Aissngment 1

Keiryn Hart, 300428418

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```
library(ggplot2)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(gridExtra)
```

```
## Warning: package 'gridExtra' was built under R version 3.6.3

##
## Attaching package: 'gridExtra'

## The following object is masked from 'package:dplyr':
##
##     combine
```

Q1: a)

```
cancer <- read.csv("cancer_reg.csv", header = TRUE)
str(cancer)
```

```
## 'data.frame':    3047 obs. of  33 variables:
##  $ avganncount            : num  1397 173 102 427 57 ...
##  $ avgdeathsperyear       : int  469 70 50 202 26 152 97 71 36 1380 ...
##  $ target_deathrate       : num  165 161 175 195 144 ...
##  $ incidencerate          : num  490 412 350 430 350 ...
##  $ medincome              : int  61898 48127 49348 44243 49955 52313 37782 40189 42579 60397 ...
##  $ popest2015             : int  260131 43269 21026 75882 10321 61023 41516 20848 13088 843954 ...
##  $ povertypercent         : num  11.2 18.6 14.6 17.1 12.5 15.6 23.2 17.8 22.3 13.1 ...
##  $ studypercap            : num  499.7 23.1 47.6 342.6 0 ...
##  $ binnedinc              : Factor w/ 10 levels "(34218.1, 37413.8]",..: 9 6 6 4 6 7 2 2 3 8 ...
##  $ medianage              : num  39.3 33 45 42.8 48.3 45.4 42.6 51.7 49.3 35.8 ...
##  $ medianagemale          : num  36.9 32.2 44 42.2 47.8 43.5 42.2 50.8 48.4 34.7 ...
##  $ medianagefemale        : num  41.7 33.7 45.8 43.4 48.9 48 43.5 52.5 49.8 37 ...
##  $ geography              : Factor w/ 3047 levels "Abbeville County, South Carolina",..: 1459 1460 14
```

```
##  $ percentmarried         : num  52.5 44.5 54.2 52.7 57.8 50.4 54.1 52.7 55.9 50 ...
##  $ pctnohs18_24           : num  11.5 6.1 24 20.2 14.9 29.9 26.1 27.3 34.7 15.6 ...
##  $ pcths18_24             : num  39.5 22.4 36.6 41.2 43 35.1 41.4 33.9 39.4 36.3 ...
##  $ pctsomecol18_24        : num  42.1 64 NA 36.1 40 NA NA 36.5 NA NA ...
##  $ pctbachdeg18_24        : num  6.9 7.5 9.5 2.5 2 4.5 5.8 2.2 1.4 7.1 ...
##  $ pcths25_over           : num  23.2 26 29 31.6 33.4 30.4 29.8 31.6 32.2 28.8 ...
##  $ pctbachdeg25_over      : num  19.6 22.7 16 9.3 15 11.9 11.9 11.3 12 16.2 ...
##  $ pctemployed16_over     : num  51.9 55.9 45.9 48.3 48.2 44.1 51.8 40.9 39.5 56.6 ...
##  $ pctunemployed16_over   : num  8 7.8 7 12.1 4.8 12.9 8.9 8.9 10.3 9.2 ...
##  $ pctprivatecoverage     : num  75.1 70.2 63.7 58.4 61.6 60 49.5 55.8 55.5 69.9 ...
##  $ pctprivatecoveragealone: num  NA 53.8 43.5 40.3 43.9 38.8 35 33.1 37.8 NA ...
##  $ pctempprivcoverage     : num  41.6 43.6 34.9 35 35.1 32.6 28.3 25.9 29.9 44.4 ...
##  $ pctpubliccoverage      : num  32.9 31.1 42.1 45.3 44 43.2 46.4 50.9 48.1 31.4 ...
##  $ pctpubliccoveragealone : num  14 15.3 21.1 25 22.7 20.2 28.7 24.1 26.6 16.5 ...
##  $ pctwhite               : num  81.8 89.2 90.9 91.7 94.1 ...
##  $ pctblack               : num  2.595 0.969 0.74 0.783 0.27 ...
##  $ pctasian               : num  4.822 2.246 0.466 1.161 0.666 ...
##  $ pctotherrace           : num  1.843 3.741 2.747 1.363 0.492 ...
##  $ pctmarriedhouseholds   : num  52.9 45.4 54.4 51 54 ...
##  $ birthrate              : num  6.12 4.33 3.73 4.6 6.8 ...
```

```r
nrow(cancer)
```

```
## [1] 3047
```

b)

```r
new_cancer <- cancer[,c(3,7,8,9,10,20,22,23)]
```

c)

```r
a<-ggplot(new_cancer,aes(x=povertypercent, y=target_deathrate))+
  geom_point() +
  geom_smooth(method='loess') +
  labs(x="percentage of poverty", y="target deathrate")+
  theme_bw()

b<-ggplot(new_cancer,aes(x=studypercap, y=target_deathrate))+
  geom_point() +
  geom_smooth(method='loess') +
  labs(x="study per capita", y="target deathrate")+
  theme_bw()

c<-ggplot(new_cancer,aes(x=binnedinc, y=target_deathrate))+
  geom_boxplot(aes(fill=binnedinc), show.legend=FALSE) +
  labs(x="binnedinc", y="target deathrate)")+
  theme_bw()

d<-ggplot(new_cancer,aes(x=medianage, y=target_deathrate))+
  geom_point() +
  geom_smooth(method='loess') +
  labs(x="medianage", y="target deathrate")+
```

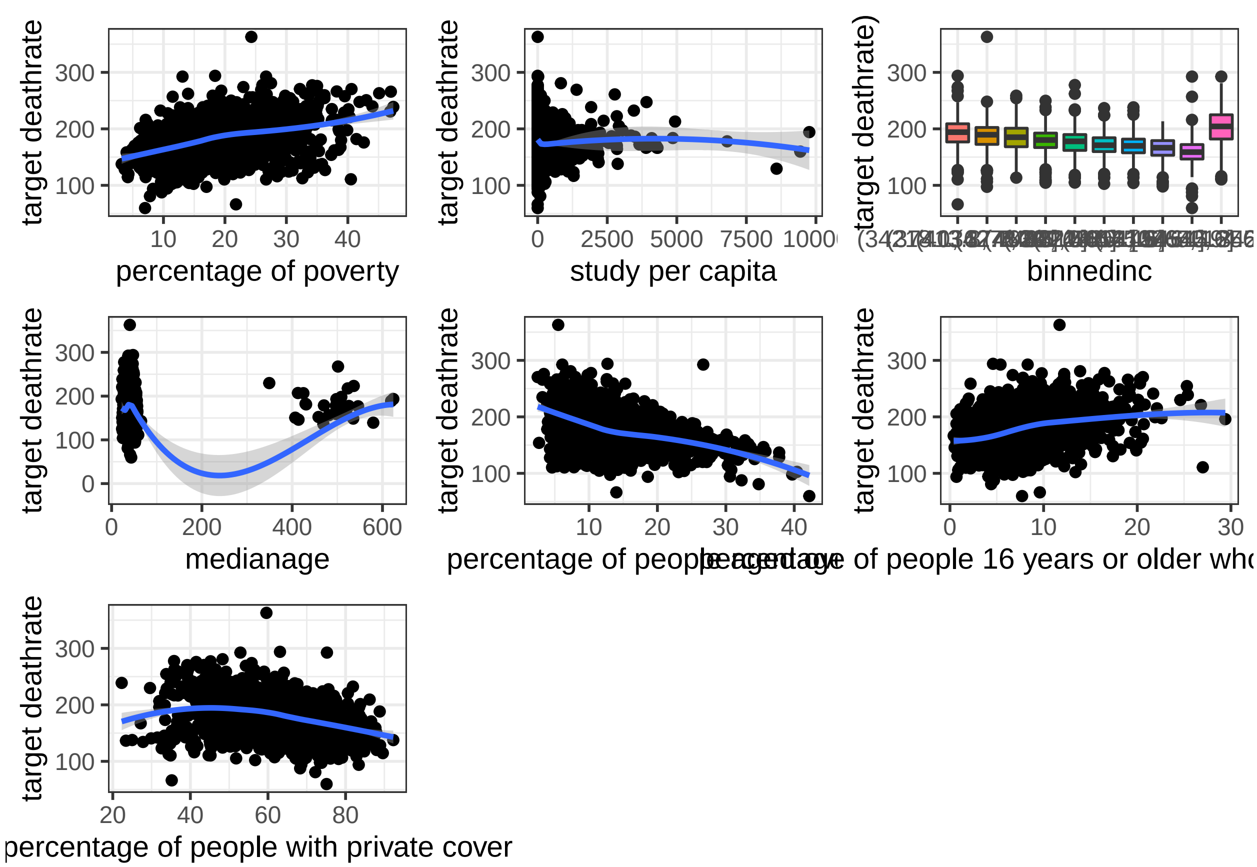
```r
  theme_bw()

e<-ggplot(new_cancer,aes(x=pctbachdeg25_over, y=target_deathrate))+
  geom_point() +
  geom_smooth(method='loess') +
  labs(x="percentage of people aged over 25", y="target deathrate")+
  theme_bw()

f<-ggplot(new_cancer,aes(x=pctunemployed16_over, y=target_deathrate))+
  geom_point() +
  geom_smooth(method='loess') +
  labs(x="percentage of people 16 years or older who are unemployed", y="target deathrate")+
  theme_bw()

g<-ggplot(new_cancer,aes(x=pctprivatecoverage, y=target_deathrate))+
  geom_point() +
  geom_smooth(method='loess') +
  labs(x="percentage of people with private cover", y="target deathrate")+
  theme_bw()

grid.arrange(a,b,c,d,e,f,g)
```



there are 2 examples of non linear relationships which are (target death rate : median age) and (target death rate : private cover)

D)

```r
cancerFilter <- new_cancer %>%
  select(povertypercent, target_deathrate, studypercap, binnedinc, medianage, pctbachdeg25_over, pctunem
  filter(medianage < 200)
nrow(cancerFilter)
```

```
## [1] 3017
```

E)

```r
str(cancerFilter)
```

```
## 'data.frame':    3017 obs. of  8 variables:
##  $ povertypercent      : num  11.2 18.6 14.6 17.1 12.5 15.6 23.2 17.8 22.3 13.1 ...
##  $ target_deathrate    : num  165 161 175 195 144 ...
##  $ studypercap         : num  499.7 23.1 47.6 342.6 0 ...
##  $ binnedinc           : Factor w/ 10 levels "(34218.1, 37413.8]",..: 9 6 6 4 6 7 2 2 3 8 ...
##  $ medianage           : num  39.3 33 45 42.8 48.3 45.4 42.6 51.7 49.3 35.8 ...
##  $ pctbachdeg25_over   : num  19.6 22.7 16 9.3 15 11.9 11.9 11.3 12 16.2 ...
##  $ pctunemployed16_over: num  8 7.8 7 12.1 4.8 12.9 8.9 8.9 10.3 9.2 ...
##  $ pctprivatecoverage  : num  75.1 70.2 63.7 58.4 61.6 60 49.5 55.8 55.5 69.9 ...
```

```r
model1 <- lm(target_deathrate ~ povertypercent + studypercap + binnedinc + medianage + pctbachdeg25_ove
nullmodel <- lm(target_deathrate ~ 1, data = cancerFilter)
summ.model1 <-summary(model1)
```

notable values:

```r
anovafit <- anova(nullmodel, model1)
sum_model1 <- summary(model1)
Fval <- anovafit$F[2]
pval <- anovafit$`Pr(>F)`[2]
RSE <- sum_model1$sigma
Rsq <- sum_model1$r.squared
adjRsq <- sum_model1$adj.r.squared
statistic <- c("F-statistic", "p-value", "RSE", "R-squared", "Adj. R-squared")
values <- c(Fval, pval, RSE, Rsq, adjRsq)
results <- data.frame(statistic, values)
results
```

```
##        statistic        values
## 1    F-statistic  8.764130e+01
## 2        p-value 1.925537e-223
## 3            RSE  2.318755e+01
## 4      R-squared  3.046190e-01
## 5 Adj. R-squared  3.011432e-01
```

```r
library(knitr)
library(kableExtra)
```

```
## Warning: package 'kableExtra' was built under R version 3.6.3
```

Table 1: Model Summary

statistic	values
F-statistic	87.641
p-value	0.000
RSE	23.188
R-squared	0.305
Adj. R-squared	0.301

Table 2: prediction Intervals

fit	lwr	upr
166.43	120.88	211.99
159.59	113.99	205.19
164.64	119.08	210.19
189.74	144.18	235.31
160.76	115.18	206.34

```
##
## Attaching package: 'kableExtra'

## The following object is masked from 'package:dplyr':
##
##     group_rows
```

```r
summ <- kable(results, caption = "Model Summary", booktabs=T, digits = 3)
kable_styling(summ)
```

looking at the F-statistic and p-value there is a very small p-value which indicates that at least one of the predictors is important in predicting the death rate.

Looking at the RSE the deviation of predicted values from true values has a percentage error relative the the mean of 0.12%

Looking at R squared with a value of 0.305 which means that the model explains 30.5% of variation in the death rate, meanwhile adjusted R squared is 0.301 which is very similar to r squared which indicates it is unlikely that we have redundant predictors. the model on represents 30.5% which is not very much.

f)

```r
predictorvalues <- subset(cancerFilter[1:5,], select = -c(target_deathrate))
confidenceInt <- predict(model1, newdata = predictorvalues, interval = "confidence")
predictionInt <- kable(predict(model1, newdata = predictorvalues, interval = "prediction"),
                        digits = 2, caption = "prediction Intervals", booktabs=T)
predictionInt
```

```r
confidenceInt
```

```
##        fit      lwr      upr
## 1 166.4344 163.5788 169.2901
```

Table 3: Regression Coefficients

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	169.842	9.011	18.848	0.000
povertypercent	0.472	0.181	2.610	0.009
studypercap	0.001	0.001	1.737	0.083
binnedinc(37413.8, 40362.7]	-2.628	1.945	-1.351	0.177
binnedinc(40362.7, 42724.4]	-4.112	2.035	-2.021	0.043
binnedinc(42724.4, 45201]	-5.510	2.148	-2.565	0.010
binnedinc(45201, 48021.6]	-6.328	2.271	-2.786	0.005
binnedinc(48021.6, 51046.4]	-10.171	2.429	-4.187	0.000
binnedinc(51046.4, 54545.6]	-9.088	2.565	-3.543	0.000
binnedinc(54545.6, 61494.5]	-9.685	2.754	-3.516	0.000
binnedinc(61494.5, 125635]	-7.885	3.260	-2.419	0.016
binnedinc[22640, 34218.1]	4.281	2.067	2.071	0.038
medianage	-0.194	0.098	-1.991	0.047
pctbachdeg25_over	-1.983	0.112	-17.720	0.000
pctunemployed16_over	1.469	0.170	8.640	0.000
pctprivatecoverage	0.443	0.077	5.719	0.000

```
## 2 159.5874 156.0809 163.0940
## 3 164.6355 161.7091 167.5618
## 4 189.7439 186.6860 192.8018
## 5 160.7593 157.4818 164.0367
```

prediction intervals are concerned with the value of specific datapoints whereas confidence intervales are concerned with the mean value of datapoint at that position, prediction intervals are therefore wider because they show the uncertainty that the interval has when prediction the specific value of that point.

g) the regression coefficients responding to pctunemployed16_over has an estimate of 1.469 this means that an increase in the percentage of people who are unemployed over the age of 16 is assiciated with an increase in the mean target death rate when all other predictors are kept constant. (1.469 * 100,000 = 146,900)

the regression coefficients corresponding to binnedinc[22640, 34218.1] has an estimate of 4.281 which is the estimated difference between binnedinc[22640, 34218.1] and [34218.1, 37413.8] being the reference level for this model. (not sure why the reference level is the bracket above?). it essentially means that the target deathrate was higher than the reference level by an estimated (4.261 * 100,000 = 428,100) when all other predictors remained constant.

```
regressionCoeff <- kable(round(coef(summ.model1), 3), caption = "Regression Coefficients", booktabs = T)
regressionCoeff
```

h)

```
model2 <- lm(target_deathrate ~ povertypercent + binnedinc + medianage + pctbachdeg25_over + pctunemplo
sum_model2 <- summary(model2)
RSE1 <- sum_model1$sigma
Rsq1 <- sum_model1$r.squared
```

Table 4: regression coefficients

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	182.352	9.805	18.598	0.000
povertypercent	0.517	0.182	2.845	0.004
binnedinc(37413.8, 40362.7]	-20.696	6.107	-3.389	0.001
binnedinc(40362.7, 42724.4]	-23.395	6.222	-3.760	0.000
binnedinc(42724.4, 45201]	-25.524	6.097	-4.186	0.000
binnedinc(45201, 48021.6]	-31.327	5.889	-5.320	0.000
binnedinc(48021.6, 51046.4]	-34.439	5.904	-5.833	0.000
binnedinc(51046.4, 54545.6]	-30.675	5.942	-5.163	0.000
binnedinc(54545.6, 61494.5]	-30.655	6.093	-5.031	0.000
binnedinc(61494.5, 125635]	-32.160	6.639	-4.844	0.000
binnedinc[22640, 34218.1]	-5.936	6.012	-0.987	0.324
medianage	-0.184	0.098	-1.877	0.061
pctbachdeg25_over	-1.974	0.112	-17.658	0.000
pctunemployed16_over	-0.297	0.431	-0.691	0.490
pctprivatecoverage	0.506	0.078	6.484	0.000
binnedinc(37413.8, 40362.7]:pctunemployed16_over	1.823	0.620	2.939	0.003
binnedinc(40362.7, 42724.4]:pctunemployed16_over	1.965	0.645	3.048	0.002
binnedinc(42724.4, 45201]:pctunemployed16_over	2.071	0.658	3.149	0.002
binnedinc(45201, 48021.6]:pctunemployed16_over	2.789	0.639	4.366	0.000
binnedinc(48021.6, 51046.4]:pctunemployed16_over	2.781	0.670	4.149	0.000
binnedinc(51046.4, 54545.6]:pctunemployed16_over	2.374	0.673	3.526	0.000
binnedinc(54545.6, 61494.5]:pctunemployed16_over	2.264	0.695	3.260	0.001
binnedinc(61494.5, 125635]:pctunemployed16_over	2.778	0.744	3.733	0.000
binnedinc[22640, 34218.1]:pctunemployed16_over	1.181	0.536	2.205	0.028

```r
adjRsq1 <- sum_model1$adj.r.squared
RSE2 <- sum_model2$sigma
Rsq2 <- sum_model2$r.squared
adjRsq2 <- sum_model2$adj.r.squared
stats <- c("RSE", "R-squared", "Adj. R-squared")
stats1 <- c(RSE1, Rsq1, adjRsq1)
stats2 <- c(RSE2, Rsq2, adjRsq2)
comparison <- data.frame(stats, stats1, stats2)
comparison
```

```
##            stats     stats1     stats2
## 1            RSE 23.1875480 23.0993555
## 2      R-squared  0.3046190  0.3117382
## 3 Adj. R-squared  0.3011432  0.3064492
```

```r
library(interactions)
```

```
## Warning: package 'interactions' was built under R version 3.6.3
```

```r
kable(round(coef(sum_model2),3),caption = "regression coefficients")
```

i) we get an f-statistic value of 3.8699 and a p-value of 0.00015, since the p value is so small there is strong evidence to suggest that the interaction term explains a significant amount of variation in the target deathrate in addition to all other predictors.

```r
likelihood <- anova(model1, model2)

likelihood
```

```
## Analysis of Variance Table
##
## Model 1: target_deathrate ~ povertypercent + studypercap + binnedinc +
##     medianage + pctbachdeg25_over + pctunemployed16_over + pctprivatecoverage
## Model 2: target_deathrate ~ povertypercent + binnedinc + medianage + pctbachdeg25_over +
##     pctunemployed16_over + pctprivatecoverage + pctunemployed16_over:binnedinc
##   Res.Df     RSS Df Sum of Sq      F    Pr(>F)
## 1   3001 1613525
## 2   2993 1597006  8     16519 3.8699 0.0001506 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

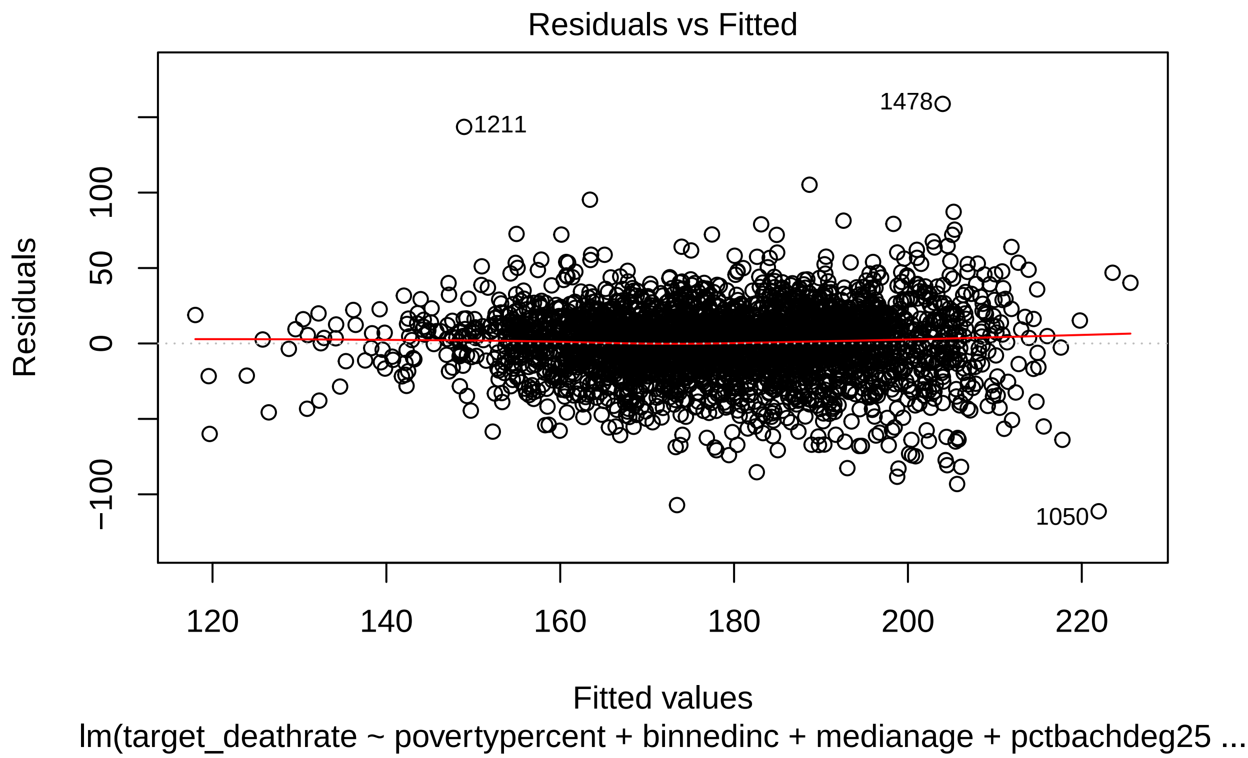
```r
Fstval <- likelihood$F[2]
pstval <- likelihood$`Pr(>F)`[2]
anovaStatistics <- c("F-statistic", "p-value")
anovaValues <- c(Fstval, pstval)
ress <- data.frame(anovaStatistics, anovaValues)
ress
```

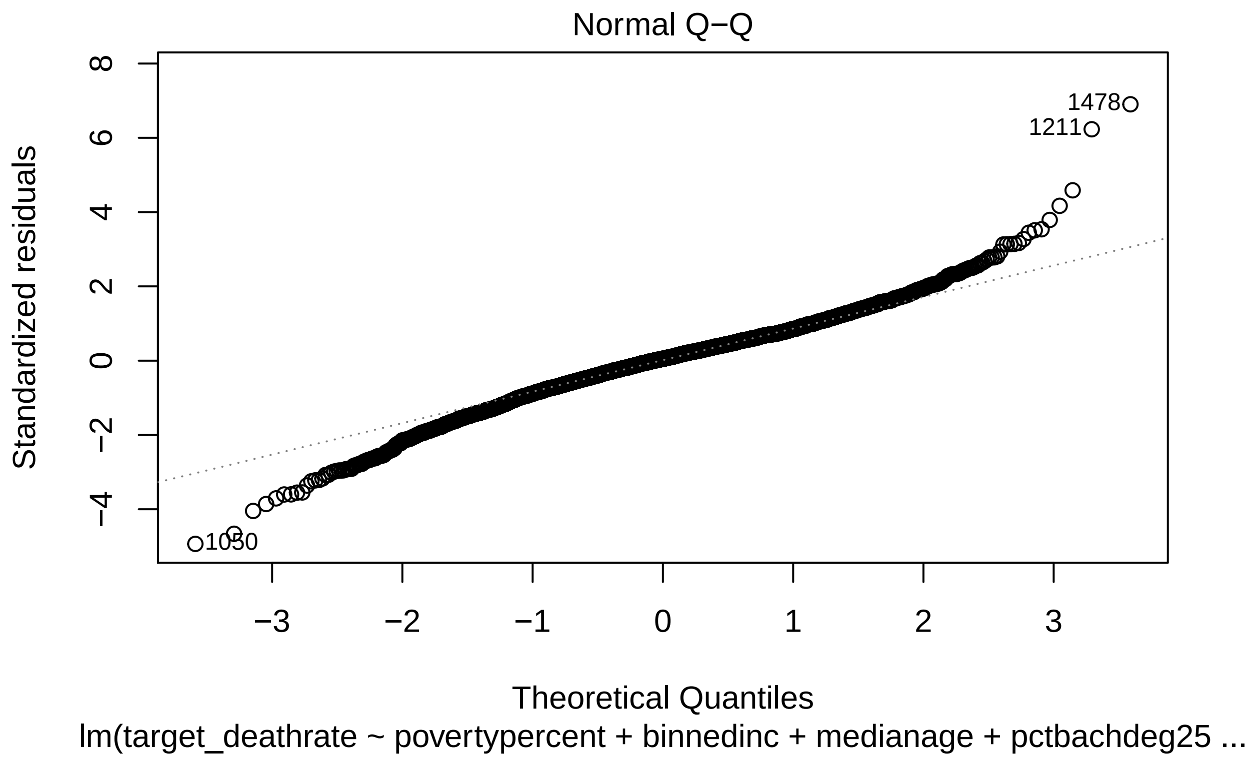
```
##   anovaStatistics  anovaValues
## 1     F-statistic 3.8698938913
## 2         p-value 0.0001505751
```

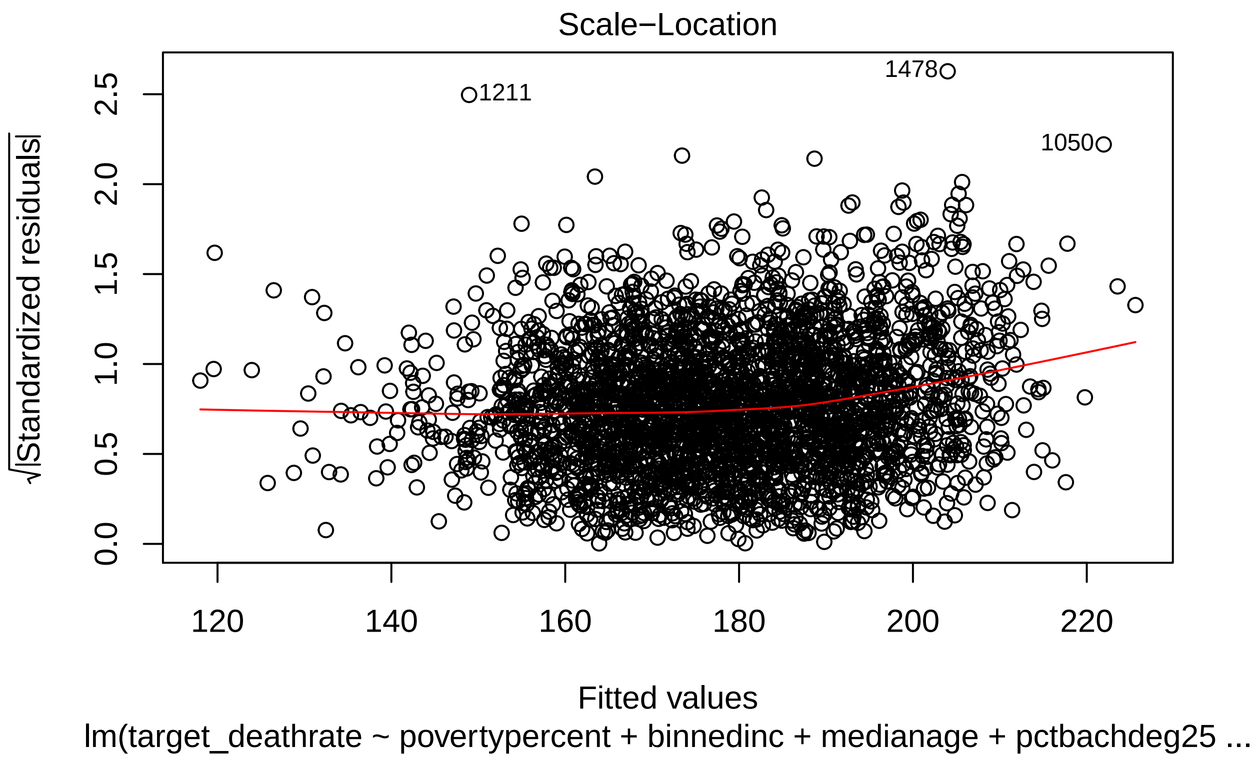
j) the interaction term indicates that one of the predictors either pctunemployed16_over or binnedinc has an effect on the other where the effect of one variable on the response variable being target death rate at different values of the other predictor variable.

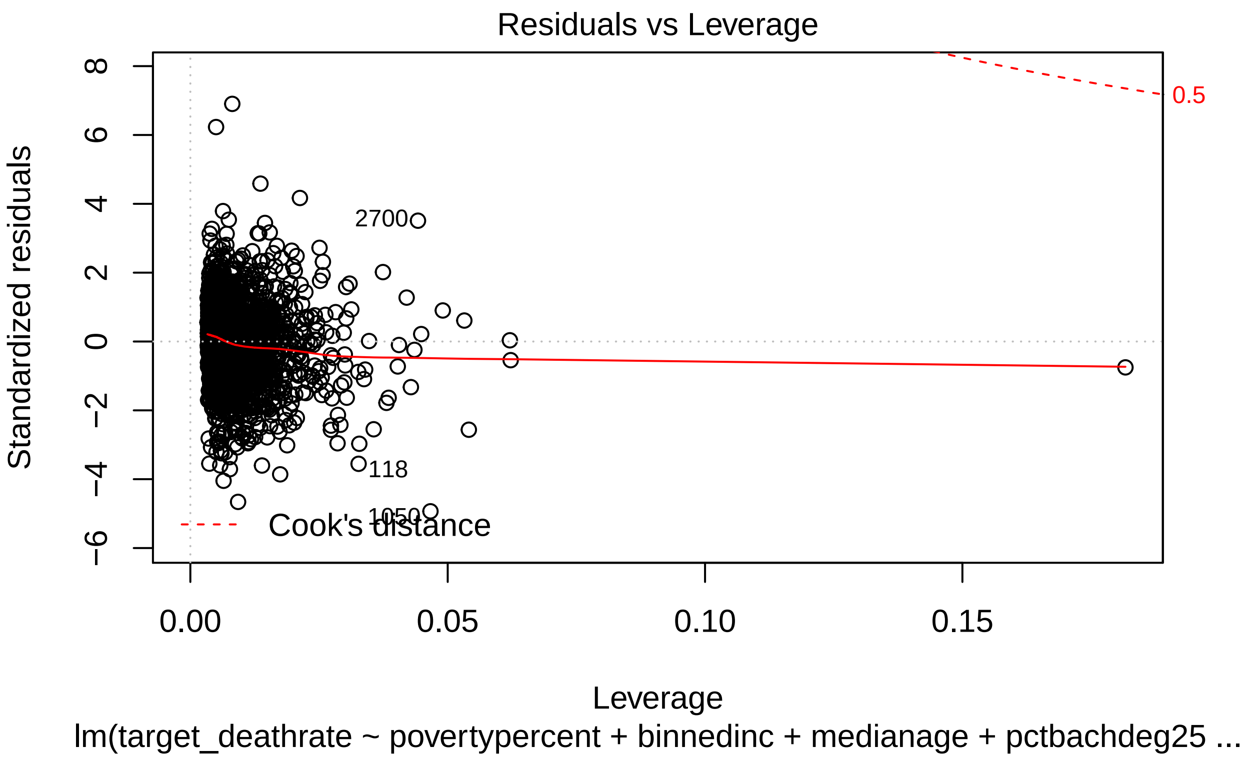
k)

```r
plot(model2)
```


Residuals vs Fitted
Residuals
100
50
0
−100
1211
1478
1050
120
140
160
180
200
220
Fitted values
lm(target_deathrate ~ povertypercent + binnedinc + medianage + pctbachdeg25 ...


Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(target_deathrate ~ povertypercent + binnedinc + medianage + pctbachdeg25 ...
1478
1211
1030
8
6
4
2
0
−2
−4
−3
−2
−1
0
1
2
3


Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
2.0
2.5
120
140
160
180
200
220
Fitted values
lm(target_deathrate ~ povertypercent + binnedinc + medianage + pctbachdeg25 ...
1211
1478
1050



comments about the individual plots go here.

residuals vs fitted: the residuals vs fitted plot shows no evidence on non-linearity as the pattern in the residuals does not indicate non-linearity, the line that has been plotted to show the relationship between the residuals and fitted values is very hirizontal.

Normal Q-Q plot: the normal Q-Q plot indicates that there is evidence of non-normality, the points do not lie on the straight line which is a clear indicator. *something that could be done is to transform the response variable, or permutation testing.

Scale Location plot: looking at the scale location plot, there seems to be a relatively even scatter of points in the plot with no clear evidence of funneling. the line plotted through the graph also seems to be relatively horizontal, both these factors indicate that there is no clear evidence of non - constant variance.

Residuals vs Leverage: there is no clear evidence of there being influencial observations, there is only one cooks distance line which also indicates that there are no influencial observations.

l)

```r
library(car)
```

```
## Warning: package 'car' was built under R version 3.6.3
```

```
## Loading required package: carData
```

```
##
## Attaching package: 'car'
```

Table 5: VIF values

	GVIF	Df	GVIF^(1/(2*Df))
povertypercent	7.70	1	2.77
binnedinc	383899350.81	9	3.00
medianage	1.46	1	1.21
pctbachdeg25_over	2.06	1	1.44
pctunemployed16_over	12.40	1	3.52
pctprivatecoverage	3.89	1	1.97
binnedinc:pctunemployed16_over	336672247.75	9	2.98

```
## The following object is masked from 'package:dplyr':
##
##     recode
```

When looking at the VIF values none of the values are larger than 10 which suggests there is no evidence of severe multicolinearity therefore there is no need for further action.

```
vif(model1)
```

```
##                          GVIF Df GVIF^(1/(2*Df))
## povertypercent       7.535408  1        2.745070
## studypercap          1.024120  1        1.011988
## binnedinc            7.000188  9        1.114168
## medianage            1.444657  1        1.201939
## pctbachdeg25_over    2.052006  1        1.432483
## pctunemployed16_over 1.917421  1        1.384710
## pctprivatecoverage   3.800720  1        1.949543
```

```
kable(vif(model2), digits=2, caption="VIF values")%>%
  kable_styling()
```

m) based on the above analysis from the second model in part h I would say that the predictions made by this model would not be very reliable as the predictions made only account for rougly 30% of the variation in the target death rate, this is only slighly better than the previous model aswell. although there are no signs of clear multicolinearity, the residual plots all look relatively good but the model is just not accurate enough to make good predictions at this stage.

Q2)

a) Y = Bo + B1X1 + B2X2 + B3X3 + B4X1X2 + B5X1X3 + E

b)

the statement (iii) is correct because this model predicts that males will earn more money than females at fixed amounts when the GPA is higher but as the GPA drops lower females tend to earn more.

c)

```r
Y <- 50 + (20 * 4) + (0.07 * 110) + (35 * 1) + (0.01 * 4 * 110) + (-10 * 4 * 1)
Y
```

```
## [1] 137.1
```

d) False, since the coefficient for GPA/IQ is very small this indicates that the interaction term explains a significant amount of variance in the starting salary of students straight out of college.

Q3)