

Colm Mooney – ST204 - 20325583

#3

```
library(readr)
```

```
 #(a)
```

```
CA3_FLU <- read_csv("CA3_Flu.csv")
```

```
CA3_FLU
```

```
 #(a) Summarise the raw data using summary statistics and graphs as appropriate
```

```
tab_overall <- xtabs(~ Strain + Time, data = CA3_FLU)
```

```
addmargins(tab_overall)
```

```
> addmargins(tab_overall)
```

	Time														
Strain	3	4	5	6	7	8	9	10	11	12	13	15	20	21	Sum
A	0	0	0	1	1	2	0	1	1	1	1	1	1	0	10
B	0	1	1	1	0	1	2	1	1	0	0	1	0	1	10
C	2	1	2	1	2	1	0	1	0	0	0	0	0	0	10
Sum	2	2	3	3	3	4	2	3	2	1	1	2	1	1	30

\* Summary stats!

```
 #From Tab overall, we can get the individual values for A,B and C.
```

```
A <- c(6,7,8,8,10,11,12,13,15,20)
```

```
B <- c(4,5,6,8,9,9,19,11,15,21)
```

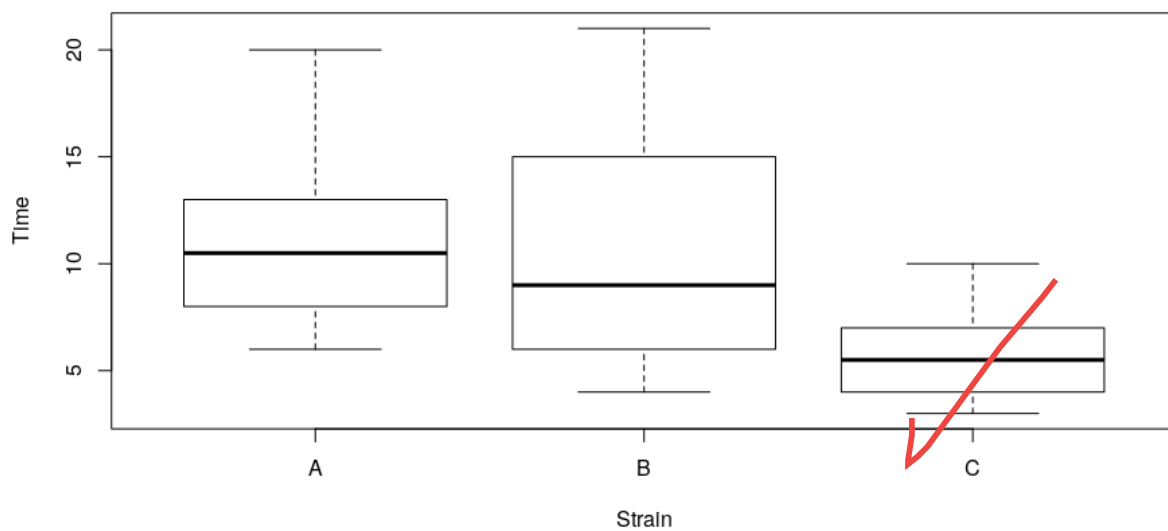
```
C <- c(3,3,4,5,5,6,7,7,8,10)
```

```
y <- c(A, B, C)
```

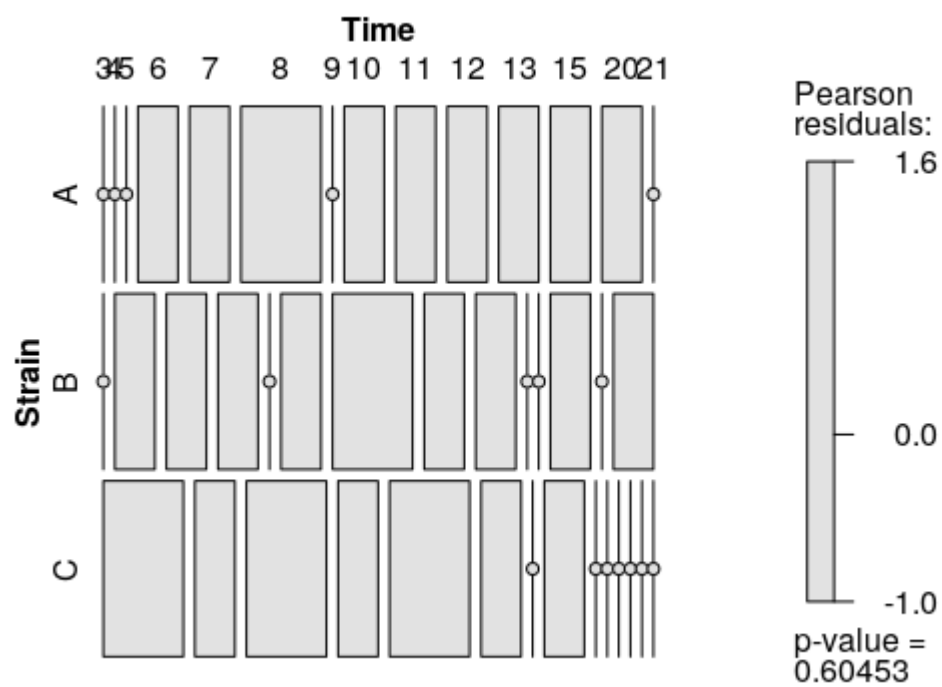
```
x <- rep(c(1,2,3), c(10,10,10))
```

```
xf <- factor(x, labels=c("A", "B", "C"))
```

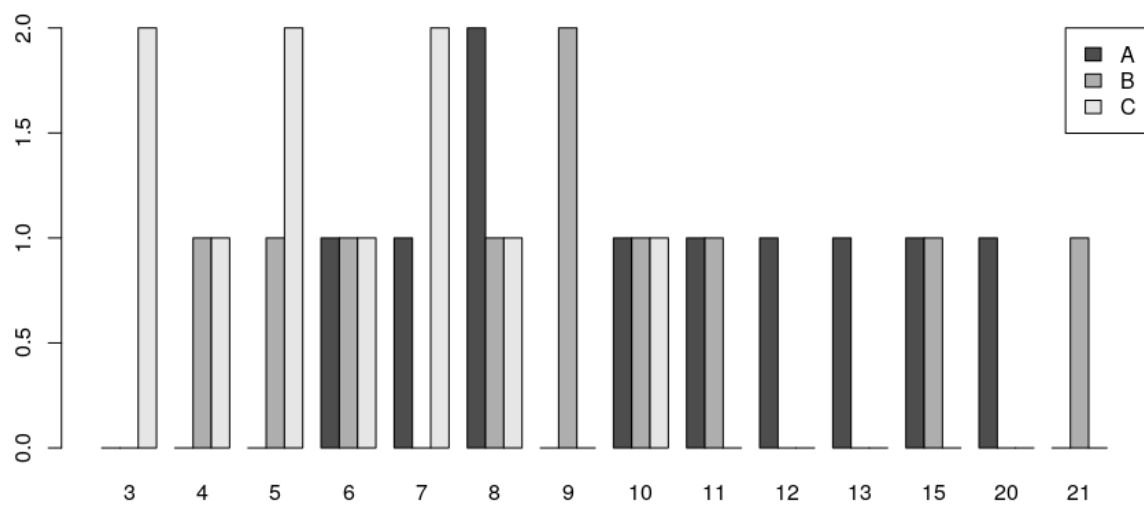
```
plot(y ~ xf, xlab = "Strain", ylab = "Time")
```



```
mosaic(~ Strain + Time, data = CA3_FLU, shade = TRUE, legend = TRUE)
```



```
barplot(tab_overall,
  legend = TRUE,
  beside = TRUE,
  args.legend = list(x = "topright"))
```



```
summary(tab_overall)
```

```
summary(CA3_FLU)
```

```
cdfA <- ecdf(A)
```

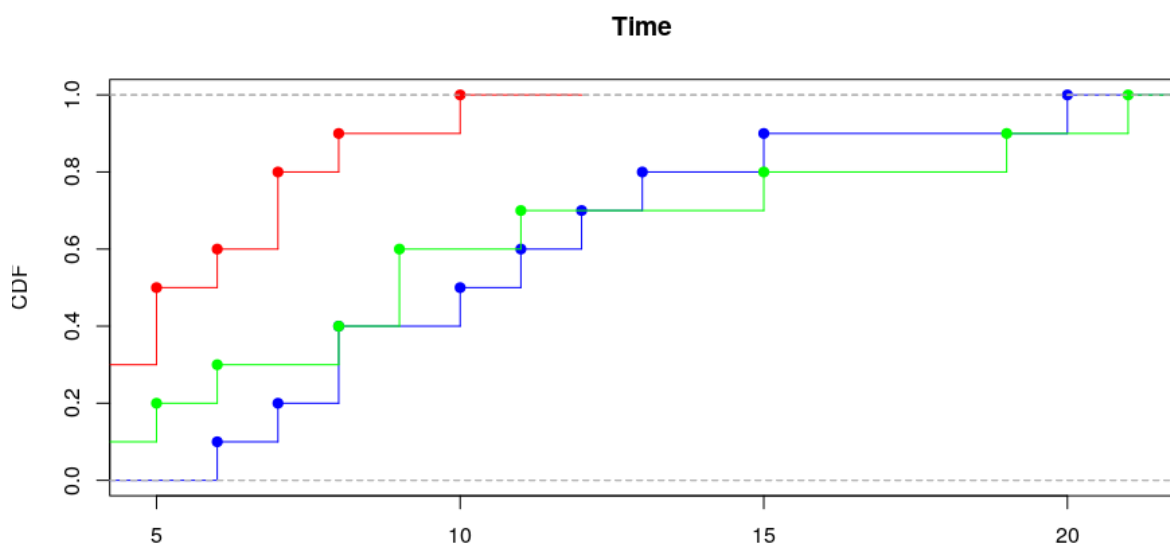
```
cdfB <- ecdf(B)
```

```
cdfC <- ecdf(C)
```

```
plot(cdfA, verticals=TRUE, col.points="blue", col="blue", main="Time", ylab="CDF", xlab="t")
```

```
lines(ecdf(B), verticals=TRUE, col.points="green", col="green")
```

```
lines(ecdf(C), verticals=TRUE, col.points="red", col="red")
```



#(b) Use a parametric test to compare the groups. State your conclusion.

#Find confidence intervals for the pairwise differences using Tukey's method.

#Assess the model fit via residual diagnostics.

#Part 1

```
A <- c(6,7,8,8,10,11,12,13,15,20)
```

```
B <- c(4,5,6,8,9,9,19,11,15,21)
```

```
C <- c(3,3,4,5,5,6,7,7,8,10)
```

```
y <- c(A, B, C)
```

```
x <- rep(c(1,2,3), c(10,10,10))
```

```
xf <- factor(x, labels=c("A", "B", "C"))
```

```
plot(y ~ xf)
```

#####FIT ONE-WAY ANOVA MODEL (i.e. APPLY F TEST)

```
f <- aov(y ~ xf) # aov fits the model
```

```
anova(f) # anova extracts the ANOVA table
```

```
summary(f) # since the model *is* an ANOVA model, the summary is the same as an ANOVA table from anova()
```

#Part 2

```
library(DescTools)
```

#Confidence Intervals are shown here:

```
TukeyHSD(f, conf.level = .95)
```

```
> TukeyHSD(f, conf.level = .95)
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = y ~ xf)

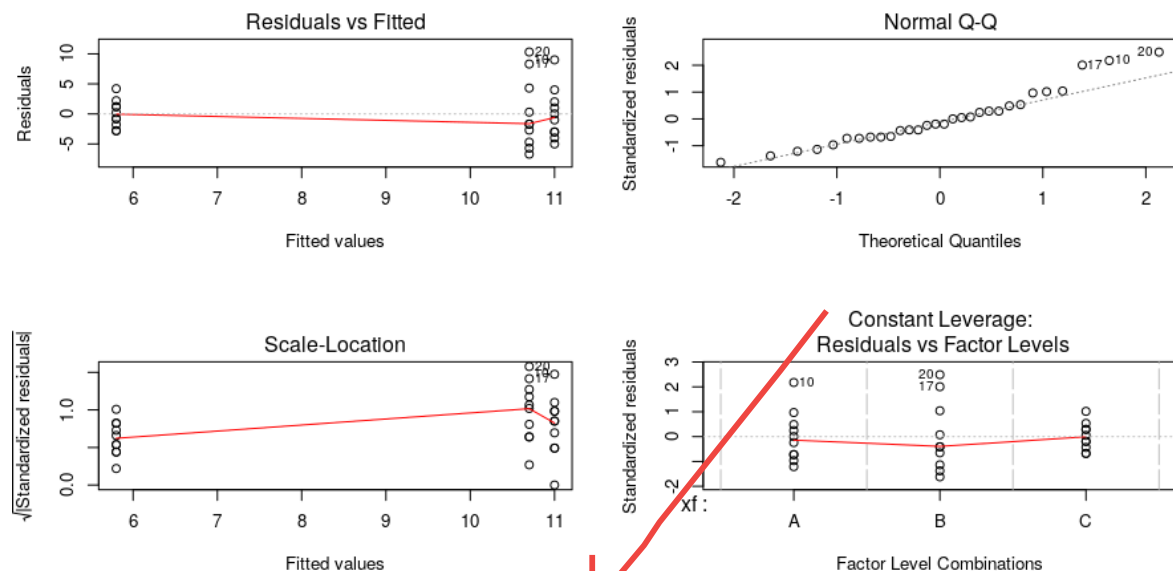
$xf
      diff       lwr       upr      p adj
B-A -0.3   -5.136571  4.53657129 0.8870516
C-A -5.2  -10.036571 -0.36342871 0.0332139
C-B -4.9   -9.736571 -0.06342871 0.0466111
```

```
hist(resid(f))
```

\* plot(f)

```
par(mfrow=c(2,2))
plot(f, conf.level = .95)
par(mfrow=c(1,1))
```

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# not normal according to QQ plot 3rd plot  
# non-constant variance according to 1st and

#(c) Use nonparametric tests to compare the groups. Look for both overall and pairwise differences.

# State all appropriate hypotheses and conclusions

# do a Kruskal-Wallis test followed by pairwise Bonferroni adjusted WMW tests.

# Kruskal Wallis.

ks.test(A,B, alternative = "greater") #p-value: .90

ks.test(A,C, alternative = "greater") #P-value: 1

ks.test(B,C, alternative = "greater") #P-value' 1

# These are for Correlation

cor.test(A, B, alternative="greater")

cor.test(A, C, alternative="greater")

cor.test(B, C, alternative="greater")

5.1

Why?

#Bonferroni Adjustments

sigma <- 0.05

bottom <- 3 \* 3(3-1)/2

sigma/bottom #Bonferroni Level of significance is 0.01666667

wilcox.test(A,B) #p = 0.7

wilcox.test(A,C) #Significance #p = 0.003461

wilcox.test(B,C) #p = 0.03362

#A is significantly different from C, but the other comparisons are not significant.

#Conclusion: There is no correlation between each of the samples.

##(d) Which approach is more appropriate here?

#I believe that using the nonparametric tests are more appropriate to use here.

#The reasons for using nonparametric tests are:

#1: The population sample size is small enough.

#2: The underlying data do not meet the assumptions about the population sample.

#3: We are dealing with Ordinal data.

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## Index of comments

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5.1      `kruskal.test(Flu$Time, Flu$Strain)`