

A Note on Estimating the Number of Free Infected Individuals

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1 Introduction

Russel et al. [1] describe a method for estimating the delay-adjusted case fatality in order to give an estimate of the Case Detection Ratio (CDR). This is useful to estimate under reporting. Russel uses the method to estimate the degree of under reporting in many countries around the world. The method has been used in Australia [2] to estimate under reporting in the different Australian states and territories. This note describes how the method can be adapted to estimate the number of Free Infected Individuals (FII), which is how many infected individuals are still in the community. In the process of developing this estimator we replicated the Russel results.

2 Replication of Russel Results

The CDR algorithm developed by Russel was coded in the R programming language, and a public version of the code was made available in a Github repository. Using the original equations described by Russel, we developed the CDR technique using the Ruby programming language and independently downloaded the data from the Johns Hopkins repository. By downloading the Russel CFR repository we were able to feed synthetic case and death data in the R version of the algorithm and our ruby version of the algorithm. The results agreed to four significant figures or better.

http://github.com/philomaths-org/covid-19/blob/master/free_infected_individuals_v2.pdf.
git-tag: fii-v2a. This study has not been peer reviewed.

Russell applied the algorithm by using case and deaths data from the Johns Hopkins web site [3], and published the results of the algorithm in table form for April 30, 2020. We independently downloaded the relevant data from the John Hopkins data and calculated the CFR for each country using our ruby code. We found the results broadly consistent, taking into account different timezones and preprocessing of the raw data.

Although the above does not represent an in-depth replication it does provide some confidence that the R implementation of the algorithm is correct and that the ruby version is consistent with the R version.

We calculate the CDR on a daily bases for all the countries in the Johns Hopkins website. Without attempting a validation, it can only be said that in most cases the results appear to be plausible. One exception is for Singapore. On June 30th, 2020, our calculation of the lower CI, estimate and upper CI was [1.00, 1.00, 1.00]. Russel reported exactly the same CDR range on that date. At that time there was significant prevalence of the disease in Singapore with roughly 400 cases a day being reported. Common sense dictates that there should have been at least some cases not being detected. This mismatch may be due to the Singapore's extraordinarily low death rate. This Strait Time [4] article explains the death rate in terms of the young demographic of infections, which is mainly amongst the migrant worker community. As well, it is claimed that it also partly due to the superior hospital care in Singapore.

3 Estimation of Free Infected Individuals

In Australia, and no doubt in many other jurisdictions, health officials endeavor to remove any infected individual as soon as they are detected. This can be done by requesting the individual self-isolates or in some cases, placing them in quarantine. This means the daily case counts gives a false impression of the number of Freely Infected Individuals (FII) who are moving about the community. We define FII as the number of individuals who are infected but who have not been detected and are not already in quarantine. Health officials are very concerned with identifying these individuals as they are source of community transmission. One indirect indicator of the number of FII is the size of community transmission, i.e. how many of the currently detected cases have an unknown source.

In the paper we propose another method of estimating the number of FII, using the CDR. Suppose we have a time series, i_0, i_1, \dots, i_N of daily new

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infected cases. Over time, the known infected individuals will recover, so the actual number of currently infected individuals on the k^{th} day, p_k is found by convolving the complimentary serial interval cumulative distribution function with the new cases i.e the prevalence on the k^{th} day is

$$p_k = \sum_{j=0}^{j=k} i_{k-j}(1 - s_j) \quad (1)$$

where s cumulative distribution function of the serial interval. For the k^{th} day the number of FII is given by

$$f_k = p_k * \left(\frac{1}{r_k} - 1 \right) \quad (2)$$

where r_k is the CDR on the k^{th} day.

4 Confidence Interval

If the estimate of the CDR also provides an upper and lower confidence interval, I_U and I_L , then the lower value of the CI for r_k can be approximated by substituting, I_U for r_k in equation 2. The use of the upper CI of the CDR to calculate the lower CI for FII is due to the reciprocal relation between CDR and FII. Similarly, the upper value for the CI can be found using substituting I_L in equation 2.

A more consistent estimate of the CI would take into account the uncertainty in calculating the prevalence. However the CI for the CDR calculated using the Russell method is dominated by the uncertainty in the case fatality ratio, so it is not clear that including the uncertainty in the prevalence would have a useful contribution to the CI.

If a country is reporting the community transmission then that provides another way of estimating FII. Suppose at any time, the number of cases of community transmission is known to be c_0, c_1, \dots, c_N . Each case of community transmission is due to a free individual, and that particular free individual was infected on average T_c days earlier. Here T_c is the mean serial interval. So, in analogy with equation 1, the number of free infected individuals would be

$$\sum_{j=0}^{j=k} c_{k-j-T_c}(1 - s_j) \quad (3)$$

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However assuming the effective reproductive ratio is constant over the period and is equal to R , then each infected individual infects R other individuals. So each case of community transmission is on average caused by $\frac{1}{R}$ individuals. So the estimate for FII using community transmission data is

$$f'_k = \frac{1}{R} \sum_{j=0}^{j=k} c_{k-j-T_c} (1 - s_j) \quad (4)$$

This approach could be useful in cases where the death rate is unusually low, as is the case of Singapore. So where community transmission data is available, a suitable estimator may be

$$\max(f_k, f'_k) \quad (5)$$

A more general approach would be to combine prevalence, the inputs to the CDR estimator, and community transmission data to a Maximum a Posteriori (MAP) estimator, and derive the CI from the error distribution of the MAP estimator.

5 Immunity

The CDR can also be used to estimate the level of immunity in a population, assuming an infected individual cannot be reinfected. Given that the CDC states that there have been no confirmed cases of reinfection [5], this assumption is reasonable. If, at any point in time, the total population is N and the total number of detected cases is C and the total number of deaths is D , then the fractional level of Immunity in the population is approximately

$$I = \frac{(\frac{C}{\text{CDR}} - D)}{N - D} \quad (6)$$

The CI for the Immunity can be calculated using the CI of the CDR, in a similar fashion to that used for the FII. The estimate of I could be improved by adjusting for the lag between detection and death. If the $D \ll N$, then I can be approximated by

$$I \approx \frac{C}{N \text{ CDR}} \quad (7)$$

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6 Conclusion

This note reports on the replication of the results of the Russel CDR estimator and then applies that to developing an estimator of the number of FII and of Immunity. It also describes an alternative estimator for FII using community transmission data. An example of the usage of the FII and Immunity estimators can be seen at this website [6] which calculates the FII and Immunity with confidence intervals for all the countries contained in the JHU database [3]. This is done on a daily basis. Compared to the Russel paper, the website uses an updated Infection Fatality Rate from Meyerowitz and Merone [7], which is also being used by the Centers for Disease Control and Prevention [8].

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