

STAT416 Assignment 4

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Question 2:

a).

```
p.values <- read.table("https://raw.githubusercontent.com/ashishjain1988/STAT416/master/HW4/hwk4_q2.txt")
p.value <- p.values[, 1]
p.adjusta <- p.adjust(p.value, method = "bonferroni")
p.adjustTa <- rep(FALSE, length(p.adjusta))
p.adjustTa[p.adjusta <= 0.05] <- TRUE
deg <- length(p.adjustTa[p.adjustTa == TRUE])
```

The number of differential expressed genes by using Bonferroni method are 4.

b).

```
p.adjust <- p.adjust(p.value, method = "holm")
p.adjustT <- rep(FALSE, length(p.adjust))
p.adjustT[p.adjust <= 0.05] <- TRUE
deg <- length(p.adjustT[p.adjustT == TRUE])
```

The number of differential expressed genes by using Holm's method are 4.

c).

```
# c.
p.adjust <- p.adjust(p.value, method = "BH")
p.adjustT <- rep(FALSE, length(p.adjust))
p.adjustT[p.adjust <= 0.05] <- TRUE
deg <- length(p.adjustT[p.adjustT == TRUE])
```

The number of differential expressed genes by using Benjamini and Hochberg's method are 177.

d).

```
# source('http://bioconductor.org/biocLite.R')
# biocLite('qvalue')
library(qvalue)
qobj <- qvalue(p.value, fdr.level = 0.05)
pi0Number <- qobj$pi0
STres <- qobj$qvalues
p.adjustTd <- rep(FALSE, length(STres))
p.adjustTd[STres <= 0.05] <- TRUE
deg <- length(p.adjustTd[p.adjustTd == TRUE])
```

The number of differential expressed genes by using Storey and Tibshirani's method are 191. The π_0 value is 0.8765903.

e).

```
getTable <- function(padjust) {  
  first200 <- padjust[1:200]  
  TP <- length(first200[first200 == TRUE])  
  FN <- 200 - TP  
  other800 <- padjust[201:1000]  
  FP <- length(other800[other800 == TRUE])  
  TN <- 800 - FP  
  return(c(TN, FN, FP, TP))  
}  
parta <- getTable(padjustTa)  
table <- data.frame(Properties = c("True Null", "False Null"),  
  `Accept Null` = c(parta[1], parta[2]), `Reject Null` = c(parta[3],  
    parta[4]))  
knitr::kable(table, caption = "Table for Part a")
```

Table 1: Table for Part a

Properties	Accept.Null	Reject.Null
True Null	799	1
False Null	197	3

```
parta <- getTable(padjustTd)  
table <- data.frame(Properties = c("True Null", "False Null"),  
  `Accept Null` = c(parta[1], parta[2]), `Reject Null` = c(parta[3],  
    parta[4]))  
knitr::kable(table, caption = "Table for Part d")
```

Table 2: Table for Part d

Properties	Accept.Null	Reject.Null
True Null	783	17
False Null	26	174