

STA305 Homework 1

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Question 1

Let y_1, y_2, y_3, y_4 be the readings from the scale for determining the unknown weights, $\beta_1, \beta_2, \beta_3, \beta_4$. The standard deviation of each weighing is denoted by σ . ϵ_1, \dots are independent errors.

(a)

$$y_1 = \beta_1 + \beta_2 + \beta_3 + \beta_4 + \epsilon_1$$

$$y_2 = \beta_1 + \beta_2 - \beta_3 - \beta_4 + \epsilon_2$$

$$y_3 = \beta_1 - \beta_2 + \beta_3 - \beta_4 + \epsilon_3$$

$$y_4 = \beta_1 - \beta_2 - \beta_3 + \beta_4 + \epsilon_4$$

(b)

View this problem as a linear regression problem: $y = X\beta + \epsilon$, where

$$y = (y_1, y_2, y_3, y_4)', X = \begin{bmatrix} 1 & 1 & 1 & 1 \\ 1 & 1 & -1 & -1 \\ 1 & -1 & 1 & -1 \\ 1 & -1 & -1 & 1 \end{bmatrix}, \beta = (\beta_1, \beta_2, \beta_3, \beta_4)'$$

The least-squares estimate of β is $\hat{\beta} = (X^T X)^{-1} X^T y$, which can be computed with the following R code:

```
1 > X <- matrix(c(1,1,1,1,1,1,-1,-1,1,-1,1,-1,1,-1,1),nrow=4,ncol=4)
2 > Y <- t(X)%*%X
3 > W <- solve(Y)
4 > W%*%t(X)
5      [,1] [,2] [,3] [,4]
6 [1,] 0.25 0.25 0.25 0.25
7 [2,] 0.25 0.25 -0.25 -0.25
8 [3,] 0.25 -0.25 0.25 -0.25
9 [4,] 0.25 -0.25 -0.25 0.25
```

So we get the least square estimates of β , specifically:

$$\begin{aligned}\hat{\beta}_1 &= \frac{1}{4} y_1 + \frac{1}{4} y_2 + \frac{1}{4} y_3 + \frac{1}{4} y_4 \\ \hat{\beta}_2 &= \frac{1}{4} y_1 + \frac{1}{4} y_2 - \frac{1}{4} y_3 - \frac{1}{4} y_4 \\ \hat{\beta}_3 &= \frac{1}{4} y_1 - \frac{1}{4} y_2 + \frac{1}{4} y_3 - \frac{1}{4} y_4 \\ \hat{\beta}_4 &= \frac{1}{4} y_1 - \frac{1}{4} y_2 - \frac{1}{4} y_3 + \frac{1}{4} y_4\end{aligned}$$

(c)

The covariance matrix of $\hat{\beta}$ is $(X^T X)^{-1} \sigma^2$.

```
1 > W
2      [,1] [,2] [,3] [,4]
3 [1,] 0.25 0.00 0.00 0.00
4 [2,] 0.00 0.25 0.00 0.00
5 [3,] 0.00 0.00 0.25 0.00
6 [4,] 0.00 0.00 0.00 0.25
```

So the standard error of each least-squares estimates of β_i is the same:
 $SD(\beta_1) = SD(\beta_2) = SD(\beta_3) = SD(\beta_4) = \sqrt{0.25\sigma^2} = 0.5\sigma$.

(d)

According to $\hat{\beta}_1 = \frac{1}{4} y_1 + \frac{1}{4} y_2 + \frac{1}{4} y_3 + \frac{1}{4} y_4$ and the other expressions of estimates of β_i ,
 $Var(\hat{\beta}_1) = Var(\hat{\beta}_2) = Var(\hat{\beta}_3) = Var(\hat{\beta}_4) = \frac{\sigma^2}{4}$ because each y_1, y_2, y_3, y_4 weighing has variance σ^2 .
 So the same precision with the design would require 4 times as many measurements (twice is not enough).

(e)

Suppose $z = (z_1, z_2, z_3, z_4)'$ are four readings from this digital scale, $\sigma/2$ is the standard deviation,
 $\epsilon_d = (\epsilon_{d1}, \epsilon_{d2}, \epsilon_{d3}, \epsilon_{d4})'$ are independent errors, so we have following:

$$\begin{aligned}z_1 &= \beta_1 + \beta_2 + \beta_3 + \beta_4 + \epsilon_{d1} \\ z_2 &= \beta_1 + \beta_2 + \epsilon_{d2} \\ z_3 &= \beta_1 + \beta_3 + \epsilon_{d3} \\ z_4 &= \beta_1 + \beta_4 + \epsilon_{d4}\end{aligned}$$

$$X_d = \begin{bmatrix} 1 & 1 & 1 & 1 \\ 1 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 \\ 1 & 0 & 0 & 1 \end{bmatrix}$$

Similarly, the least-squares estimates of the weights is represented by $\hat{\beta} = (X_d^T X_d)^{-1} X_d^T z$ and the covariance matrix is represented by $(X_d^T X_d)^{-1} \sigma^2/4$.

```

1 > Xd <- matrix(c(1,1,1,1,1,1,0,0,1,0,1,0,1,0,0,1),ncol=4,nrow=4)
2 > Xd
3      [,1] [,2] [,3] [,4]
4 [1,]    1    1    1    1
5 [2,]    1    1    0    0
6 [3,]    1    0    1    0
7 [4,]    1    0    0    1
8 > solve(t(Xd)%*%Xd) #covariance matrix
9      [,1] [,2] [,3] [,4]
10 [1,]  1.0 -0.5 -0.5 -0.5
11 [2,] -0.5  1.0  0.0  0.0
12 [3,] -0.5  0.0  1.0  0.0
13 [4,] -0.5  0.0  0.0  1.0
14 > solve(t(Xd)%*%Xd)%*%t(Xd)
15      [,1] [,2] [,3] [,4]
16 [1,] -0.5  0.5  0.5  0.5
17 [2,]  0.5  0.5 -0.5 -0.5
18 [3,]  0.5 -0.5  0.5 -0.5
19 [4,]  0.5 -0.5 -0.5  0.5

```

$$\begin{aligned}\hat{\beta}_1 &= -\frac{1}{2} z_1 + \frac{1}{2} z_2 + \frac{1}{2} z_3 + \frac{1}{2} z_4 \\ \hat{\beta}_2 &= \frac{1}{2} z_1 + \frac{1}{2} z_2 - \frac{1}{4} y_3 - \frac{1}{4} y_4 \\ \hat{\beta}_3 &= \frac{1}{2} y_1 - \frac{1}{2} z_2 + \frac{1}{2} z_3 - \frac{1}{2} z_4 \\ \hat{\beta}_4 &= \frac{1}{2} z_1 - \frac{1}{2} z_2 - \frac{1}{2} z_3 + \frac{1}{2} z_4\end{aligned}$$

$$SD(\beta_1) = SD(\beta_2) = SD(\beta_3) = SD(\beta_4) = \sqrt{1 \times \sigma^2/4} = \sigma/2$$

Since both methods have the same standard error of the weights, so they are similarly accurate, i.e. using a digital scale yields no higher precision.

Question 2

(a)

Brand A has 8 judges, there can be $\binom{15}{8}$ ways to assign judges for Brand A, and then for the rest of judges, there is only $\binom{7}{7}$ way to be assigned to Brand B, so therefore total number of ways to assign 15 judges is:

```
1 > choose(15,8)
2 [1] 6435
```

(b)

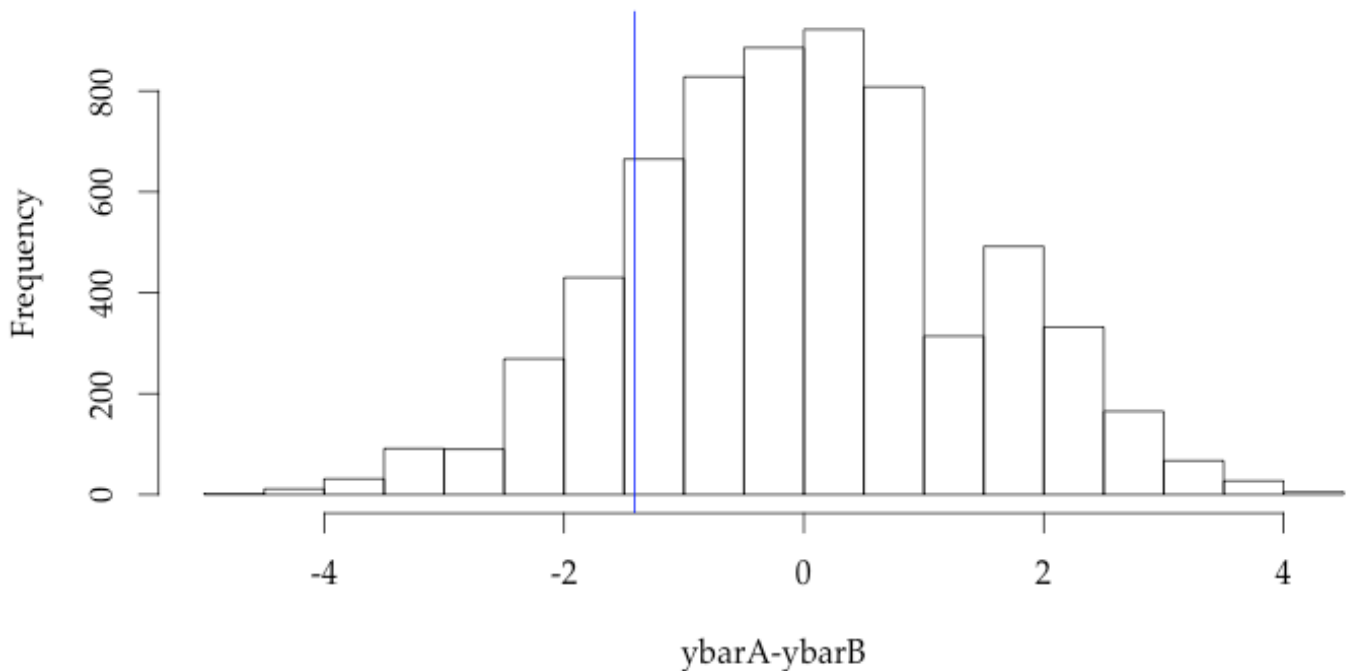
We are interested in whether Brand B tastes better than Brand A. The null and alternative hypotheses of interest are:

- H_0 : Brand B tastes the same as Brand A.
- H_1 : Brand B has a better taste than Brand A.

And we calculate one-sided randomization p-value.

```
1 > ya <- c(2,4,2,1,9,9,2,2)
2 > yb <- c(8,3,5,3,7,7,4)
3 > summary(ya);sd(ya)
4   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
5   1.000   2.000   2.000   3.875   5.250   9.000
6 [1] 3.270539
7 > summary(yb);sd(yb)
8   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
9   3.000   3.500   5.000   5.286   7.000   8.000
10 [1] 2.058663
11 > mean(ya)-mean(yb)
12 [1] -1.410714
13 > data <- c(ya,yb)
14 > N <- choose(15,8)
15 > res <- numeric(N)
16 > library(combinat)
17 > index <- combn(1:15, 8)
18 > for (i in 1:N) {res[i] <- mean(data[index[,i]])-mean(data[-index[,i]])}
19 > hist(res,xlab="ybarA-
ybarB", main="Randomization Distribution of difference in means",family="Palatino")
20 > observed <- mean(ya)-mean(yb)
21 > observed
22 [1] -1.410714
23 > abline(v=observed,col="blue")
```

Randomization Distribution of difference in means



```

1 > sum(res<=observed)
2 [1] 1225
3 > p <- sum(res<=observed)/N
4 > p
5 [1] 0.1903652

```

This means if we assume B tastes the same as A then the proportion of randomizations that would produce an observed mean difference less between A and B of at most -1.410714 is 0.1903652. That is to say, under H_0 , 19% of randomizations would produce an extreme or more extreme difference than the observed mean difference.

(c)

First we pick commonly used p-value 0.05 (significance level $\alpha = 0.05$). Since p-value from part(b) is $0.1903652 > 0.05$, observed data are consistent with H_0 , there is weak evidence against H_0 , fail to reject the null hypothesis. So there is no evidence of a significant difference between the tastes.

Question 3

(a)

Subject	Left	Right

1	A	B
2	B	A
3	B	A
4	B	A
5	B	A

(b)

Randomized paired comparison design, since each subject receives both treatment in a paired fashion.

(c)

$$Pr(\text{receive drug A in right eye}) = Pr(\text{coin toss result is Head}) = \frac{1}{2}$$

This is trivial, since the tossing has only two results: Head and tail. Head indicates drug A in right eye and correspondingly drug B in left eye. Tail indicates drug B in right eye and drug A in left eye.

(d)

The treatment allocation decided by 5 coin tossing could have $2^5 = 32$ different results.

$$Pr(4H, 1T) = \frac{5}{32}, Pr(3H, 2T) = Pr(2H, 3T) = \frac{10}{32} > Pr(4H, 1T).$$

If 1 tail is needed, it could be any of the five tosses, so the probability is $\frac{5}{32}$.

If 2 tails are needed, there are $4 + 3 + 2 + 1$ possible ways, so the probability is $\frac{10}{32}$.

And tails and heads are exchangeable, so 3 Heads 2 Tails and 2 Heads 3 Tails have the same possibility.

So this treatment allocation (4 Heads 1 Tail) is less likely than 3 Heads 2 Tails or 2 Heads 3 Tails.

(e)

As mentioned in part(d), we have 5 experimental units and we decide the drug distribution of each unit by flipping one fair coin, that makes each unit have 2 possible drug distributions. Then $2^5 = 32$ values are contained in this randomization, i.e. there are 32 possible treatment assignments. The probability of a treatment assignment is $\frac{1}{32}$.

(f)

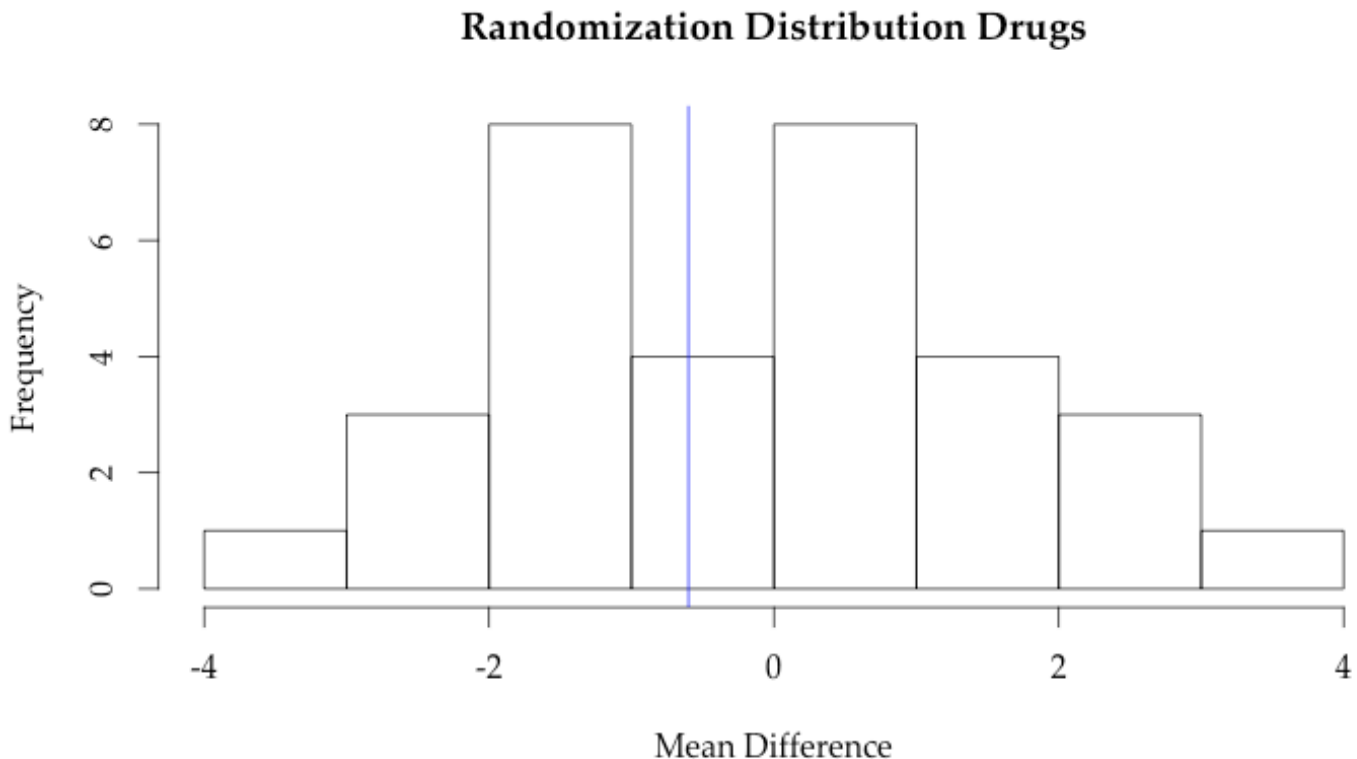
We are interested in whether there is a difference in intraocular pressure between the two drugs, so we need to calculate two-sided randomization p-value

```
1 > N <- 2^5
2 > res <- numeric(N)
3 > LR <- list(c(-1,1))
```

```

4 > trtassign <- expand.grid(rep(LR, 5))
5 > diff <- c(7-9,3-5,8-12,11-4,4-6)
6 > mean(diff)
7 [1] -0.6
8 > for(i in 1:N){res[i] <- mean(as.numeric(trtassign[i,])*diff)}
9 > hist(res,xlab="Mean Difference", main="Randomization Distribution Drugs", family="Palatino")
10 > abline(v=mean(diff),col="blue") # the line indicates observed difference -0.6, however since we consider absolute value of difference in this problem, this does not help too much
11 > tbar <- mean(res); tbar
12 [1] 0
13 > res
14 [1] 0.6 -0.2 -0.2 -1.0 -1.0 -1.8 -1.8 -2.6 3.4 2.6 2.6 1.8 1.8 1.0 1.0 0.2
15 [17] -0.2 -1.0 -1.0 -1.8 -1.8 -2.6 -2.6 -3.4 2.6 1.8 1.8 1.0 1.0 0.2 0.2 -0.6
16 > sum(abs(res-tbar)>=abs(mean(diff)-tbar))
17 [1] 26
18 > sum(abs(res-tbar)>=abs(mean(diff)-tbar))/N
19 [1] 0.8125

```



There are 26 out of 32 results having absolute mean difference larger than observed 0.6 with p-value > 0.05. We fail to reject null hypothesis, so there is no significant evidence of difference intraocular pressure between two drugs.

Question 4

(a)

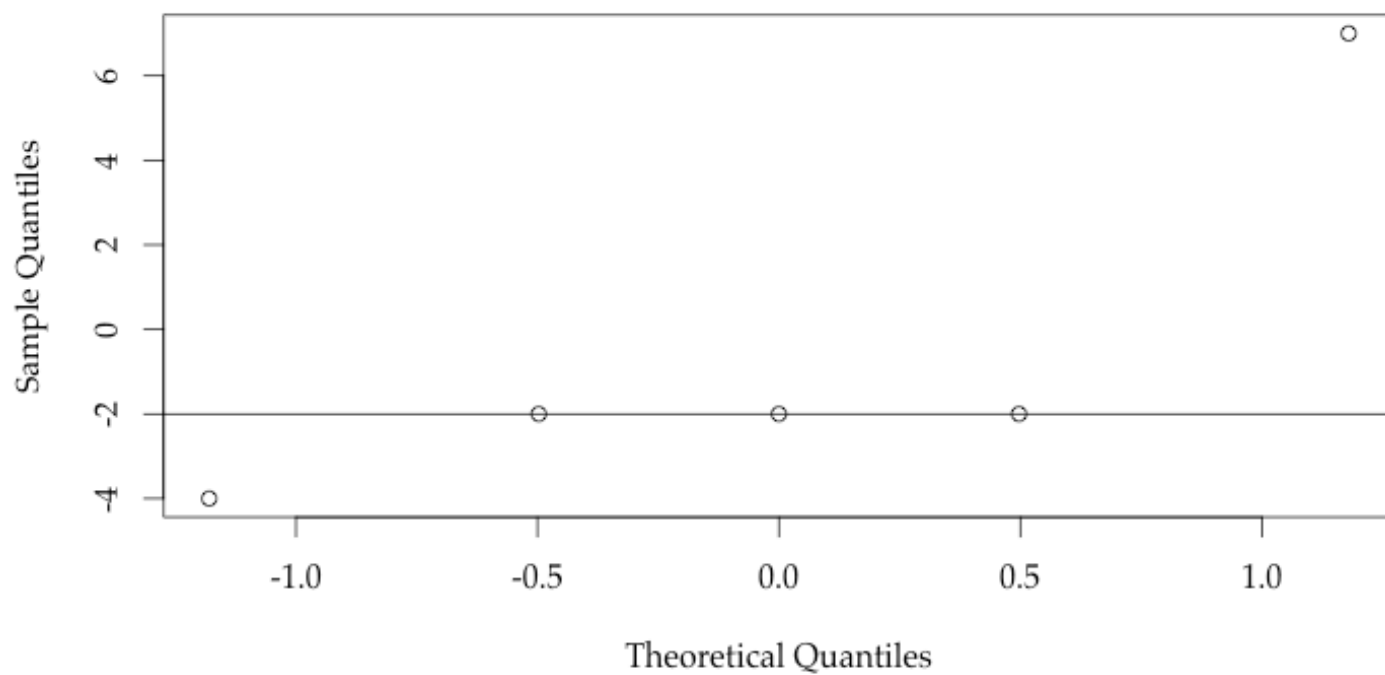
One of the assumptions of t-test is that we need the differences follow a normal distribution, so that the Q-Q Plot should be a straight diagonal line. But according to the plot shown below, it's not an ideal diagonal line. (Probably things would be better if we conduct the same method on a larger data, as the dots are more likely to be on a straight line.)

The other assumption of t-test is that the data are independently observed. In this case, the experimental subjects are 5 different, independent people, so the assumption is fulfilled.

(b)

```
1 > A <- c(7,3,8,11,4)
2 > B <- c(9,5,12,4,6)
3 > t.test(A,B,paired=TRUE,alternative="two.sided")
4
5     Paired t-test
6
7 data:  A and B
8 t = -0.30943, df = 4, p-value = 0.7724
9 alternative hypothesis: true difference in means is not equal to 0
10 95 percent confidence interval:
11  -5.983727  4.783727
12 sample estimates:
13 mean of the differences
14      -0.6
15
16 > diff <- A-B; diff
17 [1] -2 -2 -4  7 -2
18 > qqnorm(diff,family="Palatino"); qqline(diff)
```


Normal Q-Q Plot



Therefore, the p-value of two-tailed t-test (0.7724) is similar to previous one from randomization test (0.8125). We claim that two methods agree.