Stat 207 HW4

Cheng Luo 912466499
Fan Wu 912538518

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1   27.6

```
dat = read.table("CH27PR06.txt")
names(dat) = c("Y", "S", "A")
dat1 = dat
dat$A = factor(dat$A)
dat$S = factor(dat$S)
r = length(unique(dat$S))
a = length(unique(dat$A))
model = aov(Y~ A + S, data = dat)
res = resid(model)
res
```

```
##            1           2           3           4           5           6
## -1.27916667 -0.24166667  1.52083333 -0.84583333  0.69166667  0.15416667
##            7           8           9          10          11          12
##  0.62083333  0.05833333 -0.67916667  0.55416667  0.19166667 -0.74583333
##           13          14          15          16          17          18
##  0.52083333 -0.34166667 -0.17916667 -0.14583333  0.39166667 -0.24583333
##           19          20          21          22          23          24
##  0.98750000 -0.77500000 -0.21250000 -0.41250000  0.02500000  0.38750000
```
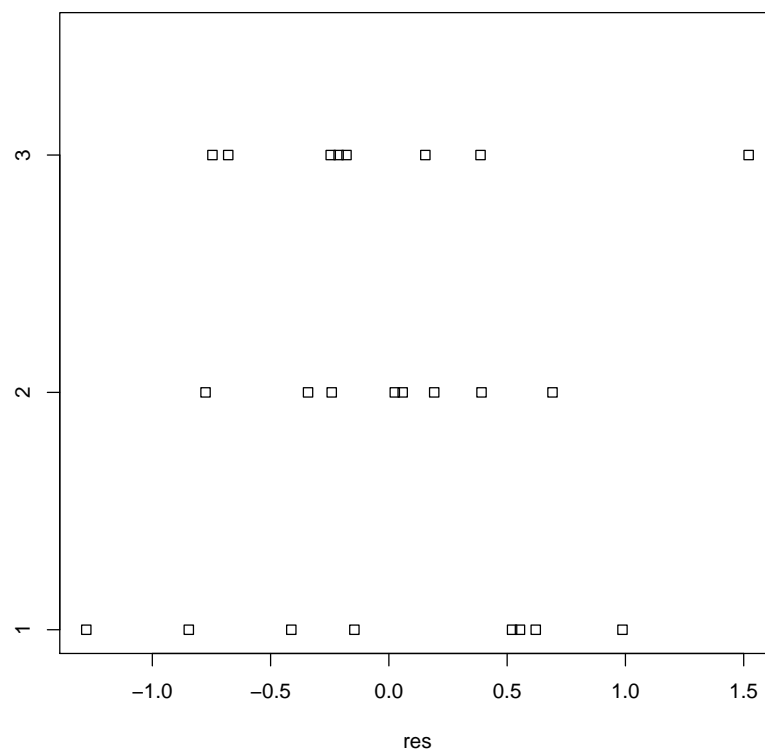
```
par(mfrow = c(1,2))
plot(model, which = 1)
plot(model, which = 2)
```
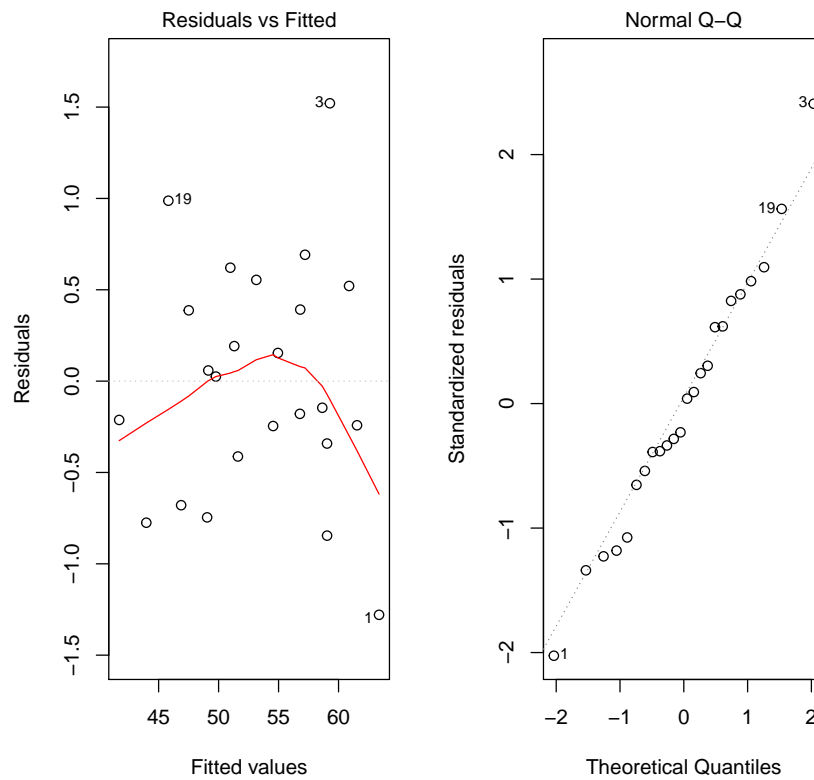
Residuals vs Fitted — Normal Q–Q

The residuals versus fitted values plots shows no sign for unequal vari-ance.And the QQ-plot indicates approximately normal distribution, so that normality assumption seems to be reasonable, we can use repeated measures model here.

(b)
```
stripchart(res ~ dat$A, method = 'stack')
```

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These plots do not indicate any correlations of the error terms within
a price level, and thus suggest that no interference effects are present.

(c)   `interaction.plot(dat$A, dat$S, dat$Y)`
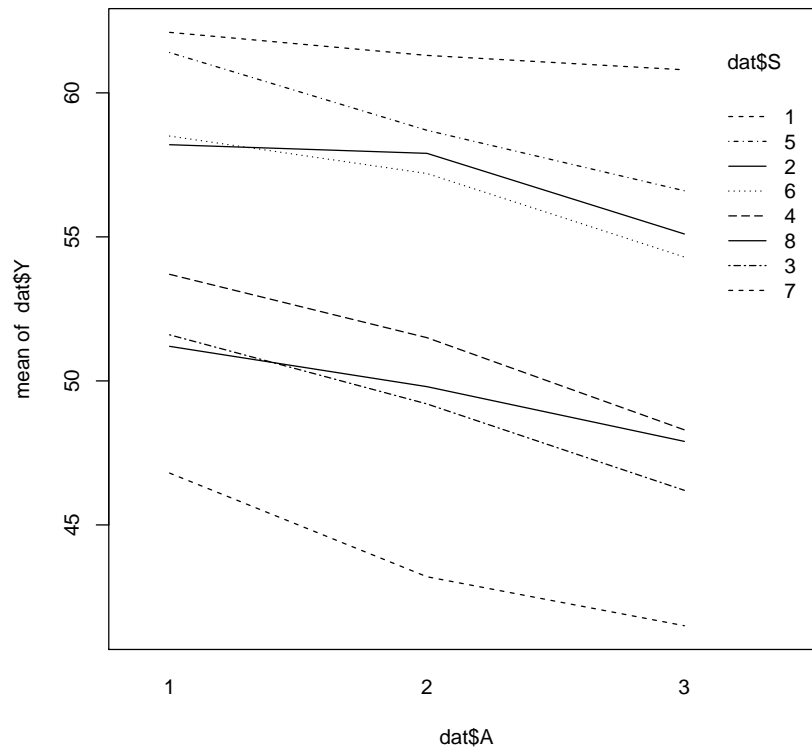
We see that the rating curves for the stores do not appear to exhibit substantial departures from being parallel, hence, the assumption of no interactions appear to be reasonable.

(d)
```
  ab = dat1$S*dat1$A
  model1 = aov(Y~factor(A)+factor(S)+ab, data = dat1)
  anova(model1)

## Analysis of Variance Table
##
## Response: Y
##            Df Sum Sq Mean Sq  F value     Pr(>F)
## factor(A)   2  67.48  33.740  52.9429 5.653e-07 ***
## factor(S)   7 745.19 106.455 167.0410 1.056e-11 ***
## ab          1   1.29   1.288   2.0204    0.1787
## Residuals  13   8.28   0.637
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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```r
qf(1-0.01, 1, 13)
```

```
## [1] 9.073806
```

```r
pf(2.0204, 1, 13, lower.tail = FALSE)
```

```
## [1] 0.1787417
```

$$H_0{:}D = 0$$
$$\text{VS. } H_1{:}D \neq 0$$
$$F^* = \frac{SSAB^*/1}{SSrem*/(13)} = 1.288/0.637 = 2.0204$$

we can reject H_0 if $F^* > F(1 - 0.01; 1, 13) = 9.073806$, otherwise reject H_1

so that reject H_1 because $F^* < 9.073806$,

therefore, our conclusion implies that D equals zero, so there's no interactions, and P-value is 0.1787417.

2 27.7

(a)
```r
model = aov(Y~ A + Error(S/A), data = dat)
summary(model)
```

```
##
## Error: S
##           Df Sum Sq Mean Sq F value Pr(>F)
## Residuals  7  745.2   106.5
##
## Error: S:A
##           Df Sum Sq Mean Sq F value    Pr(>F)
## A          2  67.48   33.74   49.35 4.57e-07 ***
## Residuals 14   9.57    0.68
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(b)
```r
qf(1-0.05, 2, 14)
```

```
## [1] 3.738892
```

```r
pf(49.35, 2, 14, lower.tail = FALSE)
```

```
## [1] 4.564874e-07
```

$$H_0\text{:all } \tau_j \text{ equal zero(j=1,2,3)}$$

$$\text{VS. } H_1\text{:not all } \tau_j \text{ equal zero}$$

$$F^* = \tfrac{MSA}{MSE} = 33.74/0.68 = 49.35$$

we can reject H_0 if $F^* > F(1-0.05;2,14) = 3.738892$,otherwise reject$H_1$

so that reject H_0 because $F^* > 3.738892$,

therefore, the mean sales of grapefruits differ for three price levels, and the P-value is 4.57e-07

(c)
```
means = with(dat, by(Y, A, mean))
D1 = means[1] - means[2]
D2 = means[1] - means[3]
D3 = means[2] - means[3]
tukey = 1/sqrt(2)*qtukey(0.95, a, (a-1)*(r-1))
tukey
```

```
## [1] 2.61728
```

```
mstr.s = 0.68
s = sqrt(2*mstr.s/(r))
s
```

```
## [1] 0.4123106
```

```
c(D1-s*tukey, D1+s*tukey)
```

```
##         1         1
## 0.7583676 2.9166324
```

```
c(D2-s*tukey, D2+s*tukey)
```

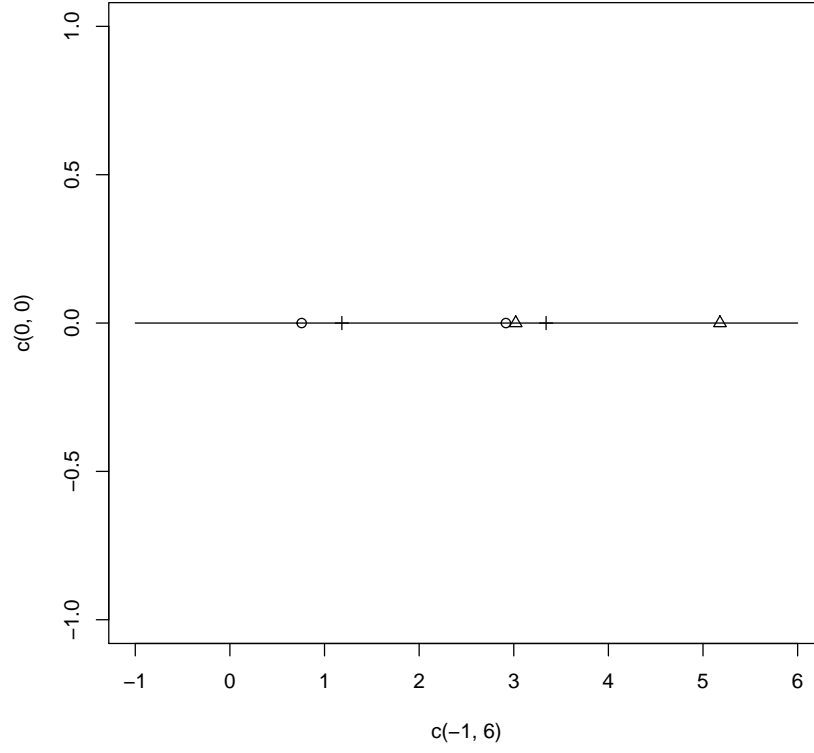```
1   1
3.020868 5.179132
```

```
c(D3-s*tukey, D3+s*tukey)
```

```
##        2        2
## 1.183368 3.341632
```

```
plot(c(-1, 6), c(0, 0), type = "l")
points(c(D1-s*tukey, D1+s*tukey), c(0, 0), pch = 1)
points(c(D2-s*tukey, D2+s*tukey), c(0, 0), pch = 2)
points(c(D3-s*tukey, D3+s*tukey), c(0, 0), pch = 3)
```

$$\bar{Y}_{1..} = 55.4375, \bar{Y}_{2..} = 53.6, \bar{Y}_{3..} = 51.3375$$

$$\hat{D}_1 = \bar{Y}_{1..} - \bar{Y}_{2..} = 1.8375, \hat{D}_2 = \bar{Y}_{1..} - \bar{Y}_{3..} = 4.1, \hat{D}_3 = \bar{Y}_{2..} - \bar{Y}_{3..} = 2.2625$$

Because we estimate all pairwise comparisons, so we use tukey procedure

$$S = \sqrt{\frac{MSTR.S}{r} * 2} = 0.4123106, Tukey = \frac{1}{\sqrt{2}}\text{qtukey}(1 - alpha, a, (a - 1) * (r - 1)) = 2.61728$$

base on $\hat{D}_i \pm S * Tukey$

$$0.7583676 \leq D_1 \leq 2.9166324$$

$$3.020868 \leq D_2 \leq 5.179132$$

$$1.183368 \leq D_3 \leq 3.341632$$

(d)

$$\hat{E} = \frac{S_r^2}{MSTR.S}$$
$$= \frac{(s-1)MSS + s(r-1)*MSTR.S}{(sr-1)*MSTR.S}$$
$$= 48.36189$$

3 27.18

(a)
```
dat = read.table("CH27PR18.txt")
names(dat) = c("Y", "S", "A", "B")
dat$S = factor(dat$S)
dat$A = factor(dat$A)
dat$B = factor(dat$B)
s = length(unique(dat$S))
a = length(unique(dat$A))
b = length(unique(dat$B))
model = aov(Y~ S+A*B+A*S+B*S, data = dat)
resid(model)
```

```
##      1       2       3       4       5       6       7       8       9      10
## -0.045   0.045   0.045  -0.045  -0.120   0.120   0.120  -0.120   0.080  -0.080
##     11      12      13      14      15      16      17      18      19      20
## -0.080   0.080  -0.045   0.045   0.045  -0.045   0.080  -0.080  -0.080   0.080
##     21      22      23      24      25      26      27      28      29      30
##  0.055  -0.055  -0.055   0.055   0.030  -0.030  -0.030   0.030  -0.045   0.045
##     31      32      33      34      35      36      37      38      39      40
##  0.045  -0.045   0.055  -0.055  -0.055   0.055  -0.045   0.045   0.045  -0.045
```
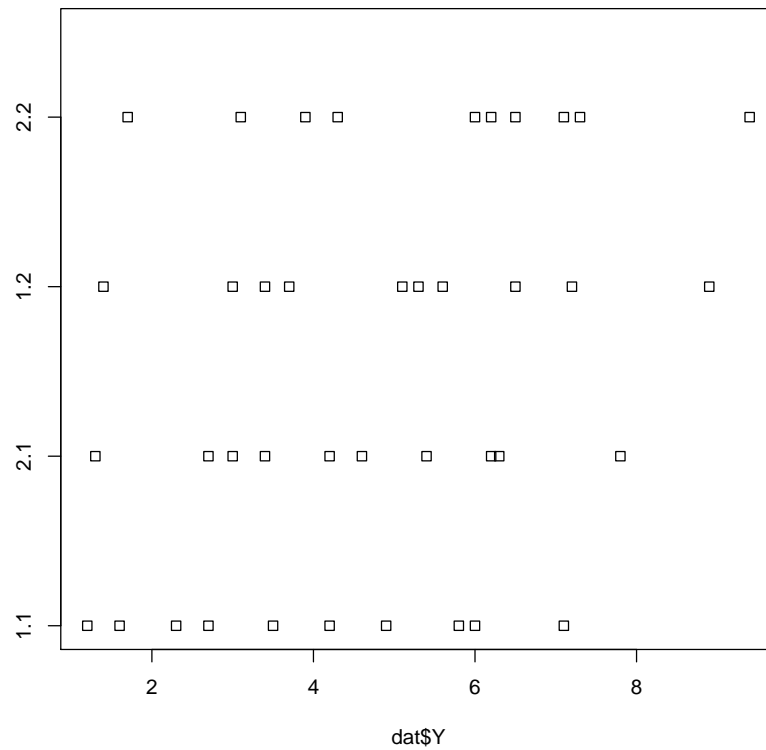
```
par(mfrow = c(1,2))
plot(model, which = 1)
plot(model, which = 2)
```
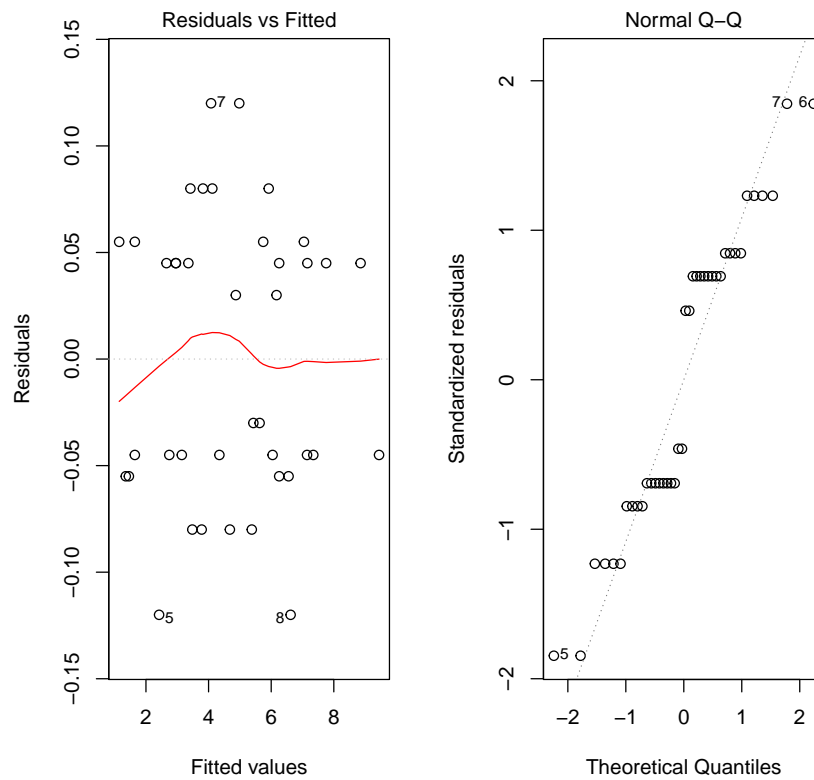
The residuals versus fitted values plots shows no sign for unequal variance.And the QQ-plot indicates approximately normal distribution with slightly light tail, so that normality assumption seems to be reasonable, we can use model here.

(b)
```r
stripchart(dat$Y ~ dat$A*dat$B, method="stack")
```

These plots do not indicate any correlations of the error terms within AB, and thus suggest that no interference effects are present.

4 27.19

(a)
```
model = aov(Y~ A*B+A*S+B*S+ Error(S/(A*B)), data = dat)
summary(model)

##
## Error: S
##   Df Sum Sq Mean Sq
## S  9  154.6   17.18
##
## Error: S:A
##     Df Sum Sq Mean Sq
## A    1  3.025  3.0250
```

```
## A:S  9  2.035  0.2261
##
## Error: S:B
##     Df Sum Sq Mean Sq
## B    1 11.449  11.449
## B:S  9  5.061   0.562
##
## Error: S:A:B
##           Df Sum Sq Mean Sq F value Pr(>F)
## A:B        1  0.001 0.00100   0.053  0.823
## Residuals  9  0.169 0.01878
```

(b)
```
interaction.plot(dat$A, dat$B, dat$Y, ylim = c(1, 8))
dat1 = dat[ which(dat$B == 1), ]
dat2 = dat[ which(dat$B == 2), ]
points(dat1$A, dat1$Y, pch = 1)
points(dat2$A, dat2$Y, pch = 2)
```
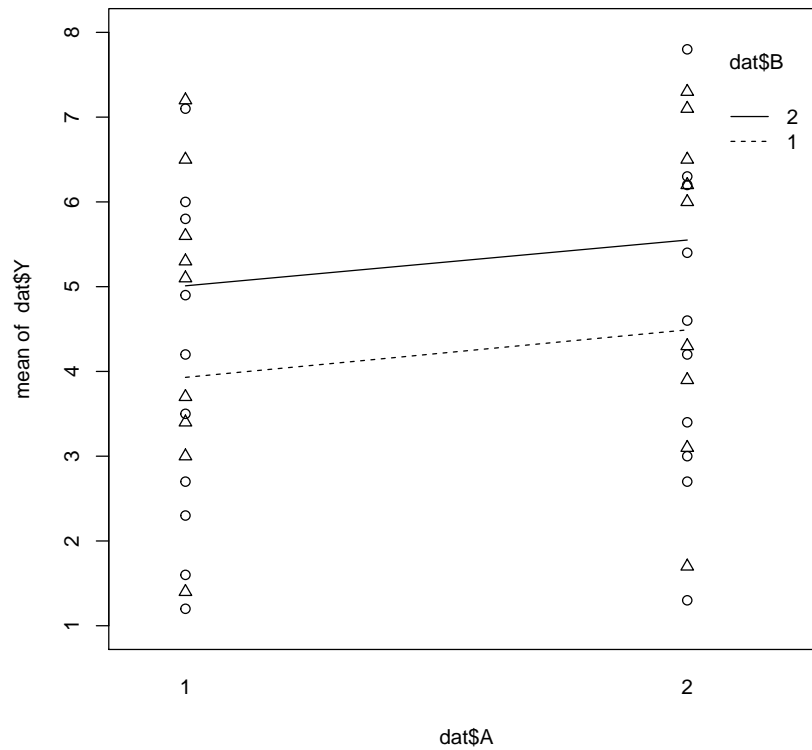
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From the plot, we know that treatment interaction effects are not present, but two treatment main effects are present.

(c)
```
qf(1-0.005, 1, 9)
```

```
## [1] 13.61361
```

```
pf(0.053, 1, 9, lower.tail = FALSE)
```

```
## [1] 0.8230705
```

$$H_0\text{:all } (\alpha\beta)_{jk} \text{ equal zero}$$
$$\text{VS. } H_1\text{:not all } (\alpha\beta)_{jk} \text{ equal zero}$$
$$F^* = \frac{MSAB}{MSABS} = 0.001/0.01878 = 0.053$$
we can reject H_0 if $F^* > F(1 - 0.005; 1, 9) = 13.61361$,otherwise reject$H_1$

so that reject H_1 because $F^* < 13.61361$,

therefore, there's no two treatment interaction effect, and the P-value is 0.823

(d)
```
qf(1-0.05, 1, 9)
```

```
## [1] 5.117355
```

```
pf(13.37904, 1, 9, lower.tail = FALSE)
```

```
## [1] 0.005253961
```

H_0: all α_i equal zero(i=1,2)

VS. H_1:not all α_i equal zero

$$F^* = \frac{MSA}{MSAS} = 3.0250/0.2261 = 13.37904$$

we can reject H_0 if $F^* > F(1-0.05; 1, 9) = 5.117355$,otherwise reject$H_1$

so that reject H_0 because $F^* > 5.117355$,

therefore, factor A main effect is present, and the P-value is 0.005253961

```
qf(1-0.05, 1, 9)
```

```
## [1] 5.117355
```

```
pf(20.37189, 1, 9, lower.tail = FALSE)
```

```
## [1] 0.001460304
```

H_0: all β_j equal zero(j=1,2)

VS. H_1:not all β_j equal zero

$$F^* = \frac{MSB}{MSBS} = 11.449/0.562 = 20.37189$$

we can reject H_0 if $F^* > F(1-0.05; 1, 9) = 5.117355$,otherwise reject$H_1$

so that reject H_0 because $F^* > 5.117355$,

therefore, factor B main effect is present, and the P-value is 0.001460304

(e)
```
  means = with(dat, by(Y, list(A,B) , mean))
  L1 = means[2,1] - means[1,1]
  L2 = means[1,2] - means[1,1]
  L3 = means[2,1] - means[1,2]
  L4 = means[2,2] - means[1,1]
  B = qt(1-0.05/(2*4), 9)
  B
```

```
## [1] 3.110935
```

```
  msabs = 0.01878
  S = sqrt(2*msabs/(s))
  S
```

```
## [1] 0.06128621
```

```
  c(L1-S*B, L1+S*B)
```

```
## [1] 0.3693426 0.7506574
```

```
  c(L2-S*B, L2+S*B)
```

```
## [1] 0.8893426 1.2706574
```

```
  c(L3-S*B, L3+S*B)
```

```
## [1] -0.7106574 -0.3293426
```

```
  c(L4-S*B, L4+S*B)
```

```
## [1] 1.429343 1.810657
```

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$$\bar{Y}_{\cdot 11} = 3.936, \bar{Y}_{\cdot 12} = 5.01,$$
$$\bar{Y}_{\cdot 21} = 4.49, \bar{Y}_{\cdot 22} = 5.55$$
$$\hat{L}_1 = \bar{Y}_{\cdot 21} - \bar{Y}_{\cdot 11} = .56, \hat{L}_2 = \bar{Y}_{\cdot 12} - \bar{Y}_{\cdot 21} = 1.08,$$
$$\hat{L}_3 = \bar{Y}_{\cdot 21} - \bar{Y}_{\cdot 12} = -.52, \hat{L}_4 = \bar{Y}_{\cdot 22} - \bar{Y}_{\cdot 11} = 1.62$$
$$S = \sqrt{\frac{MSABS}{s} * 2} = 0.06128621, B = t(1 - \alpha/(2*4), (a-1)(b-1)(s-1)) = 3.110935$$
$$\text{base on} \hat{L}_i \pm S * B$$
$$0.3693426 \le L_1 \le 0.7506574$$
$$0.8893426 \le L_2 \le 1.2706574$$
$$-0.7106574 \le L_3 \le -0.3293426$$
$$1.429343 \le L_4 \le 1.810657$$

The treatment of high dose of both drugs has the most significant reduction in pain intensity compared to the treatments of only one drug has high dose , and a significant difference exists in the mean effects of two drugs used alone.
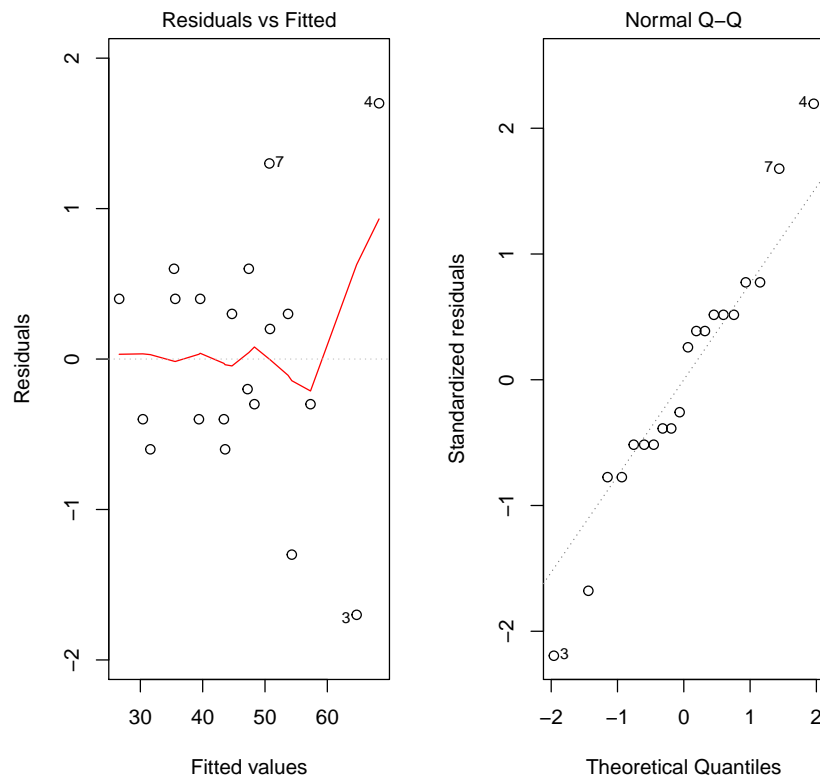
5   27.20

(a)
```
dat = read.table("CH27PR20.txt")
names(dat) = c("Y", "S", "A", "B")
dat$S = factor(dat$S)
dat$A = factor(dat$A)
dat$B = factor(dat$B)
s = length(unique(dat$S))
a = length(unique(dat$A))
b = length(unique(dat$B))
model = aov(Y~ A*B+(A/S), data = dat)
resid(model)

##    1    2    3    4    5    6    7    8    9   10   11   12   13   14   15
## -0.6  0.6 -1.7  1.7  0.4 -0.4  1.3 -1.3 -0.6  0.6  0.3 -0.3  0.4 -0.4 -0.2
##   16   17   18   19   20
##  0.2  0.4 -0.4  0.3 -0.3

par(mfrow = c(1,2))
plot(model, which = 1)
plot(model, which = 2)
```

Residuals vs Fitted | Normal Q–Q

The residuals versus fitted values plots shows no sign for unequal variance. And the QQ-plot indicates approximately normal distribution with slightly heavy tail, so that normality assumption seems to be reasonable, we can use model here.

(b)
```
dat1 = dat[ which(dat$A == 1), ]
dat2 = dat[ which(dat$A == 2), ]
par( mfrow = c(1, 2))
interaction.plot(dat1$B, dat1$S, dat1$Y)
interaction.plot(dat2$B, dat2$S, dat2$Y)
```
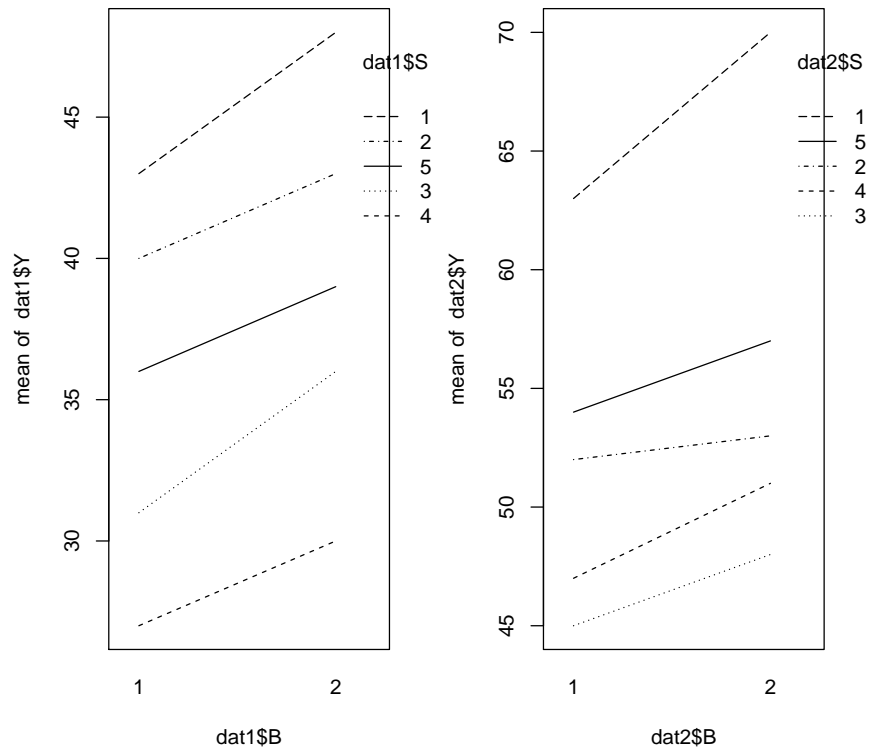
There's no evidence any interactions between field and treatments, so split-plot design can be used here.

6   27.21

(a)
```
model = aov(Y~ A*B+Error(A/S), data = dat)
summary(model)

##
## Error: A
##   Df Sum Sq Mean Sq
## A  1   1394    1394
##
## Error: A:S
##           Df Sum Sq Mean Sq F value Pr(>F)
## Residuals  8  837.6   104.7
```

```
##
## Error: Within
##           Df Sum Sq Mean Sq F value   Pr(>F)
## B          1  68.45   68.45  45.633 0.000144 ***
## A:B        1   0.05    0.05   0.033 0.859674
## Residuals  8  12.00    1.50
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(b)
```
interaction.plot(dat$A, dat$B, dat$Y, ylim = c(25, 75))
dat1 = dat[ which(dat$B == 1), ]
dat2 = dat[ which(dat$B == 2), ]
points(dat1$A, dat1$Y, pch = 1)
points(dat2$A, dat2$Y, pch = 2)
```
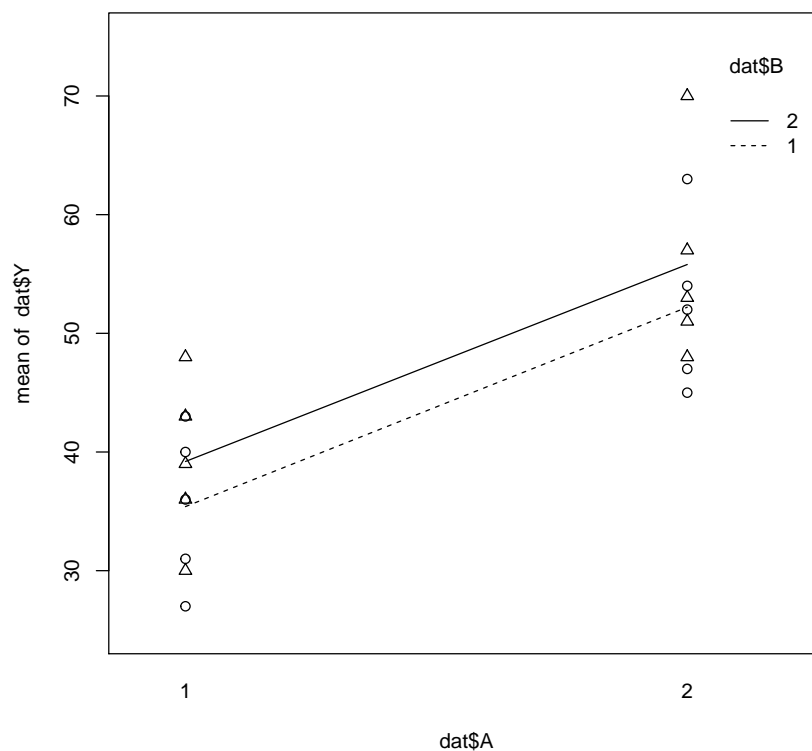

From the plot, we know that treatment interaction effects are not present, but two treatment main effects are present.

(c)
```r
qf(1-0.05, 1, 8)
```

```
## [1] 5.317655
```

```r
pf(0.033, 1, 8, lower.tail = FALSE)
```

```
## [1] 0.8603687
```

$$H_0\text{:all } (\alpha\beta)_{jk} \text{ equal zero}$$
$$\text{VS. } H_1\text{:not all } (\alpha\beta)_{jk} \text{ equal zero}$$
$$F^* = \frac{MSAB}{MSB.W(A)} = 0.05/1.5 = 0.033$$

we can reject H_0 if $F^* > F(1-0.05; 1, 8) = 5.317655$,otherwise reject$H_1$

so that reject H_1 because $F^* < 5.317655$,

therefore, there's no two treatment interaction effect, and the P-value is 0.8603687

(d)
```r
qf(1-0.05, 1, 8)
```

```
## [1] 5.317655
```

```r
pf(13.31423, 1, 8, lower.tail = FALSE)
```

```
## [1] 0.006505011
```

$$H_0\text{: all } \alpha_i \text{ equal zero(i=1,2)}$$
$$\text{VS. } H_1\text{:not all } \alpha_i \text{ equal zero}$$
$$F^* = \frac{MSA}{MSW(A)} = 1394/104.7 = 13.31423$$

we can reject H_0 if $F^* > F(1-0.05; 1, 8) = 5.317655$,otherwise reject$H_1$

so that reject H_0 because $F^* > 5.317655$,

therefore, factor A effect is present, and the P-value is 0.00650501

```r
qf(1-0.05, 1, 8)
```

```
## [1] 5.317655
```

```r
pf(45.63333, 1, 8, lower.tail = FALSE)
```

```
## [1] 0.0001442759
```

H_0: all β_j equal zero(j=1,2)

VS. H_1:not all β_j equal zero

$$F^* = \frac{MSB}{MSB.W(A)} = 68.45/1.5 = 45.63333$$

we can reject H_0 if $F^* > F(1 - 0.05; 1, 8) = 5.317655$,otherwise reject$H_1$

so that reject H_0 because $F^* > 5.317655$,

therefore, factor B main effect is present, and the P-value is 0.0001442759

(e)
```
  means1 = with(dat, by(Y, A , mean))
  means2 = with(dat, by(Y, B , mean))
  L1 = means1[1] - means1[2]
  L2 = means2[1] - means2[2]
  B = qt(1-0.1/(2*2), 8)
  B
```

```
## [1] 2.306004
```

```
  msb.wa = 1.5
  mswa = 104.7
  S1 = sqrt(2*mswa/(b*s))
  S2 = sqrt(2*msb.wa/(a*s))
  S1
```

```
## [1] 4.576024
```

```
  S2
```

```
## [1] 0.5477226
```

```
  c(L1-S1*B, L1+S1*B)
```

```
##            1           1
## -27.252331   -6.147669
```

```
  c(L2-S2*B, L2+S2*B)
```

```
##         1         1
## -4.96305 -2.43695
```

$$\bar{Y}_{.1.} = 37.3, \bar{Y}_{.2.} = 54,$$
$$\bar{Y}_{..1} = 43.8, \bar{Y}_{..2} = 47.5$$
$$\hat{L}_1 = \bar{Y}_{.1.} - \bar{Y}_{.2.} = -16.7, \hat{L}_2 = \bar{Y}_{..1} - \bar{Y}_{..2} = -3.7$$
$$B = t(1 - \alpha/(2*2), a(b-1)(s-1)) = 2.306004$$
$$S1 = \sqrt{\frac{MSW(A)}{bs} * 2} = 4.576024, S2 = \sqrt{\frac{MSB.W(A)}{as} * 2} = 0.5477226$$
$$\text{base on} \hat{L}_i \pm S * B$$
$$-27.252331 \le L_1 \le -6.147669$$
$$-4.96305 \le L_2 \le -2.43695$$

Irrigation method 2 is significantly better than Irrigation method 1, and fertilizer 2 is significantly better than fertilizer 1.

7   27.22

$$SSTO = \sum_i \sum_j (Y_{ij} - \bar{Y}_{..})^2$$
$$= \sum_i \sum_j (Y_{ij} - \bar{Y}_{i.} + \bar{Y}_{i.} - \bar{Y}_{..})^2$$
$$= \sum_i \sum_j (Y_{ij} - \bar{Y}_{i.})^2 + \sum_i \sum_j (\bar{Y}_{i.} - \bar{Y}_{..})^2 + 2 \sum_i \sum_j (Y_{ij} - \bar{Y}_{i.})(\bar{Y}_{i.} - \bar{Y}_{..})$$
$$= \sum_i \sum_j (Y_{ij} - \bar{Y}_{i.})^2 + \sum_i \sum_j (\bar{Y}_{i.} - \bar{Y}_{..})^2 + 2 \sum_i [(\bar{Y}_{i.} - \bar{Y}_{..}) * \sum_j (Y_{ij} - \bar{Y}_{i.})]$$
$$(\text{since } \sum_j (Y_{ij} - \bar{Y}_{i.}) = 0)$$
$$= \sum_i \sum_j (Y_{ij} - \bar{Y}_{i.})^2 + r \sum_i (\bar{Y}_{i.} - \bar{Y}_{..})^2$$
$$= SSS + SSW$$

8   Extra Problem

Base on:

$$Y_{ij} = \mu_{..} + \rho_i + \tau_j + \epsilon_{ij}$$
$$\bar{Y}_{i.} = \mu_{..} + \rho_i + \bar{\epsilon}_{i.}$$
$$\bar{Y}_{.j} = \mu_{..} + \bar{\rho}_{.} + \tau_j + \bar{\epsilon}_{.j}$$
$$\bar{Y}_{..} = \mu_{..} + \bar{\rho}_{.} + \bar{\epsilon}_{..}$$

So that:

$$E(SSS) = r \sum_i (E(\bar{Y}_{i\cdot} - \bar{Y}_{\cdot\cdot})^2)$$

$$= r \sum_i (Var(\bar{Y}_{i\cdot} - \bar{Y}_{\cdot\cdot}) + [E(\bar{Y}_{i\cdot} - \bar{Y}_{\cdot\cdot})]^2)$$

$$(\text{since } E(\bar{Y}_{i\cdot} - \bar{Y}_{\cdot\cdot}) = 0)$$

$$= r \sum_i (Var(\bar{Y}_{i\cdot}) + Var(\bar{Y}_{\cdot\cdot}) - 2Cov((\bar{Y}_{i\cdot}, \bar{Y}_{\cdot\cdot}))$$

$$= r \sum_i ((\sigma_\rho^2 + \frac{\sigma^2}{r}) + (\frac{\sigma_\rho^2}{s} + \frac{\sigma^2}{rs}) - 2 * (Cov(\rho_i, \bar{\rho}_\cdot) + Cov(\bar{\epsilon}_{i\cdot}, \bar{\rho}_\cdot) + Cov(\rho_i, \bar{\epsilon}_{\cdot\cdot}) + Cov(\bar{\epsilon}_{i\cdot}, \bar{\epsilon}_{\cdot\cdot}))$$

$$= rs * ((\sigma_\rho^2 + \frac{\sigma^2}{r}) + (\frac{\sigma_\rho^2}{s} + \frac{\sigma^2}{rs}) - 2 * (\frac{\sigma_\rho^2}{s} + 0 + 0 + \frac{\sigma^2}{rs}))$$

$$= (s-1)\sigma^2 + r(s-1)\sigma_\rho^2$$

$$E(MSS) = \frac{E(SSS)}{s-1}$$

$$= \sigma^2 + r\sigma_\rho^2$$

Likewise:

$$E(SSTR) = s \sum_j (E(\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot})^2)$$

$$= s \sum_j (Var(\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot}) + [E(\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot})]^2)$$

$$= s \sum_j (Var(\bar{Y}_{\cdot j}) + Var(\bar{Y}_{\cdot\cdot}) - 2Cov((\bar{Y}_{\cdot j}, \bar{Y}_{\cdot\cdot}) + \tau_j)$$

$$= s \sum_j ((\frac{\sigma_\rho^2}{s} + \frac{\sigma^2}{s}) + (\frac{\sigma_\rho^2}{s} + \frac{\sigma^2}{rs}) - 2 * (\frac{\sigma_\rho^2}{s} + 0 + 0 + \frac{\sigma^2}{rs}) + \tau_j)$$

$$= (r-1)\sigma^2 + s \sum \tau_j^2$$

$$E(MSTR) = \frac{E(SSTR)}{r-1}$$

$$= \sigma^2 + s\frac{\sum \tau_j^2}{r-1}$$

$$\begin{aligned}
E(SSTR.S) &= \sum_i \sum_j (E(Y_{ij} - \bar{Y}_{i\cdot} - \bar{Y}_{\cdot j} + \bar{Y}_{\cdot\cdot})^2) \\
&= \sum_i \sum_j (Var(Y_{ij} - \bar{Y}_{i\cdot} - \bar{Y}_{\cdot j} + \bar{Y}_{\cdot\cdot}) + [E(Y_{ij} - \bar{Y}_{i\cdot} - \bar{Y}_{\cdot j} + \bar{Y}_{\cdot\cdot})]^2) \\
&= \sum_i \sum_j (Var(Y_{ij} - \bar{Y}_{i\cdot} - \bar{Y}_{\cdot j} + \bar{Y}_{\cdot\cdot})) \\
&= (r-1)(s-1)\sigma^2 \\
E(MSTR.S) &= \frac{E(SSTR.S)}{(r-1)(s-1)} \\
&= \sigma^2
\end{aligned}$$