

Math189 Homework 2

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Problem 1

a)

```
nutrient=read.table("<https://www.math.ucsd.edu/~wez243/data/nutrient.txt>",
header = F)

# we can also save it to our working directory and use read.table("nutrient.txt")
instead

colnames(nutrient) <- c(" ", "Calcium", "Iron", "Protein", "Vitamin_A",
"Vitamin_C")

for (i in 2:6) {print (paste ('for', colnames(nutrient)[i-1], ', its mean =',
mean(nutrient[,i]), 'and standard deviation =', sd(nutrient[,i])))}
```

```
[1] "for Calcium , its mean = 624.049253731343 and standard deviation = 397.277540103266"
[1] "for Iron , its mean = 11.1298995929444 and standard deviation = 5.98419047008833"
[1] "for Protein , its mean = 65.8034409769335 and standard deviation = 30.5757564314087"
[1] "for Vitamin_A , its mean = 839.635345997286 and standard deviation = 1633.53982830006"
[1] "for Vitamin_C , its mean = 78.9284464043419 and standard deviation = 73.59527211824"
```

b)

```
> t.test(nutrient$Calcium, alternative = "t", mu = 1000, conf.level = 0.95)
```

One Sample t-test

```
data: nutrient$Calcium
t = -53.054, df = 736, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 1000
95 percent confidence interval:
 444.4321 484.0808
sample estimates:
mean of x
 464.2564
```

```
> t.test(nutrient$Iron, alternative = "t", mu = 15, conf.level = 0.95)
```

One Sample t-test

```
data: nutrient$Iron
t = 41.619, df = 736, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 15
95 percent confidence interval:
 595.3201 652.7784
sample estimates:
mean of x
 624.0493
```

```
> t.test(nutrient$Protein, alternative = "t", mu = 60, conf.level = 0.95)
```

One Sample t-test

```

data:  nutrient$Protein
t = -221.7, df = 736, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 60
95 percent confidence interval:
 10.69715 11.56265
sample estimates:
mean of x
 11.1299

> t.test(nutrient$Vitamin_A, alternative = "t", mu = 800, conf.level = 0.95)

```

One Sample t-test

```

data:  nutrient$Vitamin_A
t = -651.88, df = 736, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 800
95 percent confidence interval:
 63.59235 68.01453
sample estimates:
mean of x
 65.80344

> t.test(nutrient$Vitamin_C, alternative = "t", mu = 75, conf.level = 0.95)

```

One Sample t-test

```

data:  nutrient$Vitamin_C
t = 12.707, df = 736, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 75
95 percent confidence interval:
 721.5057 957.7650
sample estimates:
mean of x
 839.6353

```

c)

From part 2), we found that the p-values of Calcium, Iron and Protein are too small. Then, we should reject our null hypothesis which states that the amount of these three nutrients equals to the recommended intake amount. Next, we conducted a one-sided(greater) test and found out that we should reject our hypothesis for Protein amount. Therefore, we disagree that the US women meet the recommended nutrient intake amount and suggest them to take more protein but less calcium and iron.

```

> t.test(nutrient$Calcium, alternative = "greater", mu = 1000, conf.level = 0.95)

```

One Sample t-test

```
data:  nutrient$Calcium
t = -25.69, df = 736, p-value = 1
alternative hypothesis: true mean is greater than 1000
95 percent confidence interval:
 599.9483      Inf
sample estimates:
mean of x
 624.0493

> t.test(nutrient$Iron, alternative = "greater", mu = 15, conf.level = 0.95)
```

One Sample t-test

```
data:  nutrient$Iron
t = -17.557, df = 736, p-value = 1
alternative hypothesis: true mean is greater than 15
95 percent confidence interval:
 10.76687      Inf
sample estimates:
mean of x
 11.1299

> t.test(nutrient$Protein, alternative = "greater", mu = 60, conf.level = 0.95)
```

One Sample t-test

```
data:  nutrient$Protein
t = 5.1528, df = 736, p-value = 1.65e-07
alternative hypothesis: true mean is greater than 60
95 percent confidence interval:
 63.94855      Inf
sample estimates:
mean of x
 65.80344
```

Problem 2**

a)

[illegible]

```
[1] "We reject our null hypothesis with significance level 0.1."

[1] "We fail to reject our null hypothesis with significance level 0.1."

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```

```
> print(paste("In total, we reject", sum, "null hypothesis with significance
level 0.1."))
[1] "In total, we reject 14 null hypothesis with significance level 0.1."
```

b)

```
type1 <- 0
for(i in 11:50){
  ttest <- t.test(multiple[,i], conf.level = 0.9)
  pv <- ttest$p.value
  if(pv < 0.1){type1 = type1 + 1}
}
print(paste("Type 1 Error = ", type1))
[1] "Type 1 Error = 4"
```

```
type2 <- 0
for(i in 1:10){
  ttest <- t.test(multiple[,i], conf.level = 0.9)
  pv <- ttest$p.value
  if(pv > 0.1){type2 = type2 + 1}
}
print(paste("Type 2 Error = ", type2))
[1] "Type 2 Error = 0"
```

```
fwer <- 1-(1-0.01)^50
print(paste("FWER = ", fwer))
[1] "FWER = 0.99484622479268"
```

```
fdp <- type1/sum
print(paste("FDP = ", fdp))
[1] "FDP = 0.285714285714286"
```

c)

```
padj <- c(1:50)
for(i in 1:50){
  ttest <- t.test(multiple[,i], conf.level = (1-0.1/50))
  padj[i] <- ttest$p.value
  if(padj[i] < (0.1/50)){
    print("We reject our null hypothesis with significance level 0.1.")
  }else{print("We fail to reject our null hypothesis with significance level
0.1.")}
}
```

[illegible]

[illegible]


```
"FWER = 0.0952531819959643"
```

Power = 1 since number of correct rejections equals to the number of false null hypothesis.

d)

```
bh_rej <- function(p,alpha)
  \## p: vector of p-values
  \## alpha: pre-specified FDR level
{
  m <- length(p)
  l <- alpha*c(1:m)/m
  sort_p <- sort(p) # sort p in ascending order
  set <- which(l>=sort_p)
  if(length(set)==0){
    rej <- set
    pvalue <- set
  } else
    imax <- max(set)
    threshold <- sort_p[imax]
    rej <- which(p <= threshold)
    pvalue <- p[rej]
  }
  outlist<-list(pvalue=pvalue, rej=rej)
  return(outlist)
}
\## Calculate marginal p-values
\# Method 1: use for loop
p <- numeric(50)
for(j in 1:50){
  t_test <- t.test(multiple[,j], mu = 0)
  p[j] <- t_test$p.value
}
\## Apply BH method
alpha <- 0.1
bh_test <- bh_rej(p,alpha)
\## Examine conclusions
R <- length(bh_test$rej)
\# total number of rejections
V <- length(which(bh_test$rej>10))
\# number of false rejections
fdp <- V/max(1,R)
\# false discovery proportion
```

```
print(paste("FDP =", fdp))
```

```
"FDP = 0"
```

```
Power = 1 since number of false rejections(V) is 0
```