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LETTER TO THE EDITOR | COVID-19 PANDEMIC

Estimation of the Hidden Population with COVID-19 Disease

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ABSTRACT

The population with emerging diseases such as COVID-19, which is used to calculate the basic reproduction number of epidemic outbreak (R_0) cannot be simply observed. In this article, we have proposed a method for estimating the hidden population of people with COVID-19 disease. Knowing the number of people with COVID-19 disease is very important for health policy. The provision of medical equipment (e.g., masks, alcohol, ventilators, medication, etc.), the reopening of schools and universities, the start of tourism and public gatherings, the provision of medical staff and preventive planning depend on the number of patients with the disease. Therefore, it is very important to estimate the number of patients.

Key words: • Corona virus • Covid-19 • Epidemiology • Hidden population • Attack rate

In epidemiological studies, estimation of attack rate indicators such as R_0 (i.e., the basic reproduction number of epidemic outbreak) has a special place among health analysts and policymakers to estimate the rate of epidemic.[1] For example, R_0 was used in Japan[1] to measure the potential for influenza transmission, H1N1 in 2009.

Although there are different ways to estimate $R_{0.}$[2], one of the most common forms of R_0 used in epidemiological studies to estimate epidemic viability is the equation (1),

$$R_0 = -\frac{\log\left(\frac{1-AR}{S_0}\right)}{AR-(1-S_0)} \qquad \text{(Equation 1)}$$

where, AR is the percentage of the infected population and S_0 is the initial percentage of susceptible population to disease in a target population. According to Equation (1), we find that the value of S_0 cannot be easily estimated, because duration of diseases and susceptible population is exactly unknown.

Therefore, the relatively accurate method for estimating the number of susceptible (S_0) as one of the R_0 parameters is very important. However, this estimation in studies is usually not possible and its size is estimated either based on statistical distributions.[3] or determined from previous study information. Both of these strategies may cause a bias in estimating R_0.

Now, the fundamental question is "what is the way to estimate hidden population with covid-19 disease?" Another questions is, "is it possible to estimate coronavirus susceptibility population without screening and spending exorbitant CT-scan and PCR-test costs?"

Several studies[4-6] have shown that hidden population can be estimated by the network scale-up method as indirect estimation method. Therefore, we propose a network scale-up method to estimate the hidden population with COVID-19 disease.

For simplicity and adapting to Lotfi's study,[7] we can introduce the steps of estimating the hidden population of people with COVID-19 disease using the following network expansion method:

1. Estimating the average of respondents' personal network size;
2. Asking the respondents about the number of people they know in the hidden population; *i.e.*, the number of people with coronavirus in the hidden population known by respondents; and
3. Estimation of the hidden population size, *i.e.*, estimation of people with coronavirus as hidden population.

Bernard et al.[4] showed that the hidden population size can be estimated according to the Equation (2),

$$\frac{m}{C} = \frac{e}{T} \qquad \text{(Equation 2)}$$

where, T is target population or the total number of people living in a geographical area, which is determined by census information, etc.; e is the size of the total hidden population in the target group, *i.e.*, coronavirus patients; m is the average number of people with coronavirus that each person knows on their active social network; and C is average of the active social network of respondents.

Now, according to equation (1) what is unknown for us is the size of S_0 (*i.e.*, the hidden population with coronavirus), which can be replaced to in equation (2). Thus, we can estimate the indirect estimate of the hidden population with Covid-19 disease using network expansion method according to Equation (3),

$$\frac{m}{C} = \frac{S_0}{T} \qquad \text{(Equation 3)}$$

Our proposed method can answer the controversy over the estimation of the hidden population of patients with COVID-19 disease. The network scale-up methods have already been used to estimate the hidden population of drug abuse,[7] size estimation of groups at high risk of HIV/AIDS.[6] Achieving such a population plays an important role in health policy aimed at identifying the burden of the disease within groups and populations.

Compliance with Ethical Standards

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