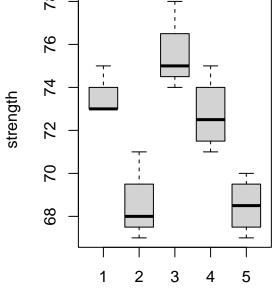
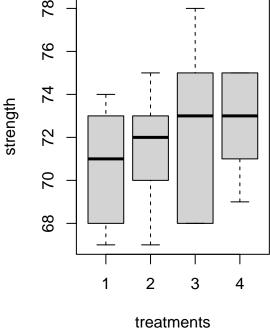
STAT 407 Homework 2

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10/8/2021



blocks



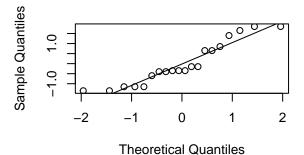
```
t<-lm(strength~trchem+blbolt)
library(car)
anova(t)</pre>
```

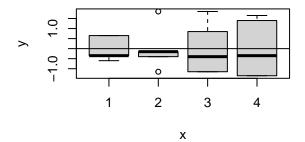
```
## Analysis of Variance Table
##
## Response: strength
```

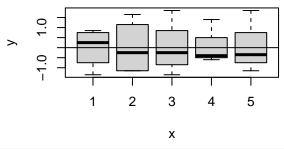
```
Df Sum Sq Mean Sq F value
          3 12.95
                       4.317 2.3761
                                         0.1211
## trchem
            4 157.00 39.250 21.6055 2.059e-05 ***
## blbolt
## Residuals 12 21.80
                       1.817
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# We fail to reject the null hypothesis at the alpha = 0.05 level. There is insufficient
# evidence (p = 0.1211) that the mean tensile strengths of the chemical agents are different.
bartlett.test(strength~trchem) # Testing normality and equal variance assumptions
##
## Bartlett test of homogeneity of variances
## data: strength by trchem
## Bartlett's K-squared = 1.1508, df = 3, p-value = 0.7648
bartlett.test(strength~blbolt)
##
## Bartlett test of homogeneity of variances
## data: strength by blbolt
## Bartlett's K-squared = 1.1175, df = 4, p-value = 0.8915
bartlett.test(t$residuals~trchem)
##
## Bartlett test of homogeneity of variances
## data: t$residuals by trchem
## Bartlett's K-squared = 2.6757, df = 3, p-value = 0.4444
leveneTest(strength~trchem)
## Levene's Test for Homogeneity of Variance (center = median)
        Df F value Pr(>F)
## group 3 0.5815 0.6357
        16
shapiro.test(t$residual)
##
## Shapiro-Wilk normality test
## data: t$residual
## W = 0.8996, p-value = 0.04054
# We should exercise caution here because the null hypothesis for the Shapiro-Wilk test is
# rejected (p = 0.04054) and the residuals may not be normally distributed.
par(mfrow=c(2,2))
qqnorm(t$residuals)
qqline(t$residuals)
plot(c(trchem),t$residuals)
abline(h=0)
plot(c(blbolt),t$residuals)
abline(h=0)
plot(t$fitted.values,t$residuals)
```

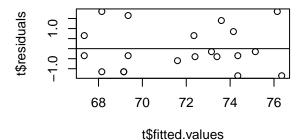
abline(h=0)

Normal Q-Q Plot







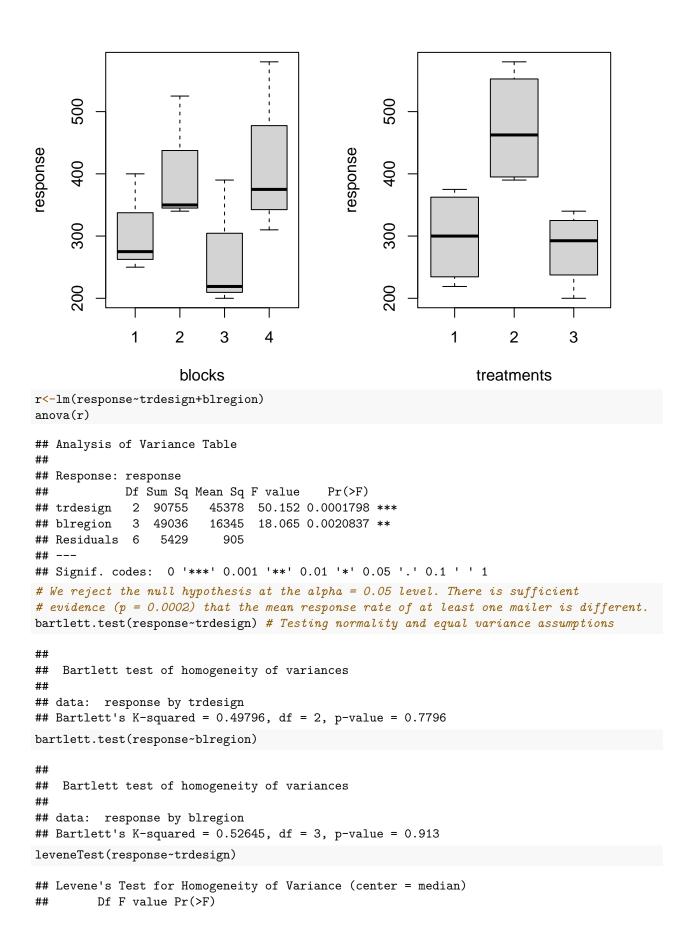


There does not appear to be any pattern in the Q-Q plot or residual plots.

Problem 4.8

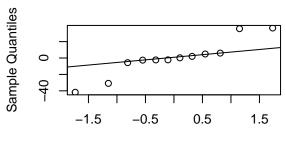
(a)

```
NE<-c(250,400,275)
NW<-c(350,525,340)
SE<-c(219,390,200)
SW<-c(375,580,310)
response<-as.vector(rbind(NE,NW,SE,SW))
blregion<-as.factor(rep(1:4,times=3))
trdesign<-as.factor(rep(1:3,each=4))
par(mfrow=c(1,2))
boxplot(response~blregion,xlab="blocks")
boxplot(response~trdesign,xlab="treatments")
```

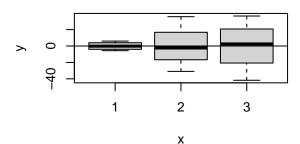


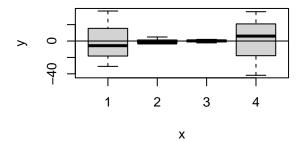
```
## group 2 1.6742 0.2409
##
 (b)
library(agricolae)
LSDr<-LSD.test(aov(response~trdesign+blregion),"trdesign")
LSDr
## $statistics
##
      MSerror Df
                                CV t.value
                                                  LSD
                     Mean
     904.8056 6 351.1667 8.565729 2.446912 52.04523
##
##
## $parameters
##
           test p.ajusted name.t ntr alpha
##
     Fisher-LSD
                   none trdesign
                                      3 0.05
##
## $means
    response
                   std r
                              LCL
                                        UCL Min Max
                                                       Q25
                                                             Q50
                                                                     Q75
       298.50 75.66814 4 261.6985 335.3015 219 375 242.25 300.0 356.25
## 1
       473.75 93.75278 4 436.9485 510.5515 390 580 397.50 462.5 538.75
       281.25 60.32896 4 244.4485 318.0515 200 340 256.25 292.5 317.50
## $comparison
## NULL
##
## $groups
    response groups
## 2
       473.75
## 1
       298.50
## 3
       281.25
##
## attr(,"class")
## [1] "group"
We can see that design 2 clearly has a different mean response rate than designs 1 and 3.
 (c)
bartlett.test(r$residuals~trdesign)
##
##
   Bartlett test of homogeneity of variances
##
## data: r$residuals by trdesign
## Bartlett's K-squared = 6.255, df = 2, p-value = 0.04383
# We should exercise caution here because the null hypothesis for the Bartlett's test
# is rejected (p = 0.04383) and the residuals may not have equal variance.
shapiro.test(r$residual)
##
##
   Shapiro-Wilk normality test
## data: r$residual
## W = 0.88867, p-value = 0.1133
```

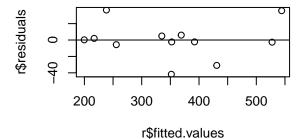
```
par(mfrow=c(2,2))
qqnorm(r$residuals)
qqline(r$residuals)
plot(c(trdesign),r$residuals)
abline(h=0)
plot(c(blregion),r$residuals)
abline(h=0)
plot(r$fitted.values,r$residuals)
abline(h=0)
```











There is some variation in the Q-Q plot, but there does not appear to be any pattern # in the residual plots.

friedman.test(response,trdesign,blregion) # Additional post-hoc analysis

```
##
## Friedman rank sum test
##
## data: response, trdesign and blregion
## Friedman chi-squared = 6.5, df = 2, p-value = 0.03877
```

TukeyHSD(aov(response~trdesign+blregion),conf.level=0.95)\$trdesign

```
## diff lwr upr p adj
## 2-1 175.25 109.98853 240.51147 0.0004235806
## 3-1 -17.25 -82.51147 48.01147 0.7104869430
## 3-2 -192.50 -257.76147 -127.23853 0.0002508095
```

Problem 4.9

(a)

```
X < -c(0.500, 0.634, 0.487, 0.329, 0.512)
Y<-c(0.535,0.675,0.520,0.435,0.540)
Z < -c(0.513, 0.595, 0.488, 0.400, 0.510)
economy <-c(X,Y,Z)
bltruck<-as.factor(rep(1:5,times=3))</pre>
troil<-as.factor(rep(1:3,each=5))</pre>
par(mfrow=c(1,2))
boxplot(economy~bltruck,xlab="blocks")
boxplot(economy~troil,xlab="treatments")
                                                                        0
     0.65
                                                     0.65
                                                               0
                                                                                  0
     0.55
                                                     0.55
                                               economy
economy
     0.45
                                                     0.45
                                                                        0
                                                                                 0
     0.35
                                                     0.35
                                                               0
              1
                   2
                         3
                              4
                                    5
                                                               1
                                                                        2
                                                                                  3
                      blocks
                                                                   treatments
e<-lm(economy~troil+bltruck)
anova(e)
## Analysis of Variance Table
##
## Response: economy
                   Sum Sq
##
              Df
                           Mean Sq F value
                                                 Pr(>F)
               2 0.006706 0.0033529 6.3527
                                                0.02229 *
## troil
               4 0.092100 0.0230249 43.6257 1.781e-05 ***
## bltruck
## Residuals 8 0.004222 0.0005278
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# We reject the null hypothesis at the alpha = 0.05 level. There is sufficient
# evidence (p = 0.0223) that the mean fuel economy of at least one oil is different.
bartlett.test(economy~troil) # Testing normality and equal variance assumptions
##
##
   Bartlett test of homogeneity of variances
##
## data: economy by troil
```

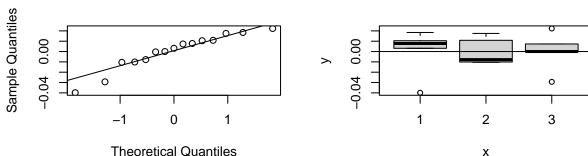
Bartlett's K-squared = 0.70349, df = 2, p-value = 0.7035

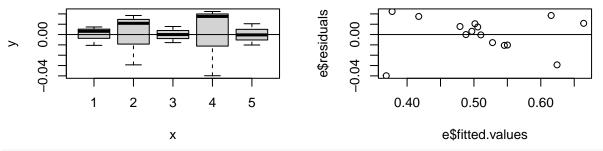
```
bartlett.test(economy~bltruck)
##
## Bartlett test of homogeneity of variances
##
## data: economy by bltruck
## Bartlett's K-squared = 3.9598, df = 4, p-value = 0.4115
leveneTest(economy~troil)
## Levene's Test for Homogeneity of Variance (center = median)
         Df F value Pr(>F)
## group 2 0.1425 0.8686
##
         12
 (b)
LSDe<-LSD.test(aov(economy~troil+bltruck), "troil")
LSDe
## $statistics
##
          MSerror Df
                                     CV t.value
                                                        LSD
                          Mean
    0.0005277833 8 0.5115333 4.491112 2.306004 0.03350564
##
## $parameters
##
           test p.ajusted name.t ntr alpha
     Fisher-LSD
                   none troil
                                   3 0.05
##
## $means
                                LCL
                                          UCL
                                                             Q25
                    std r
                                                Min
                                                      Max
                                                                   Q50
## 1 0.4924 0.10865220 5 0.4687079 0.5160921 0.329 0.634 0.487 0.500 0.512
## 2 0.5410 0.08612491 5 0.5173079 0.5646921 0.435 0.675 0.520 0.535 0.540
## 3 0.5012 0.06969720 5 0.4775079 0.5248921 0.400 0.595 0.488 0.510 0.513
##
## $comparison
## NULL
##
## $groups
## economy groups
## 2 0.5410
## 3 0.5012
                  b
## 1 0.4924
##
## attr(,"class")
## [1] "group"
We can see that oil 2 has a different mean fuel economy than oils 1 and 3.
 (c)
bartlett.test(e$residuals~troil)
##
## Bartlett test of homogeneity of variances
##
## data: e$residuals by troil
```

Bartlett's K-squared = 1.0484, df = 2, p-value = 0.592

```
shapiro.test(e$residual)
```

```
##
   Shapiro-Wilk normality test
##
##
## data: e$residual
## W = 0.91855, p-value = 0.183
# None of the null hypotheses were rejected, so the normality and
par(mfrow=c(2,2)) # equal variance assumptions appear to be met.
qqnorm(e$residuals)
qqline(e$residuals)
plot(c(troil),e$residuals)
abline(h=0)
plot(c(bltruck),e$residuals)
abline(h=0)
plot(e$fitted.values,e$residuals)
abline(h=0)
```





There does not appear to be any pattern in the Q-Q plot or residual plots. friedman.test(economy,troil,bltruck) # Additional post-hoc analysis

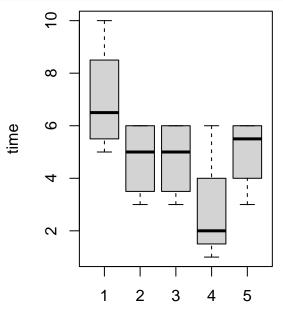
```
##
## Friedman rank sum test
##
## data: economy, troil and bltruck
## Friedman chi-squared = 7.6, df = 2, p-value = 0.02237
TukeyHSD(aov(economy~troil+bltruck),conf.level=0.95)$troil
```

diff lwr upr p adj

```
## 2-1 0.0486 0.007082078 0.090117922 0.02458094
## 3-1 0.0088 -0.032717922 0.050317922 0.82109697
## 3-2 -0.0398 -0.081317922 0.001717922 0.05949792
```

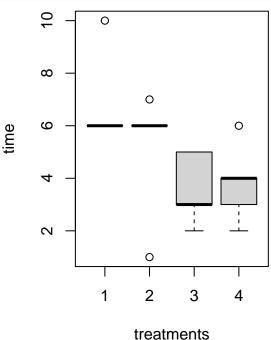
Problem 4.21

```
fou<-c(10,6,6,6,6)
six<-c(7,6,6,1,6)
eig<-c(5,3,3,2,5)
ten<-c(6,4,4,2,3)
time<-c(fou,six,eig,ten)
blsubj<-as.factor(rep(1:5,times=4))
trdist<-as.factor(rep(1:4,each=5))
par(mfrow=c(1,2))
boxplot(time~blsubj,xlab="blocks")
boxplot(time~trdist,xlab="treatments")</pre>
```



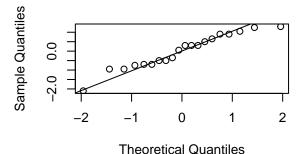
blocks

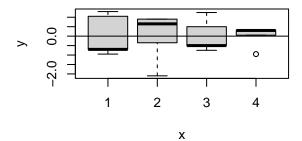
ft<-lm(time~trdist+blsubj)</pre>

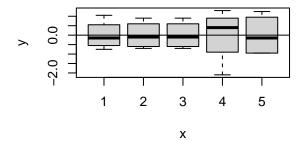


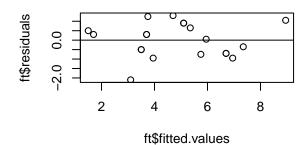
```
anova(ft)
## Analysis of Variance Table
##
## Response: time
##
            Df Sum Sq Mean Sq F value
                                        Pr(>F)
## trdist
             3 32.95 10.983 8.6144 0.002543 **
## blsubj
             4 36.30
                        9.075 7.1176 0.003548 **
## Residuals 12 15.30
                        1.275
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# We reject the null hypothesis at the alpha = 0.05 level. There is sufficient
\# evidence (p = 0.0025) that the mean focus time for at least one distance is different.
bartlett.test(time~trdist) # Testing normality and equal variance assumptions
```

```
##
## Bartlett test of homogeneity of variances
## data: time by trdist
## Bartlett's K-squared = 1.4631, df = 3, p-value = 0.6908
bartlett.test(time~blsubj)
##
## Bartlett test of homogeneity of variances
## data: time by blsubj
## Bartlett's K-squared = 1.042, df = 4, p-value = 0.9034
bartlett.test(ft$residuals~trdist)
## Bartlett test of homogeneity of variances
## data: ft$residuals by trdist
## Bartlett's K-squared = 2.6207, df = 3, p-value = 0.4539
leveneTest(time~trdist)
## Levene's Test for Homogeneity of Variance (center = median)
       Df F value Pr(>F)
## group 3 0.0539 0.9829
##
        16
shapiro.test(ft$residual)
##
## Shapiro-Wilk normality test
## data: ft$residual
## W = 0.94976, p-value = 0.3634
# None of the null hypotheses were rejected, so the normality and
par(mfrow=c(2,2)) # equal variance assumptions appear to be met.
qqnorm(ft$residuals)
qqline(ft$residuals)
plot(c(trdist),ft$residuals)
abline(h=0)
plot(c(blsubj),ft$residuals)
abline(h=0)
plot(ft$fitted.values,ft$residuals)
abline(h=0)
```









There does not appear to be any pattern in the Q-Q plot. There appears to be some # pattern in the residuals vs. fitted values plot, but remember that the sample sizes # for each distance are relatively small.

friedman.test(time,trdist,blsubj) # Post-hoc analysis

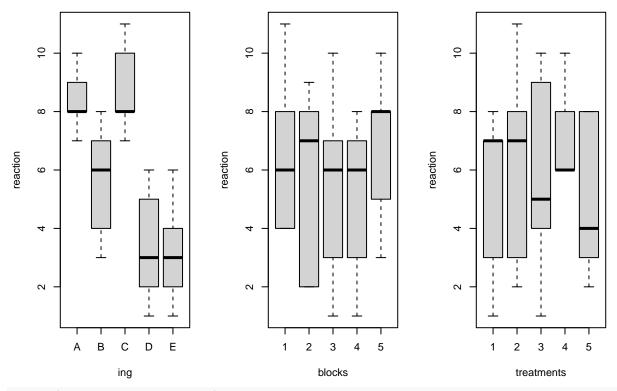
```
##
## Friedman rank sum test
##
## data: time, trdist and blsubj
## Friedman chi-squared = 9.6522, df = 3, p-value = 0.02177
LSDft<-LSD.test(aov(time~trdist+blsubj),"trdist")
LSDft</pre>
```

```
## $statistics
     MSerror Df Mean
##
                            CV t.value
                                             LSD
##
       1.275 12 4.85 23.28163 2.178813 1.555984
##
##
  $parameters
##
           test p.ajusted name.t ntr alpha
##
     Fisher-LSD
                     none trdist
##
## $means
                          LCL
                                    UCL Min Max Q25 Q50 Q75
##
     time
               std r
## 1 6.8 1.788854 5 5.699753 7.900247
                                          6
                                             10
                                                  6
                                                      6
                                                           6
                                                           6
## 2 5.2 2.387467 5 4.099753 6.300247
                                              7
                                                      6
## 3 3.6 1.341641 5 2.499753 4.700247
                                                           5
                                          2
                                              5
                                                  3
                                                      3
     3.8 1.483240 5 2.699753 4.900247
                                              6
                                                  3
##
## $comparison
```

```
## NULL
##
## $groups
    time groups
## 1 6.8
## 2 5.2
              b
## 4 3.8
              bc
## 3 3.6
              С
## attr(,"class")
## [1] "group"
TukeyHSD(aov(time~trdist+blsubj),conf.level=0.95)$trdist
##
       diff
                 lwr
                             upr
                                       p adj
## 2-1 -1.6 -3.720219 0.5202195 0.167524230
## 3-1 -3.2 -5.320219 -1.0797805 0.003615573
## 4-1 -3.0 -5.120219 -0.8797805 0.005836959
## 3-2 -1.6 -3.720219 0.5202195 0.167524230
## 4-2 -1.4 -3.520219 0.7202195 0.255437448
## 4-3 0.2 -1.920219 2.3202195 0.991929366
```

Problem 4.22

```
reaction<-c(8,7,1,7,3,11,2,7,3,8,4,9,10,1,5,6,8,6,6,10,4,2,3,8,8)
day<-as.factor(rep(1:5,times=5))
batch<-as.factor(rep(1:5,each=5))
ing<-c("A","B","D","C","E","C","E","A","D","B","B","A","C","E","D","D","C","E","B","A","E","D","B","A",
par(mfrow=c(1,3))
boxplot(reaction~ing)
boxplot(reaction~day,xlab="blocks")
boxplot(reaction~batch,xlab="treatments")</pre>
```



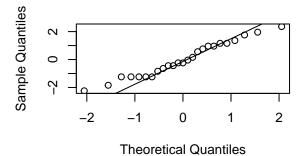
rt<-lm(reaction~ing+day+batch)
anova(rt)</pre>

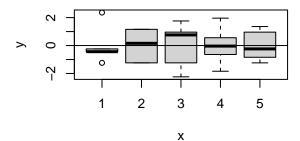
data: reaction by batch

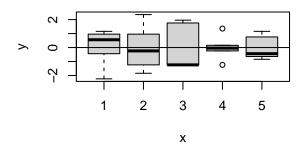
Bartlett's K-squared = 2.1504, df = 4, p-value = 0.7081

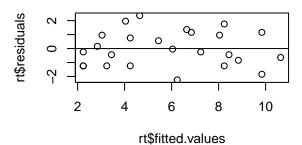
```
## Analysis of Variance Table
##
## Response: reaction
            Df Sum Sq Mean Sq F value
             4 141.44 35.360 11.3092 0.0004877 ***
## ing
                12.24
                        3.060 0.9787 0.4550143
## day
## batch
             4 15.44
                        3.860 1.2345 0.3476182
## Residuals 12 37.52
                        3.127
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# We reject the null hypothesis at the alpha = 0.05 level. There is sufficient
# evidence (p = 0.0005) that the mean reaction time for at least one ingredient is different.
bartlett.test(reaction~ing) # Testing normality and equal variance assumptions
##
## Bartlett test of homogeneity of variances
##
## data: reaction by ing
## Bartlett's K-squared = 1.5544, df = 4, p-value = 0.817
bartlett.test(reaction~batch)
##
## Bartlett test of homogeneity of variances
```

```
bartlett.test(reaction~day)
## Bartlett test of homogeneity of variances
##
## data: reaction by day
## Bartlett's K-squared = 0.29268, df = 4, p-value = 0.9903
bartlett.test(rt$residuals~batch)
##
## Bartlett test of homogeneity of variances
##
## data: rt$residuals by batch
## Bartlett's K-squared = 0.69132, df = 4, p-value = 0.9524
f<-vector() # Levene's test</pre>
for(j in c("A","B","C","D")) f[ing==j]<-abs(reaction[ing==j]-median(reaction[ing==j]))</pre>
lt<-lm(f~ing)</pre>
anova(lt)
## Analysis of Variance Table
##
## Response: f
             Df Sum Sq Mean Sq F value Pr(>F)
                  2.2 0.73333 0.5867 0.6325
             3
## Residuals 16 20.0 1.25000
shapiro.test(rt$residual)
##
##
  Shapiro-Wilk normality test
##
## data: rt$residual
## W = 0.96606, p-value = 0.5476
# None of the null hypotheses were rejected, so the normality and
par(mfrow=c(2,2)) # equal variance assumptions appear to be met.
qqnorm(rt$residuals)
qqline(rt$residuals)
plot(c(batch),rt$residuals)
abline(h=0)
plot(c(day),rt$residuals)
abline(h=0)
plot(rt$fitted.values,rt$residuals)
abline(h=0)
```









 $\mbox{\#}$ There is some variation in the Q-Q plot, but there does not appear to be any pattern $\mbox{\#}$ in the residual plots.

LSDlt<-LSD.test(aov(reaction~ing+day+batch),"ing") # Post-hoc analysis
LSDlt

```
## $statistics
      MSerror Df Mean
                             CV t.value
##
                                               LSD
##
     3.126667 12 5.88 30.07208 2.178813 2.436636
##
## $parameters
##
           test p.ajusted name.t ntr alpha
##
     Fisher-LSD
                     none
                              ing
                                    5 0.05
##
## $means
                    std r
                               LCL
                                         UCL Min Max Q25 Q50 Q75
##
     reaction
## A
          8.4 1.140175 5 6.677038 10.122962
                                                   10
                                                        8
                                                            8
                                                                 9
                                                7
          5.6 2.073644 5 3.877038 7.322962
                                                                 7
## B
                                                3
                                                    8
          8.8 1.643168 5 7.077038 10.522962
## C
                                                7
                                                   11
                                                        8
                                                                10
## D
          3.4 2.073644 5 1.677038 5.122962
                                                1
                                                    6
                                                        2
                                                            3
                                                                5
## E
          3.2 1.923538 5 1.477038 4.922962
                                                    6
                                                        2
                                                            3
##
## $comparison
## NULL
##
## $groups
##
     reaction groups
## C
          8.8
## A
          8.4
                    a
## B
          5.6
                   b
```

```
## D
          3.4
## E
          3.2
##
## attr(,"class")
## [1] "group"
TukeyHSD(aov(reaction~ing+day+batch),conf.level=0.95)$ing
##
                   lwr
                              upr
                                        p adj
## B-A -2.8 -6.3646078 0.7646078 0.153943335
## C-A 0.4 -3.1646078 3.9646078 0.996001220
## D-A -5.0 -8.5646078 -1.4353922 0.005586216
## E-A -5.2 -8.7646078 -1.6353922 0.004143094
## C-B 3.2 -0.3646078 6.7646078 0.086435305
## D-B -2.2 -5.7646078 1.3646078 0.336581142
## E-B -2.4 -5.9646078 1.1646078 0.263155088
## D-C -5.4 -8.9646078 -1.8353922 0.003082228
## E-C -5.6 -9.1646078 -2.0353922 0.002300665
## E-D -0.2 -3.7646078 3.3646078 0.999734935
Problem 4.27
SLIM<-c(1244,21,82,2221,905,839)
COCOMOA < -c(281, 129, 396, 1306, 336, 910)
COCOMOR<-c(220,84,458,543,300,794)
COCONOC<-c(225,83,425,552,291,826)
FUNCTIONPOINTS<-c(19,11,-34,121,15,103)
ESTIMALS<-c(-20,35,-53,170,104,199)
accuracy<-c(SLIM,COCOMOA,COCOMOR,COCONOC,FUNCTIONPOINTS,ESTIMALS)</pre>
blproj<-as.factor(rep(1:6,times=6))</pre>
tralgo<-as.factor(rep(1:6,each=6))</pre>
anova(lm(accuracy~tralgo+blproj))
## Analysis of Variance Table
## Response: accuracy
##
            Df Sum Sq Mean Sq F value Pr(>F)
             5 2989130 597826 5.3770 0.001720 **
## tralgo
## blproj
              5 2287339 457468 4.1146 0.007295 **
## Residuals 25 2779574 111183
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
library(dplyr) # Using Equation 4.16: var_blocks=(MSB-MSE)/a on page 152
(anova(lm(accuracy~tralgo+blproj))$"Mean Sq"[2]-anova(lm(accuracy~tralgo+blproj))$"Mean Sq"[3])/n_disti:
## [1] 57714.16
```