Ma 322: Biostatistics
Homework Assignment 7

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Due Monday, March 22nd, 2021

Read Chapter 13, "Foundations of Statistical Inference," pages 217–239 of our text.

1. Plot the F densities with every pair of numerator, denominator degrees of freedom chosen from the list 3, 10, 50, over the interval $[0, 4]$. (Hint: modify the code on page 227 of our text.)

2. This problem will illustrate the Central Limit Theorem. Let X be a random variable taking real values $x \in [-1, 0] \cup [1, 2]$ with uniform pdf

$$f(x) = \begin{cases} 1/2, & \text{if } -1 \leq x \leq 0 \text{ or } 1 \leq x \leq 2; \\ 0, & \text{otherwise.} \end{cases}$$

   (a) Generate N samples from this pdf using `runif(N)+sample(c(-1,1),N,replace=TRUE)`. Do this with $N = 500$ and plot the histogram to see how little this pdf resembles the bell-shaped curve e^{-x^2} of the normal density.

   (b) What is the exact mean μ of X? (Hint: do not use R or Calculus.)

   (c) What is the exact variance σ^2 of X? (Hint: use Calculus.)

   (d) Fix $n = 3$ and $m = 200$. Generate m vectors $\{X_i : i = 1, \ldots, m\}$ of n random samples $X_i(1), \ldots, X_i(n)$ of X and form m normalized averages

$$\bar{X}_i \stackrel{\text{def}}{=} \frac{S_i - n\mu}{\sigma\sqrt{n}}, \qquad i = 1, \ldots, m,$$

   where $S_i = \sum_{k=1}^{n} X_i(k)$, and μ and σ are from parts b and c. Plot the histogram of $\bar{X}_i$ and the quantile-quantile plot `qqnorm()` against the normal pdf.

   (e) Repeat part d with $n = 50$ and $m = 200$.

3. Alleles A and a are present in a population in unknown proportions p and $1 - p$. Assuming a Hardy-Weinberg equilibrium distribution of the resulting diploid genotypes, find the maximum likelihood estimator for p given the following experimental results:

Genotype Count Data for One Allele

Genotype	Count Data	Variable
AA	177	n_{AA}
Aa	716	n_{Aa}
aa	189	n_{aa}

4. Following are 14 samples from a population with unknown (but finite) mean μ and standard deviation σ:

```
2.59 2.67 2.16 1.95 2.61 1.11 2.62 2.06 2.06 1.66 2.16 3.35 2.46 2.55
```

   (a) Compute an estimate for σ.

   (b) Compute an estimate for μ.

   (c) Find the median of the 14 samples.

   (d) Find the quartile deviation of the 14 samples.

5. This problem will illustrate nonparametric bootstrap estimation of sample variability. First generate a 200 sample data set as follows:

```
set.seed(12345); data<- c(rnorm(90,mean=3,sd=2), rexp(110,rate=1));
```

   (a) Plot the histogram of `data`.

   (b) Find the mean and standard deviation of `data`.

   (b') Estimate the "standard error" of a 200-sample mean by $s/\sqrt{200}$ using the standard deviation from part b.

   (c) Find the median and the 1st and 3rd quartile values of `data`.

   Now apply the bootstrap method: generate 100 replications of 200 samples of `data`, with replacement, and calculate their means and medians.

   (d) Calculate the mean and standard deviation of the 100 bootstrap means.

   (d') Which is bigger, the bootstrap standard deviation of the means, or the "standard error" from part b'?

   (e) Calculate the median and the 1st and 3rd quartile values of the 100 bootstrap medians.

   (e') Compute the ratio of the differences between the 3rd and 1st quartiles for the bootstrap medians and the original data.