

Week 5

PSTAT 122C

4/24/2022

```
library(knitr) # create tables in rmd
x<-c("A","A","B","B","B","C","C","C","D","D")
y<-c(12,18,14,12,13,19,17,21,24,30)
data <- data.frame(x, y)
aov <- aov(y~x, data)
summary(aov)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## x              3     258    86.00    11.22 0.00713 **
## Residuals      6       46     7.67
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
opts <- options(knitr.kable.NA = "")
sum_aov = summary(aov)
kable(sum_aov[[1]])
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
x	3	258	86.000000	11.21739	0.0071349
Residuals	6	46	7.666667		

The table does not have a line for SS_T , but a full ANOVA table should include SS_T .

LSD method

We can use the t test for testing all pairs of mean parameters $H_0 : \mu_i = \mu_j$.

$$t_0 = \frac{\bar{y}_{i.} - \bar{y}_{j.}}{\sqrt{MS_e(\frac{1}{n_i} + \frac{1}{n_j})}} \stackrel{H_0}{\sim} t_{N-a}$$

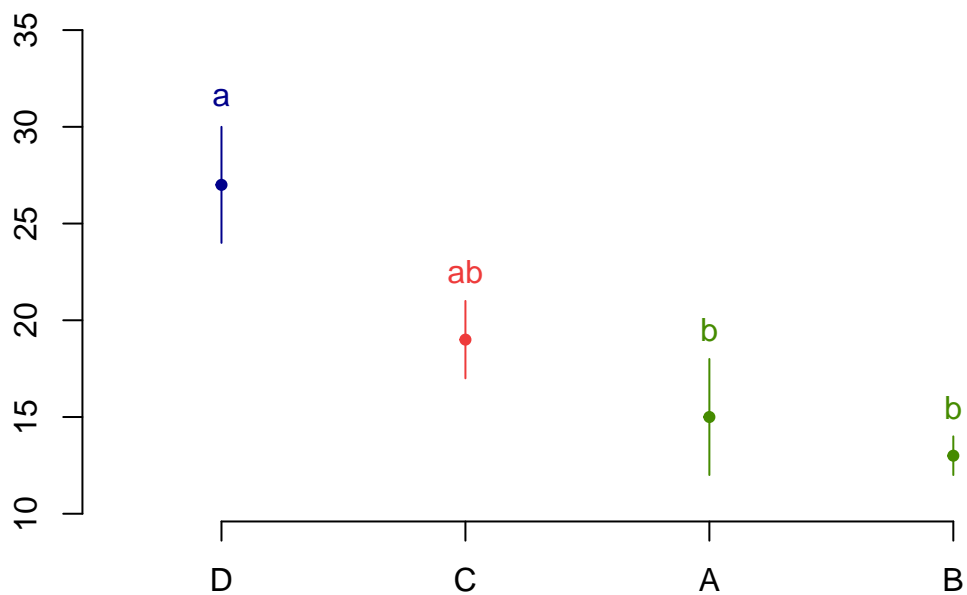
The pair of means μ_i and μ_j would be declared significantly different if $|\bar{y}_{i.} - \bar{y}_{j.}| > t_{\alpha/2, N-a} \sqrt{MS_e(\frac{1}{n_i} + \frac{1}{n_j})}$.

```
library(agricolae)
colnames(data) <- c("X", "Y")
data
```

```
##      X  Y
## 1   A 12
## 2   A 18
## 3   B 14
## 4   B 12
## 5   B 13
## 6   C 19
## 7   C 17
## 8   C 21
## 9   D 24
## 10  D 30
```

```
model <- aov(Y~X, data)
out <- LSD.test(model,"X", p.adj="bonferroni")
plot(out)
```

Groups and Range



```
print(out)
```

```
## $statistics
##      MSerror Df Mean      CV
## 7.666667  6   18 15.38264
##
## $parameters
##      test p.adjusted name.t ntr alpha
## Fisher-LSD bonferroni      X  4  0.05
```

```
##
## $means
##      Y      std r      LCL      UCL Min Max  Q25 Q50  Q75
## A 15 4.242641 2 10.209216 19.79078 12 18 13.5 15 16.5
## B 13 1.000000 3 9.088341 16.91166 12 14 12.5 13 13.5
## C 19 2.000000 3 15.088341 22.91166 17 21 18.0 19 20.0
## D 27 4.242641 2 22.209216 31.79078 24 30 25.5 27 28.5
##
## $comparison
## NULL
##
## $groups
##      Y groups
## D 27      a
## C 19     ab
## A 15      b
## B 13      b
##
## attr("class")
## [1] "group"
```

```
### compare level A and B
qt(0.975, df=6)*sqrt(7.666667*(1/2+1/3)) # > 2
```

```
## [1] 6.184876
```

```
### compare level A and D
qt(0.975, df=6)*sqrt(7.666667*(1/2+1/2)) # < 12
```

```
## [1] 6.775192
```

Residuals

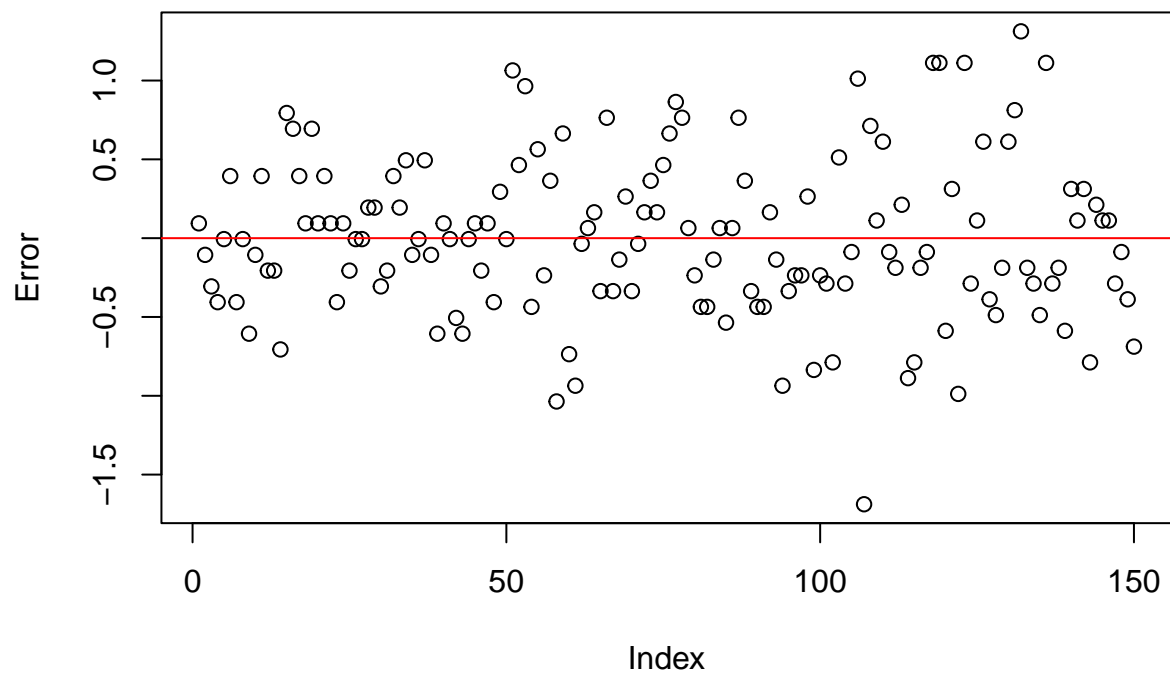
$$y_{ij} = \mu + \tau_i + \epsilon_{ij}$$

$$\epsilon_{ij} \sim N(0, \sigma^2)$$

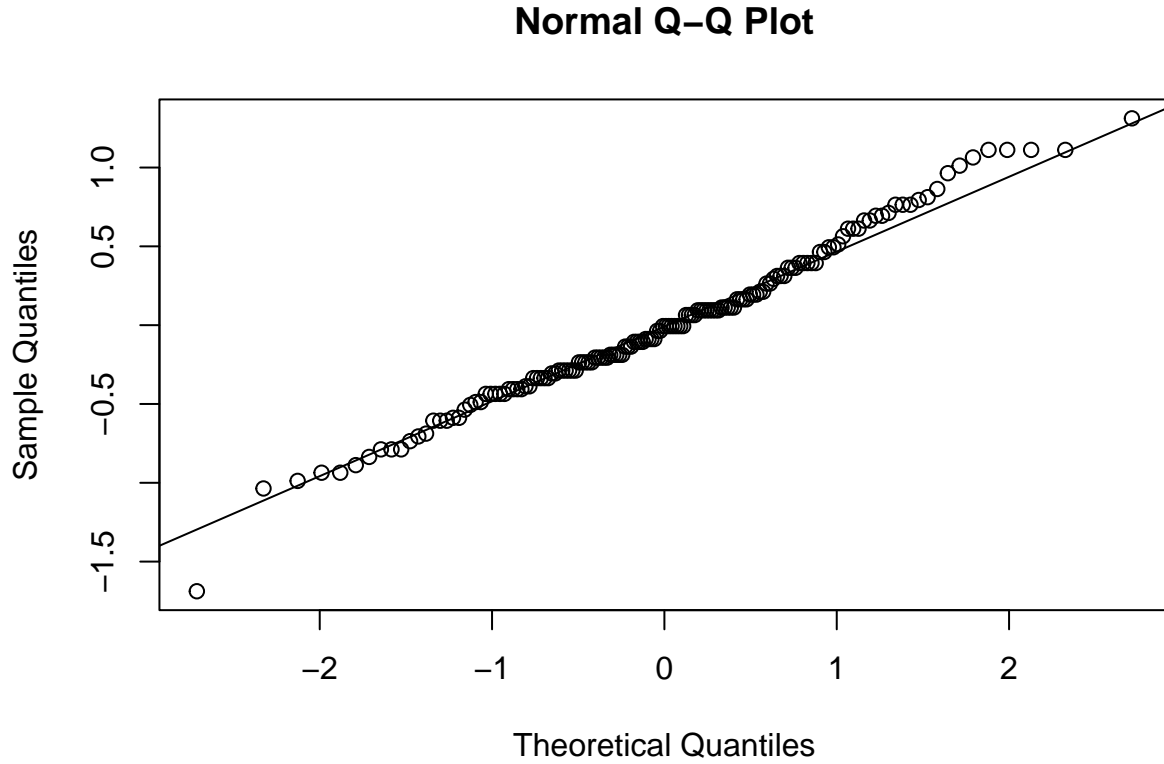
The estimates of means are $\hat{\mu}_i = \bar{y}_{i.}$, so errors (residuals) are $e_{ij} = y_{ij} - \hat{y}_{ij} = y_{ij} - \bar{y}_{i.}$. Residual analysis is not trivial for model analysis.

```
data(iris)
aov1 = aov(Sepal.Length ~ Species, iris)
res = aov1$residuals

plot(res, ylab="Error")
abline(h=0, col="red")
```



```
qqnorm(res)  
qqline(res)
```



Review the random effects model

$$\begin{aligned}
 y_{ij} &= \mu + \tau_i + \epsilon_{ij} \\
 \epsilon_{ij} &\sim N(0, \sigma^2) \\
 \tau_i &\sim N(0, \sigma_\tau^2)
 \end{aligned}$$

We have to see the treatment effect as a random variable and τ_i is independent of ϵ_{ij} . The variance of any observation is $(\sigma^2 + \sigma_\tau^2)$. The H_0 in the previous model is no longer meaningful, and the hypothesis we need to be concerned with is

$$\begin{aligned}
 H_0 : \quad &\sigma_\tau^2 = 0 \\
 H_1 : \quad &\sigma_\tau^2 > 0
 \end{aligned}$$

One can prove that we still have $SS_e = SS_T - SS_A$. Under the null hypothesis, a statistic $F_0 = \frac{SS_A/(a-1)}{SS_e/(n-a)} = \frac{MS_A}{MS_e} \sim F_{a-1, N-a}$, so we reject H_0 if $F_0 > F_{a-1, N-a}(\alpha)$

Model Parameters

$$\begin{aligned}
 \hat{\sigma}^2 &= MS_e \\
 \hat{\sigma}_\tau^2 &= \frac{MS_A - MS_e}{n} \quad (\text{balanced}) \\
 \hat{\sigma}_\tau^2 &= \frac{MS_A - MS_e}{n_0}, \quad \text{where } n_0 = \frac{1}{a-1} \left(\sum_{i=1}^a n_i - \frac{\sum_{i=1}^a n_i^2}{\sum_{i=1}^a n_i} \right) \quad (\text{unbalanced}).
 \end{aligned}$$

Note It's possible that the estimation $\hat{\sigma}_\tau^2 < 0$. If this happens, take $\hat{\sigma}_\tau^2$ to be 0.