Lab 3

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Task 1 (8 points)

(a) (1 point)

Succesfully render this file.

(b) (1 point)

```
chem_pro.df = read.table(file = chem_pro.csv, sep = ",", header = TRUE)

str(chem_pro.df)

## 'data.frame': 44 obs. of 4 variables:
## $ yield : num 55.5 54.8 52.2 50.4 49.3 ...
## $ conversion: num 11.8 11.9 12.1 12.1 12 ...
## $ flow : num 119 105 97 101 44 ...
## $ ratio : Factor w/ 40 levels "0.036","0.089",..: 16 2 3 6 5 1 7 9 11 24 ...
```

It can be seen that there are three regressors, which are yield, conversion, flow and ratio, and one response, which is yield. And since the ratio is factor, there may be some issues.

Clean ratio

```
levels(chem_pro.df$ratio)

## [1] "0.036" "0.089" "0.094" "0.097" "0.1" "0.108" "0.113" "0.116"

## [9] "0.123" "0.126" "0.135" "0.136" "0.143" "0.152" "0.153" "0.155"

## [17] "0.16" "0.161" "0.164" "0.166" "0.169" "0.17" "0.18" "0.183"

## [25] "0.184" "0.188" "0.192" "0.194" "0.195" "0.197" "0.201" "0.211"

## [33] "0.215" "0.221" "0.222" "0.223" "0.225" "0.229" "0.233" "0>163"

It can be seen that the last element in ratio seems to be a typo.

ratio_typo = which (chem_pro.df$ratio=="0>163")
    chem_pro.df$ratio = as.character(chem_pro.df$ratio)
    chem_pro.df$ratio[ratio_typo] = "0.163"
    chem_pro.df$ratio = as.double(chem_pro.df$ratio)
```

We then keep a record on the typo and then correct it. Then we take a close look at the data again.

kable(summary(chem_pro.df))

yield	conversion	flow	ratio
Min. :40.05	Min. :-11.12	Min.: 30.0	Min. :0.0360
1st Qu.:48.05	1st Qu.: 11.19	1st Qu.:221.5	1st Qu.:0.1358
Median: 51.28	Median: 11.89	Median $:325.0$	Median: 0.1675
Mean $:50.68$	Mean: 11.11	Mean $:291.9$	Mean $:0.1658$
3rd Qu.:53.91	3rd Qu.: 12.04	3rd Qu.:380.0	3rd Qu.:0.1980

yield	conversion	flow	ratio
Max. :59.34	Max.: 12.36	Max. :523.0	Max. :0.2330

It seems like that the min of conversion is far from it's $1st \ Qu$, there may be some issues. And the flow seems to be ok.

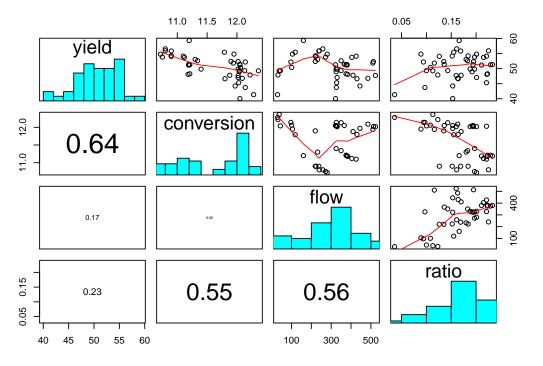
Clean conversion

```
conversion_typo = which(chem_pro.df$conversion<=-10)
chem_pro.df$conversion[conversion_typo] = -chem_pro.df$conversion[conversion_typo]</pre>
```

We keep record of the possible typo in conversion and correct it.

(c) (1 point)

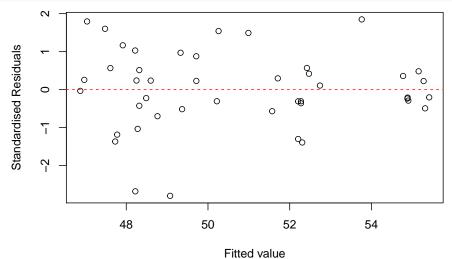
```
panel.hist <- function(x, ...)</pre>
    usr <- par("usr"); on.exit(par(usr))</pre>
    par(usr = c(usr[1:2], 0, 1.5))
    h <- hist(x, plot = FALSE)
    breaks <- h$breaks; nB <- length(breaks)</pre>
    y \leftarrow h$counts; y \leftarrow y/max(y)
    rect(breaks[-nB], 0, breaks[-1], y, col = "cyan", ...)
panel.cor <- function(x, y, digits = 2, prefix = "", cex.cor, ...)</pre>
    usr <- par("usr"); on.exit(par(usr))</pre>
    par(usr = c(0, 1, 0, 1))
    r <- abs(cor(x, y))
    txt <- format(c(r, 0.123456789), digits = digits)[1]</pre>
    txt <- paste0(prefix, txt)</pre>
    if(missing(cex.cor)) cex.cor <- 0.8/strwidth(txt)</pre>
    text(0.5, 0.5, txt, cex = cex.cor * r)
}
pairs(chem_pro.df[1:4],upper.panel = panel.smooth,lower.panel = panel.cor,
      diag.panel = panel.hist)
```



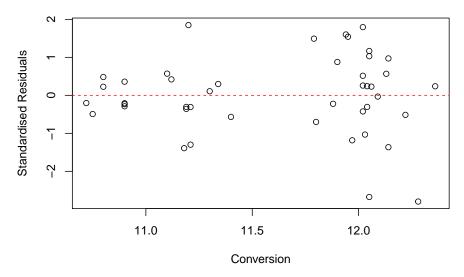
(d) (1 point)

```
chem_pro.LM = lm(yield~conversion+flow+ratio, data = chem_pro.df)
```

• Standardised residual Vs fitted value

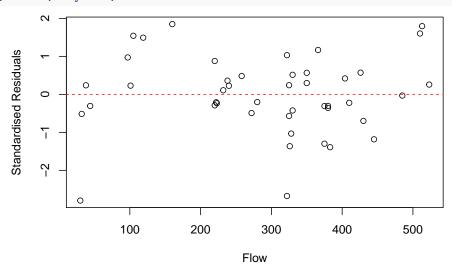


• Standardised residual Vs conversion

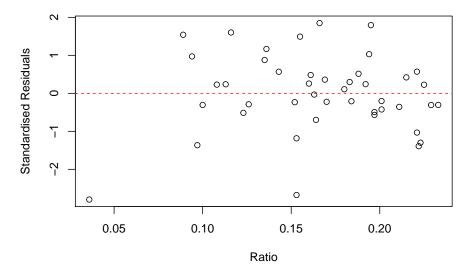


• Standardised residual Vs flow

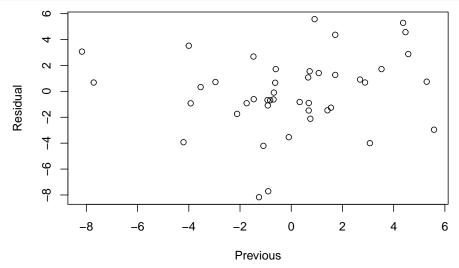
```
plot(chem_pro.df$flow,rstandard(chem_pro.LM), xlab = "Flow",ylab = "Standardised Residuals")
abline(a = 0, b = 0, lty = 2, col = "red")
```



• Standardised residual Vs ratio



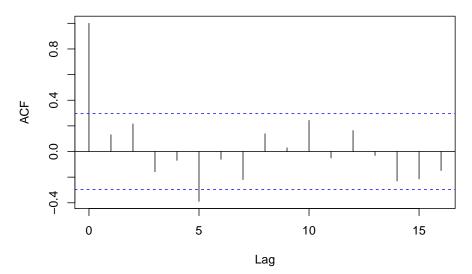
• Residual Vs Previous Residual



• Residual Autcorrelation (ACF)

acf(chem_pro.LM\$residuals, main = "ACF")

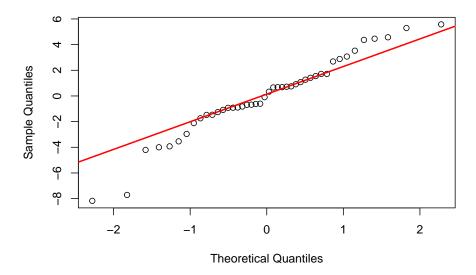




• Q-Q Normal

```
qqnorm(chem_pro.LM$residuals)
qqline(chem_pro.LM$residuals,lwd=2,col=2)
```

Normal Q-Q Plot



(e) (1 point)

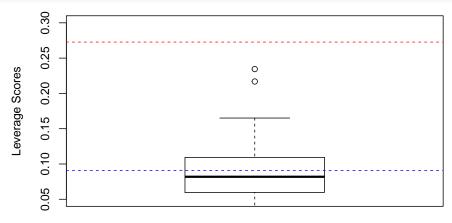
```
correlation.matrix = cor(chem_pro.df[-1])
temp = solve(correlation.matrix)
VIF.vec = c(temp[1,1],temp[2,2],temp[3,3])
names(VIF.vec) = c("conversion", "flow", "ratio")
kable(VIF.vec,col.names = "VIF")
```

	VIF
conversion	1.580323
flow	1.606860

	VIF
ratio	2.276409

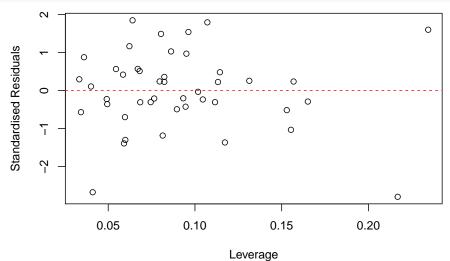
It is the same as what we found in the class.

(f) (1 point)



chem_pro.LM

(g) (1 point)

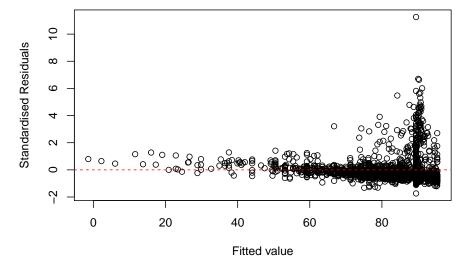


(h) (1 point)

```
im = influence.measures(chem pro.LM)
## Influence measures of
    lm(formula = yield ~ conversion + flow + ratio, data = chem_pro.df) :
##
##
                                                   cook.d
      dfb.1_ dfb.cnvr dfb.flow dfb.rati
                                       dffit cov.r
## 1
    -0.15379 0.171205 -0.37075 0.21414 0.4483 0.957 4.87e-02 0.0804
     -0.02789 0.062869 -0.12017 -0.07752 0.3146 1.111 2.48e-02 0.0951
    0.01094 -0.021314 0.06432 0.00689 -0.1070 1.234 2.93e-03 0.1116
    -0.31180 0.115894 0.17695 0.97151 -1.6193 0.592 5.41e-01 0.2169
## 6
    -0.05076  0.058095 -0.07330  0.03086  0.1015  1.305  2.64e-03  0.1569
## 8
     0.10158 -0.115249 0.17135 -0.08036 -0.2165 1.272 1.19e-02 0.1530
## 9 -0.02284 0.038443 -0.03617 -0.02638 0.1692 1.062 7.20e-03 0.0360
## 10 0.02164 -0.022460 0.01842 -0.00746 0.0546 1.135 7.61e-04 0.0333
## 11 0.19537 -0.185560 -0.28038 0.04779 0.4993 0.827 5.85e-02 0.0640
## 12 0.35865 -0.342510 0.18667 -0.38167 -0.4433 1.176 4.90e-02 0.1553
## 13 -0.05581 0.054864 -0.02031 0.04898 0.0699 1.195 1.25e-03 0.0797
## 14 -0.10685 0.105545 -0.03182 0.08916 0.1380 1.156 4.85e-03 0.0681
## 15 0.10868 -0.105522 0.04425 -0.10339 -0.1357 1.200 4.70e-03 0.0946
## 16 0.29033 -0.321183 -0.09788 -0.01622 -0.6034 0.524 7.66e-02 0.0411
## 17 -0.25558 0.250764 -0.10094 0.22932 0.3167 1.087 2.50e-02 0.0862
## 18 -0.09085 0.045557 -0.29539 0.38361 -0.5032 1.036 6.19e-02 0.1173
## 19 -0.02490 0.044340 0.17963 -0.14403 0.3021 1.027 2.26e-02 0.0622
## 20 -0.04657 0.054612
                      ## 21 0.28057 -0.240441
                      0.80109 -0.69167 0.9045 1.109 1.96e-01 0.2345
## 22 -0.28662 0.273128
                      ## 23 -0.00630 0.007837 0.08246 -0.03858 0.0987 1.265 2.50e-03 0.1313
## 24 -0.00246 -0.000810 -0.13055 0.06366 -0.1750 1.120 7.75e-03 0.0597
## 25 0.00460 -0.000362 0.01388 -0.04641 -0.1062 1.109 2.87e-03 0.0343
      ## 27 -0.01633 0.021263 -0.01283 -0.02067 -0.0806 1.149 1.66e-03 0.0494
## 28 -0.01828  0.043894 -0.01005 -0.15639 -0.3528 0.965 3.04e-02 0.0591
## 29 0.00710 0.017014 0.01493 -0.17090 -0.3307 0.991 2.69e-02 0.0599
## 30 0.00809 -0.001782 0.00932 -0.04943 -0.0825 1.177 1.74e-03 0.0685
## 31 0.01242 -0.013054 -0.02847 0.00527 -0.0501 1.158 6.43e-04 0.0492
## 32 0.00253 -0.002703 -0.00775 0.00261 -0.0107 1.232 2.94e-05 0.1018
      0.01843 -0.029428 -0.27092 0.14880 -0.3542 1.045 3.11e-02 0.0814
## 34 0.00500 -0.005066 -0.01017 0.00589 0.0218 1.151 1.21e-04 0.0401
## 35 -0.11592 0.110300 -0.03173 0.09279 -0.1270 1.314 4.13e-03 0.1651
## 36 -0.06936 0.067273 -0.00626 0.04110 -0.0790 1.229 1.60e-03 0.1045
## 37 -0.03747 0.038115 0.01600 0.00120 -0.0594 1.193 9.04e-04 0.0765
     0.01881 -0.023149 -0.03880 0.03878 0.0797 1.242 1.63e-03 0.1133
      0.08636 -0.085527 -0.00198 -0.03544 0.1066 1.190 2.91e-03 0.0823
## 40 0.15475 -0.152393 0.03017 -0.08905 0.1717 1.221 7.51e-03 0.1144
## 41 -0.10567 0.110095
                      ## 42 -0.04383 0.046000 0.00491 0.00218 -0.0645 1.215 1.06e-03 0.0933
## 43 0.03744 -0.047960 0.04730 0.02774 0.1516 1.148 5.85e-03 0.0670
## 44 0.02885 -0.035479 0.02799 0.01741 0.1034 1.155 2.73e-03 0.0585
```

Task 2 (6 points)

(a) (1 point)



It can be seen that as the fitted.value increases, the standardised residual varies in a larger range. Thus, there is a heteroskedasticity problem.

(b) (1 point)

```
z = 2 * log(abs(usare.LM$residuals))
auxiliary.LM = lm(z ~ pnh + pms, data = usare.df)
w.vec = 1 / exp(auxiliary.LM$fitted.values)
```

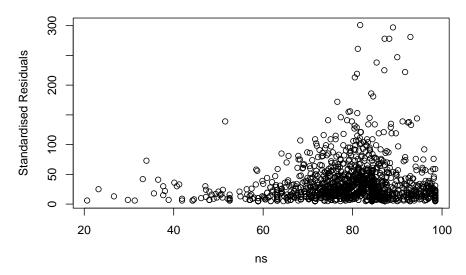
(c) (1 point)

```
usare.WLS = lm(mppsf~pnh+pms, weights = w.vec, data = usare.df)
```

(d) (1 point)

Since ns is one of the original data in the calculation of 'mppsf', it may affect the original ϵ . Then, we may choose it as a weight.

```
plot(fitted.values(usare.WLS),usare.df$ns, xlab = "ns",
    ylab = "Standardised Residuals")
```

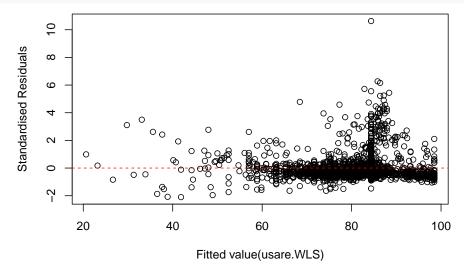


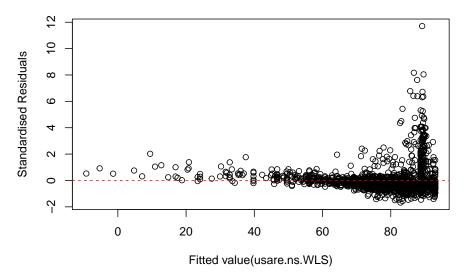
Moreover, it can be seen that the residual increase as **ns** increase, which indicates the heteroskedasticity may be solved by choosing **ns** as a weight.

(e) (1 point)

```
usare.ns.WLS = lm(mppsf~pnh+pms, weights = ns, data = usare.df)
```

(f) (1 point)





Based on the plots, we find the one of usare.WLS model has a better pattern. Thus, the usare.WLS model is better.

Task 3 (5 points)

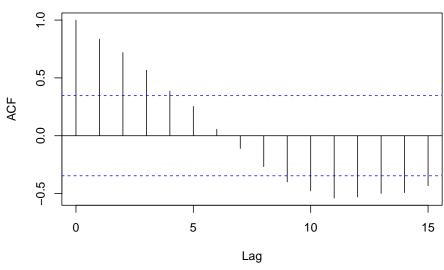
The data grossboxoffice is about yearly gross box office receipts from moives screened in Australia.

(a) (1 point)

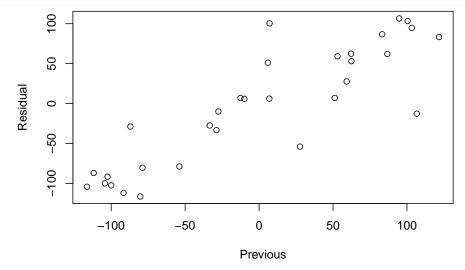
```
gbo.df = read.table("grossboxoffice.txt", header = T)
gbo.LM = lm(GrossBoxOffice ~ year, data = gbo.df)
summary(gbo.LM)
##
## Call:
## lm(formula = GrossBoxOffice ~ year, data = gbo.df)
## Residuals:
##
        Min
                  1Q
                       Median
                                     3Q
                                             Max
                        6.083
  -116.382 -79.197
                                62.260
                                        121.697
##
##
## Coefficients:
##
                 Estimate Std. Error t value Pr(>|t|)
## (Intercept) -58386.485
                            2952.825
                                       -19.77
                                                <2e-16 ***
## year
                   29.534
                                1.483
                                        19.92
                                                <2e-16 ***
##
                   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Signif. codes:
## Residual standard error: 77.44 on 30 degrees of freedom
## Multiple R-squared: 0.9297, Adjusted R-squared: 0.9274
## F-statistic: 396.8 on 1 and 30 DF, p-value: < 2.2e-16
```

acf(gbo.LM\$residuals)

Series gbo.LM\$residuals



```
plot(gbo.LM$residuals[-length(gbo.LM$residuals)],
    gbo.LM$residuals[-1],
    xlab = "Previous", ylab = "Residual")
```



Based on the acf plot and the plot of previous residual vs residual, the correlation between the residuals can be detected. Thus, gbo.LM is invalid.

(b) (1 point)

AR(1)

```
##
## Call:
## lm(formula = y ~ x1, data = res_lag.df)
##
## Residuals:
##
      Min
               1Q Median
                               3Q
                                      Max
  -88.935 -19.583 -2.572 13.908 113.918
##
## Coefficients:
##
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 4.22991
                          7.37346
                                    0.574
                                             0.571
               0.91377
                          0.09775
                                    9.348 5.91e-10 ***
## x1
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 39.63 on 27 degrees of freedom
## Multiple R-squared: 0.764, Adjusted R-squared: 0.7552
## F-statistic: 87.39 on 1 and 27 DF, p-value: 5.906e-10
```

The p-value of the F statistic indicates that there is no strong evidence that the AR(1) model is invalid. So, AR(1) model is possible.

AR(2)

```
AR2.LM = lm(y \sim x1+x2, data = res_lag.df)
summary(AR2.LM)
##
## Call:
## lm(formula = y \sim x1 + x2, data = res lag.df)
## Residuals:
##
                1Q Median
                                3Q
      Min
                                       Max
## -90.361 -20.959 -0.372 14.588 112.541
##
## Coefficients:
               Estimate Std. Error t value Pr(>|t|)
##
## (Intercept) 4.44981
                           7.53005
                                     0.591 0.559663
                                     4.311 0.000207 ***
## x1
                0.85824
                           0.19910
                0.06566
## x2
                           0.20399
                                     0.322 0.750118
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 40.31 on 26 degrees of freedom
## Multiple R-squared: 0.7649, Adjusted R-squared: 0.7468
## F-statistic: 42.3 on 2 and 26 DF, p-value: 6.702e-09
```

Compared with previoud one, the adjusted R-squared is smaller. Moreover, the p-value of the t-test of x2 is small. Based on clues above, AR(2) may not be possible.

AR(3)

```
AR3.LM = lm(y ~ ., data = res_lag.df)
summary(AR3.LM)
```

```
##
## Call:
  lm(formula = y ~ ., data = res_lag.df)
##
##
  Residuals:
##
       Min
                1Q
                    Median
                                 3Q
                                        Max
   -87.899 -18.928
                     0.656
                            15.507 113.583
##
##
  Coefficients:
##
               Estimate Std. Error t value Pr(>|t|)
##
   (Intercept)
                 3.6370
                             7.5824
                                      0.480 0.635639
                             0.1994
                 0.8660
                                      4.342 0.000205 ***
## x1
## x2
                 0.2263
                             0.2621
                                      0.863 0.396219
                -0.2007
                             0.2054
                                     -0.977 0.337898
## x3
## ---
                   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 40.34 on 25 degrees of freedom
## Multiple R-squared: 0.7736, Adjusted R-squared: 0.7464
## F-statistic: 28.47 on 3 and 25 DF, p-value: 3.16e-08
```

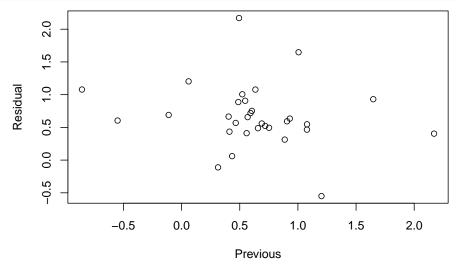
Compared with the one in AR(1) part, the adjusted R-squared is smaller. Moreover, the p-values of the t-test of x2 and x3 are small. Based on clues above, AR(2) may not be possible.

(c) (1 point)

```
gbo.final.M = arima(gbo.df$year, order = c(1,0,0),
xreg = gbo.df$GrossBoxOffice)
```

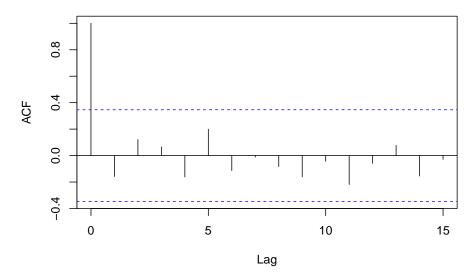
(d) (1 point)

```
plot(gbo.final.M$residuals[-length(gbo.final.M$residuals)],
    gbo.final.M$residuals[-1],
    xlab = "Previous", ylab = "Residual")
```



acf(gbo.final.M\$residuals)

Series gbo.final.M\$residuals



Based on the plot, it can be seen the residuals are independent with each other, which means the model is valid.

(e) (1 point)

Describe any weakness in your gbo.final.M.

(f) (1 point)

Use your model ${\tt gbo.final.M}$ to identify any outliers.