

Ma 3 - Problem Set 5

Marco Yang

2237027

RIP couldn't hit the buzzer beater gradescope submission so taking a 1 day extension on this.

1. (25 points) Find the MLE of θ when X_1, X_2, \dots, X_n are i.i.d. random samples and each X_i has a distribution given by the density function $f(x) = \frac{1}{2}e^{-|x-\theta|}$, $-\infty < x < \infty$.

Solution: The probability that every X_i came from this distribution is

$$P = \prod_{i=1}^N f(X_i) = \prod_{i=1}^N \frac{1}{2} e^{-|X_i - \theta|} = \frac{1}{2^N} e^{-\sum_{i=1}^N |X_i - \theta|}.$$

Maximizing this probability occurs at the critical point, e.g. when $\frac{\partial L}{\partial \theta} = 0$.

$$\begin{aligned} \frac{\partial L}{\partial \theta} &= \frac{1}{2} e^{-\sum_{i=1}^N |X_i - \theta|} \cdot \left(-\sum_{i=1}^N |X_i - \theta| \cdot \text{sign}(X_i - \theta) \right) \\ &= \frac{1}{2} e^{-\sum_{i=1}^N |X_i - \theta|} \cdot \left(-\sum_{i=1}^N (X_i - \theta) \right) \\ &= -\frac{1}{2} e^{-\sum_{i=1}^N |X_i - \theta|} \left(\sum_{i=1}^N (X_i - \theta) \right) \end{aligned}$$

We know that $\sum_{i=1}^N (X_i - \theta) = 0$ when $\theta = \sum_{i=1}^N X_i / N$. Thus, θ is the mean of the X_i .

2. (25 points) The MSE of an estimator is given by $\text{MSE}(\hat{\theta}) = \mathbb{E}[(\hat{\theta} - \theta)^2]$. Show that

$$\text{MSE}(\hat{\theta}) = \text{Var}(\hat{\theta}) + \text{Bias}(\hat{\theta})^2.$$

Solution: Note that θ , the true value, is independent of $\hat{\theta}$, our estimator. Thus, we can take it out of any expected values of γ w.r.t. $\hat{\theta}$ as if it were a constant.

$$\begin{aligned} \text{MSE}(\hat{\theta}) &= \mathbb{E}[(\hat{\theta} - \theta)^2] \\ &= \mathbb{E}[\hat{\theta}^2 - 2\theta\hat{\theta} + \theta^2] \\ &= \mathbb{E}[\hat{\theta}^2] - 2\mathbb{E}[\theta\hat{\theta}] + \mathbb{E}[\theta^2] \\ &= \mathbb{E}[\hat{\theta}^2] - 2\theta\mathbb{E}[\hat{\theta}] + \theta^2 \\ &= \theta^2 - 2\theta\mathbb{E}[\hat{\theta}] + \mathbb{E}[\hat{\theta}]^2 + \mathbb{E}[\hat{\theta}^2] - \mathbb{E}[\hat{\theta}]^2 \\ &= (\mathbb{E}[\hat{\theta}^2] - \mathbb{E}[\hat{\theta}]^2) + (\mathbb{E}[\hat{\theta}] - \theta)^2 \\ &= \text{Var}(\hat{\theta}) + \text{Bias}(\hat{\theta})^2. \end{aligned}$$

3. (25 points) Let X_1, X_2, \dots, X_n be an i.i.d. random sample where X_i are distributed according to $U(0, \theta)$, i.e. a uniform distribution on $[0, \theta]$ where θ is unknown.

(a) Find $E(X)$ if $X \sim U(0, \theta)$.

Solution:

$$E(X) = \frac{1}{N} \sum_{i=1}^N \mathbb{E}[X_i] = \frac{1}{N} \sum_{i=1}^N \mathbb{E}[U(0, \theta)] = \frac{1}{N} \sum_{i=1}^N \frac{\theta}{2} = \frac{\theta}{2}.$$

(b) Show that the estimator $\hat{\theta} = 2 \cdot \bar{x}$ is unbiased.

Solution: Plugging in $X_i \sim U(0, \hat{\theta}) = U(0, 2 \cdot \bar{x})$,

$$E(X) = \frac{1}{N} \sum_{i=1}^N \mathbb{E}[X_i] = \frac{1}{N} \sum_{i=1}^N \mathbb{E}[U(0, 2 \cdot \bar{x})] = \frac{1}{N} \sum_{i=1}^N \bar{x} = \bar{x}.$$

Since $E(X) = \bar{x}$ when $\hat{\theta} = 2 \cdot \bar{x}$, the estimator is unbiased.

(c) Find the MLE for θ .

Solution: The probability density for $U(0, \theta)$ is $\frac{1}{\theta}$. Thus, the likelihood of getting our sample X_i (or any valid sample) is

$$p = \prod_{i=1}^n \frac{1}{\theta} = \theta^{-n}.$$

Taking the derivative w.r.t. θ ,

$$\frac{dp}{d\theta} = -n\theta^{-n-1}.$$

Setting this to 0,

$$\frac{dp}{d\theta} = -n\theta^{-n-1} = 0 \implies \theta = 0.$$

However, this doesn't make sense since if $\theta = 0$, then we know that all values of X must be 0, but we are constrained by the value we sampled. What we can do is notice that p is maximized for values of θ closer to 0. Thus, we need to minimize θ given the sample, which would make $\theta = \max(X_i)$.

(d) Compare the MSE for the two estimators, which one is lower?

Solution: The MSE for $\hat{\theta} = 2 \cdot \bar{x}$ is

$$\sum_{i=1}^n \left(X_i - \frac{2}{n} \sum_{i=1}^n X_i \right)^2.$$

Let $\max(X_i) = m$. The MSE for $\theta = \max(X_i)$ is

$$\sum_{i=1}^n (X_i - m)^2.$$

Subtracting the first from the second,

$$\begin{aligned}\Delta &= \sum_{i=1}^n \left(2X_i - \frac{2}{n} \sum_{i=1}^n X_i - m \right) \cdot \left(\frac{2}{n} \sum_{i=1}^n X_i + m \right) \\ &= (2\bar{x} + m) \cdot \left(\left(2 \sum_{i=1}^n (X_i - \bar{x}) \right) - mn \right) \\ &= (2\bar{x} + m)(-mn) \\ &= -mn(2\bar{x} + m) < 0.\end{aligned}$$

Thus, $\theta = \max(X_i)$ has a lower MSE.

4. (25 points) (**Hardy-Weinberg.**) Suppose that a particular gene occurs as one of two alleles (A and a), where allele A has a frequency $\theta \in (0, 1)$ in the population. That is, a random copy of the gene is A with probability θ and a with probability $1 - \theta$. Since a diploid genotype consists of two genes, the probability of each genotype is

$$P(AA) = \theta^2 \quad P(Aa) = 2\theta(1 - \theta) \quad P(aa) = (1 - \theta)^2.$$

Suppose we test a random sample of people and find that n_1 are AA , n_2 are Aa , and n_3 are aa . Find the MLE $\hat{\theta}_n$. Make sure to verify that is indeed maximizing, by computing the second derivative of the function you are maximizing.

Solution: The probability of getting the samples n_i is

$$p = \theta^{2n_1} \cdot 2\theta(1 - \theta)^{n_2} \cdot (1 - \theta)^{2n_3} = 2\theta^{2n_1+1} (1 - \theta)^{2n_3+n_2}.$$

To maximize this likelihood, we take the derivative w.r.t. θ :

$$\frac{dp}{d\theta} = 2n_1 \theta^{2n_1-1} (1 - \theta)^{2n_3+n_2} - 2\theta^{2n_1+1} (1 - \theta)^{2n_3+n_2-1}.$$

and find where it is zero:

$$\frac{dp}{d\theta} = 0 \implies \theta = 0, 1, \frac{1}{2}.$$

Out of these candidates, only $\theta = \frac{1}{2}$ makes sense since the other are the bounds for what a probability can be.

The second derivative is

$$\frac{d^2p}{d\theta^2} = 2n_1(2n_1-1)\theta^{2n_1-2} (1 - \theta)^{2n_3+n_2} - 2(2n_1+1)\theta^{2n_1} (1 - \theta)^{2n_3+n_2-2}.$$

At $\theta = \frac{1}{2}$, the second derivative is negative, meaning it is a local maximum. At $\theta = 0, 1$, the second derivative is zero, which means we don't know if they are local minimums or maximums, but logically we can rule them out because it would be impossible to get the given genotypes if we could only have either AA or aa .