

Hw8-Solution

1)

```
Fert<-c(rep("control", 12), rep("f1", 12),
rep("f2", 12), rep("f3", 12))
Species<-c(rep(c(rep("SppA", 6), rep("SppB", 6)),4))
Height<-c(21.0, 19.5, 22.5, 21.5, 20.5, 21.0,
23.7, 23.8, 23.8, 23.7, 22.8, 24.4,
32.0, 30.5, 25.0, 27.5, 28.0, 28.6,
30.1, 28.9, 30.9, 34.4, 32.7, 32.7,
22.5, 26.0, 28.0, 27.0, 26.5, 25.2,
30.6, 31.1, 28.1, 34.9, 30.1, 25.5,
28.0, 27.5, 31.0, 29.5, 30.0, 29.2,
36.1, 36.6, 38.7, 37.1, 36.8, 37.1)
df<-data.frame(Fert=Fert, Species=Species, Height=Height)
```

A 2-way complete model for this experiment would be :

$$Y_{ijt} = \mu + \tau_{ij} + \epsilon_{ijt}, \quad i = \text{control}, f1, f2, f3 \quad j = \text{sppA}, \text{sppB} \quad t = 1, 2, 3, 4 \quad \epsilon \stackrel{iid}{\sim} N(0, \sigma^2)$$

```
model<-aov(Height~Fert+Species+Fert:Species, data=df)
anova(model)
```

```
## Analysis of Variance Table
##
## Response: Height
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Fert           3  745.44  248.479   73.0982 2.766e-16 ***
## Species        1  236.74   236.741   69.6450 2.707e-10 ***
## Fert:Species    3   50.58   16.861    4.9603 0.005081 **
## Residuals     40  135.97    3.399
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

lets look at residuals:

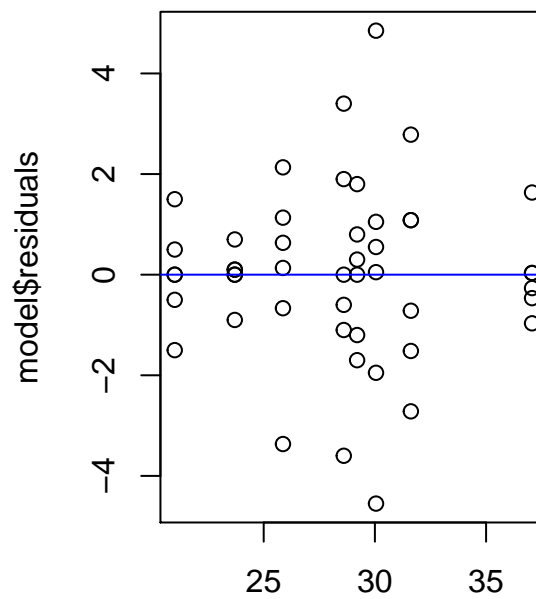
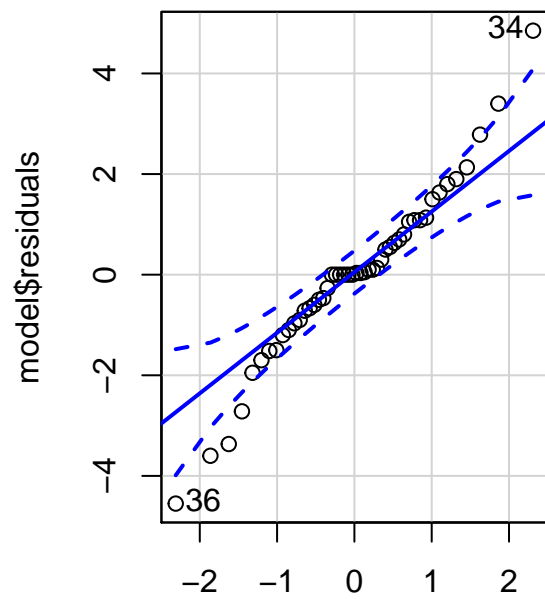
```
library("car")
```

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

```
par(mfrow=c(1,2))
qqPlot(model$residuals)
```

```
## [1] 34 36
```

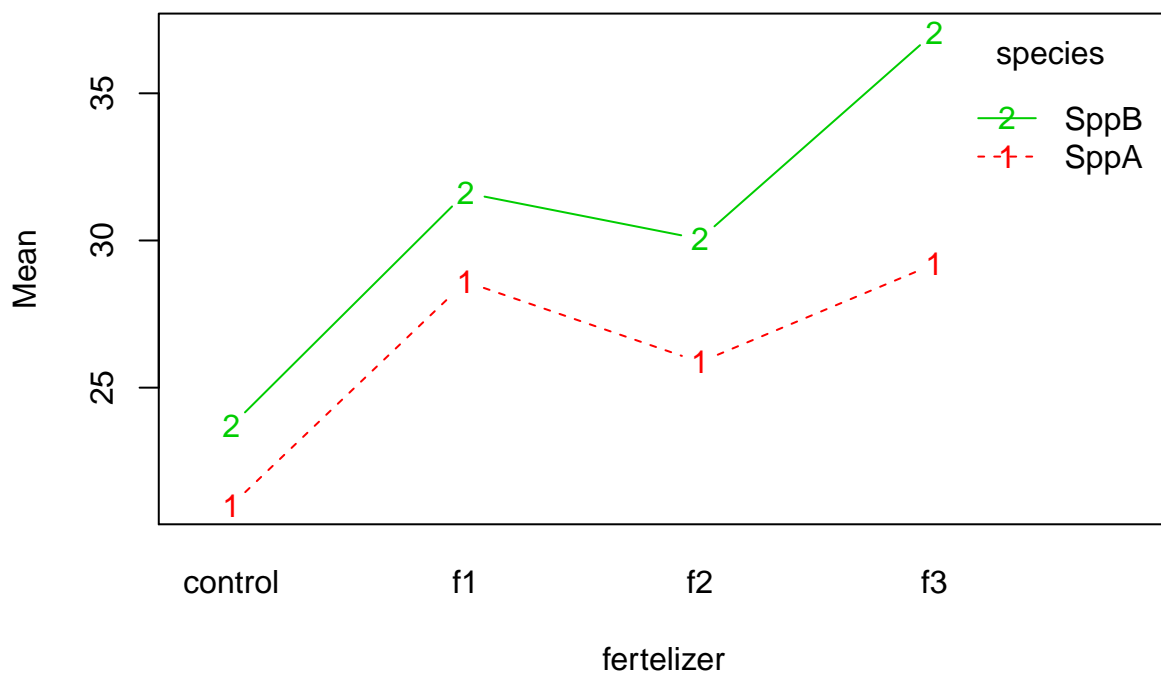
```
plot(model$fitted.values,model$residuals)
abline(h=0, col = "blue")
```



not a

big issue in residuals so we go on with our model.

```
interaction.plot(x.factor = df$Fert, trace.factor = df$Species,
response = df$Height, type = "b", col = 2:3,
xlab = "fertilizer", ylab = "Mean", trace.label = "species")
```



```
library(lsmmeans)
```

```
## The 'lsmmeans' package is being deprecated.
## Users are encouraged to switch to 'emmeans'.
## See help('transition') for more information, including how
## to convert 'lsmmeans' objects and scripts to work with 'emmeans'.
```

```
lsmsfert=lsmeans(model, ~ Fert:Species )
contrast(lsmsfert, method="pairwise")
```

```
## contrast estimate SE df t.ratio p.value
## control,SppA - f1,SppA -7.600000 1.064464 40 -7.140 <.0001
## control,SppA - f2,SppA -4.866667 1.064464 40 -4.572 0.0011
## control,SppA - f3,SppA -8.200000 1.064464 40 -7.703 <.0001
## control,SppA - control,SppB -2.700000 1.064464 40 -2.536 0.2101
## control,SppA - f1,SppB -10.616667 1.064464 40 -9.974 <.0001
## control,SppA - f2,SppB -9.050000 1.064464 40 -8.502 <.0001
## control,SppA - f3,SppB -16.066667 1.064464 40 -15.094 <.0001
## f1,SppA - f2,SppA 2.733333 1.064464 40 2.568 0.1979
## f1,SppA - f3,SppA -0.600000 1.064464 40 -0.564 0.9991
## f1,SppA - control,SppB 4.900000 1.064464 40 4.603 0.0010
## f1,SppA - f1,SppB -3.016667 1.064464 40 -2.834 0.1150
## f1,SppA - f2,SppB -1.450000 1.064464 40 -1.362 0.8685
## f1,SppA - f3,SppB -8.466667 1.064464 40 -7.954 <.0001
## f2,SppA - f3,SppA -3.333333 1.064464 40 -3.131 0.0585
## f2,SppA - control,SppB 2.166667 1.064464 40 2.035 0.4722
## f2,SppA - f1,SppB -5.750000 1.064464 40 -5.402 0.0001
## f2,SppA - f2,SppB -4.183333 1.064464 40 -3.930 0.0072
## f2,SppA - f3,SppB -11.200000 1.064464 40 -10.522 <.0001
## f3,SppA - control,SppB 5.500000 1.064464 40 5.167 0.0002
## f3,SppA - f1,SppB -2.416667 1.064464 40 -2.270 0.3345
## f3,SppA - f2,SppB -0.850000 1.064464 40 -0.799 0.9922
## f3,SppA - f3,SppB -7.866667 1.064464 40 -7.390 <.0001
## control,SppB - f1,SppB -7.916667 1.064464 40 -7.437 <.0001
## control,SppB - f2,SppB -6.350000 1.064464 40 -5.965 <.0001
## control,SppB - f3,SppB -13.366667 1.064464 40 -12.557 <.0001
## f1,SppB - f2,SppB 1.566667 1.064464 40 1.472 0.8174
## f1,SppB - f3,SppB -5.450000 1.064464 40 -5.120 0.0002
## f2,SppB - f3,SppB -7.016667 1.064464 40 -6.592 <.0001
##
## P value adjustment: tukey method for comparing a family of 8 estimates
```

2)

```
A<-c(rep(1, 10), rep(2, 10))
B<-rep(c(c(rep(1, 5), rep(2, 5))), 2)
resp<-c(12.9, 11.3, 11.7, 12.1, 12.3,
13.7, 12.8, 13.6, 13.1, 13.5,
14.2, 14.5, 13.9, 13.6, 14.4,
13.5, 13.1, 13.3, 13.1, 13.4)
df<-data.frame(A=factor(A), B=factor(B), resp=resp)
```

a) A 2-way complete model for this experiment would be :

$$Y_{ijt} = \mu + \tau_{ij} + \epsilon_{ijt}, \quad i = A1, A2 \quad j = B1, B2 \quad t = 1, \dots, 10 \quad \epsilon \stackrel{iid}{\sim} N(0, \sigma^2)$$

```
model<-aov(resp~A+B+A:B, data=df)
anova(model)
```

```
## Analysis of Variance Table
```

```
##
## Response: resp
##           Df Sum Sq Mean Sq F value    Pr(>F)
## A             1  5.000    5.000  29.4118 5.632e-05 ***
## B             1  0.242    0.242   1.4235  0.2502
## A:B           1  5.618    5.618  33.0471 2.991e-05 ***
## Residuals    16  2.720    0.170
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

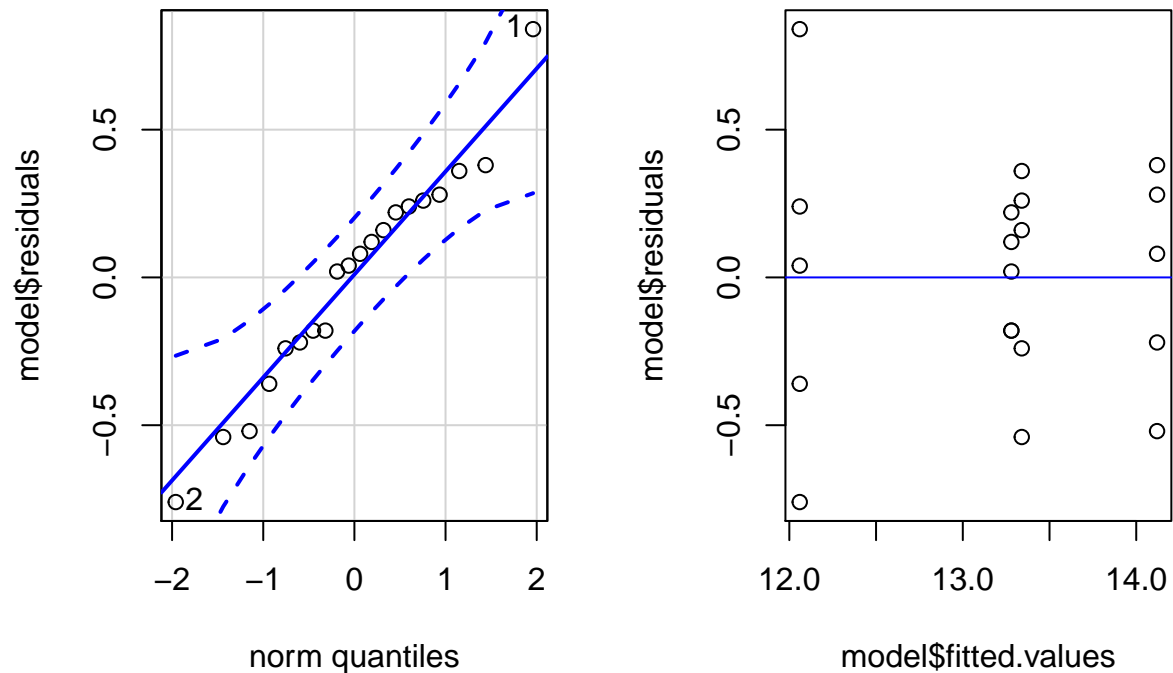
lets look at residuals:

```
library("car")

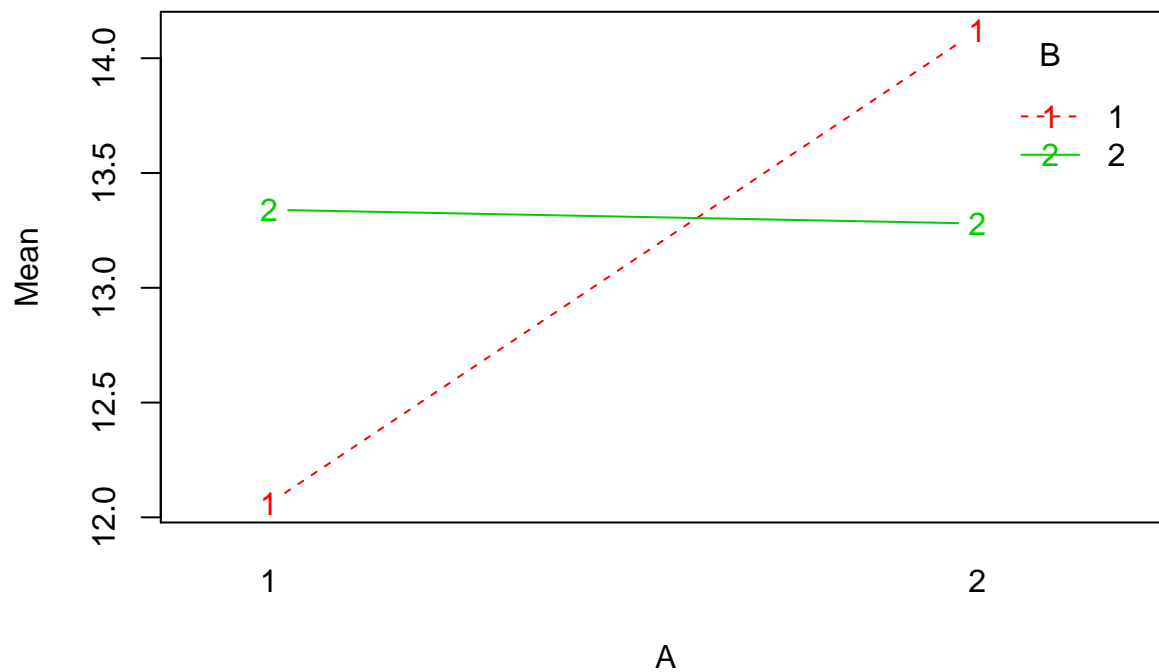
par(mfrow=c(1,2))
qqPlot(model$residuals)
```

```
## [1] 1 2
```

```
plot(model$fitted.values,model$residuals)
abline(h=0, col = "blue")
```



```
interaction.plot(x.factor = df$A, trace.factor = df$B,
response = df$resp, type = "b", col = 2:3,
xlab = "A", ylab = "Mean", trace.label = "B")
```



```
library(lsmeans)
lsms=lsmeans(model, ~ A:B )
contrast(lsms, method="pairwise")
```

```
## contrast estimate SE df t.ratio p.value
## 1,1 - 2,1 -2.06 0.2607681 16 -7.900 <.0001
## 1,1 - 1,2 -1.28 0.2607681 16 -4.909 0.0008
## 1,1 - 2,2 -1.22 0.2607681 16 -4.678 0.0013
## 2,1 - 1,2 0.78 0.2607681 16 2.991 0.0389
## 2,1 - 2,2 0.84 0.2607681 16 3.221 0.0247
## 1,2 - 2,2 0.06 0.2607681 16 0.230 0.9955
##
## P value adjustment: tukey method for comparing a family of 4 estimates
```