Homework 4

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Solution for Problem 1

1.1

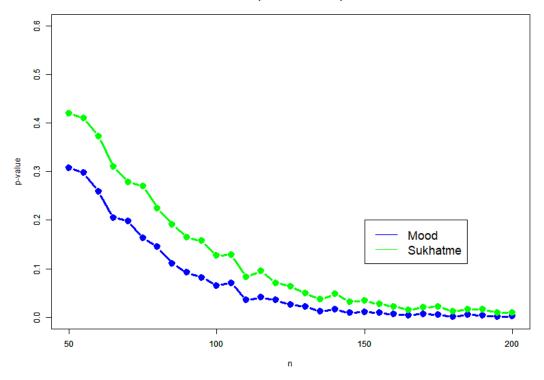
In Mood and Sukhatme test, we use normal approximation to calculate p-value.

We use random generator to generate n=100 $X_1, ..., X_n \sim N(0,1), Y_1, ..., Y_n \sim N(0,1.2)$. Simulating for 10,000 times, we get 8,805 times not to reject the null hypothesis from Mood test, 8,952 times not to reject the null hypothesis from Sukhatme test. Therefore, we **cannot reject** the null hypothesis $H_0: F_X = F_Y$ at $\alpha = 0.05$ from both Mood test and Sukhatme test.

1.2

Consider the following scenario: X and Y are from normal distribution. Without loss of generality, assume $X_1, ..., X_n \sim N(0,1), Y_1, ..., Y_n \sim N(0,1.5^2)$. We take n samples from X and Y respectively. Simulating the sampling and test process for 1,000 times for some n, we get a p-value corresponding to n from Mood test and Sukhatme test shown in the following graph.

Relationship between n and p-value

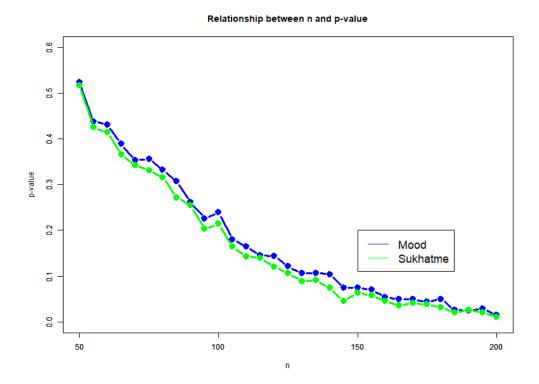


Compared to Sukhatme test, Mood test can reject the null hypothesis under the same α level from a smaller sample size in this scenario. Therefore, Mood test is more powerful than Sukhatme test in this scenario.

1.3

Consider the following scenario: X and Y are from Cauchy distribution. Without loss of generality, assume $X_1, ..., X_n \sim Cauchy(0,1), Y_1, ..., Y_n \sim Cauchy(0,1.8)$. We take n samples from

X and Y respectively. Simulating the sampling and test process for 1,000 times for some n, we get a p-value corresponding to n from Mood test and Sukhatme test shown in the following graph.



Compared to Mood test, Sukhatme test can reject the null hypothesis under the same α level from a smaller sample size in this scenario. Therefore, Sukhatme test is more powerful than Mood test in this scenario.

Solution for Problem 2

Suppose X and Y follows the same distribution F_0 . Since the median of the distribution is 0, then $F_0(0) = \frac{1}{2}$.

$$P(Y < X < 0) \cup P(0 < X < Y) = \int_{-\infty}^{0} \int_{-\infty}^{x} f_{0}(y) f_{0}(x) dy dx + \int_{0}^{\infty} \int_{x}^{\infty} f_{0}(y) f_{0}(x) dy dx$$

$$= \int_{-\infty}^{0} F_{0}(x) dF_{0}(x) + \int_{0}^{\infty} (1 - F_{0}(x)) dF_{0}(x)$$

$$= \int_{0}^{\frac{1}{2}} u du + \int_{\frac{1}{2}}^{1} (1 - u) du, \text{ where } u = F_{0}(x)$$

$$= \frac{1}{8} + \frac{1}{8}$$

$$= \frac{1}{4}$$

Therefore, $P(Y < X < 0) \cup P(0 < X < Y) = \frac{1}{4}$.

Solution for Problem 3

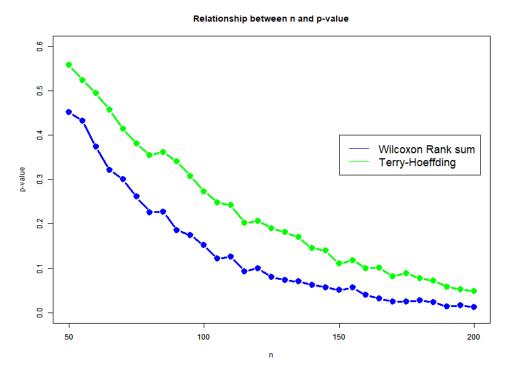
3.1

We use first approximation to approximate $E(\xi_{(i)})$, $E(\xi_{(i)}) \approx \Phi^{-1}(\frac{i}{N+1})$

We use random generator to generate n=100 $X_1, ..., X_n \sim N(0,1), Y_1, ..., Y_n \sim N(0.1,1)$. Simulating for 10,000 times, we get 8,942 times not to reject the null hypothesis from Wilcoxon Rank-sum test, 8,931 times not to reject the null hypothesis from Terry-Hoeffding test. Therefore, we **cannot reject** the null hypothesis H_0 : $F_X = F_Y$ at $\alpha = 0.05$ from both Wilcoxon Rank-sum test and Terry-Hoeffding test.

3.2

Consider the following scenario: X and Y are from Cauchy distribution. Without loss of generality, assume $X_1, ..., X_n \sim Cauchy(0,1), Y_1, ..., Y_n \sim Cauchy(0.8,1)$. We take n samples from X and Y respectively. Simulating the sampling and test process for 1,000 times for some n, we get a p-value corresponding to n from Wilcoxon Rank-sum test and Terry-Hoeffding test shown in the following graph.

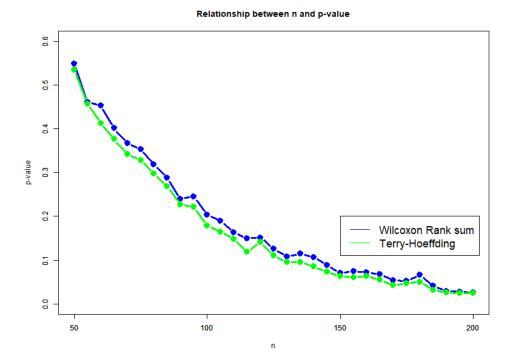


Compared to Terry-Hoeffding test, Wilcoxon Rank-sum test can reject the null hypothesis under the same α level from a smaller sample size in this scenario. Therefore, Wilcoxon Rank-sum test is more powerful than Terry-Hoeffding test in this scenario.

3.3

Consider the following scenario: X and Y are from normal distribution. Without loss of generality, assume $X_1, ..., X_n \sim N(0,1), Y_1, ..., Y_n \sim N(0,4,1)$. We take n samples from X and Y respectively. Simulating the sampling and test process for 1,000 times for some n, we get a p-value corresponding to n from Wilcoxon Rank-sum test and Terry-Hoeffding test shown in the

following graph.



Compared to Wilcoxon Rank-sum test, Terry-Hoeffding test can reject the null hypothesis under the same α level from a smaller sample size in this scenario. Therefore, Terry-Hoeffding test is more powerful than Wilcoxon Rank-sum test in this scenario.

Appendix

The following provides R code I used to complete this homework. You can also find the R code and output at https://thisiskunmeng.github.io/nonparametric/hw4.html

R code for Solution for Problem 1

```
#' rewrite Mood test
#' return True if null hypothesis is not rejected, else return False
mood_test <- function(x, y, a) {</pre>
          xy \leftarrow c(x, y)
          N <- length(x) + length(y)
          xy_sorted <- sort(xy)</pre>
          z \leftarrow rep(0, times = N)
          z[match(x, xy_sorted)] <- 1</pre>
          m_n <- 0
          for (i in 1:N) {
                     m_n \leftarrow m_n + (i - (N + 1) / 2)^2 * z[i]
           }
          e_m - (-1) = (-1) / (12)
          var_m - (-1) = var_m - (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) + (-1) 
          z_value <- (m_n - e_m_n) / sqrt(var_m_n)</pre>
          z_a \leftarrow qnorm(1 - a / 2)
          return(abs(z_value) <= z_a)</pre>
#' rewrite Sukhatme test
#' return True if null hypothesis is not rejected, else return False
sukhatme_test <- function(x, y, a) {</pre>
          t <- 0
          for (i in x) {
                     for (j in y) {
                                if ((i > j \&\& i < 0) || (i < j \&\& i > 0)) {
                                           t < -t + 1
                     }
           }
          e_t <- length(x) * length(y) / 4</pre>
          var_t \leftarrow (length(x) * length(y) * (length(x) + length(y) + 7)) / 48
          z_value <- (t - e_t) / sqrt(var_t)</pre>
          z_a \leftarrow qnorm(1 - a / 2)
          return(abs(z_value) <= z_a)</pre>
}
# 1.1
sim num <- 10000
n <- 100
a <- 0.05
x_mean <- 0
y_mean <- 0
var_x <- 1
var_y <- 1.2</pre>
mood <- c()
suk <- c()
for (i in 1:sim_num) {
          set.seed(i)
          x <- rnorm(n, mean = x_mean, sd = sqrt(var_x))</pre>
          y <- rnorm(n, mean = y_mean, sd = sqrt(var_y))</pre>
          mood <- c(mood, mood_test(x, y, a))</pre>
```

```
suk <- c(suk, sukhatme_test(x, y, a))</pre>
}
print(sum(mood)) # 8805
print(sum(suk)) # 8952
n = seq(from = 50, to = 200, by = 5)
sim num = 1000
mood_n = c()
suk_n = c()
for (i in n){
    mood <- c()
    suk <- c()
    for (j in 1:sim_num) {
        set.seed(i*j)
       x <- rnorm(i, 0, 1)
        y <- rnorm(i, 0, 1.5)
        mood <- c(mood, mood_test(x, y, a))</pre>
        suk <- c(suk, sukhatme_test(x, y, a))</pre>
    mood_n = c(mood_n, sum(mood)/sim_num)
    suk_n = c(suk_n, sum(suk)/sim_num)
png("hw4-1.2.png", width=800, height=600)
plot(n, mood_n,
    type = "b", pch = 19, xlab = "n", ylab = "p-value",
    col = "blue", ylim = c(0,0.6),
    main = "Relationship between n and p-value",
    lty = 1, lwd = 3, cex = 1.5
)
par(new=TRUE)
plot(n, suk_n,
    type = "b", pch = 19, col = "green", xlab = "", ylab = "",
    ylim = c(0,0.6),
    lty = 1, lwd = 3, cex = 1.5)
legend(150,0.2, legend=c("Mood", "Sukhatme"),
    col = c("blue", "green"), lty=c(1, 1), cex=1.5)
dev.off()
# 1.3
n = seq(from = 50, to = 200, by = 5)
sim_num = 1000
mood_n = c()
suk_n = c()
for (i in n){
    mood <- c()
    suk <- c()
    for (j in 1:sim_num) {
        set.seed(i*j)
        x \leftarrow reauchy(i, 0, 1)
        y <- rcauchy(i, 0, 1.8)</pre>
       mood <- c(mood, mood_test(x, y, a))</pre>
        suk <- c(suk, sukhatme_test(x, y, a))</pre>
    mood_n = c(mood_n, sum(mood)/sim_num)
    suk_n = c(suk_n, sum(suk)/sim_num)
png("hw4-1.3.png", width=800, height=600)
plot(n, mood_n,
```

```
type = "b", pch = 19, xlab = "n", ylab = "p-value", col = "blue",
ylim = c(0,0.6),
    main = "Relationship between n and p-value",
    lty = 1, lwd = 3, cex = 1.5
par(new=TRUE)
plot(n, suk_n,
    type = "b", pch = 19, col = "green", xlab = "", ylab = "", ylim =
c(0,0.6),
    lty = 1, lwd = 3, cex = 1.5)
legend(150,0.2, legend=c("Mood", "Sukhatme"), col = c("blue", "green"),
lty=c(1, 1), cex=1.5)
dev.off()
R code for Solution for Problem 3
#' rewrite Wilcoxon Rank-sum test
#' return True if null hypothesis is not rejected, else return False
wilcox_ranksum_test <- function(x, y, a) {</pre>
    xy \leftarrow c(x, y)
    N <- length(x) + length(y)
    xy_sorted <- sort(xy)</pre>
    z \leftarrow rep(0, times = N)
    z[match(x, xy_sorted)] <- 1</pre>
    w_n <- 0
    for (i in 1:N) {
        w_n < w_n + i * z[i]
    }
    e_{w_n} < -length(x) * (N + 1) / 2
    var_w_n \leftarrow length(x) * length(y) * (N + 1) / 12
    z_value <- (w_n - e_w_n) / sqrt(var_w_n)</pre>
    z_a \leftarrow qnorm(1 - a / 2)
    return(abs(z_value) <= z_a)</pre>
#' rewrite Terry-Hoeffding test
#' return True if null hypothesis is not rejected, else return False
terry_hoeffding_test <- function(x, y, a) {</pre>
    xy \leftarrow c(x, y)
    N <- length(x) + length(y)
    xy_sorted <- sort(xy)</pre>
    z \leftarrow rep(0, times = N)
    z[match(x, xy_sorted)] <- 1</pre>
    c1 <- 0
    e_i_all <- c()</pre>
    for (i in 1:N) {
        e_i \leftarrow qnorm(i / (N + 1))
        e_i_all <- c(e_i_all, e_i)</pre>
        c1 < -c1 + e_i * z[i]
    e c1 <- 0
    var_c1 < -length(x) * length(y) * sum((e_i_all)^2) / ((N + 1) * N)
    z_value <- (c1 - e_c1) / sqrt(var_c1)</pre>
    z_a \leftarrow qnorm(1 - a / 2)
    return(abs(z_value) <= z_a)</pre>
}
# 3.1
sim_num <- 10000
n <- 100
a <- 0.05
```

```
x_mean <- 0
y_mean <- 0.1
var_x <- 1</pre>
var_y <- 1
wilcox <- c()</pre>
terry <- c()
for (i in 1:sim_num) {
    set.seed(i)
    x <- rnorm(n, mean = x_mean, sd = sqrt(var_x))</pre>
    y <- rnorm(n, mean = y_mean, sd = sqrt(var_y))</pre>
    wilcox <- c(wilcox, wilcox_ranksum_test(x, y, a))</pre>
    terry <- c(terry, terry_hoeffding_test(x, y, a))</pre>
}
print(sum(wilcox)) # 8942
print(sum(terry)) # 8931
# 3.2
n = seq(from = 50, to = 200, by = 5)
sim_num = 1000
wilcox n = c()
terry_n = c()
for (i in n){
    wilcox <- c()
    terry <- c()
    for (j in 1:sim_num) {
        set.seed(i*j)
        x \leftarrow rcauchy(i, 0, 1)
        y <- rcauchy(i, 0.8, 1)</pre>
        wilcox <- c(wilcox, wilcox_ranksum_test(x, y, a))</pre>
        terry <- c(terry, terry_hoeffding_test(x, y, a))
    wilcox_n = c(wilcox_n, sum(wilcox)/sim_num)
    terry_n = c(terry_n, sum(terry)/sim_num)
png("hw4-3.2.png", width=800, height=600)
plot(n, wilcox_n,
    type = "b", pch = 19, xlab = "n", ylab = "p-value",
    col = "blue", ylim = c(0,0.6),
    main = "Relationship between n and p-value",
    lty = 1, lwd = 3, cex = 1.5
)
par(new=TRUE)
plot(n, terry_n,
    type = "b", pch = 19, col = "green", xlab = "", ylab = "",
    ylim = c(0,0.6),
    lty = 1, lwd = 3, cex = 1.5)
legend(150,0.4, legend=c("Wilcoxon Rank sum", "Terry-Hoeffding"),
    col = c("blue", "green"), lty=c(1, 1), cex=1.5)
dev.off()
# 3.3
n = seq(from = 50, to = 200, by = 5)
sim_num = 1000
wilcox_n = c()
terry_n = c()
for (i in n){
    wilcox <- c()
    terry <- c()
    for (j in 1:sim_num) {
        set.seed(i*j)
```

```
x <- rnorm(i, 0, 1)
       y <- rnorm(i, 0.4, 1)
       wilcox <- c(wilcox, wilcox_ranksum_test(x, y, a))</pre>
       terry <- c(terry, terry_hoeffding_test(x, y, a))</pre>
   wilcox_n = c(wilcox_n, sum(wilcox)/sim_num)
   terry_n = c(terry_n, sum(terry)/sim_num)
}
png("hw4-3.3.png", width=800, height=600)
plot(n, wilcox_n,
   type = "b", pch = 19, xlab = "n", ylab = "p-value",
   col = "blue", ylim = c(0,0.6),
   main = "Relationship between n and p-value",
   lty = 1, lwd = 3, cex = 1.5
par(new=TRUE)
plot(n, terry_n,
   type = "b", pch = 19, col = "green", xlab = "", ylab = "",
   ylim = c(0,0.6),
   lty = 1, lwd = 3, cex = 1.5)
legend(150,0.2, legend=c("Wilcoxon Rank sum", "Terry-Hoeffding"),
   col = c("blue", "green"), lty=c(1, 1), cex=1.5)
dev.off()
```