

Exercise 7C. Bleeding Time

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

1. DATA

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

```
##           Name.of.Student Age Sex Weight      Fitness ABO      Rh
## 1           Bio 122 A1   NA      NA
## 2      Perez, Maria Cristina A.  21   F 104.28 Non-athletic  B+  Positive
## 3          Tadle, Antonette    20   F 114.64 Non-athletic  O+  Positive
## 4 Genson, Julia Raphaella Genson  21   F  83.96 Non-athletic  B+  Positive
##   Bleed.NoPress Bleed.Press  Clot.Time
## 1
## 2      40.73      75.00 2 min 19 s
## 3       77      51.47 1 min 36 s
## 4       75      29.64 5 min 28 s
```

1a. Exploring Data

```
# reorganizes data for pressure vs no pressure
pres <- blood %>%
  select(Bleed.NoPress, Bleed.Press) %>%
  gather(Pressure, Bleed.Time, Bleed.NoPress, Bleed.Press) %>%
  mutate(Pressure = gsub("Bleed.NoPress", "Not Cuffed", Pressure),
         Pressure = gsub("Bleed.Press", "Cuffed", Pressure)) %>%
  mutate_all(~replace(., . == "", NA)) %>%
  drop_na()

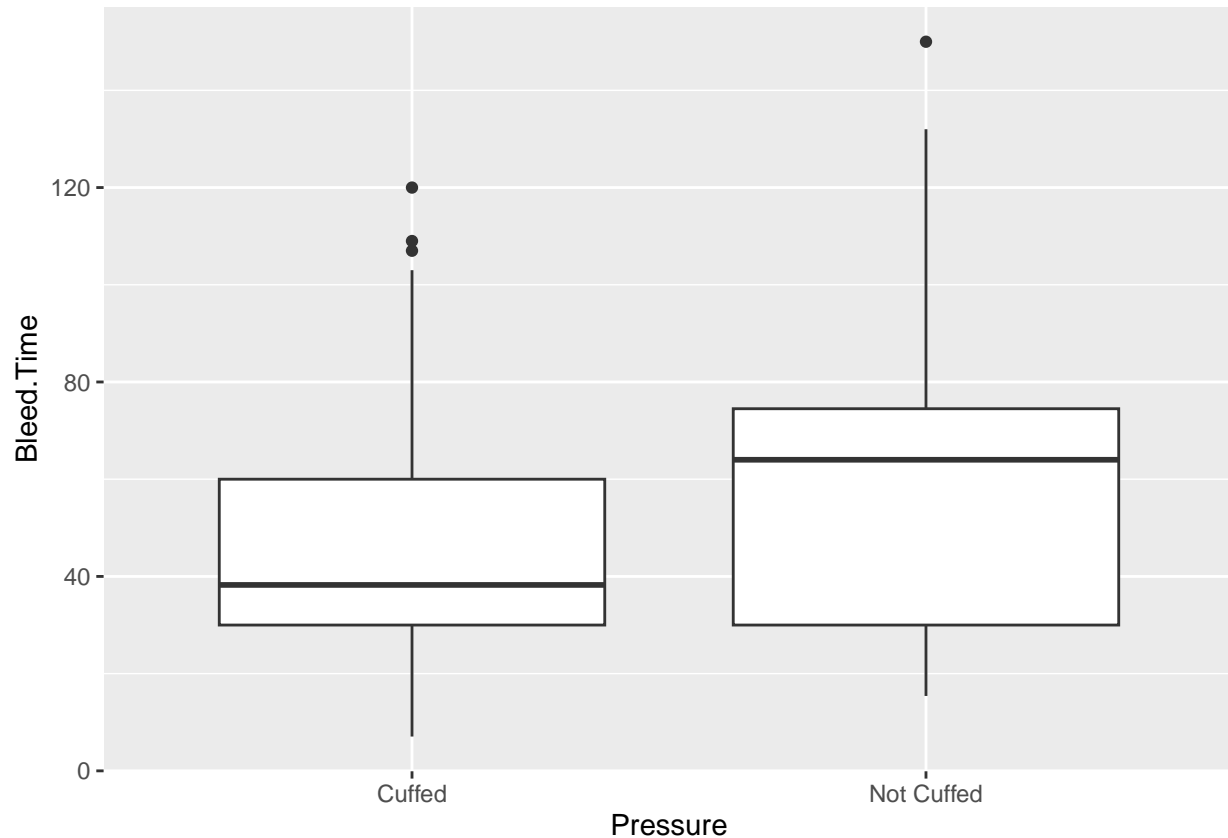
pres$Bleed.Time <- as.numeric(pres$Bleed.Time)

head(pres, n = 4)
```

```
##      Pressure Bleed.Time
```

```
## 1 Not Cuffed      40.73
## 2 Not Cuffed      77.00
## 3 Not Cuffed      75.00
## 4 Not Cuffed     109.00
```

```
## plot
ggplot(pres, aes(Pressure, Bleed.Time)) + geom_boxplot()
```



```
# reorganizes data for ABO bleed time
abo <- blood %>%
  select(ABO, Bleed.NoPress, Bleed.Press) %>%
  mutate_all(~replace(., . == "", NA)) %>%
  mutate(ABO = gsub("\\ ", "", ABO),
         Bleed.NoPress = gsub("<30", "29", Bleed.NoPress)) %>%
  drop_na()

abo$Bleed.NoPress <- as.numeric(abo$Bleed.NoPress)

head(abo, n = 4)
```

```
##   ABO Bleed.NoPress Bleed.Press
## 1  B+         40.73         75.00
## 2  O+         77.00         51.47
## 3  B+         75.00         29.64
## 4  A+        109.00         30.00
```

```
# abo but removes group with one observation (B-)
abo.b <- subset(abo, ABO!="B-")
```

```
oba <- abo %>%
  gather(Pressure, Bleed.Time, Bleed.NoPress, Bleed.Press) %>%
  mutate(Pressure = gsub("Bleed.NoPress", "Not Cuffed", Pressure),
         Pressure = gsub("Bleed.Press", "Cuffed", Pressure))

head(oba, n = 4)
```

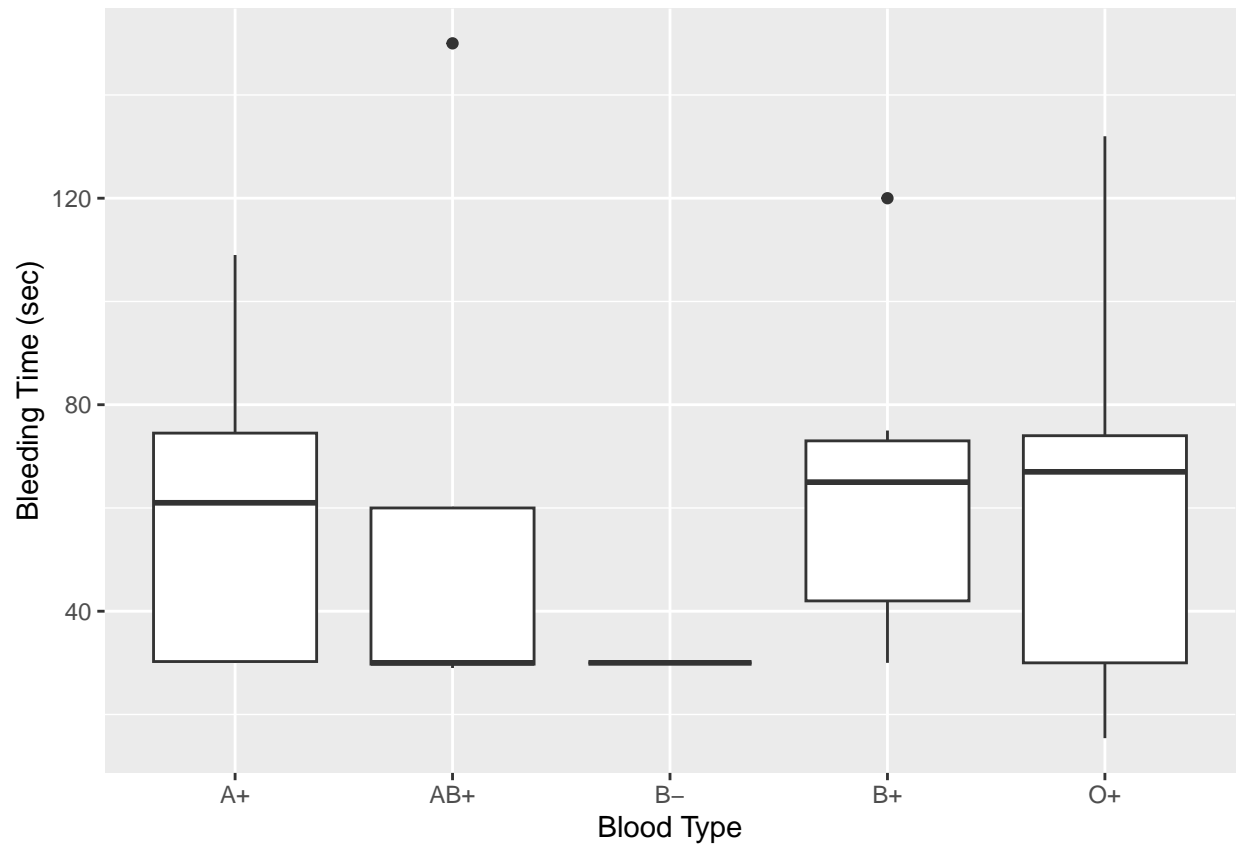
```
##   ABO   Pressure Bleed.Time
## 1  B+ Not Cuffed    40.73
## 2  O+ Not Cuffed    77.00
## 3  B+ Not Cuffed    75.00
## 4  A+ Not Cuffed   109.00
```

```
## plot
```

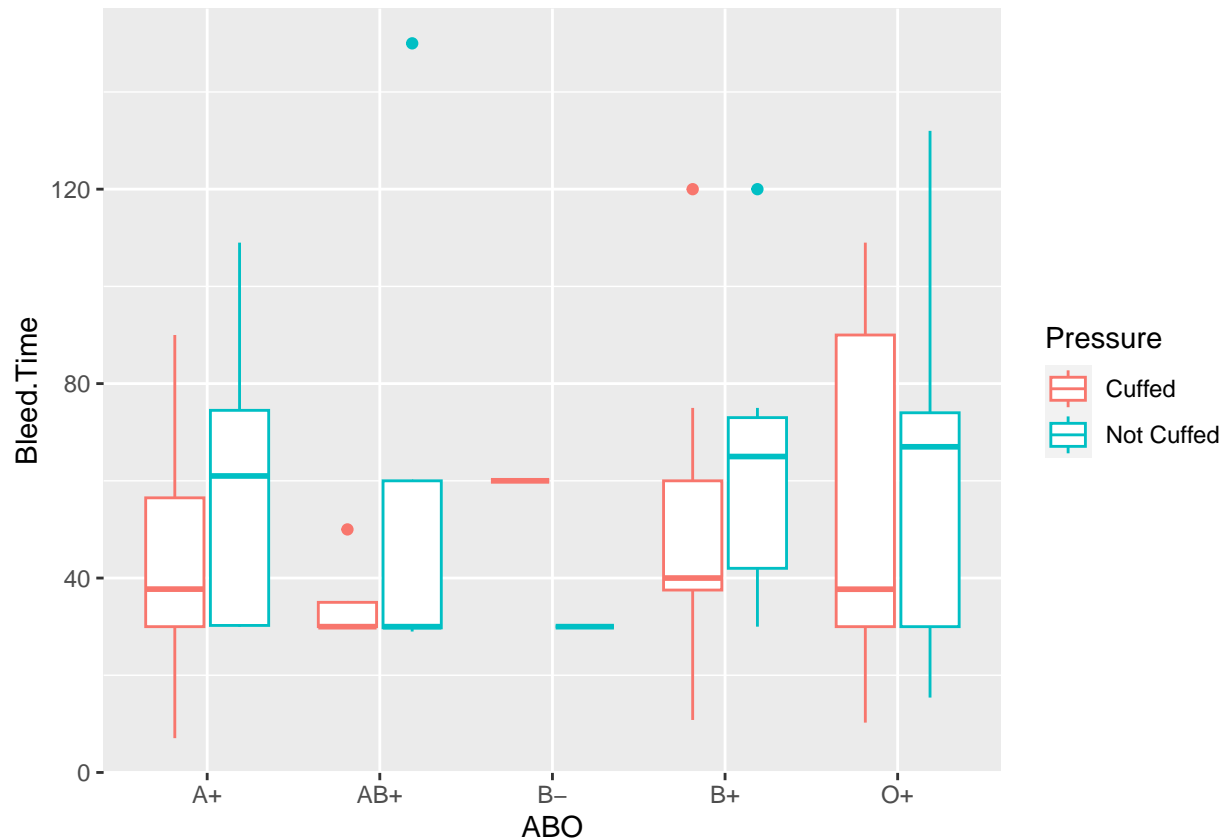
```
abo.plot <- ggplot(abo, aes(ABO, Bleed.NoPress)) + geom_boxplot() +
  xlab("Blood Type") + ylab("Bleeding Time (sec)")
```

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

```
abo.plot
```



```
## no B-  
abob.plot <- ggplot(abo.b, aes(ABO, Bleed.NoPress)) + geom_boxplot() +  
  xlab("Blood Type") + ylab("Bleeding Time (sec)")  
  
ggplot(oba, aes(ABO, Bleed.Time, col = Pressure)) + geom_boxplot()
```



2. PRESSURE VS. NO PRESSURE

2a. Test for normality of distribution

```
## Shapiro-Wilk normality Test
shapiro.test(pres$Bleed.Time[pres$Pressure == "Not Cuffed"]) # p = 0.01; not normal
```

```
##
## Shapiro-Wilk normality test
##
## data:  pres$Bleed.Time[pres$Pressure == "Not Cuffed"]
## W = 0.92943, p-value = 0.01111
```

```
shapiro.test(pres$Bleed.Time[pres$Pressure == "Cuffed"]) # p = 0.002; not normal
```

```
##
## Shapiro-Wilk normality test
##
## data:  pres$Bleed.Time[pres$Pressure == "Cuffed"]
## W = 0.91232, p-value = 0.002346
```

2b. Test for homogeneity in variances

```
## homoscedasticity
leveneTest(Bleed.Time ~ Pressure, pres) #  $p > 0.05$ ; assume equality of variance
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 1      0.49 0.4858
##      86
```

2c. Non-parametric and parametric T-test

```
## Unpaired Two-samples Wilcoxon Test
t.test(Bleed.Time ~ Pressure, data = pres,
        alternative = "two.sided", paired = FALSE, var.equal = TRUE)$p.value
```

```
## [1] 0.04328805
```

```
#  $p > 0.05$ ; reject  $H_0$ 
```

```
wilcox.test(Bleed.Time ~ Pressure, data = pres,
            exact = FALSE)$p.value
```

```
## [1] 0.04626815
```

```
#  $p > 0.05$ ; reject  $H_0$ 
```

3. PLATELET KINETICS BETWEEN BLOOD TYPES

```
# bleeding time summary
abo %>%
  group_by(ABO) %>%
  summarise(
    "Count" = n(),
    "Mean" = mean(Bleed.NoPress),
    "Minimum" = min(Bleed.NoPress),
    "Maximum" = max(Bleed.NoPress),
    "SD" = sd(Bleed.NoPress),
    "IQR" = IQR(Bleed.NoPress),
    "Sample Variance" = var(Bleed.NoPress),
    "Q1" = quantile(Bleed.NoPress, probs = c(.25)),
    "Q3" = quantile(Bleed.NoPress, probs = c(.75))
  )
```

```
## # A tibble: 5 x 10
##   ABO   Count Mean Minimum Maximum    SD   IQR 'Sample Variance'   Q1   Q3
```

```
##      <chr> <int> <dbl>    <dbl>    <dbl> <dbl> <dbl>    <dbl> <dbl> <dbl>
## 1 A+      14  58.7      30      109 27.0 44.2      727. 30.2 74.5
## 2 AB+      4  59.8      29      150 60.2 30.2     3620. 29.8 60
## 3 B-       1  30       30       30 NA    0        NA 30    30
## 4 B+       9  63.2      30      120 26.6 31       709. 42    73
## 5 O+      17  60.9     15.4     132 34.0 44      1156. 30    74
```

```
summary(abo)
```

```
##      ABO      Bleed.NoPress      Bleed.Press
## Length:45      Min.       : 15.41      Min.       : 7.06
## Class :character 1st Qu.: 30.00      1st Qu.: 30.00
## Mode  :character Median : 60.00      Median : 38.25
##              Mean  : 59.89      Mean  : 47.85
##              3rd Qu.: 74.00      3rd Qu.: 60.00
##              Max.   :150.00      Max.   :120.00
```

3a. Test for normality of distribution

```
## Shapiro-Wilk normality Test
```

```
shapiro.test(abo$Bleed.NoPress[abo$ABO == "A+"])$p.value # p = 0.08; normal
```

```
## [1] 0.08429889
```

```
shapiro.test(abo$Bleed.NoPress[abo$ABO == "B+"])$p.value # p = 0.32; normal
```

```
## [1] 0.3179248
```

```
shapiro.test(abo$Bleed.NoPress[abo$ABO == "AB+"]) # p = 0.002; not normal
```

```
##
## Shapiro-Wilk normality test
##
## data:  abo$Bleed.NoPress[abo$ABO == "AB+"]
## W = 0.63673, p-value = 0.001607
```

```
shapiro.test(abo$Bleed.NoPress[abo$ABO == "O+"]) # p = 0.27; normal
```

```
##
## Shapiro-Wilk normality test
##
## data:  abo$Bleed.NoPress[abo$ABO == "O+"]
## W = 0.93558, p-value = 0.2694
```

```
## Shapiro-Wilk normality Test (no B-)
```

```
shapiro.test(abo.b$Bleed.NoPress[abo.b$ABO == "A+"])$p.value # p = 0.08; normal
```

```
## [1] 0.08429889
```

```
shapiro.test(ab0.b$Bleed.NoPress[ab0.b$ABO == "B+"])$p.value # p = 0.32; normal
```

```
## [1] 0.3179248
```

```
shapiro.test(ab0.b$Bleed.NoPress[ab0.b$ABO == "AB+"]) # p < 0.002; not normal
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: ab0.b$Bleed.NoPress[ab0.b$ABO == "AB+"]  
## W = 0.63673, p-value = 0.001607
```

```
shapiro.test(ab0.b$Bleed.NoPress[ab0.b$ABO == "O+"]) # p = 0.27; normal
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: ab0.b$Bleed.NoPress[ab0.b$ABO == "O+"]  
## W = 0.93558, p-value = 0.2694
```

3b. Test for homogeneity in variances

```
## homoscedasticity  
leveneTest(Bleed.NoPress ~ ABO, ab0) # p > 0.05; assume equality of variance
```

```
## Levene's Test for Homogeneity of Variance (center = median)  
##      Df F value Pr(>F)  
## group 4  0.4284 0.7872  
##      40
```

```
## homoscedasticity (no B-)  
leveneTest(Bleed.NoPress ~ ABO, ab0.b) # p > 0.05; assume equality of variance
```

```
## Levene's Test for Homogeneity of Variance (center = median)  
##      Df F value Pr(>F)  
## group 3  0.2533 0.8585  
##      40
```

3c. ANOVA

```
## With B-  
  
# ANOVA  
anov <- aov(Bleed.NoPress ~ ABO, ab0) ## p = 0.92  
summary(anov) # p > 0.05; accept Ho
```



```
##           Df Sum Sq Mean Sq F value Pr(>F)
## ABO         4   1028    257.1    0.231  0.919
## Residuals   40  44480   1112.0
```

```
# Kruskal-Wallis test
kw <- kruskal.test(Bleed.NoPress ~ ABO, abo) ## p = 0.72
kw # p > 0.05; accept Ho
```

```
##
## Kruskal-Wallis rank sum test
##
## data: Bleed.NoPress by ABO
## Kruskal-Wallis chi-squared = 2.0816, df = 4, p-value = 0.7208
```

```
# multiple pairwise-comparison between groups
wx <- pairwise.wilcox.test(abo$Bleed.NoPress, abo$ABO, p.adjust.method = "BH")
wx # no sig. diff. in any group
```

```
##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: abo$Bleed.NoPress and abo$ABO
##
##      A+   AB+  B-   B+
## AB+ 0.76 -    -    -
## B-  0.76 1.00 -    -
## B+  1.00 0.76 0.76 -
## O+  1.00 1.00 1.00 1.00
##
## P value adjustment method: BH
```

```
## Without B-
```

```
# ANOVA
anov.b <- aov(Bleed.NoPress ~ ABO, abo.b) ## p = 0.991
summary(anov.b) # p > 0.05; accept Ho
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## ABO         3    115     38.2    0.034  0.991
## Residuals   40  44480   1112.0
```

```
# Kruskal-Wallis test
kw.b <- kruskal.test(Bleed.NoPress ~ ABO, abo.b) ## p = 0.80
kw.b # p > 0.05; accept Ho
```

```
##
## Kruskal-Wallis rank sum test
##
## data: Bleed.NoPress by ABO
## Kruskal-Wallis chi-squared = 0.99553, df = 3, p-value = 0.8023
```

```
# multiple pairwise-comparison between groups
wx.b <- pairwise.wilcox.test(ab0.b$Bleed.NoPress, ab0.b$AB0, p.adjust.method = "BH")
wx.b # no sig. diff. in any group
```

```
##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: ab0.b$Bleed.NoPress and ab0.b$AB0
##
##      A+   AB+   B+
## AB+ 0.91  -    -
## B+  0.95 0.91  -
## O+  0.95 0.95 0.95
##
## P value adjustment method: BH
```