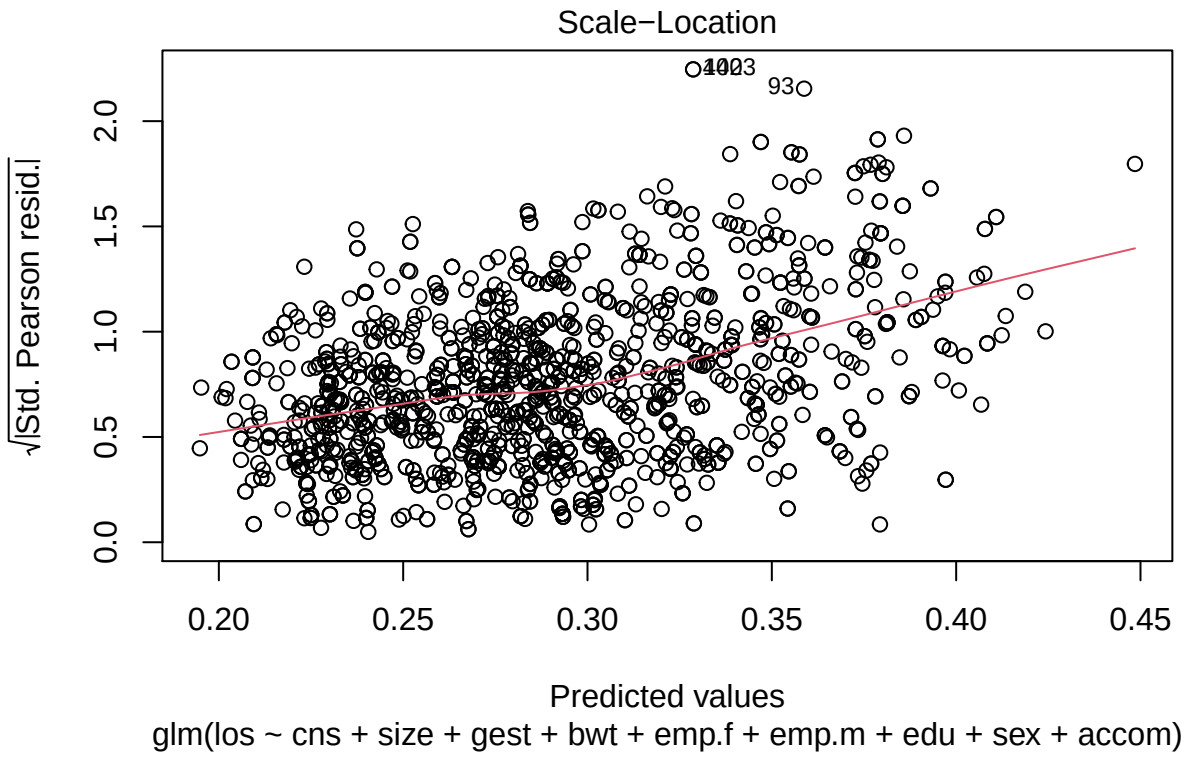
```
##
## Call:
## glm(formula = los ~ cns + size + gest + bwt + emp.f + emp.m +
##     edu + sex + accom, family = Gamma(link = inverse), data = neomod)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.62858  -0.07900  -0.00551   0.07554   0.61557
##
## Coefficients:
##             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 ***
```

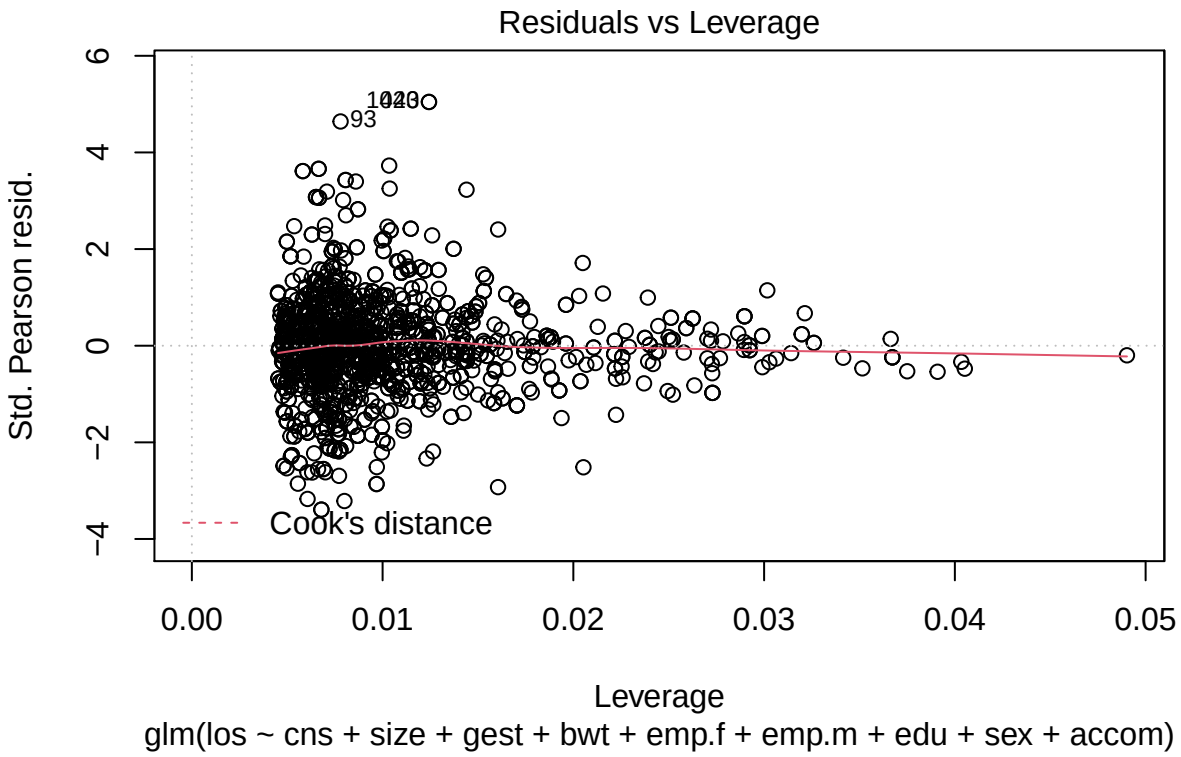
```
## emp.f1       0.006436   0.003642   1.767 0.077369 .
## emp.m1       0.004156   0.002248   1.848 0.064734 .
## edu2         0.009237   0.005032   1.836 0.066624 .
## edu3         0.001732   0.005381   0.322 0.747680
## edu4        -0.003761   0.005877  -0.640 0.522338
## sex1        -0.011305   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)
```




Normal Q−Q
Std. Pearson resid.
Theoretical Quantiles
glm(los ~ cns + size + gest + bwt + emp.f + emp.m + edu + sex + accom)
93


Scale−Location
√|Std. Pearson resid.|
0.0
0.5
1.0
1.5
2.0
0.20
0.25
0.30
0.35
0.40
0.45
93
Predicted values
glm(los ~ cns + size + gest + bwt + emp.f + emp.m + edu + sex + accom)


Residuals vs Leverage
Std. Pearson resid.
6
4
2
0
−2
−4
93
Cook's distance
0.00
0.01
0.02
0.03
0.04
0.05
Leverage
glm(los ~ cns + size + gest + bwt + emp.f + emp.m + edu + sex + accom)