BIO 122 Laboratory Exercise 4: Skeletal Muscle Contraction

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```
library(tidyverse)
library(ggpubr)
library(broom)
library(car)
library(rstatix)
library(GGally)
library(cowplot)
library(datasets)
```

Data

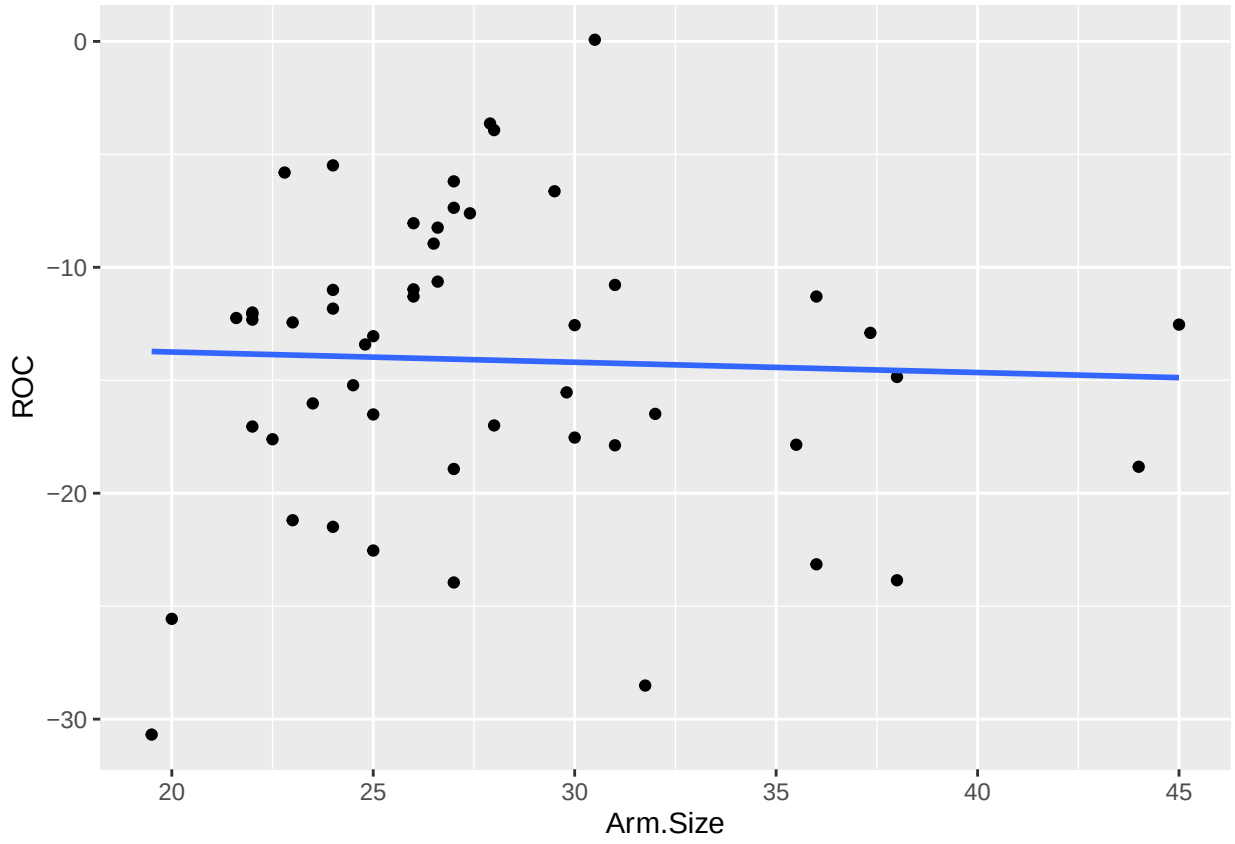
```
#  imports pooled data into R
msc <- read.csv("C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/1st Semester/BIO 118/Module 1/M

#  cleans data
msc <- msc %>%
  select(!c(Name, Section)) %>%
  mutate_all(~replace(., . == "", NA)) %>%
  mutate(Muscle.Mass = gsub("\\%", "", Muscle.Mass)) %>%
  drop_na()

msc$Muscle.Mass <- as.numeric(msc$Muscle.Mass)

#  isolates columns for arm size, arm length, and velocity
msc.cont <- msc %>%
  select(Muscle.Mass, Upper.Arm.Size, Upper.Arm.Length, Forearm.Length,
         X0.25, X0.5, X1, X1.5, X2, ROC) %>%
  gather(Load, Velocity, X0.25, X0.5, X1, X1.5, X2) %>%
  mutate(Load = gsub("\\X", "", Load),
         Muscle.Mass = gsub("\\%", "", Muscle.Mass)) %>%
  mutate_all(~replace(., . == "", NA)) %>%
  drop_na()

msc.cont$Muscle.Mass <- as.numeric(msc.cont$Muscle.Mass)

head(msc.cont)
```

```
##   Muscle.Mass Upper.Arm.Size Upper.Arm.Length Forearm.Length      ROC Load
## 1       65.67           26.0               28           23.0 -11.2927 0.25
```

```
## 2       51.43           35.5                30           23.5 -17.8537 0.25
## 3       86.45           19.5                27           23.0 -30.6829 0.25
## 4       90.39           22.0                29           23.0 -12.3171 0.25
## 5       74.84           22.8                23           24.5  -5.8049 0.25
## 6       56.03           36.0                32           24.0 -11.2927 0.25
##   Velocity
## 1       58
## 2       82
## 3       84
## 4       60
## 5       60
## 6       54
```

Exploring Data

```
roc <- read.csv("C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/1st Semester/BIO 118/Module 1/M

colnames(roc) <- c("Arm.Size", "ROC")

ggplot(roc, aes(Arm.Size, ROC)) + geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```



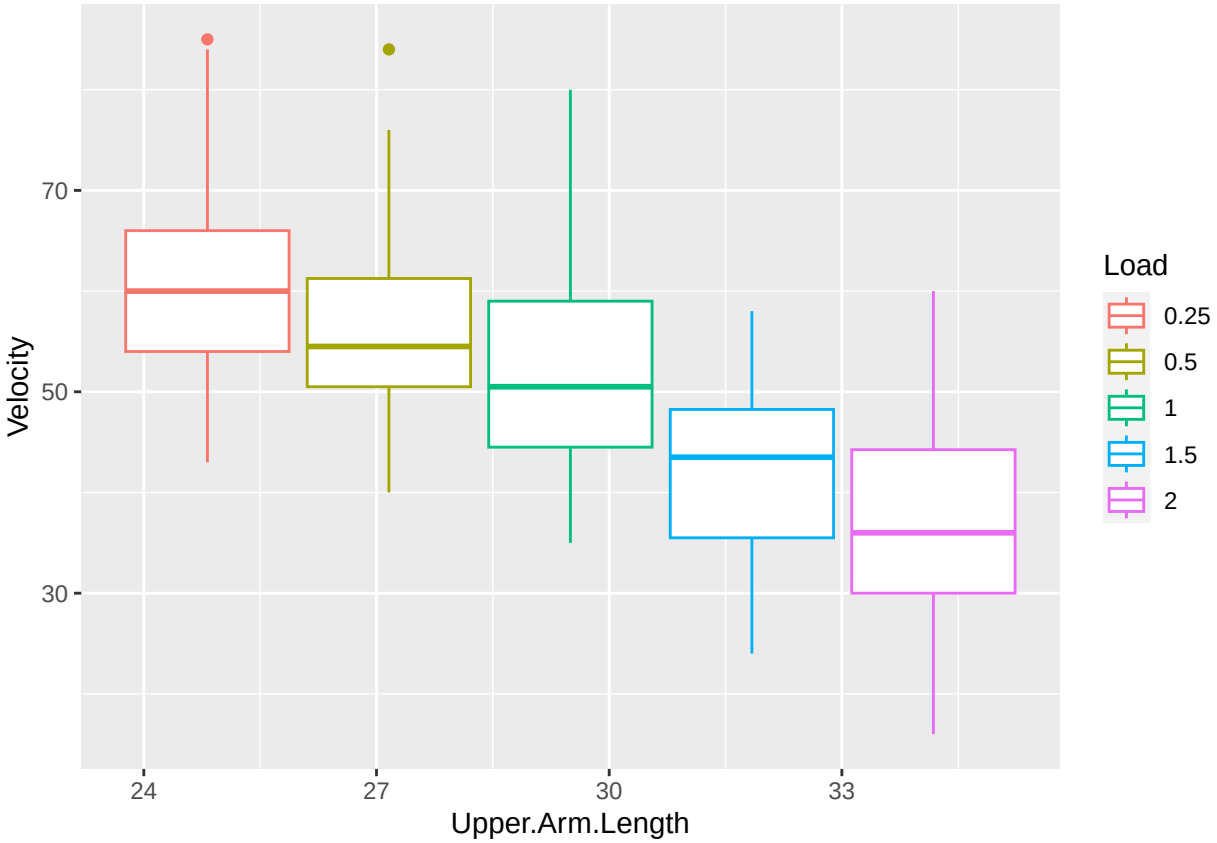
```r
roc.lm <- lm(ROC ~ Arm.Size, roc)
summary(roc.lm)
```

```
##
## Call:
## lm(formula = ROC ~ Arm.Size, data = roc)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -16.956  -3.458   1.485   3.428  14.299
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -12.84094    4.55287  -2.820  0.00686 **
## Arm.Size     -0.04541    0.16037  -0.283  0.77824
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.549 on 50 degrees of freedom
## Multiple R-squared:  0.001601,   Adjusted R-squared:  -0.01837
## F-statistic: 0.08017 on 1 and 50 DF,  p-value: 0.7782
```

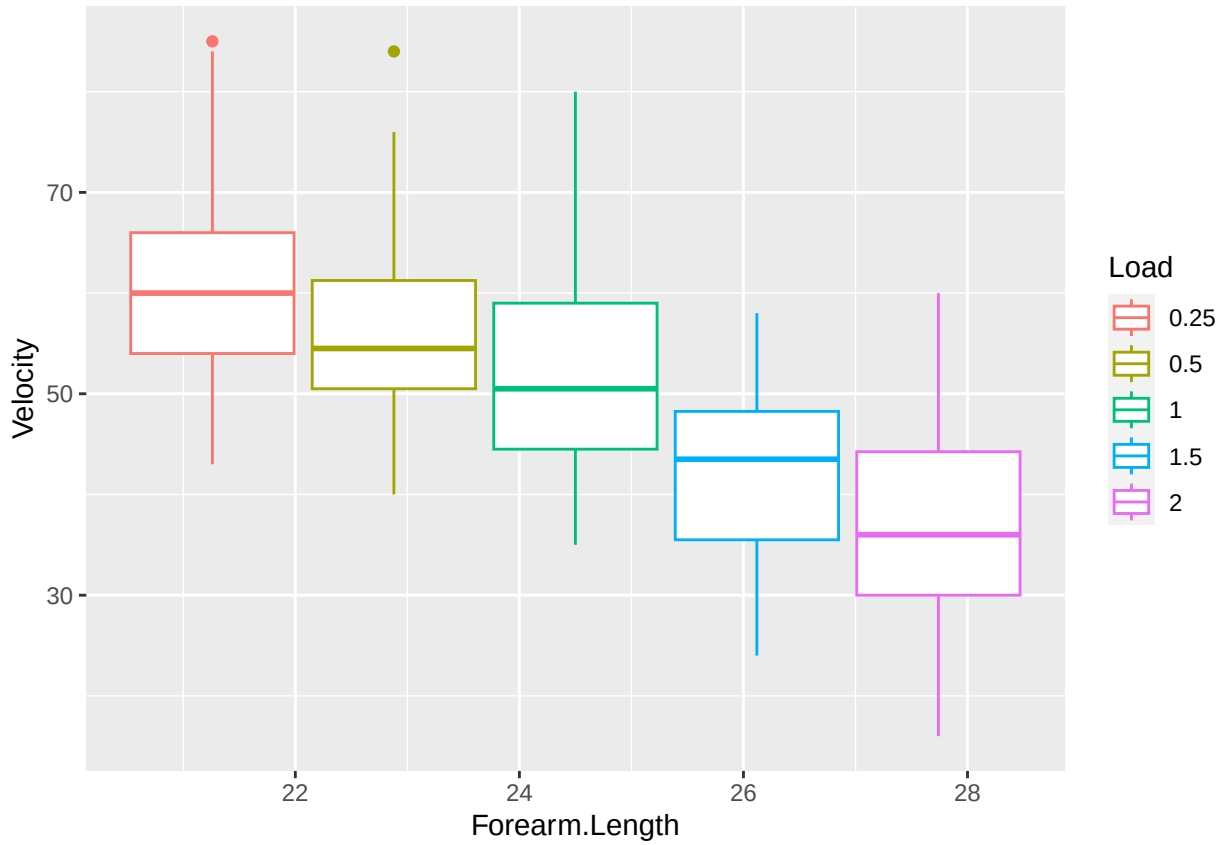
```r
cor(msc.cont$Forearm.Length, msc.cont$ROC)
```

```
## [1] 0.06927163
```

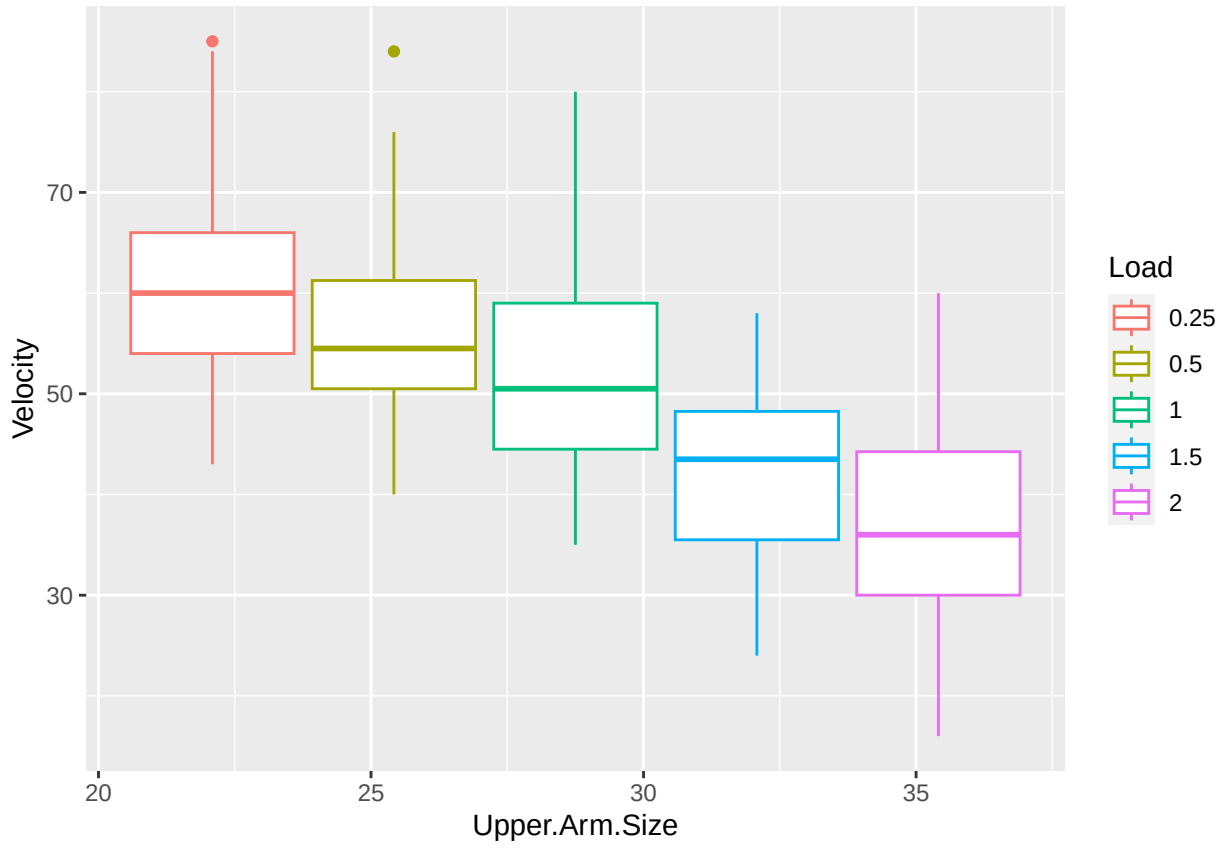
```r
bplot.ual <- ggplot(msc.cont, aes(x = Upper.Arm.Length, y = Velocity, col = Load)) +
  geom_boxplot()
bplot.ual
```




```
bplot.fore <- ggplot(msc.cont, aes(x = Forearm.Length, y = Velocity, col = Load)) +
  geom_boxplot()
bplot.fore
```




```
bplot.uas <- ggplot(msc.cont, aes(x = Upper.Arm.Size, y = Velocity, col = Load)) +
  geom_boxplot()
bplot.uas
```



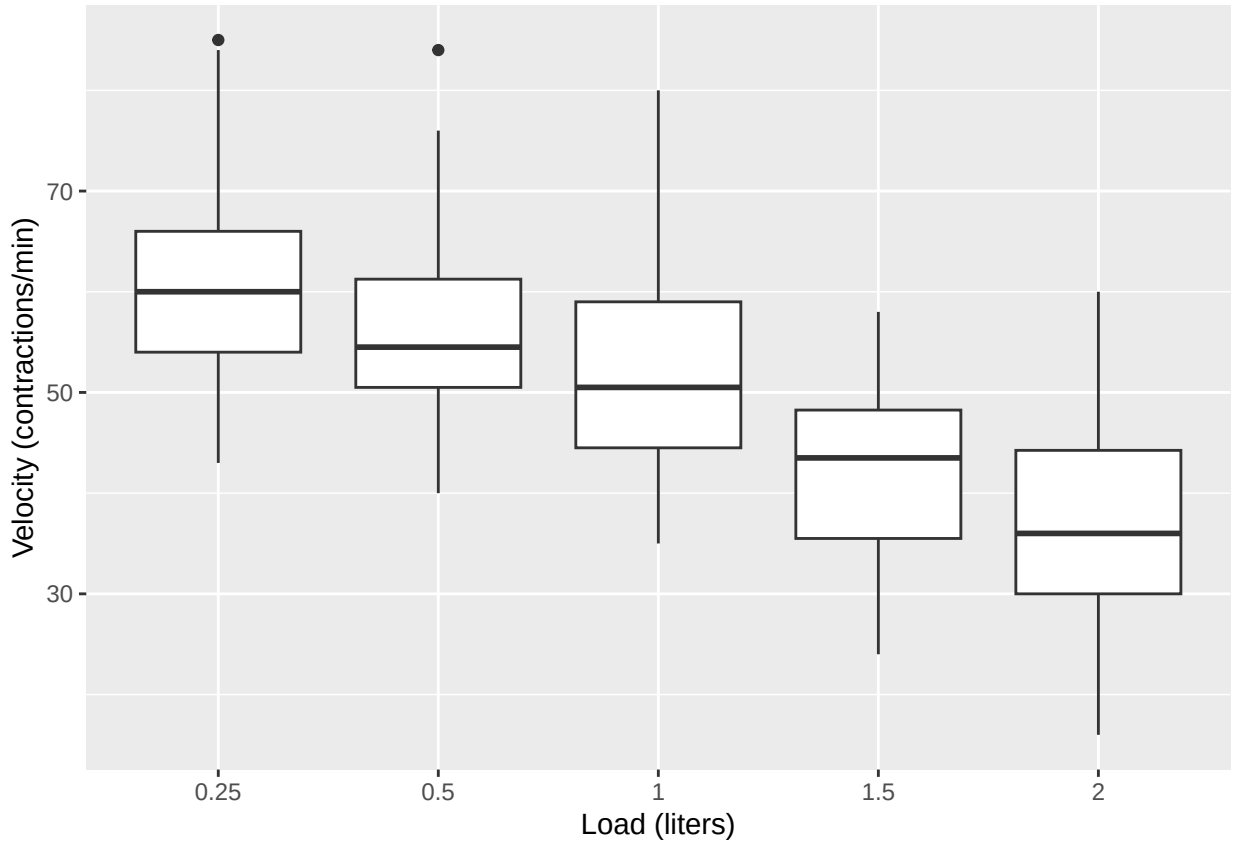
1. LOAD AND VELOCITY

1.a. Data summary and visualization

```
#  prints summary of data
msc.cont %>%
  group_by(Load) %>%
  summarise(
    Mean.Velocity = mean(Velocity),
    SD.Velocity = sd(Velocity)
  )
```

```
## # A tibble: 5 x 3
##   Load  Mean.Velocity SD.Velocity
##   <chr>         <dbl>       <dbl>
## 1 0.25           61.4       11.4
## 2 0.5            56.6       10.5
## 3 1              51.4       10.5
## 4 1.5            42.1        8.96
## 5 2              37.7       10.7
```

```
#  visualizes data
ggplot(msc.cont, aes(Load, Velocity)) + geom_boxplot() +
  ylab("Velocity (contractions/min)") + xlab("Load (liters)")
```




```
ggsave("C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/1st Semester/BIO 118/Module 1/Module 1 -
       width = 8, height = 5)

head(msc)
```

```
##   Age Sex   Prot Metabolism Muscle.Mass Upper.Arm.Size Upper.Arm.Length
## 1  21   F 14.80%     1144.1       65.67           26.0               28
## 2  22   F  7.10%     1392.8       51.43           35.5               30
## 3  21   F 26.20%      969.5       86.45           19.5               27
## 4  21   F 28.30%      948.1       90.39           22.0               29
## 5  22   F 19.80%     1051.1       74.84           22.8               23
## 6  21   F  9.50%     1294.3       56.03           36.0               32
##   Forearm.Length X0.25 X0.5 X1 X1.5 X2      ROC Grip.Left Grip.Right
## 1           23.0    58   54 49   45 37 -11.2927    0.0322     0.0241
## 2           23.5    82   62 53   49 46 -17.8537    0.0270     0.0414
## 3           23.0    84   75 64   45 30 -30.6829    0.0146     0.0176
## 4           23.0    60   54 49   46 36 -12.3171    0.0146     0.0280
## 5           24.5    60   52 51   46 49  -5.8049    0.0186     0.0210
## 6           24.0    54   49 46   42 32 -11.2927    0.0315     0.0228
##      Handedness
## 1   Left-handed
```

```
## 2  Right-handed
## 3  Right-handed
## 4 Right-handed
## 5  Right-handed
## 6  Right-handed
```

1.b. ANOVA

```
#  Assumption: homogeneity of variances
leveneTest(Velocity ~ Load, data = msc.cont)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   4  0.2202  0.927
##       195
```

```
## Accept null hypothesis (p > 0.05)
## Not enough evidence suggests that differences in variances between groups
### are statistically significant

## Assume homoscedasticity


# Assumption: normality
shapiro.test(msc.cont$Velocity[msc.cont$Load == "0.25"])  #  (p < 0.05)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  msc.cont$Velocity[msc.cont$Load == "0.25"]
## W = 0.943, p-value = 0.04369
```

```
shapiro.test(msc.cont$Velocity[msc.cont$Load == "0.5"])   #  (p > 0.05)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  msc.cont$Velocity[msc.cont$Load == "0.5"]
## W = 0.95797, p-value = 0.1427
```

```
shapiro.test(msc.cont$Velocity[msc.cont$Load == "1"])     #  (p > 0.05)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  msc.cont$Velocity[msc.cont$Load == "1"]
## W = 0.96464, p-value = 0.2406
```

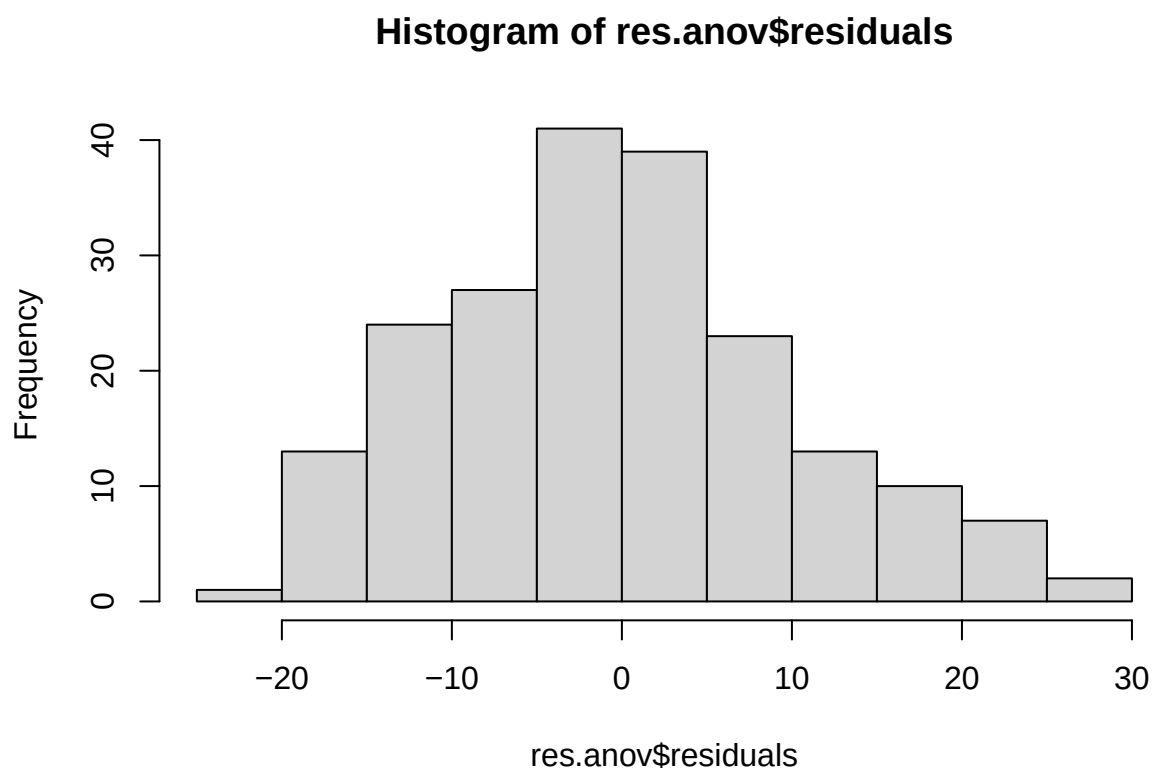
```r
shapiro.test(msc.cont$Velocity[msc.cont$Load == "1.5"])    #  (p > 0.05)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  msc.cont$Velocity[msc.cont$Load == "1.5"]
## W = 0.97269, p-value = 0.436
```

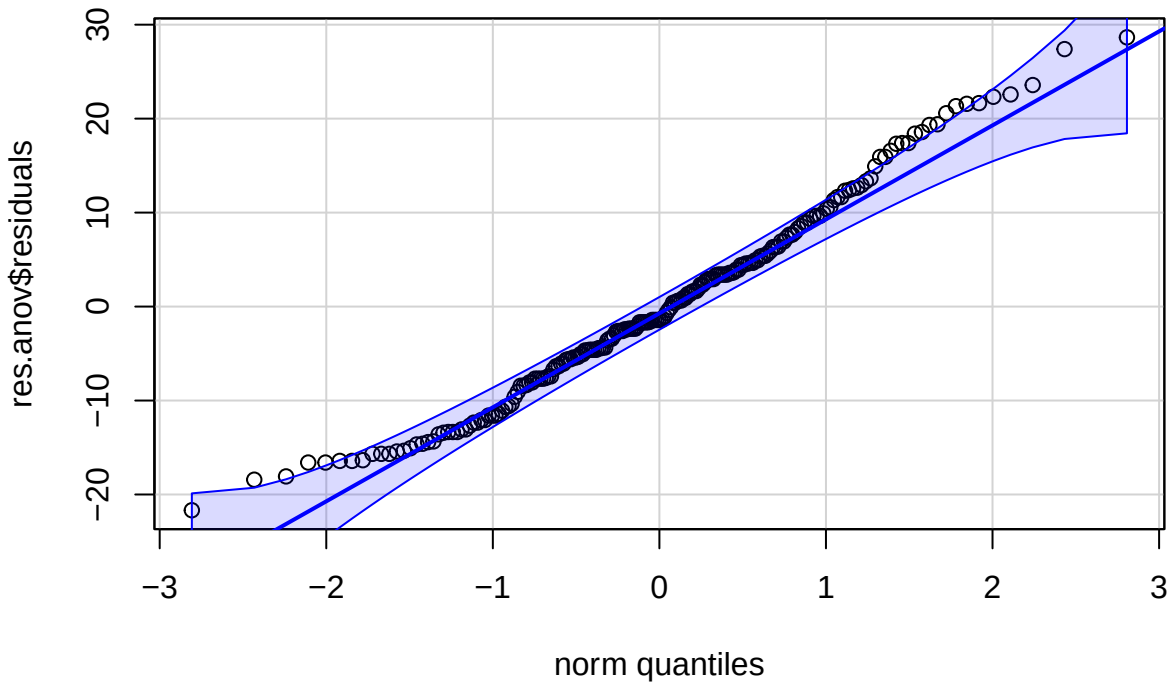
```r
shapiro.test(msc.cont$Velocity[msc.cont$Load == "2"])     #  (p > 0.05)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  msc.cont$Velocity[msc.cont$Load == "2"]
## W = 0.98043, p-value = 0.7053
```

```r
res.anov <- aov(Velocity ~ Load, msc.cont)

## histogram
hist(res.anov$residuals)
```




```r
## qqplot
qqPlot(res.anov$residuals,
  id = FALSE # id = FALSE to remove point identification
)
```



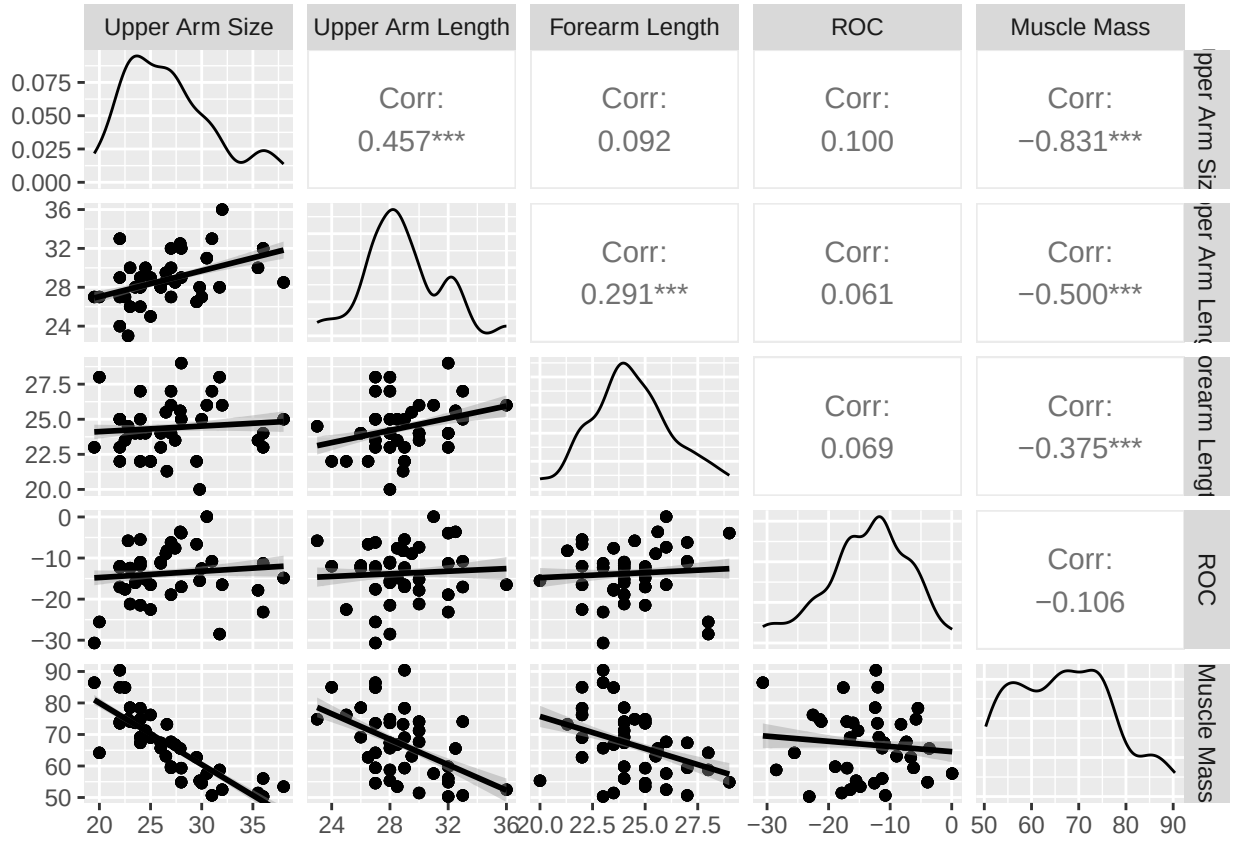

```
## histogram shows roughly a bell curve, and points in the QQ plot nearly adhere to
### a straight line and are well within the confidence bands

## We can assume normality


#  ANOVA
anov <- aov(Velocity ~ Load, msc.cont)
summary(anov)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## Load          4  15619    3905   35.78 <2e-16 ***
## Residuals   195  21282     109
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2. ARM PARAMETERS AND VELOCITY CONTROLLING FOR MUSCLE MASS

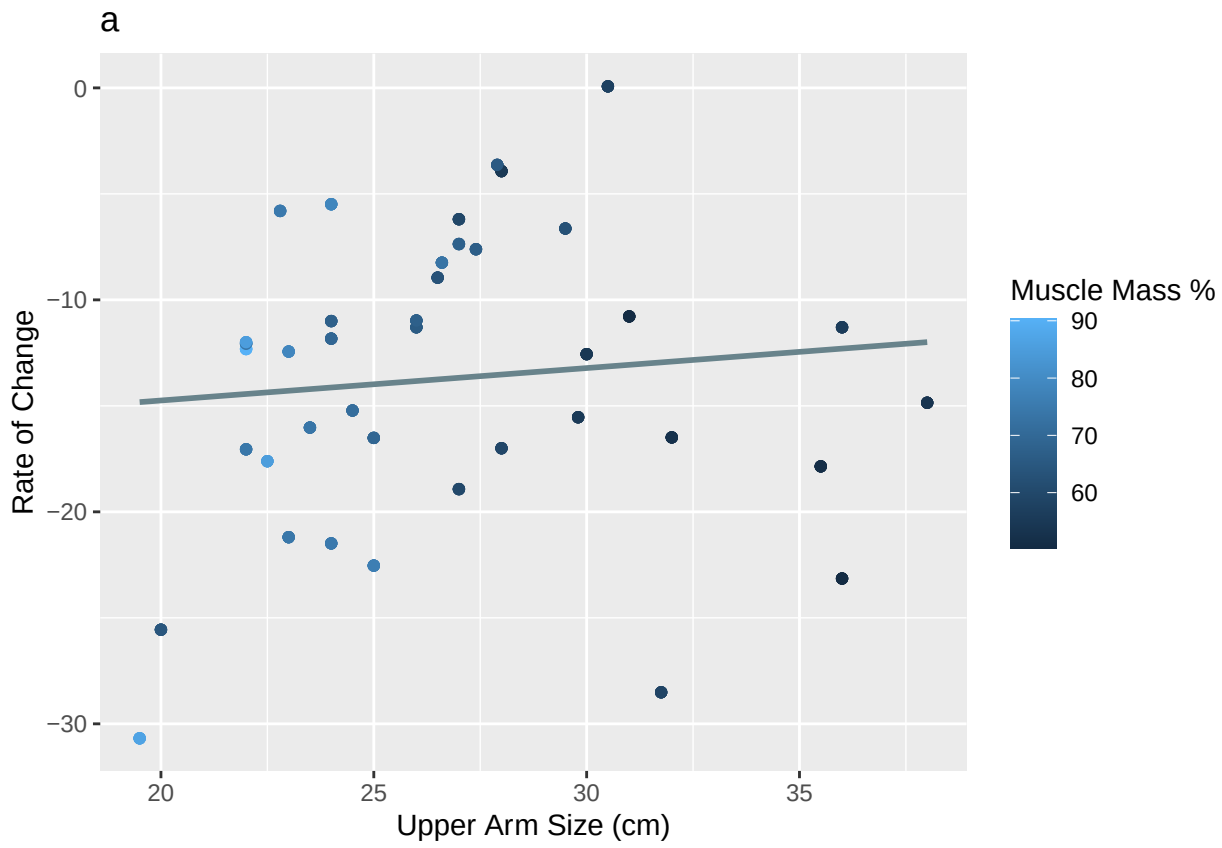
```
#  isolates columns
y <- msc.cont %>%
  select(Upper.Arm.Size, Upper.Arm.Length, Forearm.Length, ROC, Muscle.Mass)
```

```
ggsave("C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/1st Semester/BIO 118/Module 1/Module 1 -
       width = 8, height = 6)

#  visualization of correlation test (pearson)
ggpairs(y,
        lower = list(continuous = "smooth"),
        columnLabels = c("Upper Arm Size", "Upper Arm Length", "Forearm Length",
                         "ROC", "Muscle Mass"))
```



Upper Arm Size vs. Muscle Mass

```
#  Upper Arm Size vs. Muscle Mass scatter plot
plot.uas <- ggplot(msc.cont, aes(Upper.Arm.Size, ROC, color = Muscle.Mass)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, color = "lightblue4") +
  xlab("Upper Arm Size (cm)") + ylab("Rate of Change") +
  ggtitle("a")

plot.uas$labels$colour <- "Muscle Mass %"
plot.uas
```



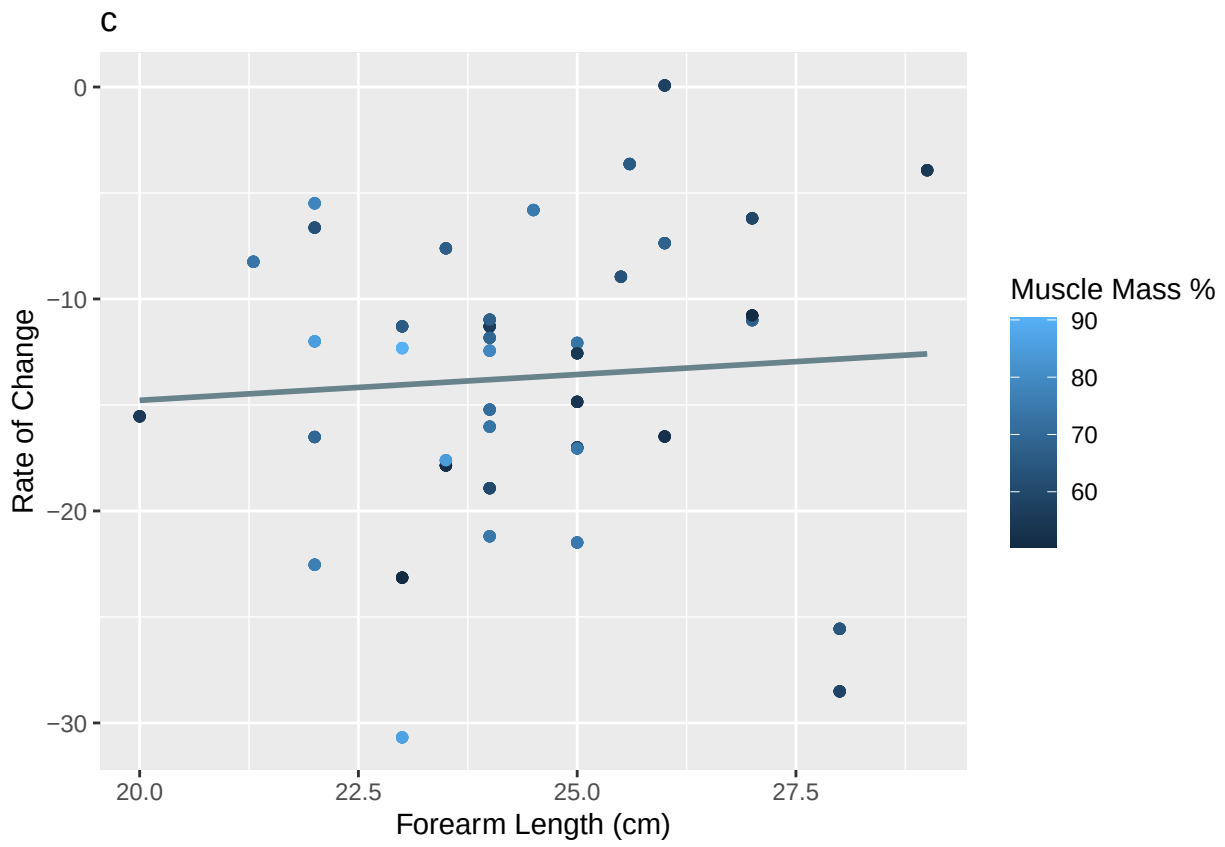

```
ggsave("C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/1st Semester/BIO 118/Module 1/Module 1 -
       width = 8, height = 5)



## linear regression

#  Upper Arm Size vs. ROC linear regression
lm.uas <- lm(ROC ~ Upper.Arm.Size + Muscle.Mass, msc.cont)
summary(lm.uas)
```

```
##
## Call:
## lm(formula = ROC ~ Upper.Arm.Size + Muscle.Mass, data = msc.cont)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -15.602  -3.727   1.633   4.899  13.126
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -12.18940   10.24041  -1.190    0.235
## Upper.Arm.Size   0.06073    0.19388   0.313    0.754
## Muscle.Mass     -0.04714    0.08239  -0.572    0.568
##
```

```
## Residual standard error: 6.8 on 197 degrees of freedom
## Multiple R-squared:  0.01172,    Adjusted R-squared:  0.001691
## F-statistic: 1.169 on 2 and 197 DF,  p-value: 0.313
```

Forearm Length vs. Muscle Mass

```
#  Forearm Length vs. Muscle Mass scatter plot
plot.fore <- ggplot(msc.cont, aes(Forearm.Length, ROC, color = Muscle.Mass)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, color = "lightblue4") +
  xlab("Forearm Length (cm)") + ylab("Rate of Change") +
  ggtitle("c")

ggsave("C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/1st Semester/BIO 118/Module 1/Module 1 -
       width = 8,
       height = 5)

plot.fore$labels$colour <- "Muscle Mass %"
plot.fore
```



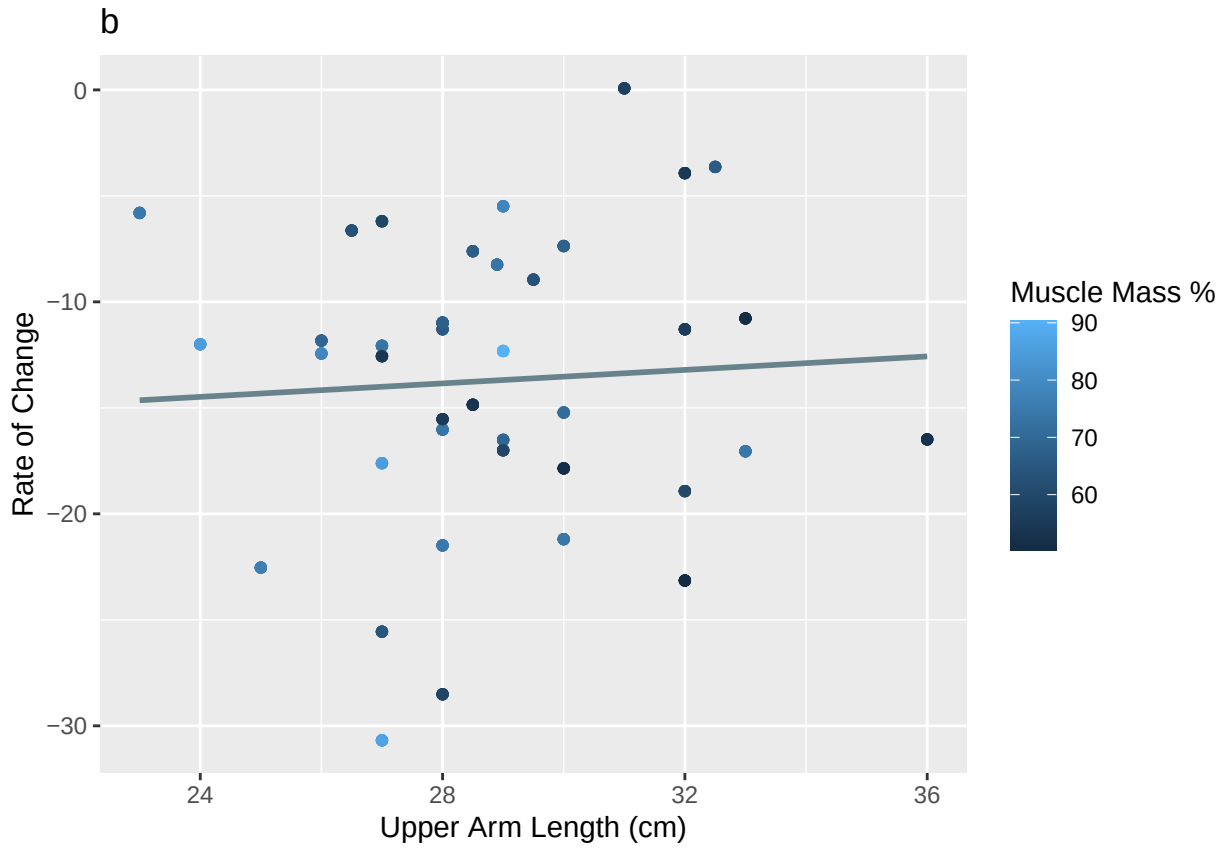

```
## linear regression

#  Forerm Size vs. ROC linear regression
```

```r
lm.fore <- lm(ROC ~ Forearm.Length + Muscle.Mass, msc.cont)
summary(lm.fore)
```

```
##
## Call:
## lm(formula = ROC ~ Forearm.Length + Muscle.Mass, data = msc.cont)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -15.720  -3.816   1.732   4.855  13.038
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -12.63267    8.38127  -1.507    0.133
## Forearm.Length   0.12072    0.26854   0.450    0.654
## Muscle.Mass     -0.06025    0.04944  -1.219    0.224
##
## Residual standard error: 6.798 on 197 degrees of freedom
## Multiple R-squared:  0.01225,    Adjusted R-squared:  0.002218
## F-statistic: 1.221 on 2 and 197 DF,  p-value: 0.2971
```

Upper Arm Length vs. Muscle Mass

```r
#  Upper Arm Length vs. Muscle Mass scatter plot
plot.ual <- ggplot(msc.cont, aes(Upper.Arm.Length, ROC, color = Muscle.Mass)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, color = "lightblue4") +
  xlab("Upper Arm Length (cm)") + ylab("Rate of Change") +
  ggtitle("b")

ggsave("C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/1st Semester/BIO 118/Module 1/Module 1 -
       width = 8, height = 5)

plot.ual$labels$colour <- "Muscle Mass %"
plot.ual
```




```
## linear regression

#  Upper Arm Size vs. ROC linear regression
lm.ual <- lm(ROC ~ Upper.Arm.Length + Muscle.Mass, msc.cont)
summary(lm.ual)
```

```
##
## Call:
## lm(formula = ROC ~ Upper.Arm.Length + Muscle.Mass, data = msc.cont)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -15.638  -3.809   1.700   4.850  13.128
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -10.13808    8.52620  -1.189    0.236
## Upper.Arm.Length   0.02712    0.21410   0.127    0.899
## Muscle.Mass       -0.06523    0.05295  -1.232    0.219
##
## Residual standard error: 6.801 on 197 degrees of freedom
## Multiple R-squared:  0.01131,    Adjusted R-squared:  0.001275
## F-statistic: 1.127 on 2 and 197 DF,  p-value: 0.3261
```

```
#  generates scatter plot grid
grid <- plot_grid(plot.uas, plot.fore, plot.ual)

ggsave("C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/1st Semester/BIO 118/Module 1/Module 1 -
       width = 8, height = 5)

print(grid)
```