STA 106 - Project 1

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I. **Introduction**

Dieting is one of the most effective forms of weight loss. With countless diets offering a variety of results a study was conducted on three different diets (referred to as diets A, B, and C) to determine which diet resulted in the most weight loss. In order to determine which of the diets resulted in the highest weight loss, we will compare the mean weight loss of each group using several ANOVA methods. We will use the F test to determine if at least one group's average weight loss is different from the rest, calculate the power of this test, and subsequently construct pairwise confidence intervals for the difference in means using the Tukey Correction and Bonferroni Correction.

II. Summary of Data

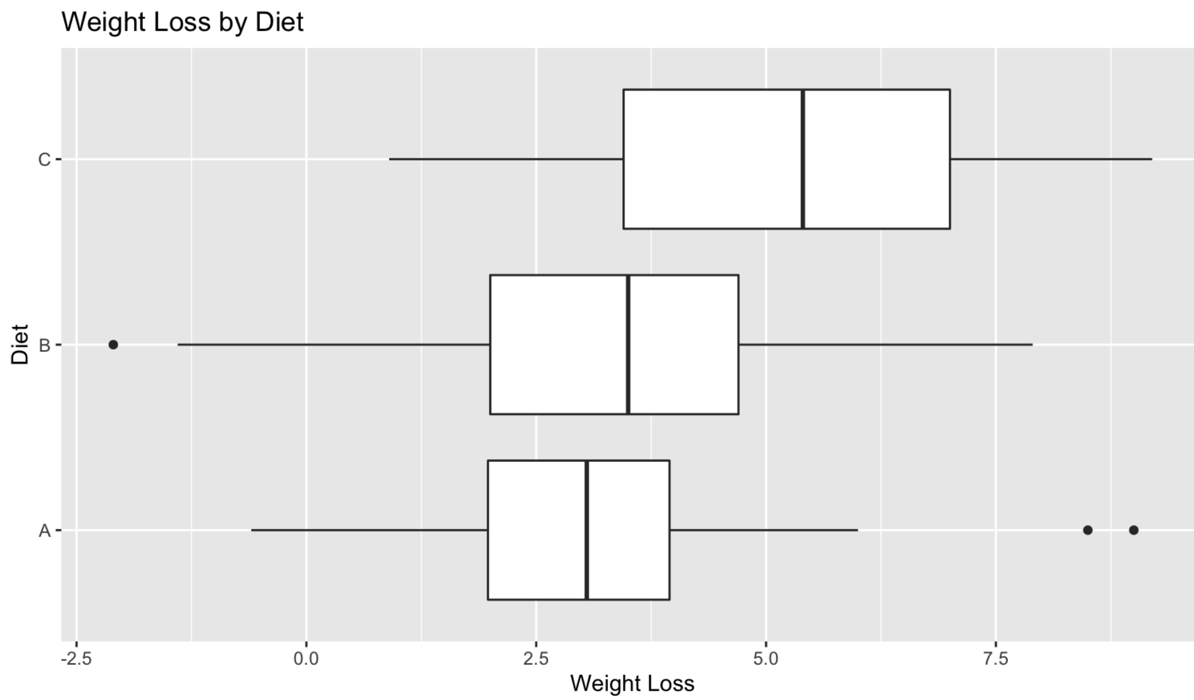

Figure 1: we see that the participants that took diet C had a higher minimum, median, and maximum than those that took diet A and B. We also observe several outliers in the groups that took diets A and B.

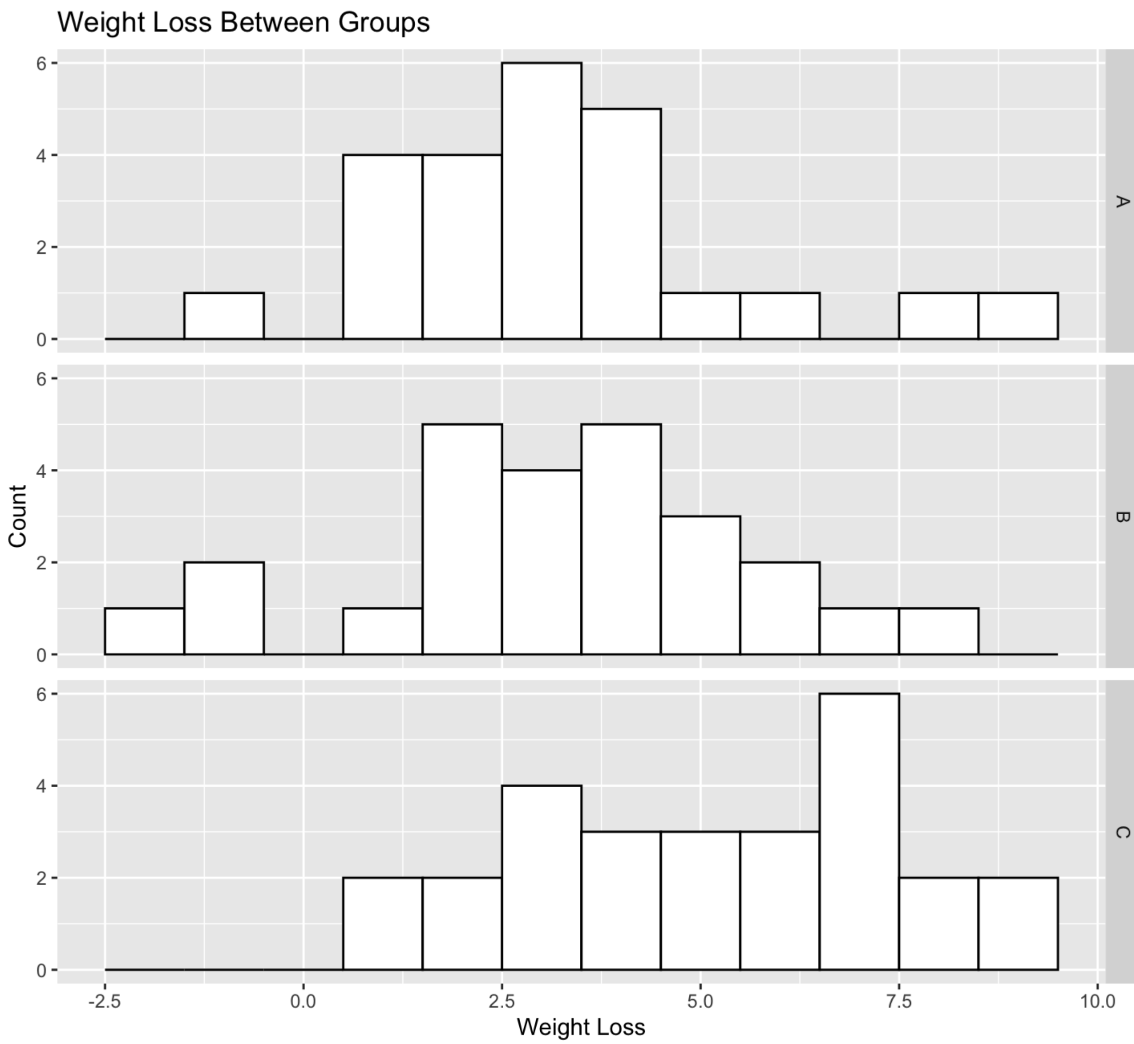

Figure 2: Looking at the above histograms, it can be seen that both diets A and B have a similar distribution of weight loss ranges, while diet C is skewed to the left. This means there were more subjects that lost a higher amount of weight when following diet C when compared to diets A and B.

Summary Statistics

	A	B	C	Overall
Sample means	2.8045	3.4916	5.2333	3.9297
Sample Std. Dev	2.2401	2.4645	2.2477	2.2850
Sample Size	22	24	27	73

III. Diagnostics

We used the Single Factor ANOVA model $Y_{ij} = \mu_i + \varepsilon_{ij}$, $\varepsilon_{ij} \sim N(0, \sigma_\varepsilon^2)$. Our assumptions for S.F. ANOVA are that it is a random sample, groups A, B, and C are independent of each other and that the errors are independent and normally distributed with mean = 0 and a constant variance of σ_ε^2. We removed three outliers from the dataset that can be seen in the figure 1 boxplot. Two outliers from group A and one outlier from group B. We did this because those outliers skewed the results of the sample means.

IV. Analysis

A. Model Fit

1. Shapiro-Wilks

In order to conduct our analysis we first need to assess the normality of our data. To do this we used the Shapiro-wilks test. The null and alternative hypotheses are as follows:

H_0: *The errors are normally distributed*

H_A: *The errors are not normally distributed*

After running the test in R, we are given a p-value of 0.9921. Since our p-value is relatively large, we fail to reject the null hypothesis at any reasonable level of significance (1%, 5%, 10%).

2. Assessing Homoscedasticity

a) Plotting Errors vs. Groups

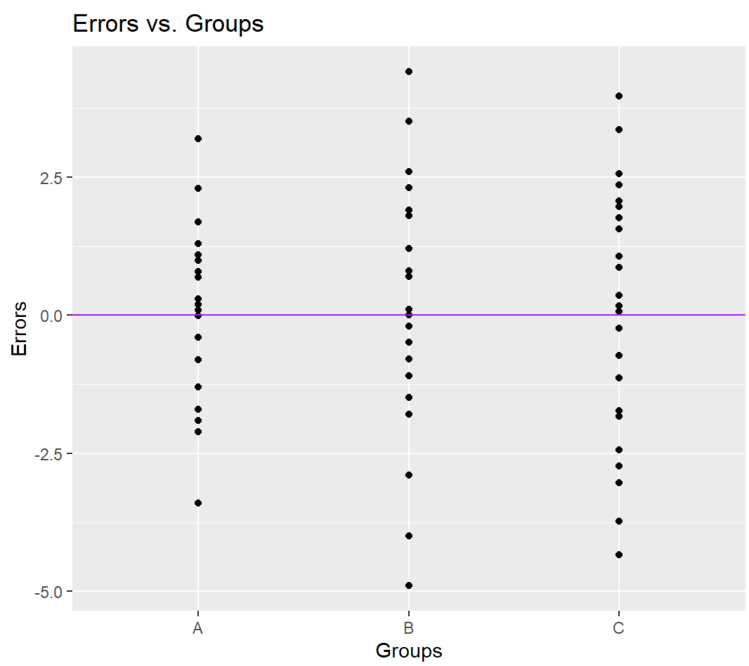

Figure 3: This plot suggests a roughly equal vertical spread.

b) **Brown-Forsythe Test**

Although Figure 3 provides a visual representation of equal variances just to be sure we will conduct a Brown-Forsythe Test. We will use the following null and alternative hypotheses.

H_0: *Population variances by group are equal*

H_A: *Population variances by group are not equal*

After performing the test we are given a test statistic value of F= 2.10 and a p-value of 0.130. Since the p-value is greater than our level of significance of 0.01 we fail to reject the null hypothesis and conclude that the population variances by groups are equal.

B. F Test

To determine if the sample means of groups A, B, and C are equal to each other, we conducted an F test with the following null and alternative hypotheses:

$$H_0:\ \mu_A = \mu_B = \mu_C$$

$$H_A\ =\ At\ least\ one\ \mu_i\ is\ not\ equal\ to\ the\ others$$

After calculating $F_{statistic}\ =\ 6.1537$, we found that the probability of calculating this value or higher is $p\ =\ 0.0034$. At $\alpha\ =\ 0.01$, we reject the null hypothesis. There is statistically significant evidence that at least one of the group means are different from each other.

C. Power of the Test

To calculate the power of the test of equal means, we used the following formulae:

$$\phi\ =\ \frac{1}{\sigma_\epsilon}\sqrt{\frac{\sum_{i=1}^{n} n_i(\mu_i-\mu_0)^2}{a}}$$

$$d.f\{numerator\}\ =\ a\ -\ 1$$

$$d.f\{denominator\}\ =\ n_t\ -\ a$$

Using the values $\phi\ =\ 2.0255$, $d.f\{numerator\}\ =\ 2$, and $d.f\{denominator\}\ =\ 73$, we calculated that $power\ =\ 0.6991$.

D. Pairwise Confidence Intervals

After calculating the F-Statistic we then calculated all of the pairwise confidence intervals for the difference in means using the equation below. Also since we are calculating multiple confidence intervals we calculated Tukey's and Bonferroni's correction multiplier and decided on using Tukey's because it is the smaller value of the two multipliers.

$$\text{Confidence Intervals } \overline{Y_{i.}} - \overline{Y_{i.}}' \pm t_{1-\frac{\alpha}{2};\, n_T-a}\sqrt{MSE\left(\frac{1}{ni} + \frac{1}{n_i'}\right)}$$

Tukey Correction = 3.01   Bonferroni Correction = 3.03

Confidence Interval for $\mu_A - \mu_B$ is (-2.519, 1.1454)

Confidence Interval for $\mu_A - \mu_C$ is (-4.2120, -0.6455)

Confidence Interval for $\mu_B - \mu_C$ is (-3.4834, 0.0001)

V. Interpretation

We first assessed how well our data fits the ANOVA model. Using the Shapiro-Wilks test, we failed to reject the null hypothesis given a large p-value of 0.9921 and thus affirmed that the errors for this dataset are normally distributed. Next, we created a plot of the error distribution by groups to see if there was equal variance. Looking at Figure 3 it suggests that there is an equal vertical spread of the errors in each of the groups. To confirm that the variances for groups A, B, and C were indeed equal, we performed the Brown-Forsythe test and found a p-value of 0.130. This p-value confirmed that the variances for all groups were equal, and that our data fits the ANOVA model.

When calculating the F-test with an alpha of 0.01, we found our p-value of 0.0034. Since our p-value is less than our alpha, we reject the null hypothesis. This means that at least one of the sample means from our diet groups is different.

The power of this F test was calculated to be 0.6991. Assuming that the average weight lost differs depending on the diet, the probability we correctly conclude that at least one of the diets has a different average in pounds lost is 0.6991.

To find which diet group had a significantly different weight loss effect from the other groups, we constructed three pairwise confidence intervals using the Tukey correction. Overall, we found that there is no significant difference in pounds of weight lost between the two diets A and B with a confidence interval of (-2.519, 1.1454), and diets B and C with a confidence interval of (-3.4834, 0.0001). However, there was a significant difference between the diets A and C with the interval (-4.2120, -0.6455), showing a net loss in weight when using diet C. Between these two diets, diet C proved to be more effective at weight loss than diet A. With 99% confidence, the largest difference in weight loss we can expect to see between diets A and C is 4.2120, and the smallest difference is 0.6455.

VI. Conclusion

In conclusion, when comparing Diets A and B and then B and C, they showed no significant difference in weight loss over the course of the experiment. Diets A and C showed a significant difference in weight loss with Diet C subjects losing more weight.

According to the results of this experiment, people looking to lose weight should choose Diet C due to it having the highest average weight loss.

Appendix

Summary of Data

```
## Boxplot

library(ggplot2)
p<-ggplot(loseit, aes(y = Loss, x = Diet))+ geom_boxplot() + ylab("Weight Loss")+ xlab("Diet") +
ggtitle("Weight Loss by Diet") + coord_flip()
p

## Histogram

ggplot(loseit, aes(x = Loss)) +
  geom_histogram(binwidth = 1, color = 'black', fill = 'white') +
  facet_grid(Diet~.) +
  ggtitle("Weight Loss Between Groups") +
  labs(x = 'Weight Loss', y = 'Count')

## Summary Statistics Values

Overall
mean(loseit$Loss)
the.sd = sd(loseit$Loss)

By group
aggregate(Loss ~ Diet, data = loseit1, mean)
aggregate(Loss ~ Diet, data = loseit1, sd)
aggregate(Loss ~ Diet, data = loseit1, length)
```

Analysis

```
##Assessing Normality with Shapiro-Wilks Test

new.model = lm(Loss ~ Diet,data = loseit)
ei = new.model$residuals
the.SWtest = shapiro.test(ei)
the.SWtest

##Assessing Homoscedasticity

Loss = `loseit1`[,2]
Diet = `loseit1`[1]
the.model = lm(Loss ~ Diet,data = loseit1)
Lost = data.frame(Loss,Diet)
Lost$ei = the.model$residuals
```

```
new.model = lm(Loss ~ Diet,data = loseit1)
ei = new.model$residuals
library(ggplot2)
qplot(Diet, ei, data = new.model) +  ggtitle("Errors vs. Groups") + xlab("Groups") + ylab("Errors")
+ geom_hline(yintercept = 0,col = "purple")

##Brown-Forsythe Test
library(car)
the.BFtest = leveneTest(ei~ Diet, data=Lost, center=median)
p.val = the.BFtest[[3]][1]
p.val

## ANOVA Table, F-Test

the.model = lm(Loss ~ Diet, data = loseit)
anova.table = anova(the.model)
Anova.table

## Power of the test

give.me.power = function(ybar,ni,MSE,alpha){
a = length(ybar) # Finds a
nt = sum(ni) #Finds the overall sample size
overall.mean = sum(ni*ybar)/nt # Finds the overall mean
phi = (1/sqrt(MSE))*sqrt( sum(ni*(ybar - overall.mean)^2)/a) #Finds the books value of phi
phi.star = a *phi^2 #Finds the value of phi we will use for R
Fc = qf(1-alpha,a-1,nt-a) #The critical value of F, use in R's function
power = 1 - pf(Fc, a-1, nt-a, phi.star)# The power, calculated using a non-central F
return(power)
}
group.means = by(loseit$Loss,loseit$Diet,mean)
group.nis = by(loseit$Loss,loseit$Diet,length)
MSE = anova.table[2,3]
the.power = give.me.power(group.means,group.nis,MSE,0.05)
the.power

## Boxplot

library(ggplot2)
p<-ggplot(loseit, aes(y = Loss, x = Diet))+ geom_boxplot() + ylab("Weight Loss")+ xlab("Diet") +
ggtitle("Weight Loss by Diet") + coord_flip()
p

## Histogram
```

```
ggplot(loseit, aes(x = Loss)) +
  geom_histogram(binwidth = 1, color = 'black', fill = 'white') +
  facet_grid(Diet~.) +
  ggtitle("Weight Loss Between Groups") +
  labs(x = 'Weight Loss', y = 'Count')

## Tukey and Bonferroni Correction

group.means = by(loseit1$Loss,loseit1$Diet,mean)
group.nis = by(loseit1$Loss,loseit1$Diet,length)
the.model = lm(Loss ~ Diet, data = loseit1)
anova.table = anova(the.model)
MSE = anova.table[2,3]
nt = sum(group.nis)
a = length(group.means)
alpha = 0.01
Tuk = qtukey(1-alpha,a,nt-a)/sqrt(2)
g=3
B = qt(1-alpha/(2*g),nt-a)

## Confidence Intervals

give.me.CI = function(ybar,ni,ci,MSE,multiplier){
if(sum(ci) != 0 & sum(ci !=0 ) != 1){
return("Error - you did not input a valid contrast")
} else if(length(ci) != length(ni)){
return("Error - not enough contrasts given")
}
else{
estimate = sum(ybar*ci)
SE = sqrt(MSE*sum(ci^2/ni))
CI = estimate + c(-1,1)*multiplier*SE
result = c(estimate,CI)
names(result) = c("Estimate","Lower Bound","Upper Bound")
return(result)
}
}

ci = c(1,-1,0)
give.me.CI(group.means,group.nis,ci,MSE,Tuk)

ci = c(1,0,-1)
give.me.CI(group.means,group.nis,ci,MSE,Tuk)

ci = c(0,1,-1)
```

```
give.me.CI(group.means,group.nis,ci,MSE,Tuk)
```