Wednesday, Oct 30

Abundance Estimation With Diagnostic Tests

Assume a simple random sampling design and the problem of estimating the number of elements in a population that have a disease. Thus y_i is defined as

 $y_i = \begin{cases} 1, & \text{if the } i\text{-th element has the disease,} \\ 0, & \text{if the } i\text{-th element does not have the disease.} \end{cases}$

The number of elements in the population that have the disease is then

$$\tau_y = \sum_{i=1}^N y_i.$$

Assume that we know the number of elements in the population (N). Two estimators we could use are

$$\hat{\tau}_y = N\bar{y}$$
 and $\hat{\tau}_y = \tau_x \bar{y}/\bar{x}$,

where x_i is some auxiliary variable. Note that \bar{y} is the *proportion* of elements in the *sample* that have the disease.

Consider using a cheap/quick diagnostic test for the auxiliary variable that can be applied to *all* elements in the population. Let x_i then be defined as

$$x_i = \begin{cases} 1, & \text{if the } i\text{-th element tests positive,} \\ 0, & \text{if the } i\text{-th element tests negative.} \end{cases}$$

Then

$$\tau_x = \sum_{i=1}^N x_i$$

is the number of elements in the population that test positive on the diagnostic test, and \bar{x} is the proportion of elements in the sample that test positive on the diagnostic test.

Note that the diagnostic test need not be perfect. Some people with the disease may test negative (a false negative), and some people without the disease may test positive (a false positive).¹

Example: Assume that the University of Idaho currently has 10000 students. Researchers want to know how many students currently have COVID-19. Assume that *all* students were administered a rapid test, and of these 300 tested positive. In a simple random sample of 1000 students, 40 are found to have COVID-19 using the highly accurate PCR test, and of these students 35 had tested positive on the rapid test. What are our estimates of the number of students that have COVID-19 using the two estimators above, where the ratio estimator uses the rapid test result as an auxiliary variable?

¹Assessing the presence of the disease to obtain y_i may use a different diagnostic test. The assumption here is that this test is (nearly) perfect — sometimes called a "gold standard" — in that it has a negligible probability of a false negative or a false positive.

Applying the rapid test would be expensive. Is it worth it? Consider the relative efficiency of the rapid test. It can be shown that in this situation

$$V(N\bar{y}) = \left(\frac{N-n}{N-1}\right) \frac{\mu_y(1-\mu_y)}{n}$$

and

$$V(\tau_x \bar{y}/\bar{x}) = \left(\frac{N-n}{N-1}\right) \left(\frac{\mu_y}{\mu_x}\right) \frac{1-\mu_y \pi_{\text{sens}} - (1-\mu_y) \pi_{\text{spec}}}{n},$$

where $\mu_y = \tau_y/N$ is the proportion of elements in the population that have COVID-19 (prevalence), $\mu_x = \tau_x/N$ is the proportion of elements in the population that would test positive on the diagnostic test, and π_{sens} and π_{sens} are the *sensitivity* and *specificity* of the diagnostic test for this population.

Sensitivity (π_{sens}) is the probability that a test will return a *positive* result when applied to someone with the disease (thereby avoiding a false negative).

Specificity (π_{spec}) is the probability that a test will return a *negative* result when applied to someone *without* the disease (thereby avoiding a false positive).

The relative efficiency of the ratio estimator (in comparison to the expansion estimator) is then

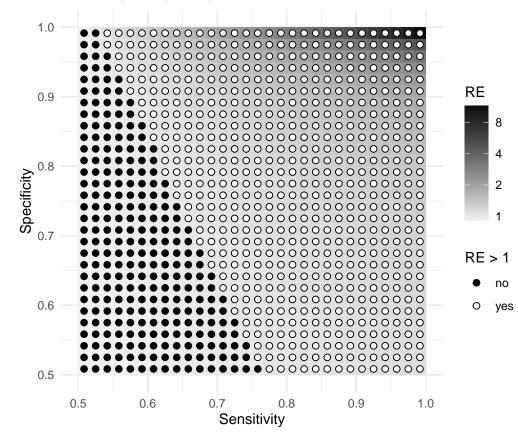
$$RE = \frac{V(N\bar{y})}{V(\mu_x \bar{y}/\bar{x})} = \frac{(1-\mu_y)\mu_x}{1-\mu_y \pi_{sens} - (1-\mu_y)\pi_{spec}}$$

where it can be shown that

$$\mu_x = \mu_y \pi_{\text{sens}} + (1 - \mu_y)(1 - \pi_{\text{spec}}).$$

Thus the relative efficiency depends on the prevalence of the disease (μ_y) , the sensitivity of the test (π_{sens}) , and the specificity of the test (π_{spec}) .

Example: The figure below shows the relative efficiency of the ratio estimator when the prevalence is $\mu_y = 0.1$ as a function of sensitivity and specificity.

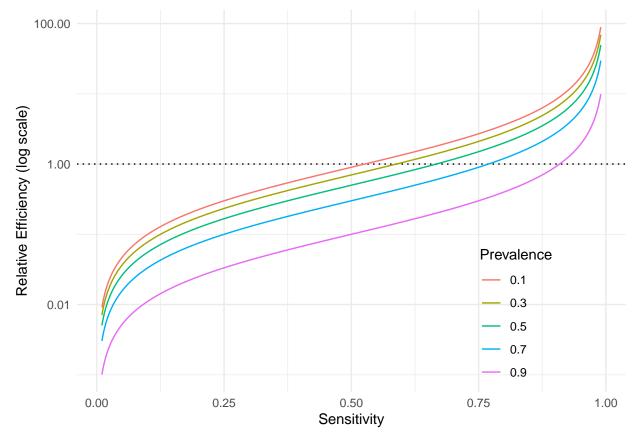


This idea can be applied to other problems where the domain is not "has disease" but there is some sort of "diagnostic test" that can be used.

Example: Assume now that researchers want to estimate the number of students at the University of Idaho that *have been vaccinated*. Based on a simple random sample of 1000 students they find that 640 of the students have been vaccinated. But they also find that of the 640 vaccinated students in the sample, 370 had already provided verification of being vaccinated so that they could earn a \$50 gift card and a chance to earn up to \$5000 in tuition credits. The researchers know that a total of 3600 students have provided proof of verification. What are our estimates of the number of vaccinated students at the University of Idaho?

What are the (estimated) sensitivity and specificity of the "diagnostic test" in the previous problem?

The plot shows the relative efficiency of the ratio estimator for the previous survey for various hypothetical values of prevalence and sensitivity.



Mark-Recapture Designs

A simple mark-recapture design is essentially a sampling design where we *create* an auxiliary variable for the purpose of estimating the number of elements in the population. This auxiliary variable is created by "marking" a subset of elements.

The Lincoln-Petersen Estimator

Consider a simple random sampling design where we have an *auxiliary variable* x_i such that

$$x_i = \begin{cases} 1, & \text{if the } i\text{-th element is marked,} \\ 0, & \text{if the } i\text{-th element is not marked,} \end{cases}$$

and so that

$$\tau_x = \sum_{i=1}^N x_i$$

is the number of marked elements in the population. As before let $y_i = 1$ for all elements in the population so that $\tau_y = N$. The ratio estimator of τ_y (and hence N) is then

$$\hat{\tau}_y = \tau_x \bar{y} / \bar{x} = \tau_x / \bar{x},$$

since $\bar{y} = 1$. We can also write this as

$$\hat{N} = \frac{\tau_x n}{m},$$

where m is the number of *marked units* in the sample because $\bar{x} = m/n$ (i.e., the proportion of elements in the sample that are marked where n is the size of the sample and m is the number of marked elements in the sample). This estimator is sometimes called the *Lincoln-Petersen estimator* (or index). There are several estimators of the variance of this estimator. One of them is

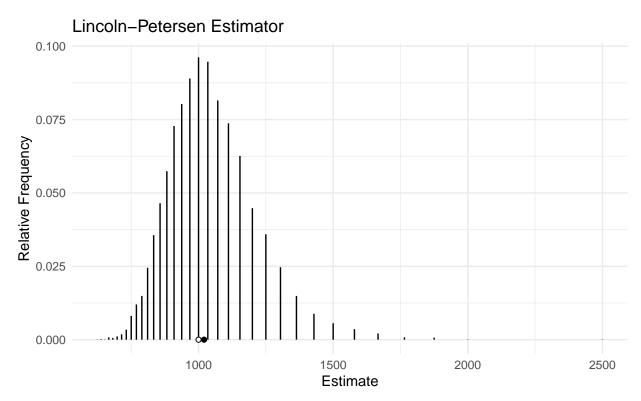
$$\hat{V}(\hat{N}) = \frac{\tau_x^2 n(n-m)}{m^3}.$$

Example: Suppose I have a large jar of jelly beans. Suppose we remove 300 jelly beans, mark them each with a pen, and then put them back in the jar. Then we shake the jar and draw a handful of 100 jelly beans. Of these we find that 30 are marked. What is our estimate of the number of jelly beans in the jar? What is the bound on the error of estimation?

The Chapman Estimator

The Lincoln-Petersen Estimator is *biased*. It can be shown that $E(\hat{N}) > N$, although the bias decreases as τ_x and/or n increase.

Example: The figure below shows the approximate sampling distribution of the Lincoln-Petersen estimator when N = 1000, $\tau_x = 300$, and n = 100.



An alternative estimator that has much less bias is the Chapman estimator

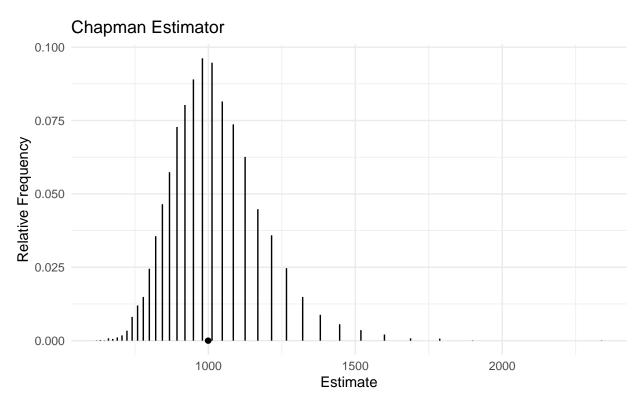
$$\hat{N} = \frac{(\tau_x + 1)(n+1)}{m+1} - 1$$

which has an estimated variance of

$$\hat{V}(\hat{N}) = \frac{(\tau_x + 1)(n+1)(\tau_x - m)(n-m)}{(m+1)^2(m+2)}.$$

The Chapman estimator is either unbiased or has relatively small bias.

Example: The figure below shows the approximate sampling distribution of the Chapman estimator when $N = 1000, \tau_x = 300$, and n = 100.



Example: Suppose I have a large jar of jelly beans. Suppose we remove 300 jelly beans, mark them each with a pen, and then put them back in the jar. Then we shake the jar and draw a handful of 100 jelly beans. Of these we find that 30 are marked. What is our estimate of the number of jelly beans in the jar? What is the bound on the error of estimation?