# Math189 HW3

# **Group Members:**

Yaqi Chen (PID: A15742547; Section: A03)

Yuetong Lyu (PID: A13779993; Section: A04)

Siyi He (PID: A13400569; Section: A03)

Zhenyuan Xu (PID: A92067995; Section: A02)

liawei Chao (PID: A13818001; Section: A02)

# **Problem 1**

#### Part a

```
Water <- read.table("water.txt", header = TRUE)
t.test(Water$bottom, Water$surface, aternative = "t", paired = T)</pre>
```

```
t.test(Water$bottom, Water$surface, aternative = "t", paired = T)

Paired t-test

data: Water$bottom and Water$surface
t = 4.8638, df = 9, p-value = 0.0008911
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
    0.043006 0.117794
sample estimates:
mean of the differences
    0.0804
```

Here we treated the dataset as a paired sample and got a small p-value that is fair enough to reject our null hypothesis. Thus, we conclude that the mean zinc concentration in bottom water is the same as that in surface.

#### Part b

The independence of the two samples can influence our t-test result. If two groups are dependent, we must use a paired t-test instead of an independent two sample t-test. Otherwise, our answer would be wrong since there are two different formulas to get the standard error in our t-test. If two samples are related, the errors will be related as well. They will form different t-distribution compared to the situation when these two samples are independent. Violation of this assumption will result in inaccurate p-value.

### **Problem 2**

#### Part a

### Setup

```
install.packages('HSAUR3')
library("HSAUR3")
data("pottery")
pottery
site1 <- subset(pottery, kiln == 1)</pre>
site2 <- subset(pottery, kiln == 2)</pre>
site4 <- subset(pottery, kiln == 4)</pre>
site5 <- subset(pottery, kiln == 5)</pre>
len1 <- length(site1$Al203)</pre>
len2 <- length(site2$Al203)</pre>
len2
len4 <- length(site4$Al203)</pre>
len5 <- length(site5$Al203)</pre>
len <- c(len1,len2,0,len4,len5)</pre>
c < -c(1,2,4,5)
mean(pottery[,1])
```

```
mean(subset(pottery, kiln == 1)[,1])
mean(subset(pottery, kiln == 5)[,1])
chemicals <- c('Al203', 'Fe203', 'Mgo', 'CaO', 'Na20', 'K2O', 'TiO2', 'MnO', 'BaO')</pre>
```

#### #f stat

```
Fstatistic <- c()</pre>
for (k in 1:9){
  error_sum <- 0
  treat sum <- 0
  whole_mean <- mean(pottery[,k])</pre>
  for (i in c){
   mean <- mean(subset(pottery, kiln == i)[,k])</pre>
    n \leftarrow len[i]
    treat_sum <- treat_sum + n * ((mean-whole_mean)^2)</pre>
    subpottery <- subset(pottery, kiln == i)</pre>
    for (j in 1:n){
      difference <- (subpottery[j,k] - mean)^2</pre>
      error_sum <- error_sum + difference</pre>
    }
  }
  treat <- treat_sum / 3</pre>
  error <- error_sum / 39
  \#print (paste(treat,error))
  ans = treat/error
```

```
print (paste(chemicals[k], ans))

Fstatistic <- c(Fstatistic, ans)
}</pre>
```

```
[1] "Al203 26.2034498265741"
[1] "Fe203 154.326776387811"
[1] "Mgo 97.9157560767963"
[1] "CaO 53.5350307231462"
[1] "Na2O 10.5266992234656"
[1] "K2O 82.3564640243008"
[1] "TiO2 14.8485513138411"
[1] "MnO 52.8034239690174"
[1] "BaO 0.480014498907605"
```

#### Part b

#### #Bonferroni

```
lower <- qf(0.05/9,3,39) #0.02537717
upper <- qf(1-0.05/9,3,39) #4.892638
for (i in 1:9){
   if ((Fstatistic[i] < upper) & (Fstatistic[i] > lower)){
      print(paste('We fail to reject the null hypothesis for', chemicals[i]))
   }
   else{print(paste('We reject the null hypothesis for', chemicals[i]))}
}
```

```
[1] "We reject the null hypothesis for Al203"
[1] "We reject the null hypothesis for Fe203"
[1] "We reject the null hypothesis for Mgo"
[1] "We reject the null hypothesis for CaO"
[1] "We reject the null hypothesis for Na20"
[1] "We reject the null hypothesis for K20"
[1] "We reject the null hypothesis for TiO2"
[1] "We reject the null hypothesis for MnO"
[1] "We fail to reject the null hypothesis for BaO"
```

Given only the F statistics of BaO is between 0.0254 and 4.893, we will still reject Ho and conclude that the first eight chemical concentrations are different among the four sites.

### Part c

#BH

```
sort_F=sort(Fstatistic,decreasing=T)
rejection<-numeric(9)
for(i in 1:9){
  lower = qf(i*0.05/9,3,39) #0.1163315
  upper=qf(1-i*0.05/9,3,39) #2.845068
  if((sort_F[i]>upper) & (sort_F[i]<lower)){
    print(paste('We reject the null hypothesis for', chemicals[i]))
    }else{
    print(paste('We fail to reject the null hypothesis for', chemicals[i]))
  }
}</pre>
```

```
[1] "We reject the null hypothesis for Al203"
[1] "We reject the null hypothesis for Fe203"
[1] "We reject the null hypothesis for Mgo"
[1] "We reject the null hypothesis for CaO"
[1] "We reject the null hypothesis for Na20"
[1] "We reject the null hypothesis for K20"
[1] "We reject the null hypothesis for TiO2"
[1] "We reject the null hypothesis for MnO"
[1] "We fail to reject the null hypothesis for BaO"
```

Still only the F statistics of BaO lies outside the critical values. Therefore, we reach the same conclusion as Bonferroni one. We reject the first eight hypothesis and Ho.