Experiment 1

```r
library(ibd)

exp1 <- read_csv("group project/group_response.csv")
bd <- bibd(6,10,5,3,2)
df <- data.frame(trt = rep(0,30), blck = rep(0,30), response = rep(0,30))
ind <- 1

for(i in 1:6){
  for(j in 1:10){
    if(bd$N[i,j] == 1){
      df$trt[ind] <- i
      df$blck[ind] <- j df$response[ind] <- exp1$y1[ind]
      ind<-ind+1}
  }
}

bd$N
df
```

```
> bd$N
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
[1,]    0    0    0    1    1    0    0    1    1     1
[2,]    1    0    0    0    0    1    1    0    1     1
[3,]    0    0    1    0    1    1    1    1    0     0
[4,]    0    1    1    1    0    1    0    0    0     1
[5,]    1    1    1    0    0    0    0    1    1     0
[6,]    1    1    0    1    1    0    1    0    0     0
> df
   trt blck response
1    1    4    226.4
2    1    5    232.6
3    1    8    234.0
4    1    9    220.7
5    1   10    219.8
6    2    1    163.8
7    2    6    179.4
8    2    7    168.6
9    2    9    173.4
10   2   10    157.8
11   3    3    238.3
12   3    5    231.7
13   3    6    227.7
14   3    7    237.2
15   3    8    232.9
16   4    2    184.4
17   4    3    180.6
18   4    4    179.5
19   4    6    186.2
20   4   10    161.8
21   5    1    240.5
22   5    2    246.9
23   5    3    240.3
24   5    8    244.7
25   5    9    237.6
26   6    1    179.0
27   6    2    168.0
28   6    4    165.2
29   6    5    156.5
30   6    7    160.3
```

6 treatments, 10 blocks, 3 runs in each block, 5 replicates, and lambda equals to 2.

```
df$trt<-as.factor(df$trt)
df$blck<-as.factor(df$blck)
anal1 <- aov(data=df, response ~ blck + trt)
summary(anal1)

anal2 <- aov(data=df, response ~ trt + blck)
summary(anal2)
```

```
> summary(anal1)
            Df Sum Sq Mean Sq F value   Pr(>F)
blck         9   7601     845   21.53 5.15e-07 ***
trt          5  23980    4796  122.28 1.32e-11 ***
Residuals   15    588      39
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> anal2 <- aov(data=df, response ~ trt + blck)
> summary(anal2)
            Df Sum Sq Mean Sq F value   Pr(>F)
trt          5  30914    6183  157.64 2.05e-12 ***
blck         9    667      74    1.89    0.132
Residuals   15    588      39
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

anova table shows block and treatment are significant, so reject H0, there is a difference between different groups.

```
residuals<-anal1$residuals
fitted<-anal1$fitted.values
fitres<-cbind(df, data.frame(fitted, residuals))
```

```
ggplot(data=fitres, aes(sample=residuals)) + geom_qq() + geom_qq_line()
ggplot(data=fitres, aes(x=residuals)) + geom_histogram(color="white")
```
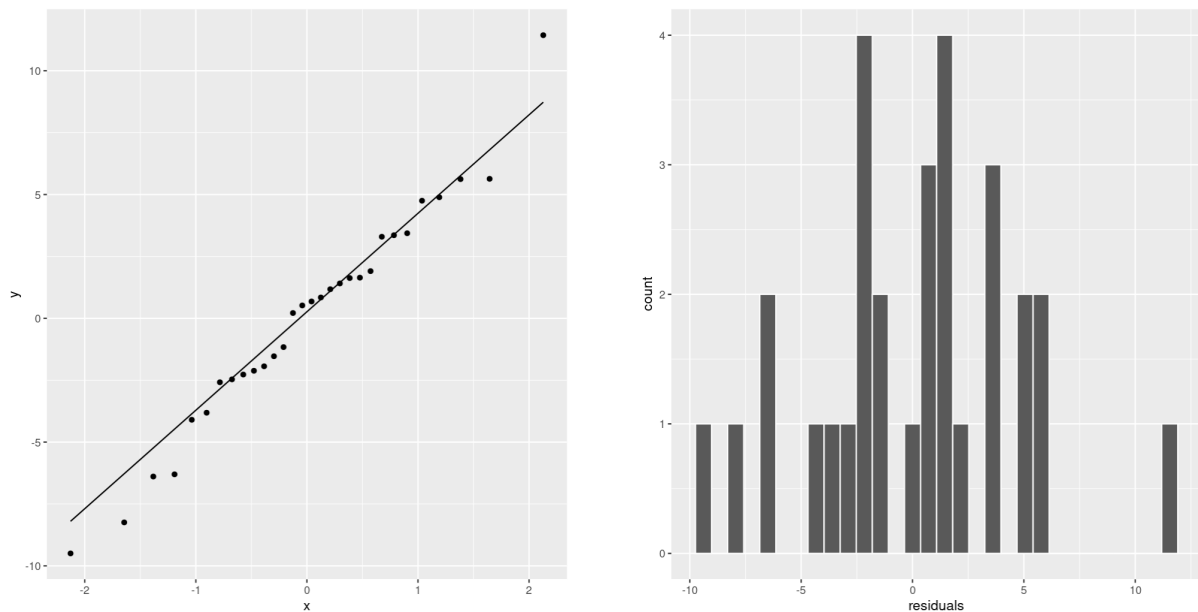

There is no violation of the normally distributed residual.

fitted vs residual plot shows that residuals has no obvious violation for mean 0 and constant variance.

```
shapiro.test(fitres$residuals)
```

Shapiro-Wilk normality test

data: fitres$residuals
W = 0.98071, p-value = 0.8442