

Assignment 7

- 1) Identify one positive and one negative correlate of the number of specialist species found in each tree.

One positive correlate of the number of specialist species found in a tree is temperature. The correlation coefficient is 0.3538. One negative correlate is precipitation. The correlation coefficient is -0.473. The specialist species, temperature, and precipitation data all required log transformation to meet the assumption of normality for Pearson's Correlation Test. See the transformations and correlation data below.

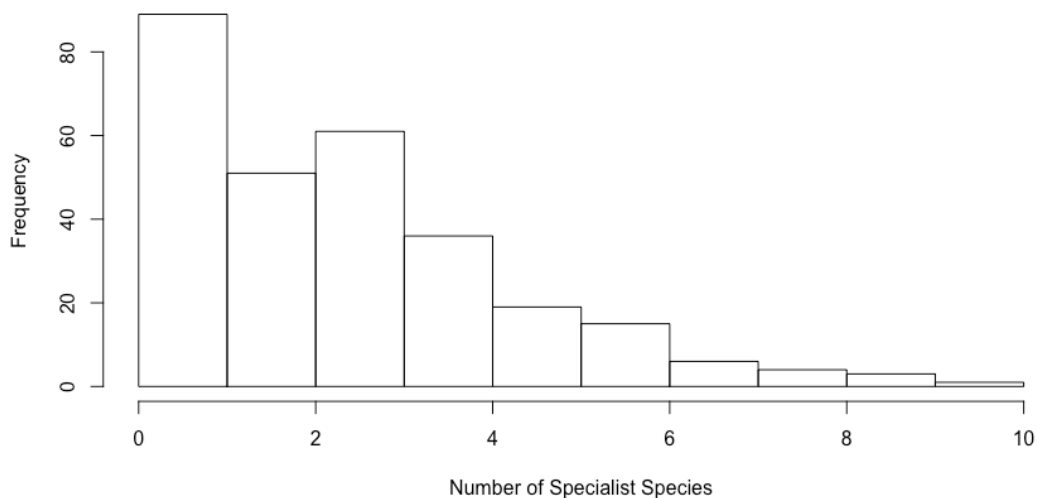
```
Pearson's product-moment correlation

data: log(Data$specialist + 1) and log(Data$MeanTempWarmestQuart + 1)
t = 6.365, df = 283, p-value = 7.85e-10
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.2478807 0.4514993
sample estimates:
      cor 
0.353876

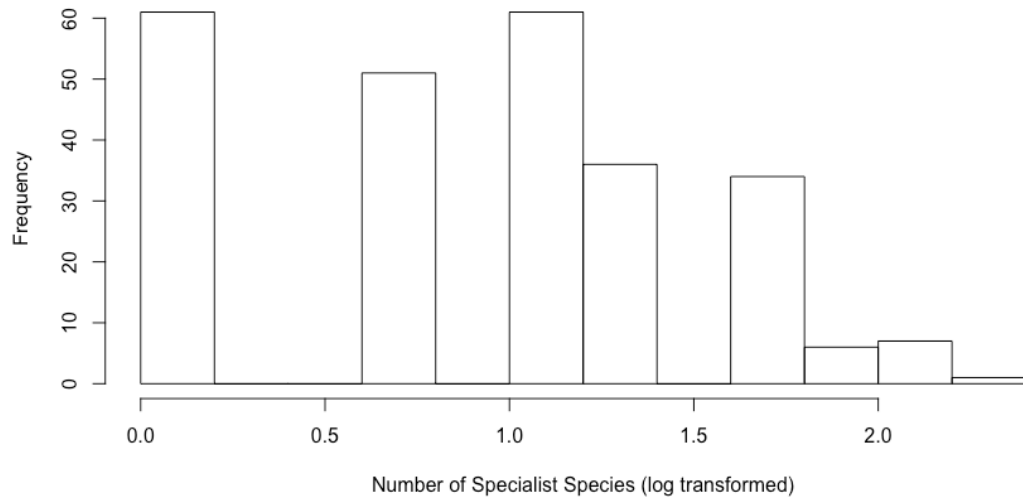
Pearson's product-moment correlation

data: log(Data$specialist + 1) and log(Data$MeanPrecipWarmestQuart + 1)
t = -9.0409, df = 283, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
-0.5588421 -0.3779960
sample estimates:
      cor 
-0.4733925
```

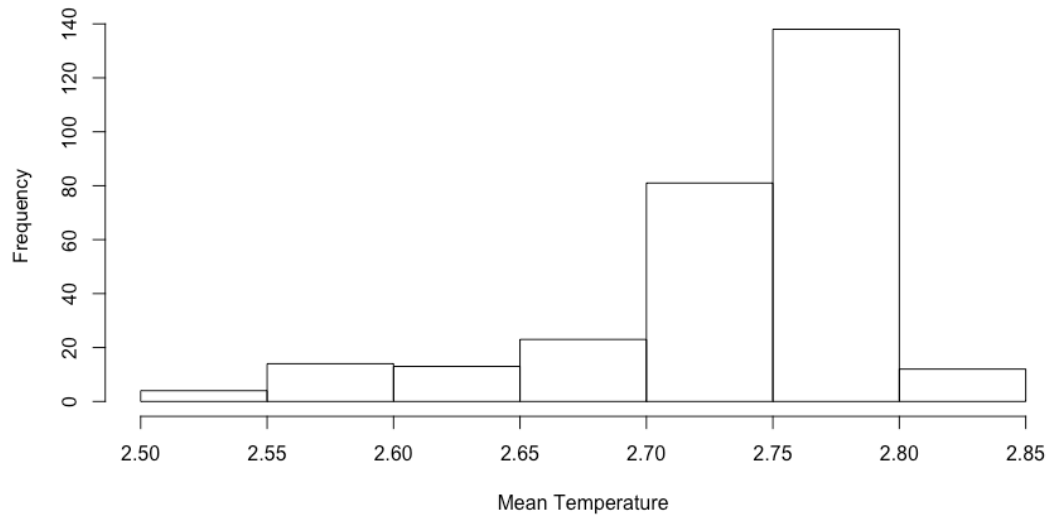
Specialist Species



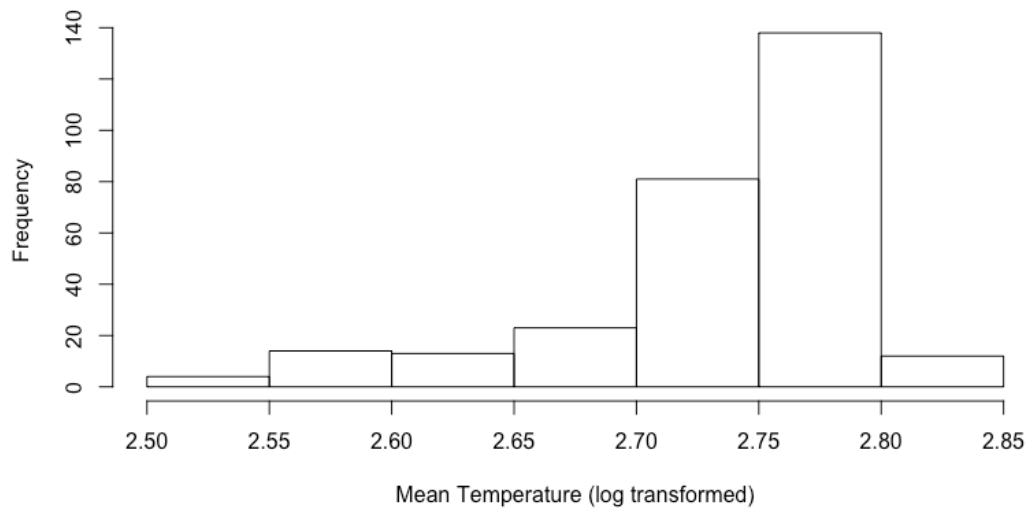
Specialist Species

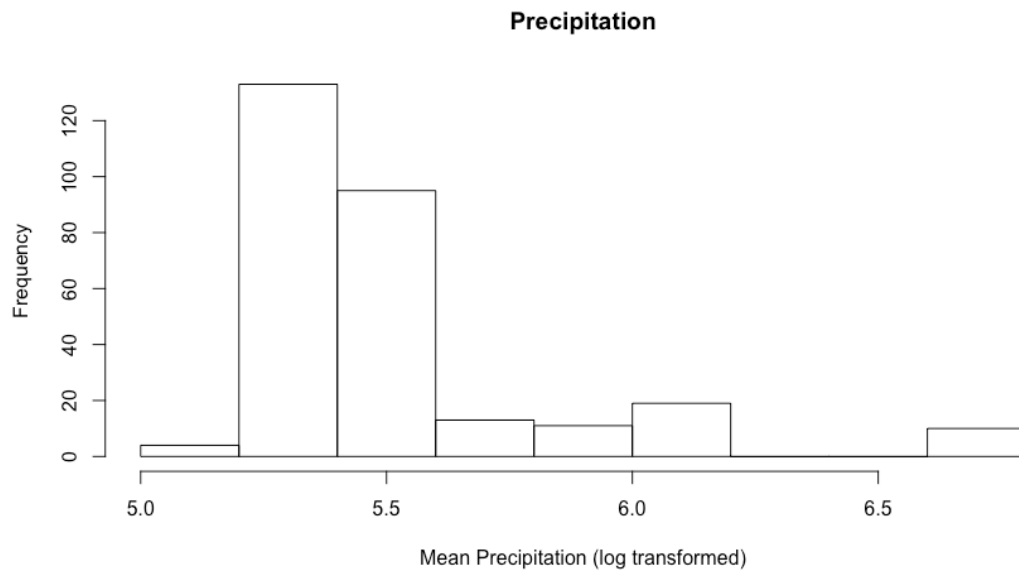
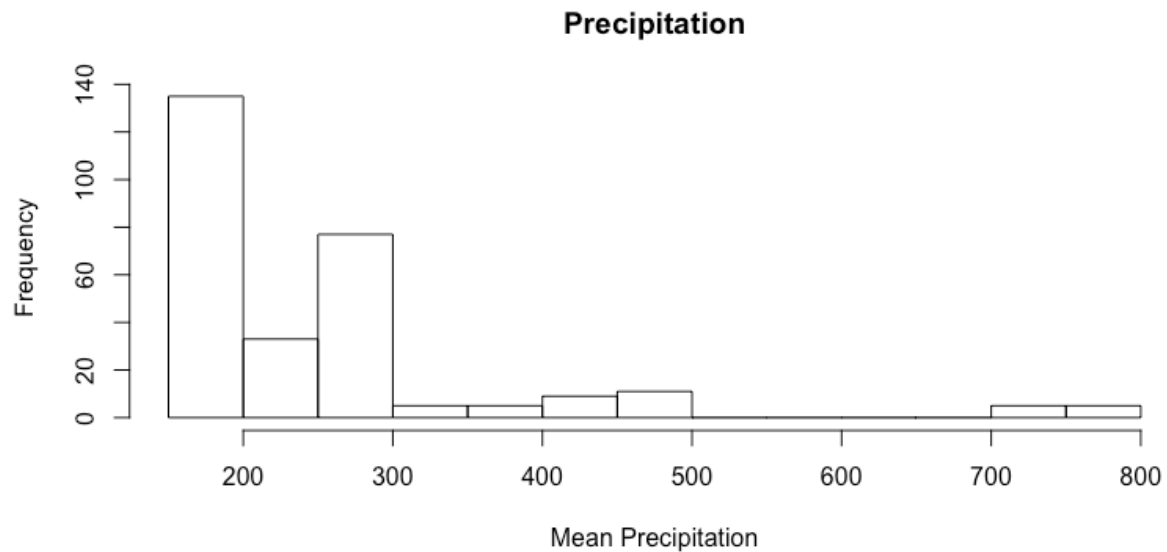


Temperature



Temperature



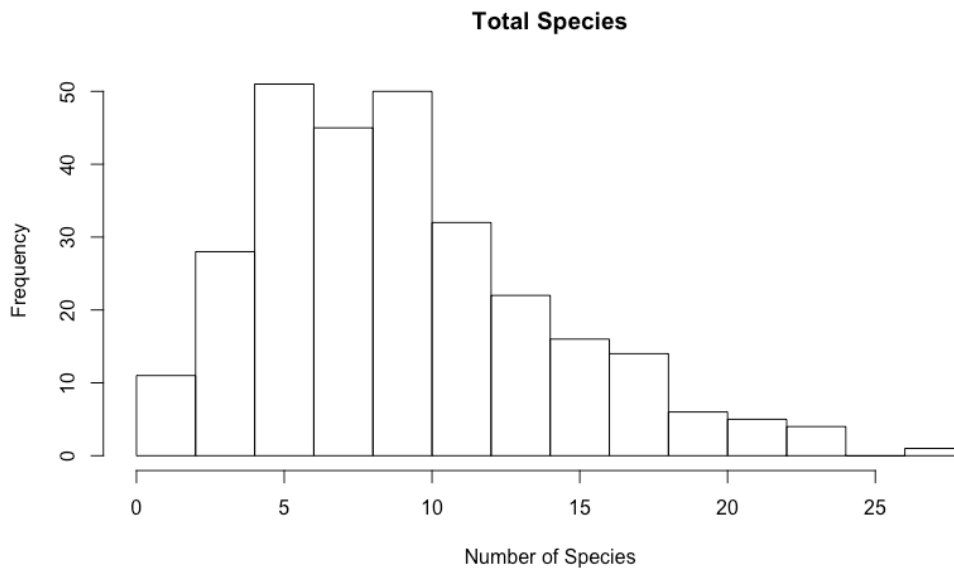


2) Find the strongest correlate of total number of species found on a tree. Plot your result and report your statistical test.

This total species data is normally distributed, so there is no need to transform this. The strongest correlate is precipitation. This yields a correlation value of -0.331849. This offers evidence for a moderate negative correlation between total species and precipitation.

```
Pearson's product-moment correlation

data: (Data$specialist + Data$generalist) and log(Data$MeanPrecipWarmestQuart)
t = -5.9179, df = 283, p-value = 9.404e-09
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
-0.4314027 -0.2243106
sample estimates:
cor
-0.331849
```



3) Use what you have learned to analyze this dataset and make a statement about the impact of macroinvertebrates on leaf litter decay.

An ANOVA generates a low p-value, indicating that at least one of the comparisons has a difference of means. To find the specific differences, Tukey's should be used. Tukey's indicates there is a difference between "none" and "small, as well as "small" and "large". So, we can conclude that the presence of macroinvertebrates has an effect on leaf litter decay. The "small" treatment has increased difference in mean (weight final – weight initial) when compared to "large" and "none", demonstrating that the most decay occurred in this treatment type. (This doesn't really make sense though, as I would have predicted this would have the smallest change in weight due to the fact that it excludes all macroinvertebrates.)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
DataLitter\$treatment	2	8016	4008	16.943	1.76e-06 ***
DataLitter\$block	1	234	234	0.989	0.324
Residuals	56	13248	237		

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

	diff	lwr	upr	p adj
none-large	-1.069	-12.77235	10.63435	0.9737293
small-large	-25.037	-36.74035	-13.33365	0.0000100
small-none	-23.968	-35.67135	-12.26465	0.0000222

4) What is the name for this type of experimental design?

Reciprocal experimental design

5) Is there an interaction between the type of habitat fish are from and their performance in a new habitat?

An ANOVA does indicate that there are differences in the fitness of individuals dependent on their original habitat and the habitat in which they are moved. Conducting a Tukey Test shows where these differences are. The following categories were analyzed by a pairwise comparison:

- A: open to open
- B: open to shallow
- C: shallow to open
- D: shallow to shallow

The following conclusions can be made from Tukey's test:

- The growth resulting from the movement of fish from open water to open water habitat is significantly larger than moving the fish from open to shallow, shallow to open, or shallow to shallow.
- The growth resulting from the movement of fish from open to shallow is significantly larger than shallow to open.
- The growth resulting from shallow to shallow is larger than shallow to open.

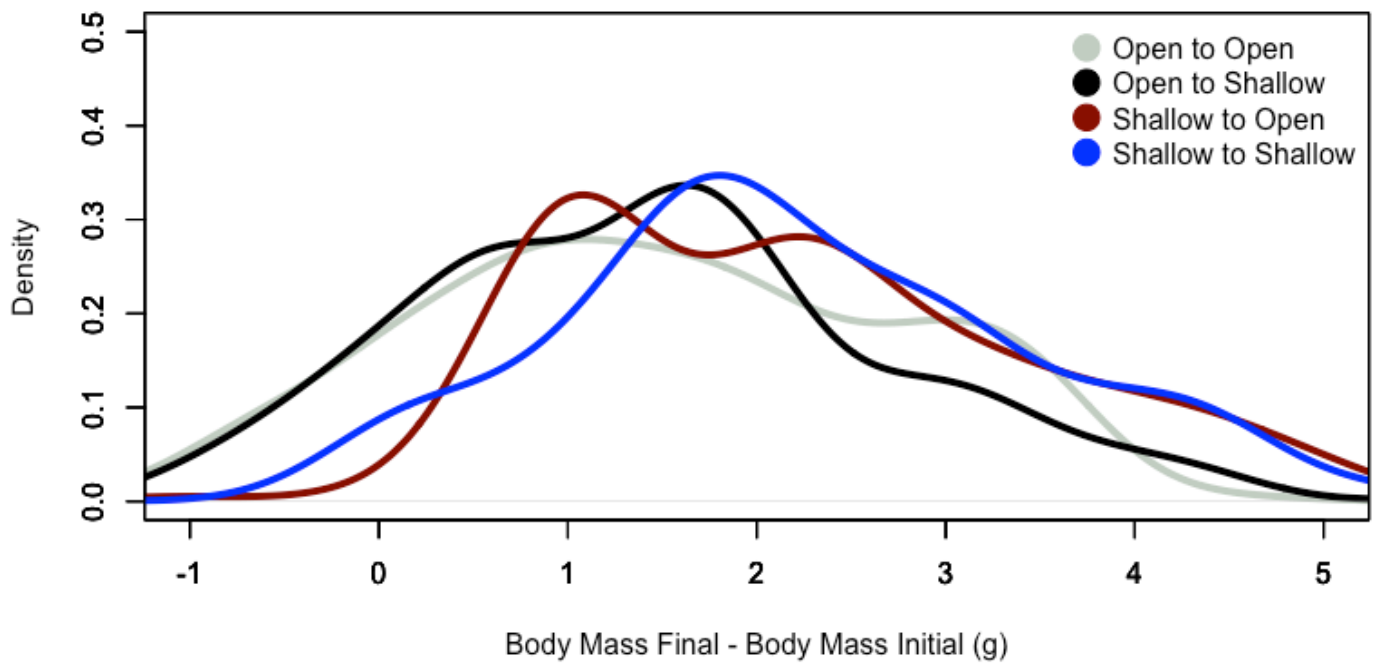
In conclusion, the fish have the best fitness when they go to the habitat similar to where they were collected. However, the fish going from open to shallow do better than those going from shallow to open.

```
              Df Sum Sq Mean Sq F value Pr(>F)
DataFish$Group  3 110.18   36.73   94.66 <2e-16 ***
Residuals      196  76.05    0.39
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

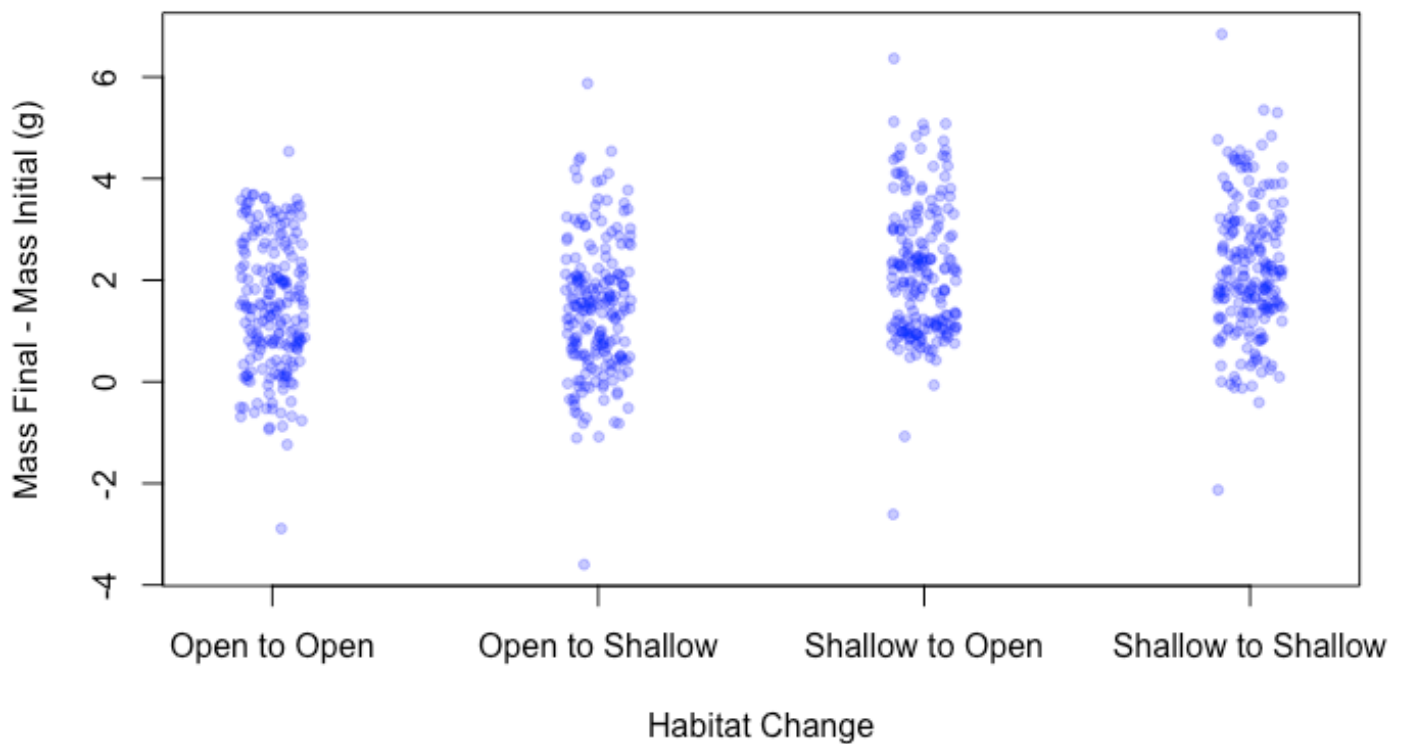
```
$`DataFish$Group`
      diff      lwr      upr      p adj
B-A -1.4100811 -1.7328923 -1.0872698 0.0000000
C-A -2.0446431 -2.3674544 -1.7218319 0.0000000
D-A -1.2834638 -1.6062751 -0.9606525 0.0000000
C-B -0.6345620 -0.9573733 -0.3117508 0.0000049
D-B  0.1266173 -0.1961940  0.4494285 0.7400685
D-C  0.7611793  0.4383681  1.0839906 0.0000000
```

6) Plot this dataset. Prepare a document with your answers to these questions and turn it in by Tuesday. If there are specific topics you would like to go over prior to the midterm please let me know in the next couple of days.

Effect of Habitat Change on Fitness in Fish



Effect of Habitat Change on Fitness in Fish



R-Code:

```
DataLitter <- read.csv("litter.csv")
```

```
diff <- DataLitter$final_mass - DataLitter$initial_mass  
result <- lm(diff ~ DataLitter$treatment)  
anova <- aov(result)  
summary(anova)  
TukeyHSD(aov(result))
```

```
DataFish <- read.csv("fish.csv")
```

```
Graph_Title = "Effect of Habitat Change on Fitness in Fish"
```

```
X_Axis = c(-1,5)  
Y_Axis = c(0, .5)  
X_Label = "Body Mass Final - Body Mass Initial (g)"  
Y_Label = "Density"
```

```
Color1 = (col="honeydew3")
```

```
Color2 = (col="black")
```

```
Color3 = (col="darkred")
```

```
Color4 = (col="blue")
```

```
plot(density(DataFish$mass_2-DataFish$mass_1 [1:50], na.rm=TRUE),  
     main = Graph_Title,  
     ylim = Y_Axis,  
     xlim = X_Axis,  
     xlab = X_Label,  
     ylab = Y_Label,  
     col = Color1,  
     lwd = 4)
```

```
par(new=TRUE)
```

```
plot(density(DataFish$mass_2-DataFish$mass_1 [51:100], na.rm=TRUE),  
     main = "",  
     ylim = Y_Axis,  
     xlim = X_Axis,  
     xlab = "",  
     ylab = "",  
     col = Color2,  
     lwd = 4)
```

```
par(new=TRUE)
```

```
plot(density(DataFish$mass_2-DataFish$mass_1 [101:150], na.rm=TRUE),
```

```

main = "",
ylim = Y_Axis,
xlim = X_Axis,
xlab = "",
ylab = "",
col = Color3,
lwd = 4)

```

```

par(new=TRUE)

```

```

plot(density(DataFish$mass_2-DataFish$mass_1 [151:200], na.rm=TRUE),
     main = "",
     ylim = Y_Axis,
     xlim = X_Axis,
     xlab = "",
     ylab = "",
     col = Color4,
     lwd = 4)

```

```

legend("topright",
      legend = c("Open to Open",
                  "Open to Shallow",
                  "Shallow to Open",
                  "Shallow to Shallow"),
      col = c(Color1, Color2, Color3, Color4),
      pch = c(19,19),
      bty = "n",
      pt.cex = 2,
      cex = 1,
      text.col = "black",
      horiz = F)

```

```

diff2 <- (DataFish$mass_2 - DataFish$mass_1)
anova <- aov(diff2 ~ DataFish$Group)
summary(anova)

```

```

TukeyHSD(anova)

```

```

a <- DataFish$mass_2-DataFish$mass_1 [1:50]
b <- DataFish$mass_2-DataFish$mass_1 [51:100]
c <- DataFish$mass_2-DataFish$mass_1 [101:150]
d <- DataFish$mass_2-DataFish$mass_1 [151:200]

```

```

x <- list("Open to Open" = a,
          "Open to Shallow" = b,
          "Shallow to Open" = c,
          "Shallow to Shallow" = d)

```

```

stripchart(x,

```



```
main = "Effect of Habitat Change on Fitness in Fish",  
method = "jitter",  
ylab = "Mass Final - Mass Initial (g)",  
pch = 20,  
col = rgb(0,0,1,.25),  
xlab = "Habitat Change",  
vertical = TRUE)
```