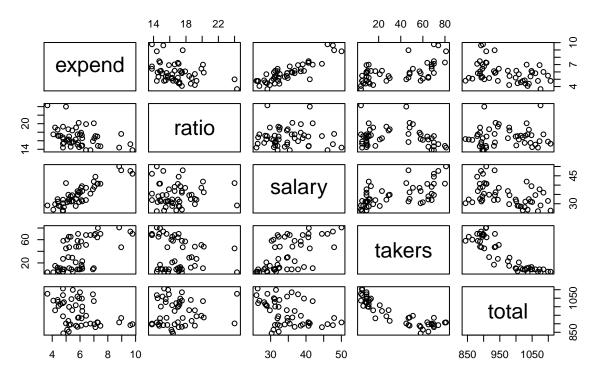
Homework 2

Netid: ghosh17
Subhankar Ghosh

Question 1

```
library(faraway)
data(sat)
satdata = sat
#Looking at the data
head(satdata)
##
              expend ratio salary takers verbal math total
## Alabama
               4.405 17.2 31.144
                                       8
                                            491
                                                 538
## Alaska
               8.963 17.6 47.951
                                      47
                                                        934
                                            445
                                                  489
## Arizona
               4.778 19.3 32.175
                                      27
                                            448
                                                  496
                                                        944
## Arkansas
               4.459 17.1 28.934
                                            482
                                                 523
                                                       1005
                                       6
## California 4.992 24.0 41.078
                                            417
                                                  485
                                                        902
## Colorado
               5.443 18.4 34.571
                                      29
                                            462
                                                 518
                                                        980
# Looking at the scatterplot of all data
pairs(~expend + ratio + salary + takers + total, data = satdata, main = "scatterplot matrix")
```

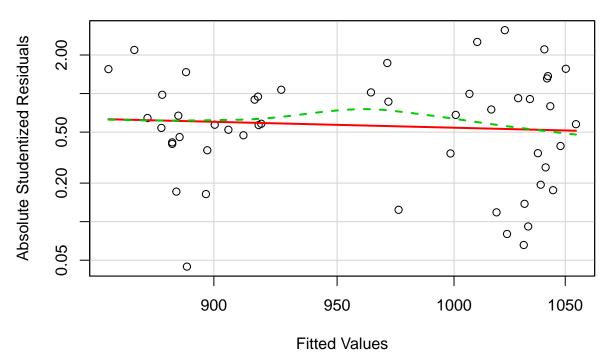
scatterplot matrix



```
model = lm(total ~ expend + ratio + salary + takers, data = satdata)
summary(model)
##
## lm(formula = total ~ expend + ratio + salary + takers, data = satdata)
##
## Residuals:
##
       Min
                1Q Median
                                3Q
                                       Max
## -90.531 -20.855 -1.746 15.979
                                    66.571
##
## Coefficients:
##
                Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1045.9715
                            52.8698 19.784 < 2e-16 ***
                                     0.423
                                                0.674
## expend
                  4.4626
                            10.5465
## ratio
                 -3.6242
                             3.2154 -1.127
                                                0.266
## salary
                 1.6379
                             2.3872
                                     0.686
                                                0.496
                 -2.9045
                             0.2313 -12.559 2.61e-16 ***
## takers
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 32.7 on 45 degrees of freedom
## Multiple R-squared: 0.8246, Adjusted R-squared: 0.809
## F-statistic: 52.88 on 4 and 45 DF, p-value: < 2.2e-16
a. Check the constant variance assumption.
car::ncvTest(model)
## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
                                       p = 0.4037221
## Chisquare = 0.6972119
                            Df = 1
In this hypothesis testing the H_0: Variance is constant and since p-value=0.403 is greater that \alpha=0.05
we can accept the null hypothesis that the Variance is actually constant.
```

car::spreadLevelPlot(model)

Spread-Level Plot for model

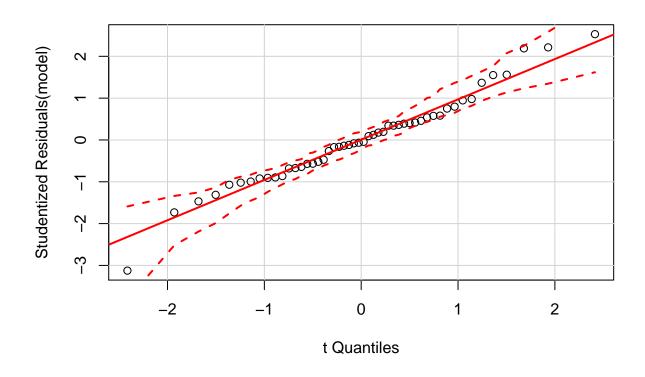


##
Suggested power transformation: 2.006009

There is very slight evidence of variance going down with the mean but it is not statistically significant.

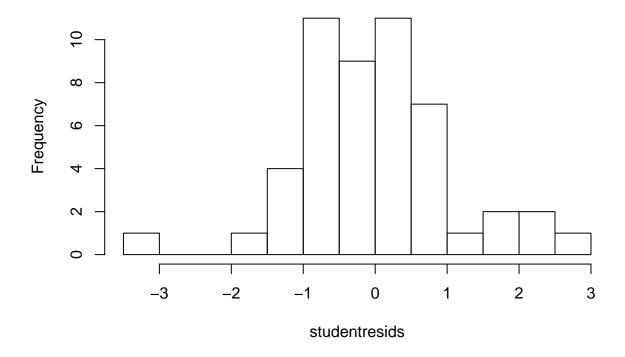
b. Check the normality assumption.

car::qqPlot(model)



studentresids=rstudent(model)
hist(studentresids,nclass=12)

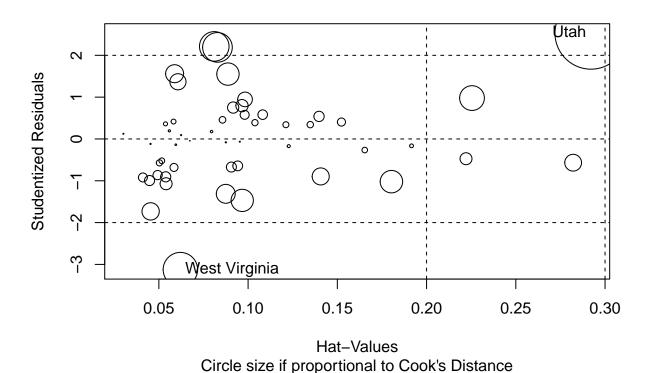
Histogram of studentresids



From the plot we can conclude that the residuals are normally distributed.

c. Check for large leverage points.

car::influencePlot(model, main="Influence Plot", sub="Circle size if proportional to Cook's Distance")



West Virginia and Utah have quite large leverage points.

d) Check for outliers.

car::outlierTest(model)

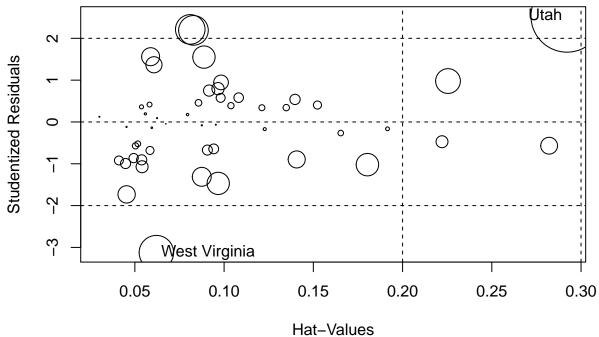
```
##
## No Studentized residuals with Bonferonni p < 0.05
## Largest |rstudent|:</pre>
```

rstudent unadjusted p-value Bonferonni p
West Virginia -3.124428 0.0031496 0.15748

There appears to be no evidence of outliers

e. Check for influential points.

car::influencePlot(model, main="Influence Plot", sub="Circle size if proportional to Cook's Distance")



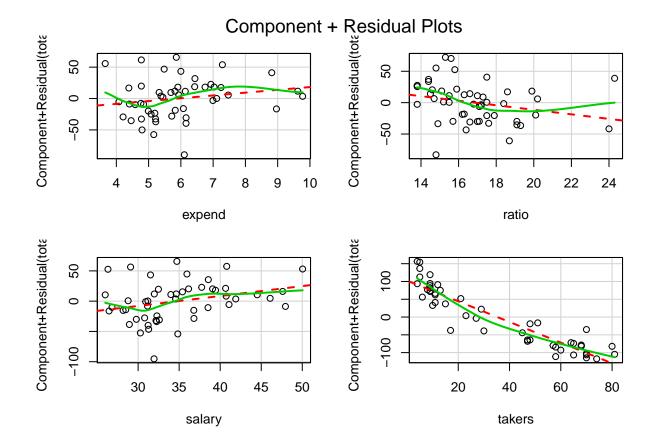
Circle size if proportional to Cook's Distance

##			StudRes	Hat	CookD
##	Utah		2.529587	0.29211280	0.4715287
##	West	Virginia	-3.124428	0.06206536	0.1081395

West Virginia and Utah are quite influential points.

f. Check the functional form of the relationship between the predictors and the response.

car::crPlots(model)

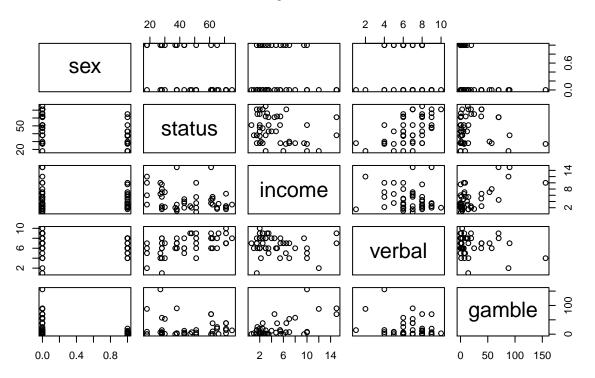


From the functional form plots we can notice that there is slight curvature in all the predictors (expend, ratio, salary, takers)

Question 2

```
data("teengamb")
teengamb = teengamb
#Looking at the data
head(teengamb)
     sex status income verbal gamble
##
                   2.00
                              8
                                   0.0
##
             51
  1
       1
##
   2
       1
             28
                   2.50
                              8
                                   0.0
              37
                   2.00
                              6
                                   0.0
##
  3
       1
## 4
       1
              28
                   7.00
                              4
                                   7.3
## 5
       1
             65
                   2.00
                              8
                                  19.6
## 6
       1
             61
                   3.47
                              6
                                   0.1
# Looking at the scatterplot of all data
pairs(~sex + status + income + verbal + gamble, data = teengamb, main = "scatterplot matrix")
```

scatterplot matrix



```
model1 = lm(gamble ~ sex + status + income + verbal, data = teengamb)
summary(model1)
```

```
##
## Call:
## lm(formula = gamble ~ sex + status + income + verbal, data = teengamb)
##
## Residuals:
                1Q Median
                               3Q
                                      Max
  -51.082 -11.320 -1.451
                            9.452 94.252
##
## Coefficients:
               Estimate Std. Error t value Pr(>|t|)
                          17.19680
                                    1.312
                                             0.1968
## (Intercept) 22.55565
## sex
               -22.11833
                           8.21111 -2.694
                                             0.0101 *
## status
                0.05223
                           0.28111
                                     0.186
                                             0.8535
## income
                4.96198
                           1.02539
                                    4.839 1.79e-05 ***
               -2.95949
## verbal
                           2.17215 -1.362
                                             0.1803
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 22.69 on 42 degrees of freedom
## Multiple R-squared: 0.5267, Adjusted R-squared: 0.4816
## F-statistic: 11.69 on 4 and 42 DF, p-value: 1.815e-06
```

a. Check the constant variance assumption.

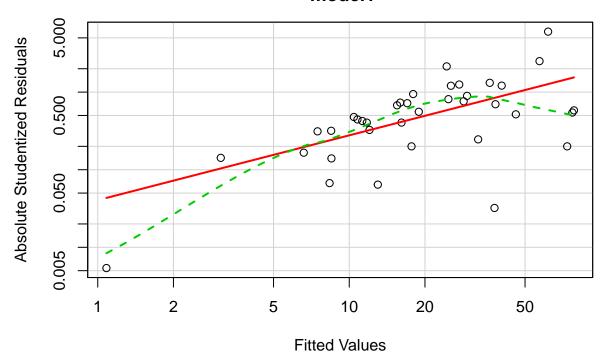
car::ncvTest(model1)

In this hypothesis testing the H_0 : Variance is constant and since p-value is less than $\alpha=0.05$ we cannot accept the null hypothesis. That is the *Variance is actually not constant*.

```
car::spreadLevelPlot(model1)
```

Warning in spreadLevelPlot.lm(model1): 10 negative fitted values removed

Spread-Level Plot for model1



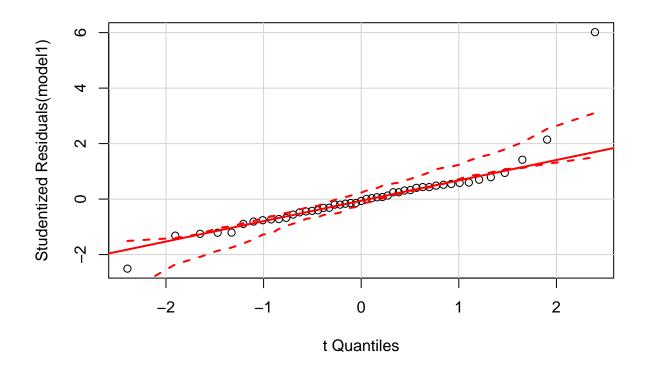
##

Suggested power transformation: 0.1646836

There is strong evidence of variance going up with the mean.

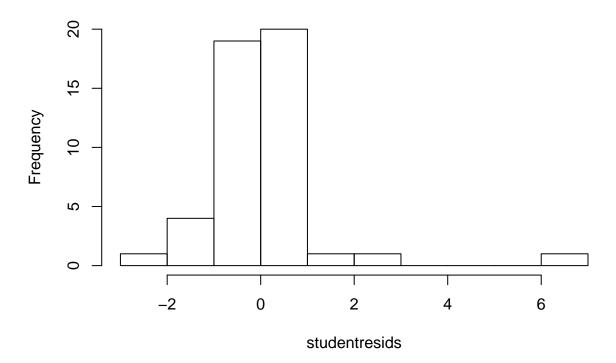
b. Check the normality assumption.

car::qqPlot(model1)



studentresids=rstudent(model1)
hist(studentresids,nclass=10)

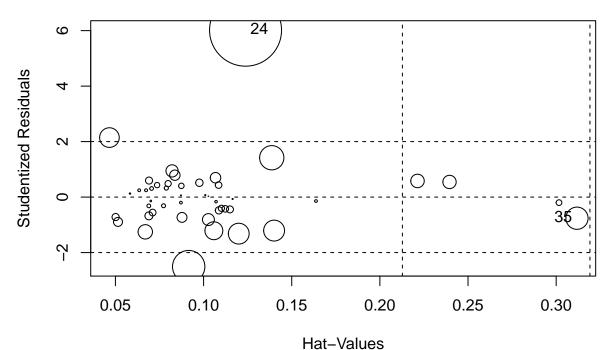
Histogram of studentresids



From the plot we can conclude that the residuals are not normally distributed as the histogram does not correspond to bell shape and qqPlot does not correspond to a straight line.

c. Check for large leverage points.

car::influencePlot(model1, main="Influence Plot", sub="Circle size if proportional to Cook's Distance")



Circle size if proportional to Cook's Distance

```
## StudRes Hat CookD
## 24 6.0161163 0.1238046 0.55650113
## 35 -0.7612557 0.3118029 0.05304304
```

24 and 35 have quite large leverage points.

d) Check for outliers.

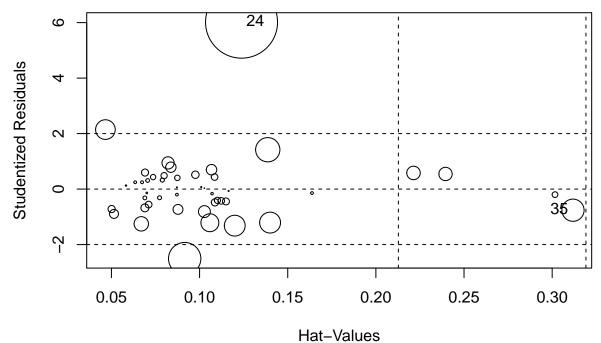
```
car::outlierTest(model1)
```

```
## rstudent unadjusted p-value Bonferonni p
## 24 6.016116 4.1041e-07 1.9289e-05
```

There appears to be strong evidence of outliers.

e. Check for influential points.

car::influencePlot(model1, main="Influence Plot", sub="Circle size if proportional to Cook's Distance")



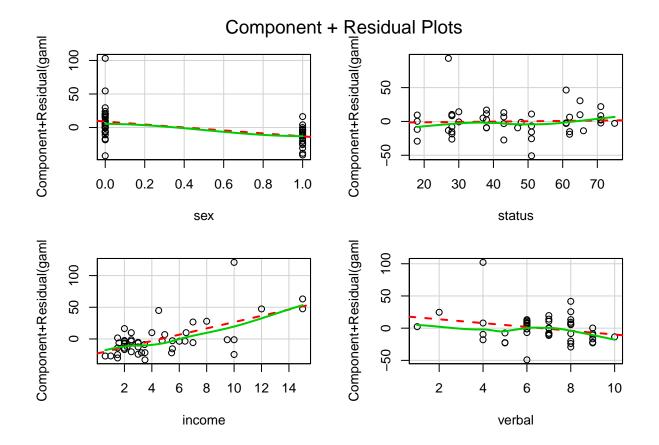
Circle size if proportional to Cook's Distance

```
## StudRes Hat CookD
## 24 6.0161163 0.1238046 0.55650113
## 35 -0.7612557 0.3118029 0.05304304
```

24 and 35 seem to be quite influencial points.

f. Check the functional form of the relationship between the predictors and the response.

car::crPlots(model1)



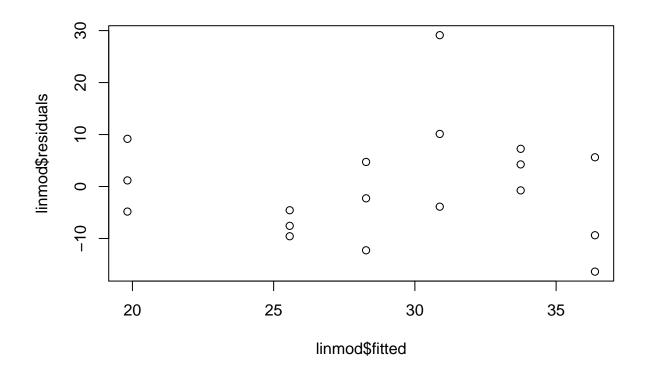
From the functional form plots we can notice that there is slight curvature in verbal and income predictors.

Question 3

head(salmonella)

```
colonies dose
##
## 1
            15
                   0
## 2
            21
                   0
## 3
            29
                   0
            16
## 4
                  10
## 5
            18
                  10
## 6
            21
                  10
```

```
linmod=lm(colonies~log(dose + 1), data = salmonella)
plot(linmod$fitted,linmod$residuals)
```



The lack of constant variance is quite evident from the residual vs fitted plot but let is run a test

```
car::ncvTest(linmod)
## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 0.825563
                           Df = 1
                                       p = 0.3635587
genmod=lm(colonies~factor(log(dose + 1)), data = salmonella)
summary(genmod)
##
## Call:
## lm(formula = colonies ~ factor(log(dose + 1)), data = salmonella)
##
  Residuals:
##
       Min
                1Q
                    Median
                                 3Q
                                        Max
  -15.667
           -3.917
                    -0.500
                              3.417
                                    17.333
##
## Coefficients:
##
                                          Estimate Std. Error t value Pr(>|t|)
                                            21.667
                                                                 3.935
                                                                        0.00198
## (Intercept)
                                                         5.506
## factor(log(dose + 1))2.39789527279837
                                            -3.333
                                                         7.787
                                                                -0.428
                                                                        0.67617
## factor(log(dose + 1))3.52636052461616
                                             3.333
                                                         7.787
                                                                 0.428
                                                                        0.67617
## factor(log(dose + 1))4.61512051684126
                                            21.000
                                                         7.787
                                                                 2.697
                                                                        0.01942
## factor(log(dose + 1))5.8111409929767
                                            15.667
                                                         7.787
                                                                 2.012
                                                                        0.06722
## factor(log(dose + 1))6.90875477931522
                                             8.000
                                                         7.787
                                                                 1.027
                                                                        0.32449
##
```

```
## (Intercept)
## factor(log(dose + 1))2.39789527279837
## factor(log(dose + 1))3.52636052461616
## factor(log(dose + 1))4.61512051684126 *
## factor(log(dose + 1))5.8111409929767
## factor(log(dose + 1))6.90875477931522
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.536 on 12 degrees of freedom
## Multiple R-squared: 0.5475, Adjusted R-squared: 0.359
## F-statistic: 2.904 on 5 and 12 DF, p-value: 0.06047
anova(linmod, genmod)
## Analysis of Variance Table
##
## Model 1: colonies ~ log(dose + 1)
## Model 2: colonies ~ factor(log(dose + 1))
    Res.Df
              RSS Df Sum of Sq
                                    F Pr(>F)
## 1
        16 1881.1
## 2
                        789.73 2.1709 0.1342
         12 1091.3 4
```

In this hypothesis test the H_0 : No lack of fit, P value is 0.1342 so we cannot reject the null no lack of fit and conclude that there is no lack of fit