

▼ Statistical Data Analysis Problem sheet 3

1. Exercise 1

```
✓ [37] 1 #importing all the libraries  
Ds      2 import pandas as pd  
        3 import numpy as np
```

```
✓ [38] 1 #getting the X values as a dataframe  
Ds      2 dfx = pd.read_csv('/content/drive/MyDrive/1-DS/X.txt', sep=",", header=None)
```

```
✓ [39] 1 #getting the Y values as a dataframe  
Ds      2 dfy = pd.read_csv('/content/drive/MyDrive/1-DS/Y.txt', header= None)
```

Now we need to convert them into matrix

```
[40] 1 #converting to numpy array to get matrix  
      2 x = dfx.to_numpy()  
      3 y = dfy.to_numpy()
```

```
✓ [41] 1 #adding an identity column to the x to equalize the full rank p + 1  
Ds      2 x = np.insert(x, 0, 1.0, axis=1)
```

As the LS estimator is equivalent to the ML estimator based on the maximization of the log likelihood, we can estimate the beta hat from it.

```
✓ [42] 1 #beta hat estimating  
Ds      2 xt = np.transpose(x)  
        3 xtx = xt.dot(x)  
        4  
        5 beta = np.linalg.inv(xtx).dot(xt).dot(y)  
        6 beta
```

```
[42] 1 #beta hat estimating
      2 xt = np.transpose(x)
      3 xtx = xt.dot(x)
      4
      5 beta = np.linalg.inv(xtx).dot(xt).dot(y)
      6 beta
```

```
array([[ -0.00800698],
       [  0.88161162],
       [-2.45938171],
       [-0.97715699]])
```

- Here we get B_0, B_1, B_2 and B_3 for the multiple linear regression model
- As the mean is 0 and the constant variance is 1 which gives us that N is a standard normal distribution.



```
1 #now we can get the sigma hat square in the multiple linear regression model
2 sgms = (np.transpose(y-x.dot(beta))*(y-x.dot(beta))) / 201
3 sgms
```

```
array([[ 1.43756944e-04, -2.60179376e-04,  4.88288715e-05, ...,
        -8.27929177e-04, -5.93215518e-04, -6.80968604e-04],
       [-2.60179376e-04,  4.70887219e-04, -8.83732288e-05, ...,
        1.49843263e-03,  1.07363470e-03,  1.23245515e-03],
       [ 4.88288715e-05, -8.83732288e-05,  1.65853462e-05, ...,
        -2.81216658e-04, -2.01493183e-04, -2.31299633e-04],
       ...,
       [-8.27929177e-04,  1.49843263e-03, -2.81216658e-04, ...,
        4.76823381e-03,  3.41646407e-03,  3.92185420e-03],
       [-5.93215518e-04,  1.07363470e-03, -2.01493183e-04, ...,
        3.41646407e-03,  2.44791410e-03,  2.81002872e-03],
       [-6.80968604e-04,  1.23245515e-03, -2.31299633e-04, ...,
        3.92185420e-03,  2.81002872e-03,  3.22571018e-03]])
```

```
[44] 1 #now we can also get the adjusted estimator of the variance hat
      2 sgad = ((np.transpose(y).dot(y))- (np.transpose(beta).dot(xt).dot(y))) / (201 - 3 - 1)
      3 sgad
```

```
array([[0.97422819]])
```

Statistical Data Analysis

problem sheet 3



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2)

i) Here,

least squares estimator $\hat{\beta} = (X^T X)^{-1} X^T y$

and REML estimator $\hat{\sigma}_{ad}^2 = \frac{1}{n-p-1} \hat{e}^T \hat{e}$

Now, $\text{Cov}(\hat{\beta}) = \text{Cov}((X^T X)^{-1} X^T y)$ [Plugging $\hat{\beta}$ value]

We know, $\text{Cov}(xy) = E[(xy - E[xy])(xy - E[xy])^T]$ ⁽ⁱ⁾

$$= E[x(y - E[y]) - (y - E[y])^T x^T]$$

$$= X E[(y - E[y])(y - E[y])^T] X^T$$

$$= X \text{Cov}(y) X^T \quad [\text{putting value of } \text{Cov}(y)]$$

By using (ii) in (i), we get,

$$\text{Cov}(\hat{\beta}) = (X^T X)^{-1} X^T \text{Cov}(y) [(X^T X)^{-1} X^T]^T$$

$$= (X^T X)^{-1} X^T \text{Cov}(y) X [(X^T X)^{-1}]^T$$

$$= (X^T X)^{-1} X^T X [(X^T X)^{-1}]^T \text{Cov}(y)$$

$$= (X^T X)^{-1} (X^T X) (X^T X)^{-1} \text{Cov}(y)$$

$$= (X^T X)^{-1} \text{Cov}(y)$$

$$\therefore \text{Cov}(\hat{\beta}) = \sigma^2 (X^T X)^{-1} \quad [\text{Cov}(y) = \sigma^2 I]$$

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(ii)

Here, $\hat{e} = y - X\hat{\beta}$ [with respect to ϵ]

$$= y - X(X^T X)^{-1} X^T y$$

$$= y(I_n - X(X^T X)^{-1} X^T)$$

$$= (X\beta + \epsilon)(I_n - X(X^T X)^{-1} X^T)$$

$$= X\beta - X(X^T X)^{-1} X^T X\beta + (I_n - X(X^T X)^{-1} X^T)\epsilon$$

Now,

$$(X^T X)^{-1} X^T X = I_{p+1}$$

$$= X\beta - X\beta + (I_n - X(X^T X)^{-1} X^T)\epsilon$$

$$= (I_n - X(X^T X)^{-1} X^T)\epsilon \quad \left[\text{linear properties of } \epsilon \right]$$

$$= M\epsilon$$

Here, $M = (I_n - X(X^T X)^{-1} X^T)$ is a symmetric and idempotent matrix.

$$\hat{e}^T \hat{e} = \epsilon^T M^T M \epsilon = \epsilon^T M \epsilon$$

here we get a scalar. Using trace operators 'tr' we get,

$$E[\hat{e}^T \hat{e}] = E[\epsilon^T M \epsilon]$$

$$= E[\text{tr}(\epsilon^T M \epsilon)]$$

$$= E[\text{tr}(M \epsilon \epsilon^T)]$$

$$= \text{tr}(M E[\epsilon \epsilon^T])$$

$$= \text{tr}(M \sigma^2 I_n)$$

$$= \sigma^2 \text{tr}(M)$$



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Now, plugging the value of M ,

$$E[\hat{\epsilon}^T \hat{\epsilon}] = \sigma^2 \text{tr}(\mathbf{I}_n - \mathbf{X}(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T)$$

$$= \sigma^2 [\text{tr}(\mathbf{I}_n) - \text{tr}(\mathbf{X}(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T)]$$

$$= \sigma^2 (n-p-1) \quad [\text{using } \text{tr}(A+B) \dots \textcircled{1}]$$

$$\text{So, } E[\hat{\sigma}^2] = E\left[\frac{1}{n-p-1} \hat{\epsilon}^T \hat{\epsilon}\right]$$

$$= E\left[\frac{1}{n-p-1} \cdot \sigma^2 (n-p-1)\right] \quad [\text{using } \textcircled{1}]$$

$$= \sigma^2 \quad (\text{shown})$$

③ The corresponding statistical model is the Hardy-Weinberg model. It is used to compare gene frequencies in each population over a period of time. According to its principle, at equilibrium, the gene or the allele frequencies within a population will be same in each all generations. A population of alleles must meet five rules to be considered "in equilibrium":

- ① No occurrences of allele changes
- ② No migration in or out of the population.
- ③ Random mating must occur.



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④ No genetic drift

⑤ No natural selection.

environmental change may occur. In this rules.

To solve the equilibrium question we need,

$$p + q = 1$$

$$p^2 + 2pq + q^2 = 1$$

Here, p is the frequency of the dominant allele.

q is the frequency of the recessive allele.

p^2 is the frequency of individuals with the homozygous dominant genotype.

$2pq$ is the frequency of individuals with the heterozygous genotype.

q^2 is the frequency of individuals with the homozygous recessive genotype.

Now, Given, alleles are AA, Aa, aa .

there, allele frequencies are equal to the products of the corresponding allele frequencies.

Thus, $p_{AA} = p_x = p^2$

$$p_{Aa} = p_y = 2p(1-p)$$

$$p_{aa} = p_z = (1-p)^2$$



Now, the likelihood of P is:

$$L(P) = \frac{n!}{x!y!z!} (p^x)^x [2p(1-p)]^y [(1-p)^2]^z$$

The natural log likelihood of ~~P~~ P is

$$l(P) = \ln(n!) - \ln(x!) - \ln(y!) - \ln(z!) + \ln(p^{2x}) \\ + \ln 2p^y + \ln(1-p)^y + \ln(1-p)^{2z}$$

$$= \ln(n!) - \ln(x!) - \ln(y!) - \ln(z!) + 2x \ln(p)$$

$$+ \ln(2) + y \ln(p) + y \ln(1-p) + 2z \ln(1-p)$$

..... (i)

Now, we will take a derivative respect to P .

$$\therefore \frac{d}{dp} l(P) = \frac{d}{dp} [2x \ln(p)] + \frac{d}{dp} [y \ln(p)] + \frac{d}{dp} [y \ln(1-p)] \\ + \frac{d}{dp} [2z \ln(1-p)]$$

$$= \frac{2x}{p} + \frac{y}{p} - \frac{y}{(1-p)} - \frac{2z}{(1-p)}$$

$$= \frac{2x+y}{p} - \frac{2z+y}{1-p} \dots \dots \dots (ii)$$

To estimate p , the derivative = 0.

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$$\therefore \frac{2x+y}{p} - \frac{2z+y}{1-p} = 0$$

$$\text{or, } \frac{2x+y}{p} = \frac{2z+y}{1-p}$$

$$\text{or, } (1-p)(2x+y) = 2zp + py$$

$$\text{or, } 2x+y - 2xp - py - py = 2zp$$

$$\text{or, } 2p(x+y+z) = 2x+y$$

$$\text{or, } p = \frac{2x+y}{2(x+y+z)} \quad [\because x+y+z=n]$$

\therefore Maximum likelihood estimator for $p = \frac{2x+y}{2n}$.