Laboratory Exercise 2

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```
library(tidyverse)
library(ggpubr)
library(reshape2)
library(car)
library(rstatix)
library(cowplot)
```

VISION

```
# imports data
vis <- read.csv("C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/1st Semester/BIO 118/Module 1/M</pre>
# organizes data
vis.eye <- vis %>%
  filter(!row_number() %in% c(1, 2, 39)) %>%
  mutate(VisualAcuity = map_dbl(X.4, ~eval(parse(text = .x)))) %>%
  select(X, X.1, VisualAcuity)
# renames columns
colnames(vis.eye) <- c("Names", "Sex", "VisualAcuity")</pre>
# renames rows
vis.eye$Sex[vis.eye$Sex == "F"] <- "Female"</pre>
vis.eye$Sex[vis.eye$Sex == "M"] <- "Male"</pre>
# prints summary of data
group_by(vis.eye, Sex) %>%
  summarise(
   count = n(),
   mean = mean(VisualAcuity, na.rm = TRUE),
    sd = sd(VisualAcuity, na.rm = TRUE)
 )
## # A tibble: 2 x 4
##
   Sex count mean
## <chr> <int> <dbl> <dbl>
## 1 Female 35 0.654 0.489
## 2 Male 17 1.01 0.661
```

Plots

```
# generates box plot
visplot <- ggplot(vis.eye, aes(x = Sex, y = VisualAcuity)) +
   geom_boxplot() +
   ylab("Visual Acuity")

# saves .png of plot
ggsave("C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/1st Semester/BIO 118/Module 1/Module 1 -</pre>
```

T-test

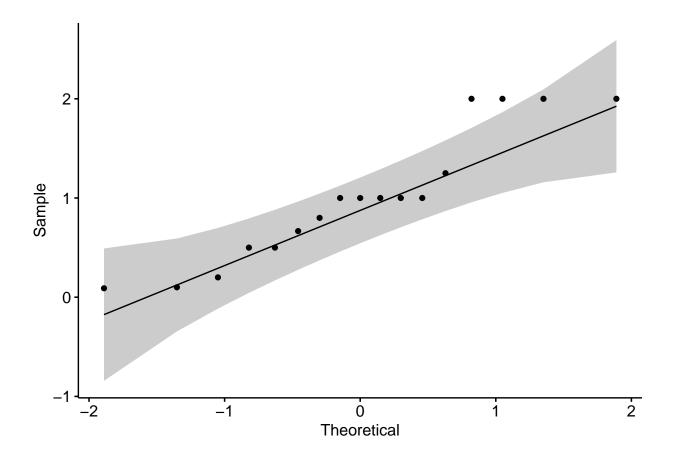
```
# Shapiro-Wilk normality test
shapiro.test(vis.eye$VisualAcuity[vis.eye$Sex == "Female"]) # p < 0.05

##
## Shapiro-Wilk normality test
##
## data: vis.eye$VisualAcuity[vis.eye$Sex == "Female"]
## W = 0.90125, p-value = 0.004274

shapiro.test(vis.eye$VisualAcuity[vis.eye$Sex == "Male"]) # p < 0.05

##
## Shapiro-Wilk normality test
##
## data: vis.eye$VisualAcuity[vis.eye$Sex == "Male"]
## W = 0.88785, p-value = 0.04271

## QQ
ggqqplot(vis.eye$VisualAcuity[vis.eye$Sex == "Male"])</pre>
```



ggqqplot(vis.eye\$VisualAcuity[vis.eye\$Sex == "Female"])

```
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```

alternative hypothesis: true difference in means between group Female and group Male is not equal to

##

##

Two Sample t-test

-0.6788540 -0.0255318 ## sample estimates:

data: VisualAcuity by Sex

95 percent confidence interval:

t = -2.1655, df = 50, p-value = 0.03514

```
## mean in group Female mean in group Male ## 0.6540816 1.0062745 # p < 0.05 # Reject Ho; there is a significant difference between male and female vision acuity
```

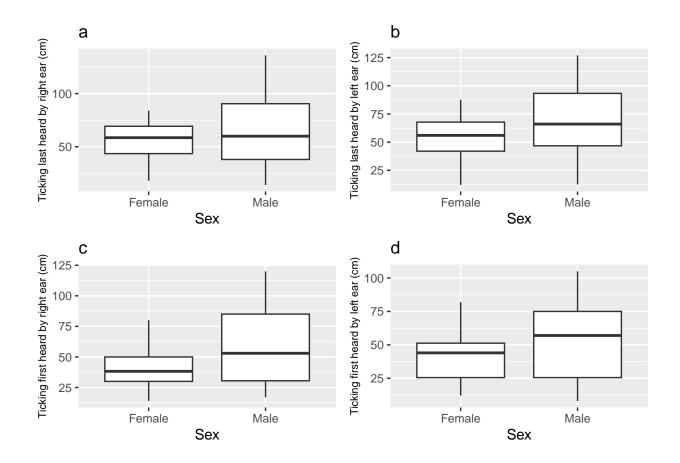
AUDITORY

T-test

Plots

```
# box plot for right ear away
r.away <- ggplot(ear.lr, aes(x = Sex, y = Away.Right)) +</pre>
```

```
geom_boxplot() +
  ggtitle("a") +
  ylab("Ticking last heard by right ear (cm)") +
  theme(axis.title.y = element_text(size = 8))
# box plot for left ear away
1.away \leftarrow ggplot(ear.lr, aes(x = Sex, y = Away.Left)) +
  geom_boxplot() +
  ggtitle("b") +
  ylab("Ticking last heard by left ear (cm)") +
  theme(axis.title.y = element_text(size = 8))
# box plot for right ear towards
r.towards \leftarrow ggplot(ear.lr, aes(x = Sex, y = Towards.Right)) +
  geom_boxplot() +
  ggtitle("c") +
  ylab("Ticking first heard by right ear (cm)") +
  theme(axis.title.y = element_text(size = 8))
# box plot for left ear towards
1.towards <- ggplot(ear.lr, aes(x = Sex, y = Towards.Left)) +
  geom_boxplot() +
  ggtitle("d") +
  ylab("Ticking first heard by left ear (cm)") +
  theme(axis.title.y = element_text(size = 8))
# arranges plots into grid
hearing <- plot_grid(r.away, l.away, r.towards, l.towards)</pre>
hearing
```

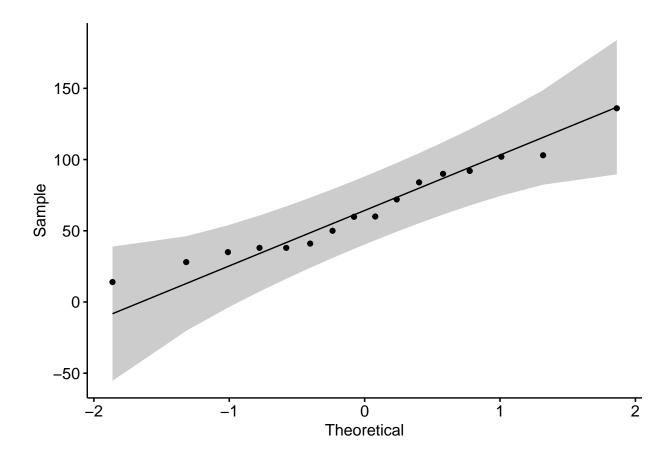


```
# saves .png of plots
ggsave("C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/1st Semester/BIO 118/Module 1/Module 1 -
## Shapiro-Wilk normality test
# Away.Right
shapiro.test(ear.lr$Away.Right[ear.lr$Sex == "Female"]) # p < 0.05; not normal</pre>
##
    Shapiro-Wilk normality test
##
##
## data: ear.lr$Away.Right[ear.lr$Sex == "Female"]
## W = 0.92737, p-value = 0.02624
shapiro.test(ear.lr$Away.Right[ear.lr$Sex == "Male"]) # p > 0.05; normal
##
##
    Shapiro-Wilk normality test
##
## data: ear.lr$Away.Right[ear.lr$Sex == "Male"]
## W = 0.95831, p-value = 0.6312
# Away.Left
```

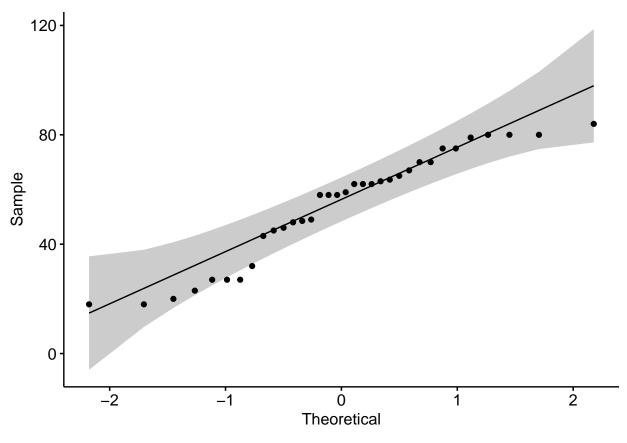
shapiro.test(ear.lr\$Away.Left[ear.lr\$Sex == "Female"]) # p > 0.05; normal

```
##
## Shapiro-Wilk normality test
##
## data: ear.lr$Away.Left[ear.lr$Sex == "Female"]
## W = 0.97406, p-value = 0.5818
shapiro.test(ear.lr$Away.Left[ear.lr$Sex == "Male"]) # p > 0.05; normal
##
          Shapiro-Wilk normality test
##
##
## data: ear.lr$Away.Left[ear.lr$Sex == "Male"]
## W = 0.97013, p-value = 0.8406
# Towards.Right
shapiro.test(ear.lr$Towards.Right[ear.lr$Sex == "Female"]) # p > 0.05; normal
##
##
          Shapiro-Wilk normality test
## data: ear.lr$Towards.Right[ear.lr$Sex == "Female"]
## W = 0.9752, p-value = 0.618
shapiro.test(ear.lr$Towards.Right[ear.lr$Sex == "Male"]) # p > 0.05; normal
##
##
          Shapiro-Wilk normality test
## data: ear.lr$Towards.Right[ear.lr$Sex == "Male"]
## W = 0.93697, p-value = 0.3135
# Towards.Left
shapiro.test(ear.lr\$Towards.Left[ear.lr\$Sex == "Female"]) \ \# \ p > 0.05; \ normal \ normal
##
        Shapiro-Wilk normality test
##
## data: ear.lr$Towards.Left[ear.lr$Sex == "Female"]
## W = 0.97039, p-value = 0.4723
shapiro.test(ear.lr$Towards.Left[ear.lr$Sex == "Male"]) # p > 0.05; normal
##
        Shapiro-Wilk normality test
## data: ear.lr$Towards.Left[ear.lr$Sex == "Male"]
## W = 0.93461, p-value = 0.2881
```

```
## QQ
ggqqplot(ear.lr$Away.Right[ear.lr$Sex == "Male"])
```



ggqqplot(ear.lr\$Away.Right[ear.lr\$Sex == "Female"])



```
# homoscedasticity
## Away.Right
leveneTest(Away.Right ~ Sex, ear.lr)
## Levene's Test for Homogeneity of Variance (center = median)
        Df F value Pr(>F)
## group 1 5.9973 0.01803 *
##
        48
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
# p < 0.05
# reject null hypo that variances between two groups are not significantly different
# assume hetero
## Away.Left
leveneTest(Away.Left ~ Sex, ear.lr)
## Levene's Test for Homogeneity of Variance (center = median)
        Df F value Pr(>F)
## group 1 5.8569 0.01935 *
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
```

```
# reject null hypo that variances between two groups are not significantly different
# assume hetero
## Towards.Right
leveneTest(Towards.Right ~ Sex, ear.lr)
## Levene's Test for Homogeneity of Variance (center = median)
        Df F value
                      Pr(>F)
## group 1 16.173 0.0002036 ***
##
        48
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# p < 0.05
# reject null hypo that variances between two groups are not significantly different
# assume hetero
## Towards.Left
leveneTest(Towards.Left ~ Sex, ear.lr)
## Levene's Test for Homogeneity of Variance (center = median)
       Df F value
                    Pr(>F)
## group 1 8.2653 0.006007 **
##
        48
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
# p < 0.05
# reject null hypo that variances between two groups are not significantly different
# assume hetero
## Welch's T-test for non-equal variance
#Away.Right
t.test(Away.Right ~ Sex, data = ear.lr, alternative = "two.sided", var.equal = FALSE)
##
## Welch Two Sample t-test
##
## data: Away.Right by Sex
## t = -1.2147, df = 20.292, p-value = 0.2384
## alternative hypothesis: true difference in means between group Female and group Male is not equal to
## 95 percent confidence interval:
## -29.861302 7.870126
## sample estimates:
## mean in group Female mean in group Male
              54.17941
                                   65.17500
##
\# p > 0.05
```

Accept; there is no sign diff bet male and female aud. acuity for right away

```
#Away.Left
t.test(Away.Left ~ Sex, data = ear.lr, alternative = "two.sided", var.equal = FALSE)
##
##
  Welch Two Sample t-test
##
## data: Away.Left by Sex
## t = -1.8768, df = 20.395, p-value = 0.07492
## alternative hypothesis: true difference in means between group Female and group Male is not equal to
## 95 percent confidence interval:
## -35.227865
                1.837424
## sample estimates:
## mean in group Female
                        mean in group Male
##
              53.77353
                                    70.46875
\# p > 0.05
# Accept; there is no sign diff bet male and female aud. acuity for left away
\#Towards.Right
t.test(Towards.Right ~ Sex, data = ear.lr, alternative = "two.sided", var.equal = FALSE)
##
##
   Welch Two Sample t-test
##
## data: Towards.Right by Sex
## t = -2.0473, df = 18.528, p-value = 0.05507
## alternative hypothesis: true difference in means between group Female and group Male is not equal to
## 95 percent confidence interval:
## -35.0306667
                 0.4166961
## sample estimates:
## mean in group Female
                         mean in group Male
##
               40.26176
                                    57.56875
\# p > 0.05
# Accept; there is no sign diff bet male and female aud. acuity for right towards
#Towards.Left
t.test(Towards.Left ~ Sex, data = ear.lr, alternative = "two.sided", var.equal = FALSE)
##
##
  Welch Two Sample t-test
##
## data: Towards.Left by Sex
## t = -1.7381, df = 19.705, p-value = 0.09779
## alternative hypothesis: true difference in means between group Female and group Male is not equal to
## 95 percent confidence interval:
## -31.579461
                2.887549
## sample estimates:
## mean in group Female
                         mean in group Male
                                    55.18125
##
               40.83529
```

```
# p > 0.05
# Accept; there is no sign diff bet male and female aud. acuity for left towards
```

Organizes data for export

```
library(writexl)
ra.ear <- ear.lr %>%
  select(c(1,2,3)) %>%
  spread(Sex, Away.Right) %>%
  select(c(2,3))
write_xlsx(ra.ear, "C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/2nd Semester/BIO 122/lab/Exe
la.ear <- ear.lr %>%
  select(c(1,2,4)) %>%
  spread(Sex, Away.Left) %>%
  select(c(2,3))
write_xlsx(la.ear, "C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/2nd Semester/BIO 122/lab/Exe
rt.ear <- ear.lr %>%
  select(c(1,2,5)) %>%
  spread(Sex, Towards.Right) %>%
  select(c(2,3))
write_xlsx(rt.ear, "C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/2nd Semester/BIO 122/lab/Exe
lt.ear <- ear.lr %>%
  select(c(1,2,6)) %>%
  spread(Sex, Towards.Left) %>%
  select(c(2,3))
write_xlsx(lt.ear, "C:/Users/Xyrine/Documents/School Stuff/BS BIO 4th Year/2nd Semester/BIO 122/lab/Exe
```