REGRESSION ASSIGNMENT 2

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```
1)
A)
       mpg_wt_cyl = lm(mpg \sim wt + cyl, data = mtcars2)
       summary(mpg_wt_cyl)
       int_4cyl = coef(mpg_wt_cyl)[1]
       int_6cyl = coef(mpg_wt_cyl)[1] + coef(mpg_wt_cyl)[3]
       int_8cyl = coef(mpg_wt_cyl)[1] + coef(mpg_wt_cyl)[4]
       slope\_all\_cyl = coef(mpg\_wt\_cyl)[2]
       fit=(3*slope_all_cyl+int_6cyl)
       fit
wt
19.95467
We need to test H_0: \beta_{cvl} = 0
   null=lm(mpg~wt,data=mtcars2)
   full=lm(mpg~wt+cyl,data=mtcars2)
   anova(null,full)
Analysis of Variance Table
Model 1: mpg \sim wt
Model 2: mpg \sim wt + cyl
 Res.Df RSS Df Sum of Sq
                                F Pr(>F)
    23 200.88
1
    21 139.62 2 61.253 4.6063 0.02194 *
2
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' '1
P-value is smaller than 0.05 → hypothesis is rejected because → the reduced model is rejected, fu
Il model is accepted. \rightarrow cyl should be in the model and it is significant at 0.05.
C)
       mpg_wt_cyl = lm(mpg \sim wt + cyl + wt:cyl, data = mtcars2)
```

```
slope_8cyl = coef(mpg_wt_cyl)[2] + coef(mpg_wt_cyl)[6] # slope 3
fit1=(int_8cyl+3*slope_8cyl)
fit1
```

Call:

 $lm(formula = mpg \sim wt + cyl + wt:cyl, data = mtcars2)$

Residuals:

Min 1Q Median 3Q Max -3.6507 -1.1242 -0.5088 1.4086 5.2918

Coefficients:

Estimate Std. Error t value Pr(>ltl) 3.7624 10.280 3.37e-09 *** (Intercept) 38.6787 wt -5.4880 1.5419 -3.559 0.00209 ** -4.3800 16.9168 -0.259 0.79849 cyl6 -16.2269 5.7241 -2.835 0.01059 * cyl8 5.2116 0.166 0.86995 wt:cyl6 0.8649 3.7042 1.8856 1.964 0.06427. wt:cyl8

Signif. codes: 0 '*** '0.001 '** '0.01 '* '0.05 '.' 0.1 ' '1

Residual standard error: 2.466 on 19 degrees of freedom

Multiple R-squared: 0.8452, Adjusted R-squared: 0.8045

F-statistic: 20.75 on 5 and 19 DF, p-value: 4.241e-07

(Intercept)

17.10022



Null hypothesis: "There is no significant interaction effect between two predictors." In the part (C) P-value for $\beta_{wt:cyl6}$ and $\beta_{wt:cyl8}$ is larger than 0.05 \rightarrow there not significant interaction effect between two predictors.

```
By the way we can test H_0: \beta_{wt:cyl6} = \beta_{wt:cyl8} = 0 as follows nullmpg_wt_cyl = lm(mpg ~ wt + cyl, data = mtcars2) fullmpg_wt_cyl = lm(mpg ~ wt + cyl + wt:cyl, data = mtcars2) anova(nullmpg_wt_cyl,fullmpg_wt_cyl)
```

Analysis of Variance Table

Model 1: mpg \sim wt + cyl Model 2: mpg \sim wt + cyl + wt:cyl Res.Df RSS Df Sum of Sq F Pr(>F)

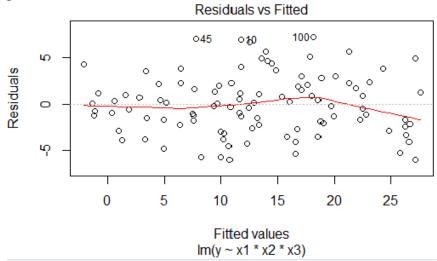
- 1 21 139.62
- 2 19 115.54 2 24.086 1.9804 0.1655

we fail to reject null hypothesis is rejected \rightarrow the reduced model can be accepted \rightarrow there is no significant interaction effect between two predictors.

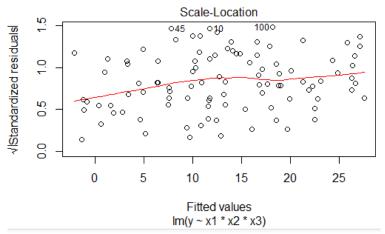
 $model1 = lm(y \sim x1*x2*x3, data = hw2_data_1)$ summary(model1) $E(y \mid x_2 = 50, x_3 = 7) = 7.327393 + 1.709184x_1 - 0.166497x_2 + 0.561826x_3$ $+0.038134x_1x_2 + 0.1217x_1x_3 - 0.003239x_2x_3 - 0.001350x_1x_2x_3 =$ $7.327393 + 1.709184x_1 - 8.32485 + 3.932782 + 1.9067x_1 + 0.8519x_1$ $-1.13365 - 0.4725x_1 = 1.801675 + 3.995284x_1$ $x^2 = 50$ and $x^3 = 7$ one unit increase in x_1 increases the estimated mean of y by 3.995284 units.

B)

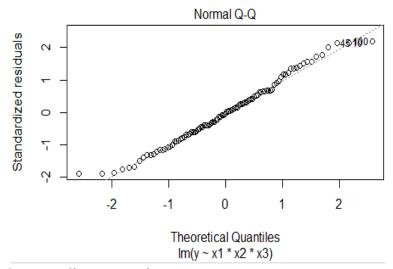
plot(model1)



The red line should be horizontal at zero → there is no fitted pattern. It means we can accept linearity assumption.



residuals are spread equally along the ranges of predictors, the variances of the residual points is fairly constant \rightarrow assume equality of variance.



we can accept the normality assumption.



$$datahw2 = lm(y \sim x1*x2*x3, data = hw2_data_1)$$

summary(datahw2)

Call:

$$lm(formula = y \sim x1 * x2 * x3, data = hw2_data_1)$$

Residuals:

```
Coefficients:
```

Estimate Std. Error t value Pr(>|t|) (Intercept) 7.327393 3.559242 2.059 0.0424 * x1 1.709184 1.251519 1.366 0.1754 -0.166497 0.059186 -2.813 0.0060 ** x2**x**3 $0.561826 \quad 0.312254 \quad 1.799 \quad 0.0753$. 0.038134 0.020579 1.853 0.0671. x1:x20.121700 0.110824 1.098 0.2750 x1:x3 -0.003239 0.005007 -0.647 0.5193 x2:x3 x1:x2:x3 -0.001350 0.001735 -0.778 0.4385 Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' '1

Residual standard error: 3.336 on 92 degrees of freedom

Multiple R-squared: 0.8574, Adjusted R-squared: 0.8466

F-statistic: 79.04 on 7 and 92 DF, p-value: < 2.2e-16

 $H_0: \beta_{x,x_2,x_3} = 0$ P-value is more than 0.05 \rightarrow we fail to reject $H_0 \rightarrow$ three way interaction is not significant in the model.



We are going to test
$$H_0$$
: $\beta_4 = \beta_5 = B_6 = \beta_7 = 0$. null_datahw2= lm(y ~ x1+x2+x3, data = hw2_data_1) full_datahw2 = lm(y ~ x1*x2*x3, data = hw2_data_1) anova(null_datahw2,full_datahw2)

Analysis of Variance Table

Model 1: $y \sim x1 + x2 + x3$ Model 2: $y \sim x1 * x2 * x3$ Res.Df RSS Df Sum of Sq F Pr(>F) 96 1240.8 92 1023.6 4 217.16 4.8795 0.001297 ** Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' '1 p-value is less than $0.05 \rightarrow H_0$ is rejected \rightarrow at least there is at least one of the $\beta_4, \beta_5, B_6, \beta_7$ which is not zero and it is not significant at 0.05.

3-

$$model2 = lm(y \sim x, data = hw2_data_2)$$

 $summary(model2)$

Call:

 $lm(formula = y \sim x, data = hw2_data_2)$

Residuals:

Min 1Q Median 3Q Max -1.99865 -0.65994 -0.02829 0.75697 2.07659

Coefficients:

Estimate Std. Error t value Pr(>ltl) (Intercept) 2.01828 0.20149 10.02 <2e-16 *** X

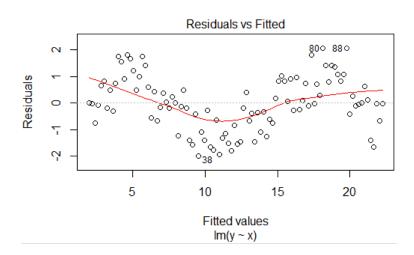
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' '1

Residual standard error: 1.015 on 98 degrees of freedom

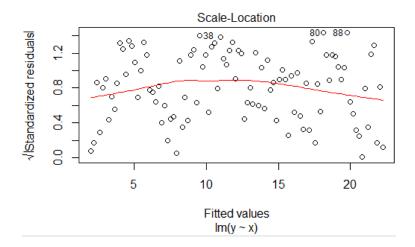
Multiple R-squared: 0.9717, Adjusted R-squared: 0.9714

F-statistic: 3368 on 1 and 98 DF, p-value: < 2.2e-16

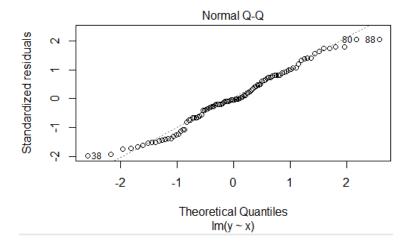
$$\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 x = 2.01828 + 2.02023(x)$$



Residuals vs Fitted: linearity assumption is not valid.



Equality of variance: the distribution of residuals has the same variance > level of error in the model is approximately the same regardless of the value of the predictor variable



Normal Q-Q:

all the points fall approximately along the reference line, so we
normality is hold and normality assumption is accepted.

4-

 $model4 = lm(y \sim x, data = hw2_data_3)$ summary(model4)

Call:

 $lm(formula = y \sim x, data = hw2_data_3)$

Residuals:

Min 1Q Median 3Q Max -42.505 -6.346 -1.484 7.156 41.962

Coefficients:

Estimate Std. Error t value Pr(>ltl)
(Intercept) -4.5459 3.3358 -1.363 0.176
x 3.8815 0.2443 15.887 <2e-16 ***

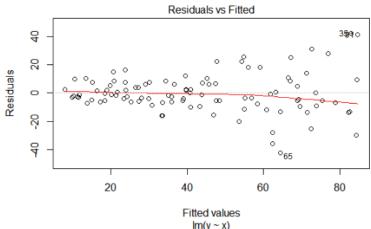
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1

Residual standard error: 13.88 on 98 degrees of freedom

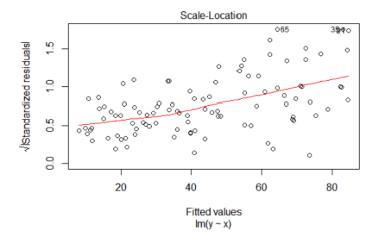
Multiple R-squared: 0.7203, Adjusted R-squared: 0.7175

F-statistic: 252.4 on 1 and 98 DF, p-value: < 2.2e-16

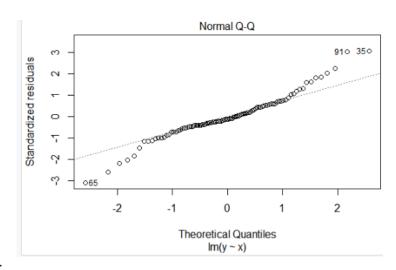
$$\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 x = -4.5459 + 3.8815(x)$$



Residuals vs Fitted: we can accept linearity assumption.



Equality of variance: distribution of residuals does not have the same variance \Rightarrow assumption of equality of variances is rejected.



Normal Q-Q:

The pattern is non-linear, so plot give evidence against assume normality → Normality assumption is rejected.

```
5-
a)
lev_fit = lm(y \sim x, data = mydata)
leverages = hatvalues(lev_fit)
hatvalues(lev_fit) > 2 * mean(hatvalues(lev_fit))
             4
                  5
                     6
         3
                         7
                             8
                                  9 10
FALSE FALSE TRUE FALSE FALSE FALSE FALSE FALSE
It means C and E have a high leverage.
b)
lev_fit1 = lm(y \sim x, data = newmydata)
> leverages = hatvalues(lev_fit1)
> leverages
                              5
                                    6
                                                 8
                                                              10
0.1609862\ 0.1261784\ 0.4655547\ 0.1011603\ 0.5525743\ 0.1026106\ 0.1087745\ 0.1319797\ 0.1490
210 0.1011603
       It means it has not changed.
> leverages.df <- as.data.frame(t(leverages))
 > leverages.df [, c (2,3,5,8)]
           3
    2.021882 -0.6087305 -2.093985 -0.9718407
d)
 cooks.distance(lev_fit)
   cooks.distance.df <- as.data.frame(t(cooks.distance(lev_fit)))</pre>
   cooks.distance.df [, c (2,3,5,8)]
              3
                      5
    0.2951508  0.1613941  2.707616
                                         0.07180215
> newdata <- cooks.distance.df [, c (2,3,5,8)]
  newdata > 4 / length(newdata)
            3
                 5
[1,] FALSE FALSE TRUE FALSE
```

Only E is an influential point.