

Exercise 8A: Changes in the Thoracic Activity

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```
library(tidyverse)
library(car)
library(ggpubr)
```

1.DATA

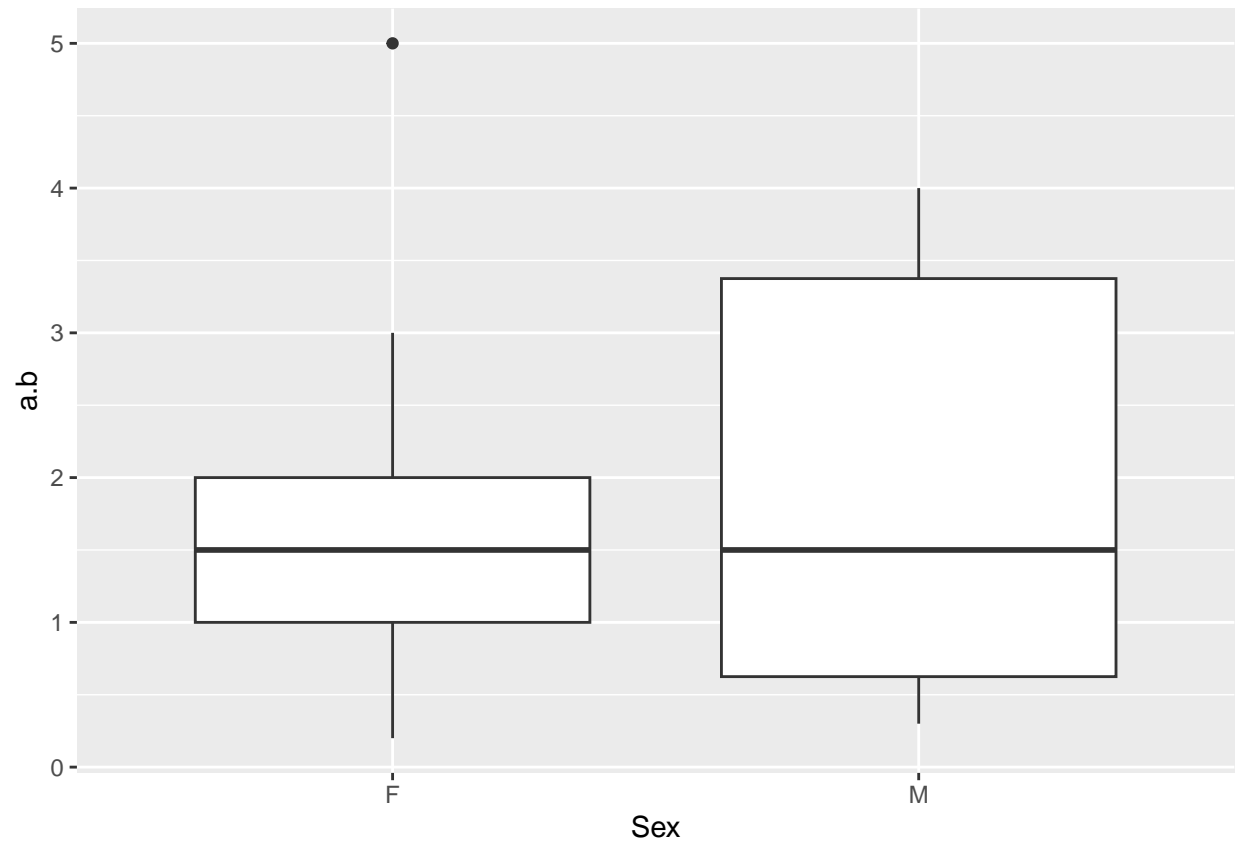
```
# imports data into R
ex08a <- read.csv("C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/1st Semester/BIO 118/Module 1/
head(ex08a, head = 5)
```

```
##           DataSource Age Sex a.TI b.TE c.FI.TE d.FE.TI e.FI.FE
## 1           Bio 122 A1  NA      NA      NA      NA      NA
## 2      Perez, Maria Cristina A.  21  F    80 78.5    82.0    78.0    82.0
## 3          Tadle, Antonette    20  F    93 90.0    93.5    92.5    94.0
## 4 Genson, Julia Raphaella Genson  21  F    76 74.5    78.5    70.9    77.5
## 5      Mejias, Mafe Nenia A.    21  F    99 97.0   102.5    94.5   102.0
## 6      Cena, Hannah Trisha A.    21  F    79 77.0    80.0    76.5    81.0
##   f.FE.FI a.b c.d e.d c.f
## 1      NA  NA  NA  NA  NA
## 2    77.0 1.5 4.0 4.0 5.0
## 3    91.0 3.0 1.0 1.5 2.5
## 4    71.5 1.5 7.6 6.0 7.0
## 5   100.0 2.0 8.0 2.0 2.5
## 6    77.5 2.0 3.5 4.5 2.5
```

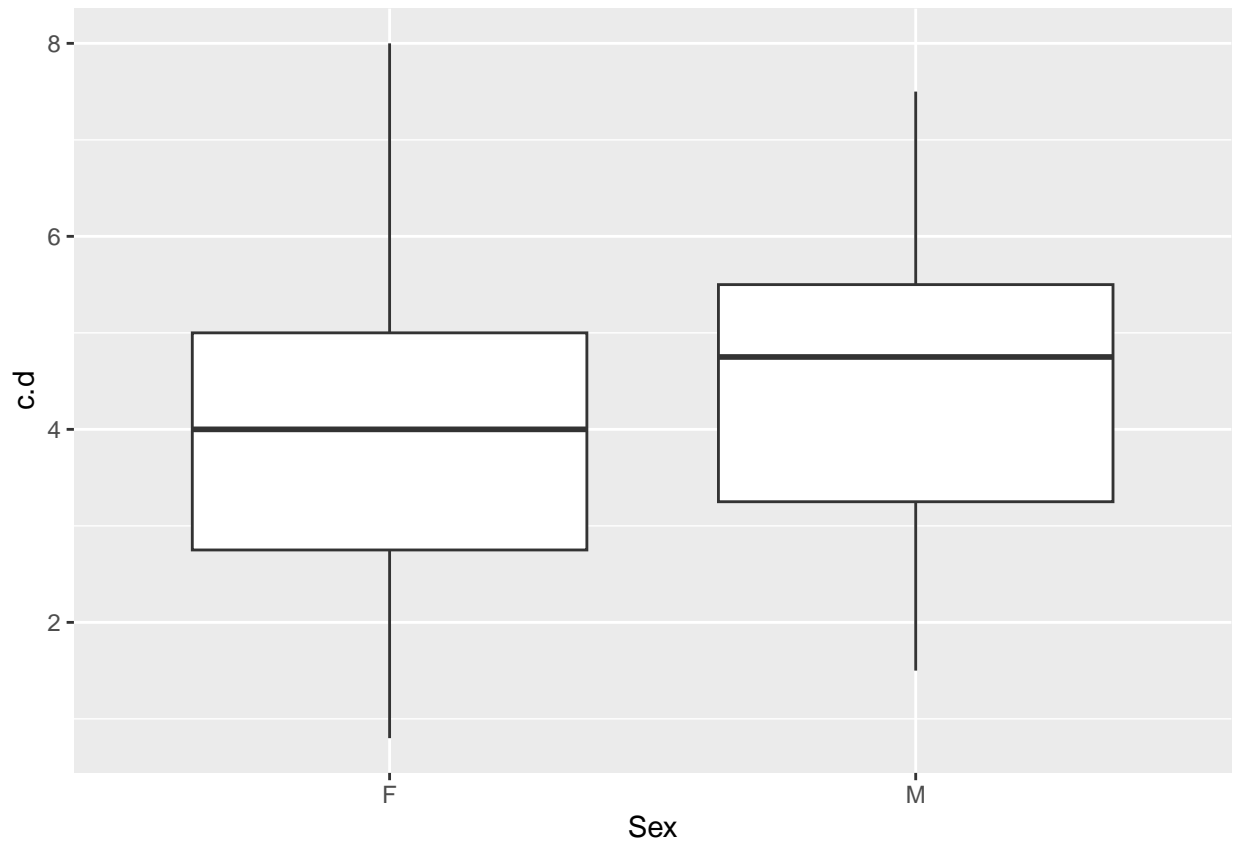
```
# cleans data
cav <- ex08a %>%
  select(!DataSource) %>%
  drop_na()
```

1a. Exploring Data

```
## INFLUENCE OF SEX ON CHEST EXPANSION
# generates box plot male vs. female tidal insp. and exp.
sex.t <- ggplot(cav, aes(Sex, a.b)) + geom_boxplot()
sex.t
```



```
# generates box plot male vs. female forceful insp. and exp.  
sex.f <- ggplot(cav, aes(Sex, c.d)) + geom_boxplot()  
sex.f
```

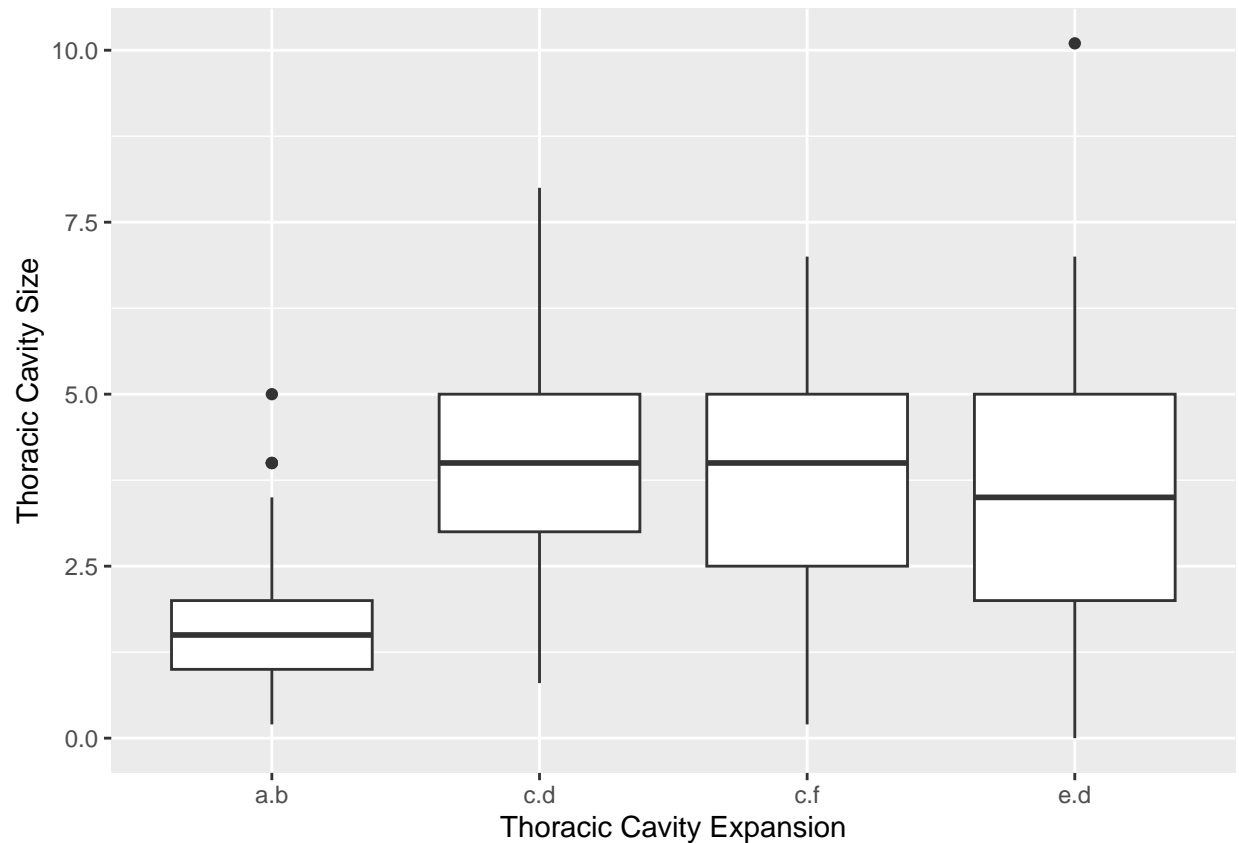


DIFFERENCES IN CAVITY CHANGES

```
# rearranges data
thor <- cav %>%
  select(a.b, c.d, e.d, c.f) %>%
  gather(Breathe, Cav.Size, a.b, c.d, e.d, c.f)
head(thor, n = 5)
```

```
##   Breathe Cav.Size
## 1    a.b      1.5
## 2    a.b      3.0
## 3    a.b      1.5
## 4    a.b      2.0
## 5    a.b      2.0
```

```
# generates plot
thor.plot <- ggplot(thor, aes(Breathe, Cav.Size)) + geom_boxplot() +
  ylab("Thoracic Cavity Size") + xlab("Thoracic Cavity Expansion")
thor.plot
```



```
thor.line <- ggline(thor, x = "Breathe", y = "Cav.Size",
  add = c("mean_se", "jitter"),
  order = c("a.b", "c.d", "e.d", "c.f"),
  ylab = "Change in Cavity Size", xlab = "Breathing")
```

```
## BETWEEN c.f and e.d
force <- cav %>%
  select(c.f, e.d) %>%
  gather(Breathe, Cav.Size, c.f, e.d) %>%
  drop_na()
head(force, head = 5)
```

```
##   Breathe Cav.Size
## 1    c.f      5.0
## 2    c.f      2.5
## 3    c.f      7.0
## 4    c.f      2.5
## 5    c.f      2.5
## 6    c.f      2.5
```

```
## BETWEEN c.d and e.d
force.b <- cav %>%
  select(c.d, e.d) %>%
```

```
gather(Breathe, Cav.Size, c.d, e.d) %>%
drop_na()
head(force.b, head = 5)
```

```
##   Breathe Cav.Size
## 1      c.d      4.0
## 2      c.d      1.0
## 3      c.d      7.6
## 4      c.d      8.0
## 5      c.d      3.5
## 6      c.d      2.0
```

```
## BETWEEN c.d and c.f
force.c <- cav %>%
  select(c.d, c.f) %>%
  gather(Breathe, Cav.Size, c.d, c.f) %>%
  drop_na()
head(force.c, head = 5)
```

```
##   Breathe Cav.Size
## 1      c.d      4.0
## 2      c.d      1.0
## 3      c.d      7.6
## 4      c.d      8.0
## 5      c.d      3.5
## 6      c.d      2.0
```

```
## BETWEEN a.b and c.d
force.d <- cav %>%
  select(a.b, c.d) %>%
  gather(Breathe, Cav.Size, a.b, c.d) %>%
  drop_na()
head(force.d, head = 5)
```

```
##   Breathe Cav.Size
## 1      a.b      1.5
## 2      a.b      3.0
## 3      a.b      1.5
## 4      a.b      2.0
## 5      a.b      2.0
## 6      a.b      0.5
```

```
## BETWEEN a.b and c.f
force.e <- cav %>%
  select(a.b, c.f) %>%
  gather(Breathe, Cav.Size, a.b, c.f) %>%
  drop_na()
head(force.e, head = 5)
```

```
##   Breathe Cav.Size
## 1      a.b      1.5
```

```
## 2      a.b      3.0
## 3      a.b      1.5
## 4      a.b      2.0
## 5      a.b      2.0
## 6      a.b      0.5
```

```
## BETWEEN a.b and e.d
force.f <- cav %>%
  select(a.b, e.d) %>%
  gather(Breathe, Cav.Size, a.b, e.d) %>%
  drop_na()
head(force.f, head = 5)
```

```
##      Breathe Cav.Size
## 1      a.b      1.5
## 2      a.b      3.0
## 3      a.b      1.5
## 4      a.b      2.0
## 5      a.b      2.0
## 6      a.b      0.5
```

2. T-TEST (Sex influence on chest expansion)

2a. Test for normality of distribution

```
## Shapiro-Wilk normality Test
# Tidal Inspiration and Tidal Expiration
shapiro.test(cav$a.b[cav$Sex == "F"]) # p = 0.0001968; not normal
```

```
##
## Shapiro-Wilk normality test
##
## data:  cav$a.b[cav$Sex == "F"]
## W = 0.84695, p-value = 0.0001968
```

```
shapiro.test(cav$a.b[cav$Sex == "M"]) # p = 0.01; not normal
```

```
##
## Shapiro-Wilk normality test
##
## data:  cav$a.b[cav$Sex == "M"]
## W = 0.84457, p-value = 0.01876
```

```
# Forceful Inspiration and Forceful Expiration
shapiro.test(cav$c.d[cav$Sex == "F"]) # p = 0.4; normal
```

```
##
## Shapiro-Wilk normality test
##
## data:  cav$c.d[cav$Sex == "F"]
## W = 0.97085, p-value = 0.467
```

```
shapiro.test(cav$c.d[cav$Sex == "M"]) # p = 0.6; normal
```

```
##  
## Shapiro-Wilk normality test  
##  
## data:  cav$c.d[cav$Sex == "M"]  
## W = 0.95564, p-value = 0.6511
```

2b. Test for homogeneity in variances

```
## homoscedasticity  
# a.b  
leveneTest(a.b ~ Sex, cav) # p < 0.05; heteroscedastic
```

```
## Levene's Test for Homogeneity of Variance (center = median)  
##      Df F value Pr(>F)  
## group 1  7.3941 0.00914 **  
##      47  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# c.d  
leveneTest(c.d ~ Sex, cav) # p > 0.05; assume equality of variance
```

```
## Levene's Test for Homogeneity of Variance (center = median)  
##      Df F value Pr(>F)  
## group 1  0.0401 0.8422  
##      47
```

2c. Non-parametric and parametric T-test

```
## Unpaired Two-samples Wilcoxon Test  
# a.b  
sx.tt <- t.test(cav$a.b ~ Sex, data = cav,  
                alternative = "two.sided", paired = FALSE, var.equal = FALSE)  
sx.tt # p > 0.05; accept Ho
```

```
##  
## Welch Two Sample t-test  
##  
## data:  cav$a.b by Sex  
## t = -1.0135, df = 17.342, p-value = 0.3248  
## alternative hypothesis: true difference in means between group F and group M is not equal to 0  
## 95 percent confidence interval:  
## -1.3150394  0.4607537  
## sample estimates:  
## mean in group F mean in group M  
##      1.522857      1.950000
```

```

sx.wxt <- wilcox.test(cav$a.b ~ Sex, data = cav,
                      exact = FALSE)
sx.wxt    # p > 0.05; accept Ho

```

```

##
## Wilcoxon rank sum test with continuity correction
##
## data:  cav$a.b by Sex
## W = 224, p-value = 0.6426
## alternative hypothesis: true location shift is not equal to 0

```

```

# c.d
sx.tf <- t.test(cav$c.d ~ Sex, data = cav,
                alternative = "two.sided", paired = FALSE, var.equal = TRUE)
sx.tf # p > 0.05; accept Ho

```

```

##
## Two Sample t-test
##
## data:  cav$c.d by Sex
## t = -1.0768, df = 47, p-value = 0.2871
## alternative hypothesis: true difference in means between group F and group M is not equal to 0
## 95 percent confidence interval:
##  -1.7537284  0.5308713
## sample estimates:
## mean in group F mean in group M
##      3.888571      4.500000

```

```

sx.wxf <- wilcox.test(cav$c.d ~ Sex, data = cav,
                      exact = FALSE)
sx.wxf    # p > 0.05; accept Ho

```

```

##
## Wilcoxon rank sum test with continuity correction
##
## data:  cav$c.d by Sex
## W = 193, p-value = 0.2519
## alternative hypothesis: true location shift is not equal to 0

```

3. ANOVA (Cavity Size)

3a. Test for normality of distribution

```

## Shapiro-Wilk normality Test
shapiro.test(thor$Cav.Size[thor$Breathe == "a.b"])$p.value # p = 0.00013; not normal

```

```

## [1] 0.0001279188

```



```
shapiro.test(thor$Cav.Size[thor$Breathe == "c.d"])$p.value #  $p = 0.40$ ; normal
```

```
## [1] 0.3991751
```

```
shapiro.test(thor$Cav.Size[thor$Breathe == "c.f"])$p.value #  $p = 0.167$ ; normal
```

```
## [1] 0.1671073
```

```
shapiro.test(thor$Cav.Size[thor$Breathe == "e.d"])$p.value #  $p = 0.072$ ; normal
```

```
## [1] 0.07190357
```

3b. Test for homogeneity in variances

```
## homoscedasticity
```

```
leveneTest(Cav.Size ~ Breathe, thor) #  $p < 0.05$ ; assume hetero
```

```
## Levene's Test for Homogeneity of Variance (center = median)
```

```
##      Df F value Pr(>F)
```

```
## group 3  3.8603 0.01033 *
```

```
##      192
```

```
## ---
```

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

3c. ANOVA and T-test

```
# ANOVA
```

```
anov <- aov(Cav.Size ~ Breathe, thor) ##  $p = 3.22e-12$ 
```

```
summary(anov) #  $p < 0.05$ ; reject  $H_0$ 
```

```
##      Df Sum Sq Mean Sq F value    Pr(>F)
```

```
## Breathe      3  186.9    62.30    21.85 3.22e-12 ***
```

```
## Residuals   192  547.4     2.85
```

```
## ---
```

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

```
# Kruskal-Wallis test
```

```
kw <- kruskal.test(Cav.Size ~ Breathe, thor) ##  $p = 3.842e-12$ 
```

```
kw #  $p > 0.05$ ; accept  $H_0$ 
```

```
##
```

```
## Kruskal-Wallis rank sum test
```

```
##
```

```
## data: Cav.Size by Breathe
```

```
## Kruskal-Wallis chi-squared = 56.182, df = 3, p-value = 3.842e-12
```

```
# t-test between c.f and e.d
force.2 <- t.test(Cav.Size ~ Breathe, data = force,
                  alternative = "two.sided", paired = FALSE, var.equal = FALSE)
force.2$p.value # p > 0.05; accept Ho
```

```
## [1] 0.6305018
```

```
# t-test between c.d and e.d
force.3 <- t.test(Cav.Size ~ Breathe, data = force.b,
                  alternative = "two.sided", paired = FALSE, var.equal = FALSE)
force.3$p.value # p > 0.05; accept Ho
```

```
## [1] 0.3359047
```

```
# t-test between c.d and c.f
force.4 <- t.test(Cav.Size ~ Breathe, data = force.c,
                  alternative = "two.sided", paired = FALSE, var.equal = FALSE)
force.4$p.value # p > 0.05; accept Ho
```

```
## [1] 0.6130356
```

```
# t-test between a.b and c.d
force.5 <- t.test(Cav.Size ~ Breathe, data = force.d,
                  alternative = "two.sided", paired = FALSE, var.equal = FALSE)
force.5$p.value # p < 0.05; reject Ho
```

```
## [1] 7.699216e-12
```

```
# t-test between a.b and c.f
force.6 <- t.test(Cav.Size ~ Breathe, data = force.e,
                  alternative = "two.sided", paired = FALSE, var.equal = FALSE)
force.6$p.value # p < 0.05; reject Ho
```

```
## [1] 9.630893e-11
```

```
# t-test between a.b and e.d
force.7 <- t.test(Cav.Size ~ Breathe, data = force.f,
                  alternative = "two.sided", paired = FALSE, var.equal = FALSE)
force.7$p.value # p < 0.05; reject Ho
```

```
## [1] 9.710989e-09
```