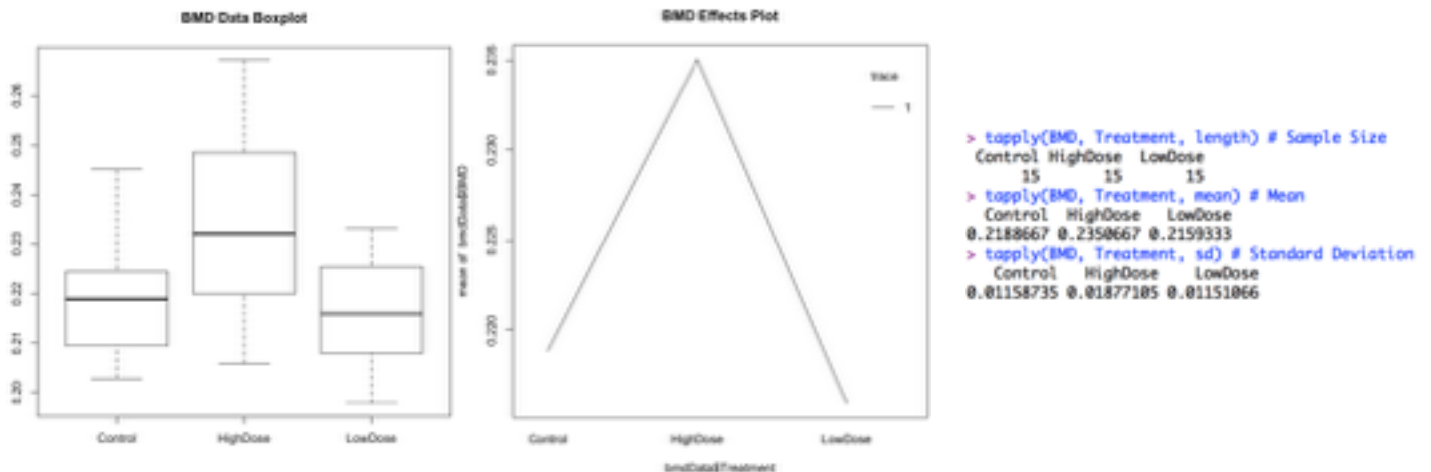


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STAT350 - Lab 7
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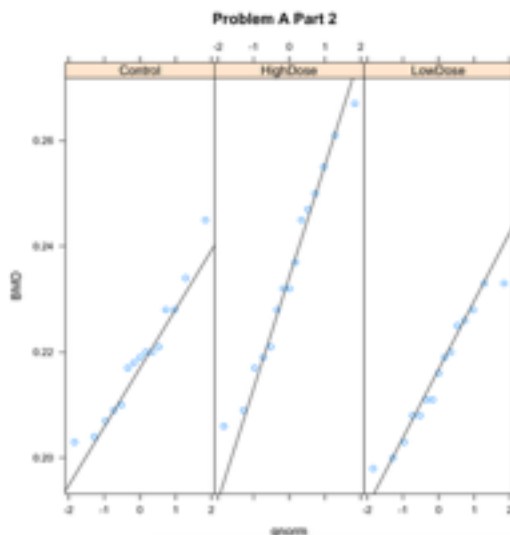
A. Isoflavones and Bone Mineral Density (Code can be found in appendix)

1.



From the above data, I believe the means for the control and low dose are the same, however the high dose has a higher mean. This is because all three results point to similar results for control and low dose, but higher values for the high dose.

2.



Based on the data, it should be appropriate to continue the analysis. The data includes independence, normality, and constant variance. This is shown in the graph to the left, as the data is evenly distributed around each qqline. The data is normal, and the standard deviation is constant.

3.

```
> summary(fit)
      Df Sum Sq Mean Sq F value Pr(>F)
Treatment  2 0.003186  0.0015928   7.718 0.0014 **
Residuals 42 0.008668  0.0002064
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

μ_B is the population mean BMD value for the Basal method.

μ_D is the population mean BMD value for the Basal method.

μ_S is the population mean BMD value for the Basal method.

Hypotheses:

$H_0: \mu_B = \mu_D = \mu_S$

H_a : At least one is different

Test Statistic:

$F_t = 7.718$

$DF_1 = p-1 = 3-1 = 2$, $DF_2 = n - p = 45 - 3 = 42$

P-Value = 0.0014

Conclusion: Since $0.0014 < 0.05$, we should reject H_0 and conclude that at least one is different. This is the same conclusion we came to in A.1., concluding that the High Dose has a substantially different mean.

4.

```
> pairwise.t.test(bmdData$BMD, bmdData$Treatment, p.adjust="bon")

Pairwise comparisons using t tests with pooled SD

data:  bmdData$BMD and bmdData$Treatment

      Control HighDose
HighDose 0.0107  -
LowDose  1.0000  0.0022

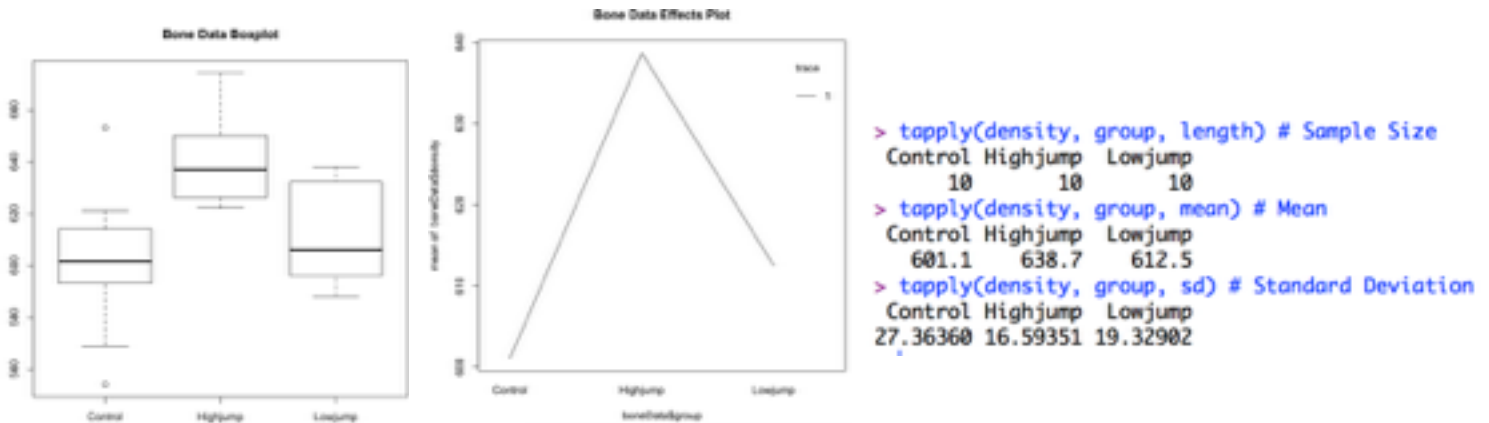
P value adjustment method: bonferroni
```

This test shows that Control and HighDose are different ($.0107 < 0.05$), and HighDose and LowDose are different ($.0022 < 0.05$) while Control and LowDose are the same ($1 > 0.05$) I chose this test method because it directly compares each of the response variables and determines which are the same and which are different.

5. The results show that high doses of kudzu have an impact on the rat, while low doses do not.

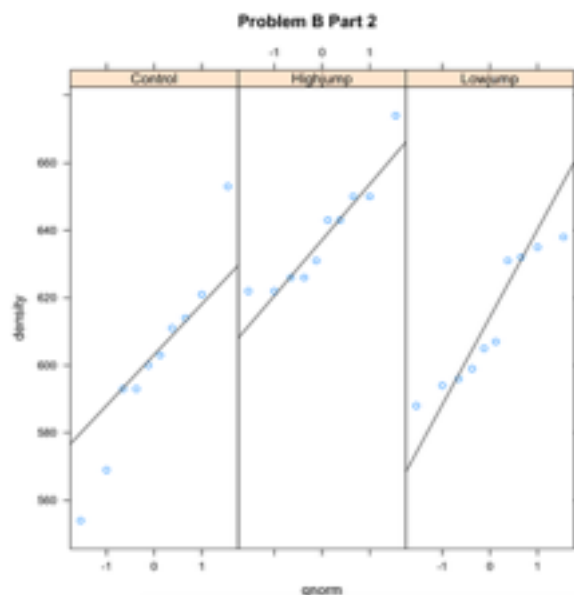
B. Exercise and Healthy Bones

1.



From the above data, I believe the means for all three groups are different. This is because all three results point to different means for each of the three groups.

2.



Based on the data, it should be appropriate to continue the analysis. The data includes independence, normality, and constant variance. This is shown in the graph to the left, as the data is evenly distributed around each qqline. The data is normal, and the standard deviation is constant.

3.

```
> summary(fit)
      Df Sum Sq Mean Sq F value Pr(>F)
group    2   7434    3717   7.978  0.0019 **
Residuals 27  12579     466

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

μ_B is the population mean treatment value for the Basal method.

μ_D is the population mean treatment value for the Basal method.

μ_S is the population mean treatment value for the Basal method.

Hypotheses:

$H_0: \mu_B = \mu_D = \mu_S$

H_a : At least one is different

Test Statistic:

$F_t = 7.978$

$DF_1 = p-1 = 3-1 = 2$, $DF_2 = n - p = 30 - 3 = 27$

P-Value = 0.0019

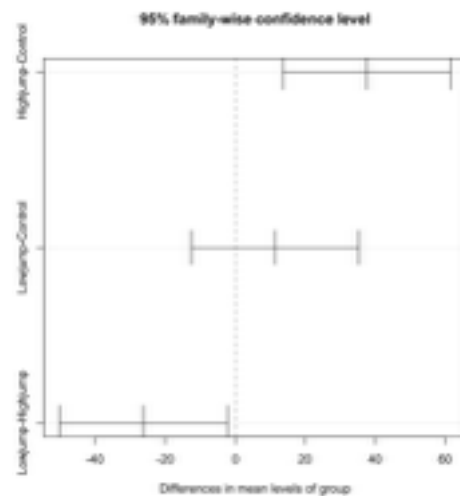
Conclusion: Since $0.0019 < 0.05$, we should reject H_0 and conclude that at least one is different. This is the same conclusion we came to in B.1., concluding that all three means are different.

4.

```
> test.Tukey
Tukey multiple comparisons of means
95% family-wise confidence level

Fit: aov(formula = density ~ group, data = boneData)

$group
      diff      lwr      upr    p adj
Highjump-Control 37.6 13.66604 61.533957 0.0016388
Lowjump-Control  11.4 -12.53396 35.333957 0.4744032
Lowjump-Highjump -26.2 -50.13396 -2.266043 0.0297843
```



This test shows that all three groups have substantially different means. I chose this test method because it clearly shows that all three groups are substantially different.

5. The results show that there is a substantial difference between the control, low jump and high jump.

Appendix:

```
##### Problem A #####
```

```
bmdData <- read.table(file="ex12-45bmd.txt",header=T)
```

```
##### Part 1 #####
```

```
boxplot(BMD~Treatment,bmdData,main="BMD Data Boxplot") # Boxplot
```

```
# Effects Plot
```

```
trace <-rep(1,length(bmdData$Treatment))
```

```
interaction.plot(bmdData$Treatment,trace,bmdData
  $BMD,fun=mean,lengend=F,main="BMD Effects Plot")
```

```
# Info Table
```

```

attach(bmdData)
tapply(BMD, Treatment, length) # Sample Size
tapply(BMD, Treatment, mean) # Mean
tapply(BMD, Treatment, sd) # Standard Deviation

##### Part 2 #####
library(lattice)
qqmath(~BMD | Treatment, data = bmdData, layout=c(3,1), panel =
  function(x) {
    panel.qqmath(x)
    panel.qqmathline(x)
  }, main="Problem A Part 2")

##### Part 3 #####
fit <- aov(BMD ~ Treatment, bmdData)
summary(fit)

##### Part 4 #####
pairwise.t.test(bmdData$BMD, bmdData$Treatment, p.adjust="bon")

##### Problem B #####
boneData <- read.table(file="ex12-47jump.txt",header=T)

##### Part 1 #####
boxplot(density~group,boneData,main="Bone Data Boxplot") # Boxplot
# Effects Plot
trace <-rep(1,length(boneData$group))
interaction.plot(boneData$group,trace,boneData
  $density,fun=mean,lengend=F,main="Bone Data Effects Plot")
# Info Table
attach(boneData)
tapply(density, group, length) # Sample Size
tapply(density, group, mean) # Mean
tapply(density, group, sd) # Standard Deviation

##### Part 2 #####
library(lattice)
qqmath(~density | group, data = boneData, layout=c(3,1), panel =
  function(x) {
    panel.qqmath(x)
    panel.qqmathline(x)
  }, main="Problem B Part 2")

```

Part 3

```
fit <- aov(density ~ group, boneData)
summary(fit)
```

Part 4

```
test.Tukey <- TukeyHSD(fit, conf.level=0.95)
test.Tukey
plot(test.Tukey)
```