HW2

Runye Hu A13410385 Yijie Fan A13485989 Xinyi He A13561164 Yifan Wu A14060535 Yiwen Cai A13530685

Problem1

Nutrient data

```
nutrient=read.table("https://www.math.ucsd.edu/~wez243/data/nutrient.txt")
nutrient$V1=NULL
colnames(nutrient)=c("Calcium", "Iron", "Protein", "Vitamin A", "Vitamin C")
```

Q1:

```
means <- colMeans(nutrient, na.rm = TRUE)
print(means)</pre>
```

```
## Calcium Iron Protein Vitamin A Vitamin C
## 624.04925 11.12990 65.80344 839.63535 78.92845
```

```
sd <- apply(nutrient, 2, function(x) sd(x, na.rm = TRUE))
print(sd)</pre>
```

```
## Calcium Iron Protein Vitamin A Vitamin C
## 397.27754 5.98419 30.57576 1633.53983 73.59527
```

Q2:

```
intake = c(1000,15,60,800,75)
p_val = c();
for (i in 1:ncol(nutrient)){
   p = t.test(nutrient[i],alternative = c("two.sided"),mu = intake[i], paired = FALSE,con
   f.level = 0.95)$p.value
   p_val = c(p_val,p)
}
p_val
```

```
## [1] 2.108727e-104 6.654391e-58 3.299706e-07 5.102954e-01 1.477297e-01
```

```
ans = p_val > matrix(0.05,1,ncol(nutrient))
ans
```

```
## [,1] [,2] [,3] [,4] [,5]
## [1,] FALSE FALSE TRUE TRUE
```

Q3:

For Calcium, Iron, Protein we reject the hypotheses that the population mean of that variable equals the recommended values because their p-value are less than significance level.

For VitaminA and VitaminC, we don't have enough evidence to reject because their p-value are larger than significance level. Therefore, we conclude that the US women don't meet the recommended nutrient intake amount.

My recommendation is that US women should intake more food with rich Calcium and Iron while intaking a little bit less protein.

Problem2

Multiple data

```
multiple = read.table("~/Downloads/multiple.txt");
```

Q1:

```
p_val = c()
ans = c()
for (i in 1:50){
   p = t.test(multiple[i], alternative = c("two.sided"), mu = 0, paired = FALSE, conf.level
   = 0.9)$p.value
   p_val = c(p_val,p)
}
p_val
```

```
## [1] 7.477468e-34 1.030644e-32 1.613953e-33 5.107798e-37 4.299681e-35
## [6] 4.181053e-33 1.782424e-39 2.281744e-34 4.767758e-34 9.020768e-42
## [11] 8.501800e-01 3.387655e-01 8.433591e-01 2.353081e-01 8.346443e-01
## [16] 3.410084e-01 4.495285e-01 8.988573e-01 4.855360e-01 8.298508e-02
## [21] 7.435778e-01 4.344605e-01 5.521855e-01 4.775194e-01 7.573900e-01
## [26] 1.354197e-01 9.927262e-01 2.944327e-01 6.783256e-01 1.898939e-01
## [31] 4.716828e-01 9.302681e-02 4.736660e-01 9.189993e-01 2.138515e-01
## [36] 6.519921e-01 3.408716e-01 2.211123e-01 8.806238e-01 7.315268e-02
## [41] 7.171567e-01 6.472996e-01 6.915055e-01 2.475067e-02 2.191321e-01
## [46] 7.678119e-01 3.489369e-01 1.367531e-01 8.886784e-01 7.316609e-01
```

```
ans = p_val > matrix(0.1,1,50)
ans
```

So the population mean vector doesn't equal to a vector whose elements are all zeros.

Q2:

```
type1 = 4
type1

## [1] 4

type2 = 0
type2

## [1] 0

FWER = 1-(1-0.1)^50
FWER

## [1] 0.9948462

FDP = type1/(50-sum(ans))
FDP

## [1] 0.2857143
```

Number of Type 1 Error: 4 Number of Type 2 Error: 0

FWER: 0.9948462 FDP: 0.2857143

Q3:

```
p_B = c()
ans_B = c()
for (i in 1:50){
   p = t.test(multiple[i], alternative = c("two.sided"), mu = 0, paired = FALSE, conf.level
   = 0.9)$p.value
   p_B = c(p_B,p)
}
p_B
```

```
## [1] 7.477468e-34 1.030644e-32 1.613953e-33 5.107798e-37 4.299681e-35
## [6] 4.181053e-33 1.782424e-39 2.281744e-34 4.767758e-34 9.020768e-42
## [11] 8.501800e-01 3.387655e-01 8.433591e-01 2.353081e-01 8.346443e-01
## [16] 3.410084e-01 4.495285e-01 8.988573e-01 4.855360e-01 8.298508e-02
## [21] 7.435778e-01 4.344605e-01 5.521855e-01 4.775194e-01 7.573900e-01
## [26] 1.354197e-01 9.927262e-01 2.944327e-01 6.783256e-01 1.898939e-01
## [31] 4.716828e-01 9.302681e-02 4.736660e-01 9.189993e-01 2.138515e-01
## [36] 6.519921e-01 3.408716e-01 2.211123e-01 8.806238e-01 7.315268e-02
## [41] 7.171567e-01 6.472996e-01 6.915055e-01 2.475067e-02 2.191321e-01
## [46] 7.678119e-01 3.489369e-01 1.367531e-01 8.886784e-01 7.316609e-01
```

```
ans_B = p_B > matrix(0.1/50,1,50)
ans_B
```

```
FWER = 1-(1-0.1/50)^50
FWER
```

```
## [1] 0.09525318
```

```
power = 10/10
power
```

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

FWER:0.09525318

power:1

Q4:

```
p_value = c()
ans BH = c()
for (i in 1:50){
  p = t.test(multiple[i], alternative = c("two.sided"),mu = 0,paired = FALSE,conf.level
 = 0.9), "p.value"
 p_value = c(p_value,p)
}
bh <- function(p,alpha)</pre>
  m <- length(p)</pre>
  1 <- alpha*c(1:m)/m
  result <- matrix(TRUE,1,m)
  sort_p <- sort(p)</pre>
  set <- which(l>=sort_p)
  if(length(set)==0){
    rej <- set
  } else{
    imax <- max(set)</pre>
    threshold <- sort_p[imax]</pre>
    rej <- which(p <= threshold)</pre>
  result[rej] = FALSE;
  outlist<-list(result = result)</pre>
  return(outlist)
}
bh test <- bh(p value, 0.1)
p_value
```

```
## [1] 7.477468e-34 1.030644e-32 1.613953e-33 5.107798e-37 4.299681e-35
## [6] 4.181053e-33 1.782424e-39 2.281744e-34 4.767758e-34 9.020768e-42
## [11] 8.501800e-01 3.387655e-01 8.433591e-01 2.353081e-01 8.346443e-01
## [16] 3.410084e-01 4.495285e-01 8.988573e-01 4.855360e-01 8.298508e-02
## [21] 7.435778e-01 4.344605e-01 5.521855e-01 4.775194e-01 7.573900e-01
## [26] 1.354197e-01 9.927262e-01 2.944327e-01 6.783256e-01 1.898939e-01
## [31] 4.716828e-01 9.302681e-02 4.736660e-01 9.189993e-01 2.138515e-01
## [36] 6.519921e-01 3.408716e-01 2.211123e-01 8.806238e-01 7.315268e-02
## [41] 7.171567e-01 6.472996e-01 6.915055e-01 2.475067e-02 2.191321e-01
## [46] 7.678119e-01 3.489369e-01 1.367531e-01 8.886784e-01 7.316609e-01
```

```
ans_BH = bh_test$result
ans_BH
```

```
##
              [,2] [,3] [,4] [,5] [,6] [,7] [,8]
        [,1]
                                                     [,9] [,10] [,11]
## [1,] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE TRUE
##
       [,12] [,13] [,14] [,15] [,16] [,17] [,18] [,19] [,20] [,21] [,22]
## [1,] TRUE
             TRUE
                   TRUE
                        TRUE
                              TRUE
                                    TRUE
                                          TRUE
                                               TRUE
                                                     TRUE
                                                           TRUE
                                                                TRUE
##
       [,23] [,24] [,25] [,26] [,27] [,28] [,29] [,30] [,31] [,32] [,33]
## [1,] TRUE
             TRUE
                   TRUE
                        TRUE
                               TRUE
                                    TRUE
                                          TRUE
                                               TRUE
                                                     TRUE
                                                           TRUE
                                                                TRUE
##
       [,34] [,35] [,36] [,37] [,38] [,39] [,40] [,41] [,42] [,43] [,44]
                                          TRUE
                                               TRUE
## [1,] TRUE TRUE
                   TRUE
                        TRUE
                               TRUE
                                    TRUE
                                                      TRUE
                                                           TRUE
                                                                 TRUE
##
       [,45] [,46] [,47] [,48] [,49] [,50]
## [1,] TRUE TRUE
                   TRUE
                        TRUE
                               TRUE
                                    TRUE
```

```
FDP = 0/sum(ans_BH)
FDP
```

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

```
power = 10/10
power
```

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

FDP: 0 power:1

By using BH method, we improve from the result of naive multiple testing and multiple testing with Bonferroni method.

In 2.1(naive multiple testing part), we have 4 Type I error, while we make no Type I error using BH method. For 2.3 and 2.4, type I and type II errors are the same(we make no errors), and thus they both work good for this case.