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2023-02-16

Question 1

The following is the code for the 1st question.

```
p_values <- c(0.0050, 0.0010, 0.0100, 0.0005, 0.0009, 0.0400, 0.0560, 0.0500, 0.0480, 0.0130, 0.0370, 0

p_values <- sort(p_values)

p_bonferroni <- p.adjust(p_values, method = "bonferroni", n = length(p_values))

p_hochberg <- p.adjust(p_values, method = "hochberg", n = length(p_values))


print(p_values)
```

```
##  [1] 0.0005 0.0009 0.0010 0.0020 0.0050 0.0100 0.0130 0.0250 0.0370 0.0400
## [11] 0.0430 0.0480 0.0500 0.0560 0.0700 0.0800 0.1100
```

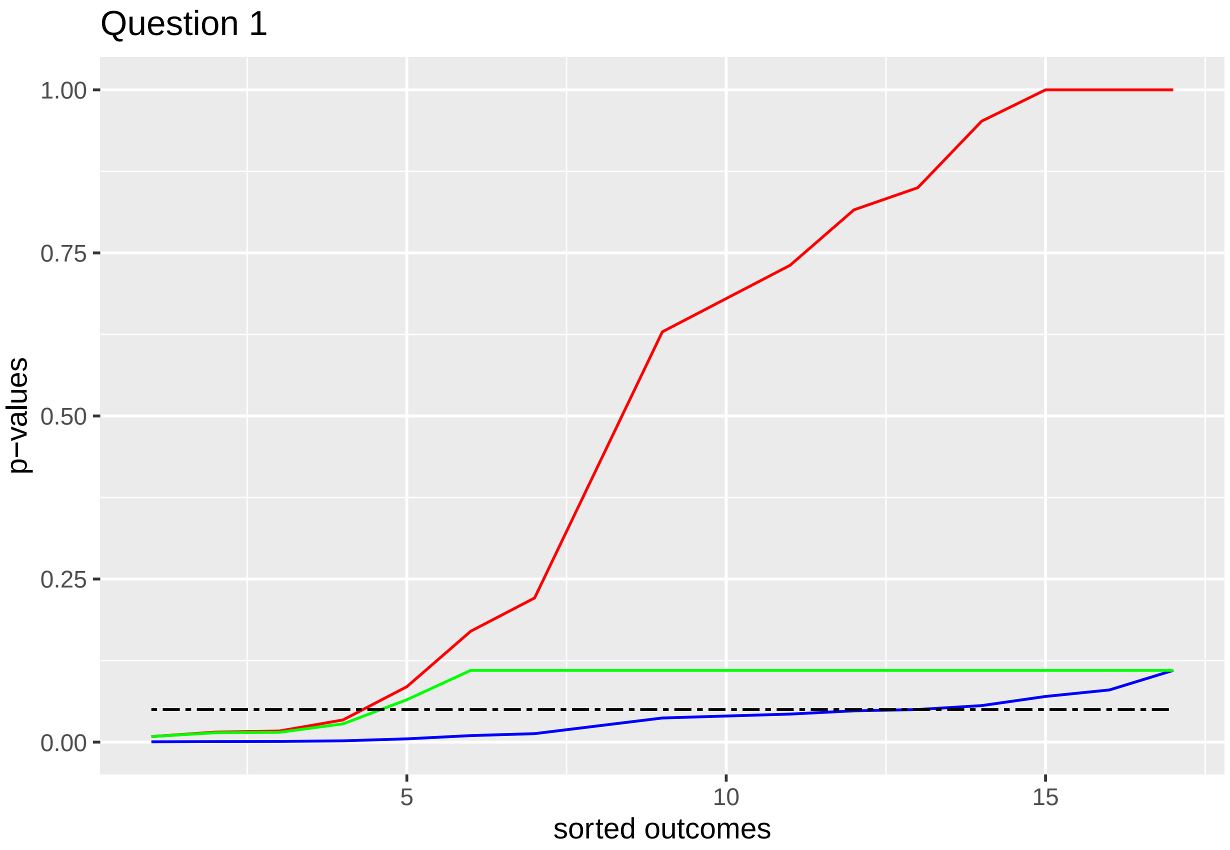
```
print(p_bonferroni)
```

```
##  [1] 0.0085 0.0153 0.0170 0.0340 0.0850 0.1700 0.2210 0.4250 0.6290 0.6800
## [11] 0.7310 0.8160 0.8500 0.9520 1.0000 1.0000 1.0000
```

```
print(p_hochberg)
```

```
##  [1] 0.0085 0.0144 0.0150 0.0280 0.0650 0.1100 0.1100 0.1100 0.1100 0.1100
## [11] 0.1100 0.1100 0.1100 0.1100 0.1100 0.1100 0.1100
```

```
library(reshape2)
library(ggplot2)

data <- data.frame(x = c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17), y1 = p_values, y2 =

gfg_plot <- ggplot(data, aes(x)) +
    geom_line(aes(y = y1), color = "blue") +
     geom_line(aes(y = y2), color = "red") +
    geom_line(aes(y = y3), color = "green")+
    geom_line(aes(y = y4), color = "black", linetype = "twodash")+ labs(title="Question 1", x = "sorted

gfg_plot
```



```
#+geom_line(aes(color=c("Unadjusted", "Bonferroni", "Hochberg")))
```

The following is the inference from the graph:

High adjusted p values for the earlier experiments show that there is not enough data to conclusively demonstrate an effect. The more severe Bonferroni correction produces bigger adjusted p values. It is less rigorous since the Hochberg adjustment correlates to lower adjusted p values for the experiment than our alpha. The bonferroni test is a conservative test since it has a high probability of rejecting the null hypothesis.

Question 2

The following is the code for the second question.

Part A

```
library(readxl)
mydataq2 <- read_excel("./BRSM_Results_Visualization.xlsx", 1)

print(mydataq2)
```

```
## # A tibble: 43 x 2
##    Group ‘No. of Mosquitoes‘
##    <chr>                <dbl>
##  1 Beer                    27
##  2 Beer                    19
##  3 Beer                    20
##  4 Beer                    20
##  5 Beer                    23
##  6 Beer                    17
##  7 Beer                    21
##  8 Beer                    24
##  9 Beer                    31
## 10 Beer                    26
## # i 33 more rows
```

```
beer <- mydataq2[mydataq2$Group == "Beer", ]
print(beer)
```

```
## # A tibble: 25 x 2
##    Group ‘No. of Mosquitoes‘
##    <chr>                <dbl>
##  1 Beer                    27
##  2 Beer                    19
##  3 Beer                    20
##  4 Beer                    20
##  5 Beer                    23
##  6 Beer                    17
##  7 Beer                    21
##  8 Beer                    24
##  9 Beer                    31
## 10 Beer                    26
## # i 15 more rows
```

```
water <- mydataq2[mydataq2$Group == "Water", ]
print(water$`No. of Mosquitoes`)
```

```
##  [1] 21 19 13 22 15 22 15 22 20 12 24 24 21 19 18 16 23 20
```

```
beer_mean <- mean(beer$`No. of Mosquitoes`)
print(beer_mean)
```

```
## [1] 23.6
```

```
water_mean <- mean(water$`No. of Mosquitoes`)
print(water_mean)
```

```
## [1] 19.22222
```

```
test.stat.1 <- abs(water_mean - beer_mean)

beer_median <- median(beer$`No. of Mosquitoes`)
water_median <- median(water$`No. of Mosquitoes`)
test.stat.2 <- abs(beer_median - water_median)
print(test.stat.2)
```

```
## [1] 4
```

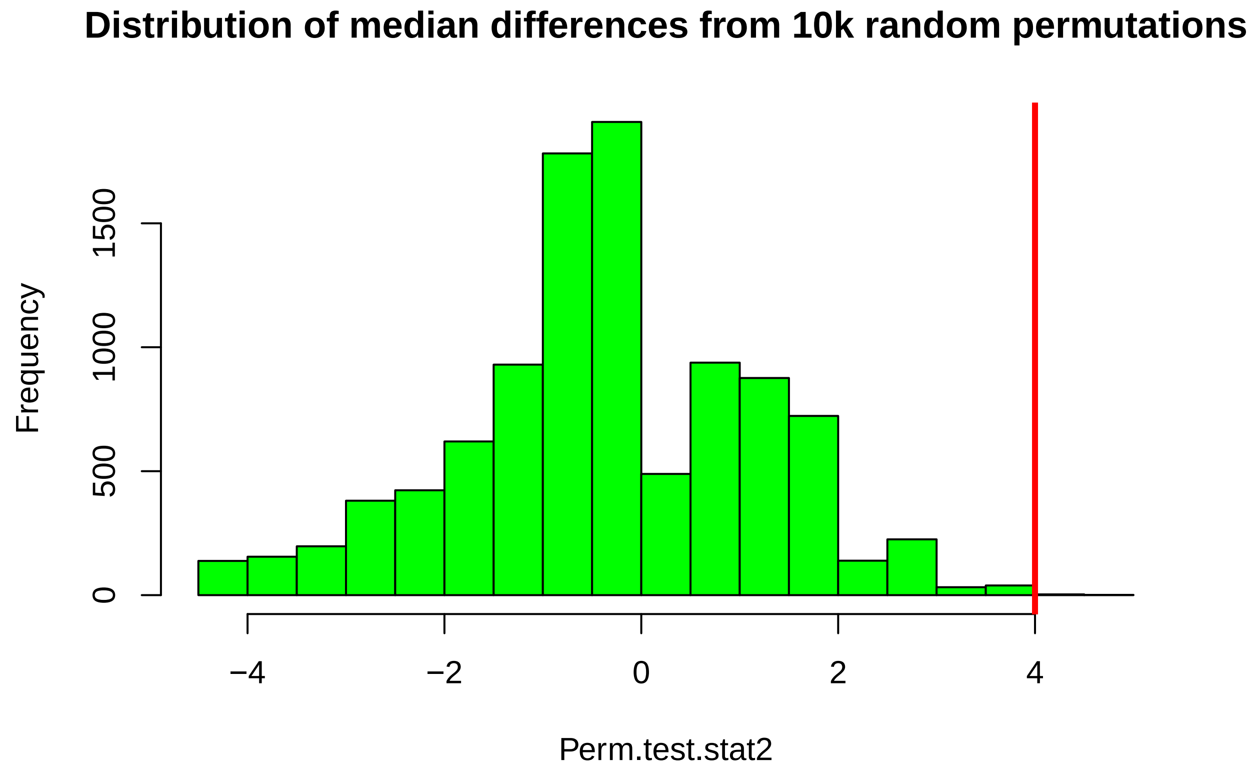
```
cat("The difference between the group medians is", test.stat.2)
```

```
## The difference between the group medians is 4
```

```
set.seed(1979)

n <- length(mydataq2$Group)
P <- 10000
var <- mydataq2$`No. of Mosquitoes`

PermSamples <- matrix(0, nrow = n, ncol = P)

for(i in 1:P)
{
  PermSamples[, i] <- sample(var, size = n, replace = FALSE)
}


Perm.test.stat1 <- rep(0, P)
Perm.test.stat2 <- rep(0, P)

for (i in 1:P)
{
    Perm.test.stat1[i] <- mean(PermSamples[mydataq2$Group == "Beer", i]) - mean(PermSamples[mydataq2$Gr

    Perm.test.stat2[i] <- median(PermSamples[mydataq2$Group == "Beer", i]) - median(PermSamples[mydataq

}

print(mean(Perm.test.stat2 >= test.stat.2))
```

```
## [1] 0.0043
```

```
hist(Perm.test.stat2, col = "green", main="Distribution of median differences from 10k random permutati
abline(v=test.stat.2, lwd=3, col="red")
```



```r
p_value = sum(Perm.test.stat2 >= test.stat.2)/P
print(p_value)
```

```
## [1] 0.0043
```

```r
cat("The p_value obtained is ", p_value)
```

```
## The p_value obtained is  0.0043
```

We observe that the p-value is less than 0.05 which brings to us a very high possibility of the alternate directional hypothesis to be true and the observed statistic is significant.

Part B

```r
t <- t.test(beer$`No. of Mosquitoes`, water$`No. of Mosquitoes`, var.equal = TRUE)
t <- t$statistic[['t']]
cat("The initial t-score is ", t)
```

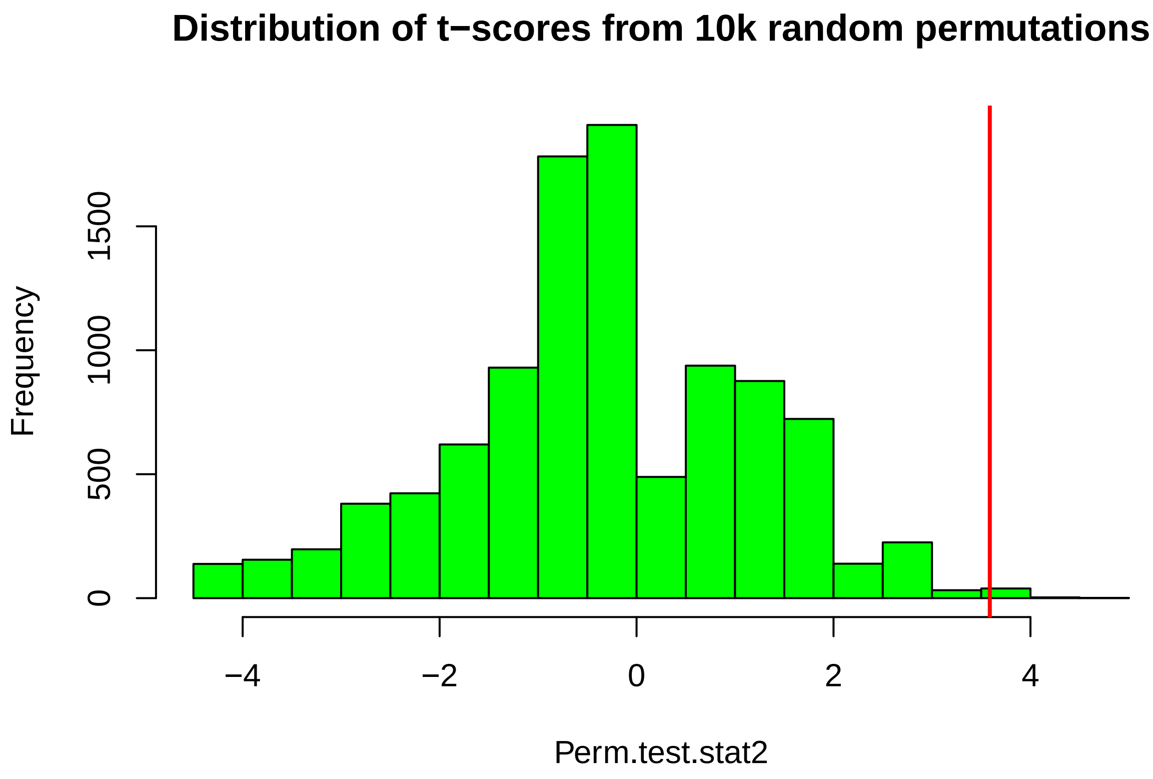
```
## The initial t-score is  3.586984
```

```
p2_perm = rep(0, P)

for(i in 1:P)
{
  temp_t <- t.test(head(PermSamples[, i], 25), tail(PermSamples[,i], 18), var.equal = TRUE)
  p2_perm[i] <- temp_t$statistic[['t']]
}

p_value_2 = sum(p2_perm >= t)/P
cat("The observed p_value is ", p_value_2)
```

```
## The observed p_value is  3e-04
```

The observed p_value is less than 0.05 which confirms that the alternate hypothesis is true and the observed statistic is significant.

```
hist(Perm.test.stat2, col="green", main = "Distribution of t-scores from 10k random permutations")
abline(v=t, lwd=2, col="red")
```



Part C

Since, we are calculating the p-value assuming that the hypothesis is non-directional, therefore we need to calculate the p-value with the absolute value of the differences of the medians.

```r
p_value_3 = sum(abs(Perm.test.stat2) >= test.stat.2)/P
cat("The p-value is this case is ", p_value_3)
```

```
## The p-value is this case is  0.0181
```

The p-value is observed to be less than 0.05 which implies that the non-directional hypothesis is true and the observed statistic is significant.

Question 3

Following is the code for the third question.

```r
mydataq3 <- read_excel("./IQ.xlsx", 1)
```

```
## New names:
## * ‘‘ -> ‘...1‘
```

```r
q3_p <- cor(mydataq3$IQ, mydataq3$TESTSCORE)
print("The intial correlation value is ")
```

```
## [1] "The intial correlation value is "
```

```r
print(q3_p)
```

```
## [1] 0.4931479
```

```r
n <- length(mydataq3$IQ)
P <- 10000
iq <- mydataq3$IQ
test_scores <- mydataq3$TESTSCORE

iq_samples <- matrix(0, nrow = n, ncol = P)
test_scores_samples <- matrix(0, nrow = n, ncol = P)

for(i in 1:P)
{
  iq_samples[, i] <- sample(iq, size = n, replace = FALSE)
  test_scores_samples[, i] <- sample(test_scores, size = n, replace = FALSE)
}

p3_perm = rep(0, P)

for(i in 1:P)
{

  p3_perm[i] = cor(iq_samples[, i], test_scores_samples[, i])
}

p_value_4 <- sum(p3_perm >= q3_p)/P
print(p_value_4)
```

```
## [1] 0
```

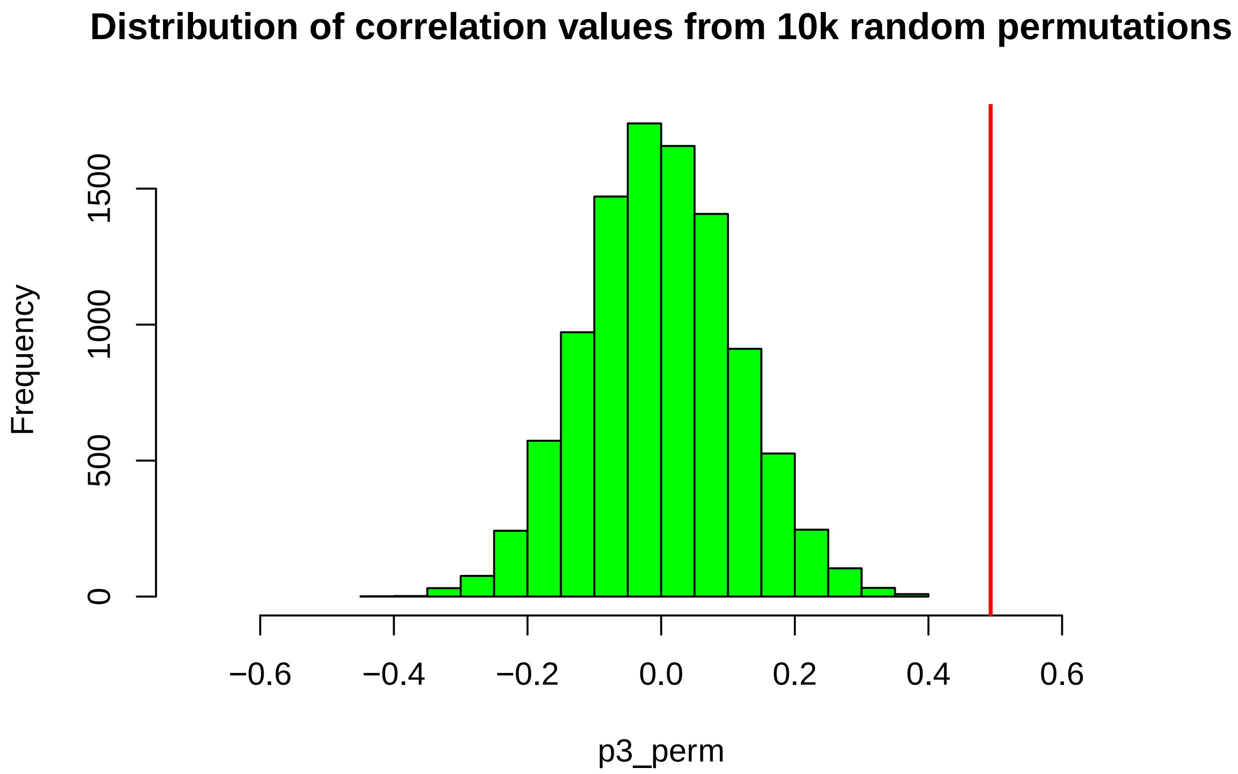
```
print(paste("The observed p-value is ", p_value_4))
```

```
## [1] "The observed p-value is  0"
```

The p-value that is being obtained as I run the code above oscillates between 0 and 1e-04. At the very moment, the p-value from the code above is 1e-04, but for some reason it is getting rendered as 0 in the pdf.

We observe that the p-value is much less than 0.05 based on our observed statistic. Therefore, we can safely assume that we can reject the null hypothesis, since there exists a correlation between IQ and Test scores.

```
hist(p3_perm, col="green", main = "Distribution of correlation values from 10k random permutations", xli
abline(v=q3_p, lwd=2, col="red")
```


Distribution of correlation values from 10k random permutations
Frequency
p3_perm