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The behaviour of infection, survival and testing effort variables of SARS-CoV-2: A theoretical modelling based on optimization technique

Subhasis Bhattacharya\textsuperscript{a,}\textsuperscript{*}, Suman Paul\textsuperscript{b}

\textsuperscript{a} Department of Economics, Sidho-Kanho-Birsha University, Purulia, West Bengal, India
\textsuperscript{b} Department of Geography, Sidho-Kanho-Birsha University, Purulia, West Bengal, India

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\textbf{ABSTRACT}

\textbf{Background:} The experiences of SARS-CoV-2 are different in nature among the different states of the world. Studies on survival analysis of such pandemic mainly based on differential equation analysis, but the main limitation of such models is non-universal applicability. Consideration of improper functional relation in case of identification, survival and testing effort variables of the disease may be the cause of such non-universal applicability.

\textbf{Methods:} Present study using optimization techniques try to find the general functional form for the variables like identification of the carrier’s and testing effort. The study uses both the discrete and continuous time procedure of optimization technique. The main objective of the study is to institute relation between the identified carrier’s and effort taken for identification.

\textbf{Results:} The study considers test as the pseudo variable for effort of identification. The study found that the relationship between test and identified is not a linear one, rather it is nonlinear quadratic type. The study does not go for using data driven methods to verify the results.

\textbf{Introduction:}

In the end of 2019 the novel Corona virus first time identified in Wuhan, China \cite{1}. The SARS-CoV-2, also known as Covid-19 virus had been spread in some Chinese provinces and then transmitted to the rest of world mainly through air routes \cite{2}. Most of the countries over the globe already made huge sacrifice in terms of human loss and economic loss and still now, some countries are within the sacrifice process. The experience from the countries identifies that to manage the infection, identification of the infected is a major significant variable and tests of non-infected or those who have some close contact with the already infected are found as pragmatic sources. World Health Organisation generates some guidelines for the states to avoid the infection, but it is frequently found that countries do not strictly follow those guidelines. Countries with huge population density and poor health practices may be in crucial positions under such pandemic. Differential equation based modelling like SIR model, Richard Model and also some difference equation based techniques are found in the literature to forecast the behaviour of the growth pattern of endemic. Present study considers the natural resource economics based modelling to elucidate the behaviour of infection, survival and test pattern to identification of the carriers and under such contemplation both the static and dynamic optimization techniques are used by the study. Bio-economic models like fisheries economics, the study considers the variables like stock of infected, production of test for identification of infected and supply of survival. The basic aim is to amplify the amount of survival over time. The study does not use any data driven application of the model, rather it can be viewed as different form of modelling than commonly used differential equation technique.

\textbf{Background:}

The studies by Murray \cite{4} and Hethcote \cite{5} are measured as pioneering in the field of epidemiological mathematics. The data driven approaches have also used to explain the behaviour pattern of an endemic and these techniques mostly forecast the future estimates of infection. Logistic growth model approach followed by a series of studies \cite{6–9}. The epidemiological models are categorised into two group’s namely deterministic and stochastic models. Some studies are found to estimate the relation between rates of infection with the demographic variables \cite{10}. Studies like Riley et al. \cite{11} observed that hospital transmission is one prime issue during the epidemic syndrome. Other
study considers the process of reproduction of epidemic caused by virus is the main factor [12]. The studies based on logistic growth model over different regions found that variable rates of infection forces are acting on different regions [13]. Studies on generation of infection variance between low and high immunity difference found a major cause [14]. In some studies on South Korea the transmission process identifies different reproduction rate for different types of hosts [15]. Such reproduction rate may depend upon human behaviour and heterogeneous contact [16]. Khan and Gomez-Aguilar [17] studied nonlocal conformable derivative to explain the disease dynamics of tuberculosis. Some study uses fractional derivative model in Caputo sense to explain the dynamics of Zika virus in terms of Lyapanov function theory [18]. Khan et al. [19] discussed the movement of infected from symptomatic phase to asymptomatic phase in case of HIV/AIDS infection with the help of Liouville-Caputo and Atangana-Baleanu-Caputo (ABC) derivatives. The nonlinear dynamic model under fuzzy Caputo fractional derivative tries to investigate the disease dynamics for Covid-19 [20]. Some studies considers HIV-TB coinfection model in terms of fractional differential form to discuss the existence and uniqueness of the solution in terms of Hyers-Ullam (HU) stability [27]. Present study considers the general optimization technique to determine the number of survival, infected and required number of test to maximise the survival population. The environment economics and resource economics very frequently used such optimization technique to consider the sustainability issue of environment [22]. But just moving in the reverse direction of the research methods followed by resource economist [23], present study attempts to derive the number of survival. In more general sense, in fishery economics, over-fishing is always avoided as per the sustainability issue [24], but in case of epidemic estimation, identification of last infected is very much sustainable. To understand the pattern of disease dynamics, some study on controlling Tuberculosis used deterministic model with control variable under optimal control theory [25]. Studies used optimal control theory in case of non-pharmaceutical intervention for novel coronavirus identified some key parameters as a control tool of the disease [26]. Khan et al. [21] formulate the disease dynamics model with and without control variable to calculate the basic reproduction rate. Finally the study identified the effectiveness of the control variable.

The model

As an unknown virus like SARS-CoV-2 is spread over the environment, primarily its diffusion process is mysterious. In this time, the infection grows naturally by its instantaneous process. After some time observing the health shocks, the support level contemplates to take measures for the virus, and in this phase the growth of the disease will be interrupted by the human intervention. Thus, initially we consider a break free growth of such virus. Let $X$ denote the stock of infected at some time. Thus $\dot{X} = \frac{dX}{dt}$ denote the changes of infected stock over time.

Let such instantaneous natural growth of infected population before any policy intervention is

$$\dot{X} = F(X, M)$$

where $F(X, M)$ is the gross biological growth function of the virus or it may be supplemented as gross growth function of infection. In epidemiology there may be difference between these two growth i.e virus growth function and gross growth function of infection, but here for the simplicity we assume these two are same. Here, $M$ signifies the factors which are accountable for diffusion of the disease like total population, population densities, even the western pattern of welcome thorough body contact.

The study assumes biological growth function of infected population is assumed as logistic because it will represented by a parabola when it is measured in terms of $X$ and started from zero.

Then we can write

$$F(X, M) = rX \left(1 - \frac{X}{K}\right)M$$

(1a)

Here, $r(>0)$ is the intrinsic instantaneous rate of growth of the infection, if the intrinsic growth of infection becomes closure to zero, then we found $K = X$, that means total population will be infected and infection carries the maximum carrying capacity. Now, for better understanding in case of SARS-CoV-2, such $X$ compiled of both the symptomatic and asymptomatic population group. As the disease appears for the first time in a state, some symptomatic carriers are identified not the asymptomatic, but the asymptomatic carriers are still in the population.

With the initiation of human intervention, the natural gross biological growth of infected population is to be affected and the net rate of growth of infected population can be expressed as the difference between gross biological growth of infected population and identification function of the asymptomatic carriers. In case of SARS-CoV-2, as the asymptomatic are identified (mainly by test) then they can be separate from existing population, so the reproduction rate can be checked.

$$\dot{X} = F(X, M) - I$$

(2)

Here, $I$ denote the identification function of the disease. Starting with small but positive values of infection, the infected population will grow initially and reach maximum and then decline till the environment reaches its infection carrying capacity. The biological equilibrium means that a specific value of infected population stock $X$, after which no further growth of infection will be possible, i.e. $X = 0$, that implies $F(X, M) = I$, and this level of $X$ is to be termed as maximum sustainable infection (MSI). Thus the MSI of infected stock is achieved when identification of the infected (asymptomatic) is equal to gross biological growth of infected population.

To improve the identification function $I$, the study first assumes the general Gordon [28] and Schaefer [29] type production function for identification, which mainly used by the resource economics.

$$I = qXE$$

(3)

where $q(>0)$ the identification rate from the infected people, and $E$ is the effort taken for identification. Thus, $I(X, E)$, can be recognized as the identification function of the infection and it depends on infected amount and the effort taken to reduce the infection. The effort can be written as the form of health support services or health provision availability during the pandemic, which help us to identify the cases smoothly. Surely test (antibody testing or polymerise chain reaction) is the most effective instrument under such concern. The study observes that at the very initial phase some countries tries to capture the past footprints of the symptomatic carriers but that may not always provide ideal figures due to low information criteria. Under such construction the study considers the following restrictions on the growth function of infection and identification function of infection. In case of growth function the restrictions can be stated as follows.

$$\frac{\partial F}{\partial X} > 0, \frac{\partial^2 F}{\partial X^2} < 0, \frac{\partial F}{\partial M} > 0.$$

From the diffusion behaviour of SARS-CoV-2 (like other epidemic virus) it is observed from various countries that initial growth rate of infection is tremendous but after a stage the rate of growth is diminishing, that means it depicts concave downward growth function, once which will reach maximum and then it will reduces. $M$ is the combined index of some demographical factors (supplied from World Bank data set) which comprises of relative population density ranking (with respect to highest population density country, $\frac{\text{density}}{\text{world}}$), relative population ranking (with respect to highest populace country, $\frac{\text{population}}{\text{world}}$), common safety practices (health), national welcome behaviour etc. Thus, $M$ is considered as such a variable or factor, which promotes infection. Regarding identification function, the study considers such restrictions as follows. It is understandable that as the effort to identify the infected increases
(like test), more infected can be identified. Similarly, as the volume of infected people increases, to check the danger of infection, more effort will be necessary from the governance to check the growth of infection. Thus identification becomes significant instrument to check the infection. Since, the identification considered as linear in terms of \( X \), thus the last condition directly derived from this.

\[
\frac{dl}{dE} > 0, \frac{dl}{dN} > 0, \frac{d^2l}{dX^2} = 0.
\]

Now to derive the effort function the study assumes specific form of the function is considered as follows.

\[
E = E(T_0, T)
\]  

(5)

Here, \( T_0 (> 0) \) is the instantaneous stringency effort measured by the state to tackle the situation, someone may supplement this by the effort like lock-down of different economic and social activities and it is treated purely autonomous. The other part of the effort function can be expressed in terms of test (\( T \)). The present study observes over different countries of the world that volume of tests are organised in heterogeneous pattern and surely they have some strong logical grounds to do such performance. In theoretical sense, the test pattern will be ideal if it captures the maximum number of infection (asymptomatic) cases and that will also be expressed as the best effort. To find the required test of any particular time, the study considers that will also be expressed as the best effort. To find the required test of such performance. In theoretical sense, the test pattern will be ideal if it expresses in terms of test (\( T \)).

\[
I = \frac{qK}{rM} (qK)T - \frac{qK}{rM} T = \gamma_1 - \gamma_2 T.
\]

Thus, \( \gamma \) can be expressed as identification-test function and this is a linear function of test performance. From the before constructed identification function (7) the maximum sustainable identification will be possible by

\[
\frac{dl}{dT} = \gamma_1 - 2\gamma_2 T = 0.
\]

Solving \( T \) from here and substituting that in \( I \) equation (7) we get maximum sustainable identified infection (MSII)

\[
I = \frac{\gamma_1^2}{4\gamma_2}.
\]

Thus, from such optimization of \( X \), the study observes that all the values of infected population and identification of infected are expressed as a function of test performance. Now under the situation of a pandemic like SARS-CoV-2 where the vaccine for the disease is still not available and the countries depend on two things majorly one is identification of the infected and the other is stringency measures adopted to reduce the chance of mixing of the infected with others. Follows from equation (6) huge test means huge identification possibilities and the state can quickly separate the infected and the pandemic will be recovered quickly. For better understanding of such logic, the study considers some graphical demonstrations (Fig. 1). In the horizontal axis of Fig. 1, the study measures the stock of infection and in the vertical axis we measure the identification, effort (Test) and growth of infection.

Now consider that various level of effort (tests) are to be employed like \( T_1, T_2, T_3 \), and as per these effort, the stocks of infected are \( X_1, X_2, X_3 \). The \( I = qX(T_0 + T) \) line can be represented as \( qX(T_0 + T_1) \), \( qX(T_0 + T_2) \) and \( qX(T_0 + T_3) \). Thus, the identification lines are drawn as origin passing straight lines and suppose \( T_1 < T_2 < T_3 \). Thus the interaction between the \( f(X, M) \) function and the survival line gives us amount of infection as well as identification of the infected as per the different efforts adopted. From such analysis study found that as per our assumption \( T_1 < T_2 < T_3 \) but we get \( I_1 < I_2 < I_3 \). This implies that identification-test or effort curve will also be inverted U shaped (Fig. 2) not linear which support our previous assumption (Fig. 3).

Here, the interesting feature is that an effort (test) level \( T_2 \) exceeds the maximum sustainable effort \( T_{\text{max}} \), but the same amount of identification of infected can be represented by taking the effort \( T_2 \). Why such things is occur may be a basic asking but that can be answered as follows. At the \( T_2 \) level of effort or test surely infected stock will be higher so when we make fewer tests like \( T_2 \) huge infected are found and identification will be high. From such observations the study may conclude that when infected stock becomes lower huge test also be

\[
\dot{I} = \frac{\gamma_1^2}{4\gamma_2}.
\]

Fig. 1. Effort changing behaviour of infection. Source: Author Construction.
necessary to find the rare infected. From the above figure the study arrives in the conclusion that identification of infected function follows a concave functional form.

The study added that at the outset when the infection increases, it is apparent that in every day the number of infected are found doubling or more than doubling than any previous date. So, up to when such doubling number of infection will be continued. That can be determining from the inflexion point of the growth curve of infected person, i.e. setting \( \frac{dI}{dt} = 0 \). This implies \( X = \frac{E}{q} \left[ 1 + \frac{q(T_0 + T)}{rM} \right] \), which is just half of the value of \( X \) when \( X \) is maximum (6a). The number of infected is less than the half of maximum number of infected, i.e. at the left side of point of inflexion, doubling rate of infection will continue. Doubling of infection can be regarded as a signal that the country or state may not still cross its point of inflexion. The amount of identified infected through effort or test also can also be estimated from the setting and that will be \( I = \frac{qT_0}{2} \left( T_0 + T \right) - \frac{n(T_0 + T)^2}{TM} \). As expected it is also found as half of \( I \) what we receive during \( X \) is maximum (6b).

As the states are distributed unevenly as per their per-capita GDP, thus effort to control the epidemic are also varies over the countries due to shortages of resources. Arrangements of huge test kits without foreign intervention in a short interval may be a delusion to the low income countries. During SARS-CoV-2 several examples in this regards are commonly visible considering the point of intervention or volume of measures adopted by different nations. Thus, to approve stringency measures and to arrange ample of tests, efficiency may have a significant role. The economic efficiency can be expressed in terms of the benefits derived from test or identification of the infected (asymptomatic) and the cost to apply such effort or test or identification of the infected. \( X \) is the amount of infected which is a combination of symptomatic and asymptomatic. Through identification as promptly as we identified the asymptomatic carriers, we can reduce the chance of future growth of infection. This is the most positive aspect of test/identification. Thus, the study has to constructs an infected and identification/test relationship which truly brings out the relation between net benefits and cost aspects as a function of effort of identification/test. The revenue can be expressed as a product of number of identified infected through test with the price of test/identification. The test types are also heterogeneous over the globe and commonly known as Polymerase Chain Reaction (PCR), TR-PCR, qPCR, Isothermal amplification as says Antigen test, Medical imaging, serology test etc. [3]. The price of identification is a grey area of literature, and there may be the chances of differences of opinions. This net benefit function is build up in terms of societies need, and as fast as the country removes the infected case through identification it will return back quickly to its normal way of economic cycle, and less internal boost-up policies will be required. Thus, elongated the disease endemic span, the country will have to pay higher for identification. So, the study can argue that price is inversely proportional to the time span of SARS-CoV-2. The total cost for identification can be easily estimated in terms of applied effort multiplied by per unit cost of effort. From such construction, the study consider net benefit from the effort applied for the identification of the infected is

\[
\pi = pI - cE.
\]

Here, \( p (> 0) \) is the price of identification, where \( p > 0 \); and \( n \) is the SARS-CoV-2 ailments episode, \( c (> 0) \) is the per-unit cost of effort, which can be easily supplemented by price or cost of test kit. Thus, \( p \) is the revenue from identification and \( cE \) is the cost of effort. We have to remind that identification \( I \) depends upon the effort from the identification effort relationship (equation 3). For simplicity the study assumes \( p \) and \( c \) as constant. Identification-effort relation already established that identification curve is inverted U shaped, hence the total revenue will also be inverted U shaped curve, whereas the cost of effort is linear upward rising and passing through the origin. Initially as effort increases, total revenue from identification increases and reaches maximum then decreases. Continuous increase in effort will bring optimum for the total revenue of identification. Optimum can be received by the maximisation of the difference between total revenue of the identification and the cost of effort line. One may termed this as economic optimum. Here,

\[
\frac{\partial \pi}{\partial E} = 0, \quad \frac{\partial I}{\partial E} = \frac{c}{p}
\]

But from the biological point of view, during epidemic this may not regarded as the desirable solutions. In the figure at \( e_1 \) the maximum economic net benefit of the identification problem is occur, but this is not a socially optimum because some infected still persist within the set and that will sustain the possibility of further infection. Social optimal can be achieved like open access equilibrium of environmental resources.

Situation like \( e_2 \) entail that still the total revenue from the identification is greater than the total cost, but in compare to \( e_1 \) more infected can be identified by the adopted effort. At \( e_3 \) the situation realise that total revenue for the identification is equal with the total cost of effort and the level of effort is maximum. The point like \( e_3 \) will generate maximum sustainable identification for taking such effort. At \( e_3 \), the total revenue from the identification intersects the total cost of effort line. That means here, \( \pi = pI - cE = 0 \), otherwise we may write it as \( pI = cE \).

The study starts with the logistic type growth function of infection and linear identification function, where \( I = qXE \), and we can define the net benefit equation. At equilibrium we already get \( X = 0 \), so \( X = K \left[ 1 + \frac{q(T_0 + T)}{rM} \right] \). Putting this in the net benefit equation and considering

\[
E = T_0 + T \text{ when } \pi = 0
\]

\[
q(T_0 + T)K \left( 1 - \frac{q(T_0 + T)}{rM} \right) - c(T_0 + T) = 0.
\]
Solving this equation for $E$, the study found,
\[ E = \left( T_0 + T \right) = \frac{rM}{q} \left( 1 - \frac{c}{pqK} \right) = E'. \]

This is the optimal level of efforts at equilibrium. Like before considering $T_0 = 0$, the level of test at equilibrium level of effort can be defined as
\[ T = \frac{rM}{q} \left( 1 - \frac{c}{pqK} \right). \]

Similarly, the optimal level of infected and identification for test at equilibrium can be determined.
\[ X = \frac{c}{pq} = X'. \]
\[ I = \frac{cM}{pq} \left( 1 - \frac{c}{pqK} \right) = I'. \]

Such concept of net benefit and from it the derivations of identification of infected and applied effort are all the part of static analysis. Let us consider the matter with dynamic behaviour modelling.

The net benefit function as derived earlier as
\[ \pi = pI - cE = pI - cI \frac{q}{qX} = \left( p - \frac{c}{qX} \right) I. \]

The functional form can be stated as maximisation of the net benefit in terms of identification. We are going to be maximising this net benefit as follows.

\[ \text{MaxNPV} = \int_0^T [pI(t) - C(t)]e^{-\delta t}dt. \]

Here $\delta$ is the discounting factor.

The subjective restrictions are $\dot{X} = rX(t) \left( 1 - \frac{X(t)}{K} \right) M - qX(t)E(t)$.

Where $I(t) = qX(t)E(t)$ and $C(t) = cE(t)$ and given $X(0) = X_0$. Thus, we can write the problem in more arranged form as

\[ \text{Max} \int_0^T [pqX(t)E(t) - cE(t)]e^{-\delta t}dt. \]

Subject to
\[ \dot{X} = rX(t) \left( 1 - \frac{X(t)}{K} \right) M - qX(t)E(t). \]

This is purely a problem of dynamic optimization and the current value Hamiltonian of the problem
\[ H_1(t) = [pqX(t)E(t) - cE(t)] + \varphi(t) \left[ rX(t) \left( 1 - \frac{X(t)}{K} \right) M - qX(t)E(t) \right]. \]

Here, $\varphi$ is the adjoint or costate variable which represents the current value shadow price associated with the incremental change in the stock of infected. Effort(E(t)) is the control variable and infected population $\{X(t)\}$ is the state variable.

Thus the first order necessary condition for maximum
\[ \frac{\partial H_1}{\partial \varphi} = [pqX - c] - q\varphi X = 0. \]

Solving the value of $\varphi$ from here, we get $\varphi = p - \frac{c}{qX}$. Similarly,
\[ \frac{\partial H_1}{\partial \varphi} = pqE + \varphi rM - 2\varphi M \frac{X}{K} - qE. \]

Again,
\[ \frac{\partial H_1}{\partial \varphi} = \left[ rX(t) \left( 1 - \frac{X(t)}{K} \right) M - qX(t)E(t) \right] = \hat{X}. \]

Now as per condition of Hamiltonian
\[ \hat{\varphi} = \delta \varphi - \frac{\partial H}{\partial X}. \]
\[ \hat{\varphi} = \delta \varphi - \left[ pqE + \varphi rM - 2\varphi M \frac{X}{K} - q\varphi E \right]. \]

The steady state will be follows only when $\hat{\varphi} = \hat{X} = 0$. Thus $\hat{\varphi} = 0$ means
\[ \delta \varphi - \left[ pqE + \varphi rM - 2\varphi M \frac{X}{K} - q\varphi E \right] = 0. \]

Earlier we get $\varphi = p - \frac{c}{qX}$ and putting the value of $\varphi$ in the steady state condition, the result follows as
\[ \delta \left( p - \frac{c}{qX} \right) - \left[ pqE + \left( p - \frac{c}{qX} \right) rM - 2\frac{MX}{K} \left( p - \frac{c}{qX} \right) \right] = 0. \]
\[ \delta \left( p - \frac{c}{qX} \right) - \left[ \left( p - p + \frac{c}{qX} \right) qE + \left( rM - 2\frac{MX}{K} \right) \left( p - \frac{c}{qX} \right) \right] = 0. \]
\[ \frac{cE}{X} = \delta \left( \frac{p - \frac{c}{qX}}{qX} \right) \left( rM - 2\frac{MX}{K} \right) \left( p - \frac{c}{qX} \right). \]
\[ \frac{cE}{X} = \frac{\left( pqX - c \right)}{qX} \left[ \delta \left( r - 2\frac{X}{K} \right) M \right] \]
\[ E = \frac{\left( pqX - c \right)}{qX} \delta \left( r - 2\frac{X}{K} \right) M. \]

Now the steady state situation for infected person implies that $X = 0$.
\[ qXE = rX \left( 1 - \frac{X}{K} \right) M. \]

From this relation we can also solve the value of effort and get
\[ E = \frac{r}{q} \left( 1 - \frac{X}{K} \right) M. \]

Equating equation (8) and (9) we get
\[ \frac{r}{q} \left( 1 - \frac{X}{K} \right) M = \frac{\left( pqX - c \right)}{qX} \delta \left( r - 2\frac{X}{K} \right) M. \]

Now solving this equation in terms of $X$ we get
\[ X^2 + \left[ \delta - \frac{rM}{2M} \right] - \frac{c(2 - r)}{2pq} X - \frac{c\delta K}{2pqM} = 0. \]

Consider this equation as
\[ X^2 + AX + B = 0. \]

Where, $A = \left[ \frac{\delta - rM}{2M} - \frac{c(2 - r)}{2pq} \right]$ and $B = -\frac{c\delta K}{2pqM}$

Thus, the $X$ can be solve from here as follows
\[ X = \frac{1}{2} \left( -A \pm \sqrt{A^2 - 4B} \right). \]

Solving this we get
\[ X = \frac{1}{2} \left[ - \left[ \frac{\delta - rM}{2M} - \frac{c(2 - r)}{2pq} \right] + \sqrt{\left[ \frac{\delta - rM}{2M} - \frac{c(2 - r)}{2pq} \right]^2 - 4 \left( -\frac{c\delta K}{2pqM} \right)} \right] \]
\[ = \frac{\sqrt{A^2 - 4B}}{2}. \]

The study can also determine the optimum level of efforts and op-
timum level of identification.
\[
\tilde{E} = \frac{q}{\dot{V}} \left( 1 - \frac{\dot{X}}{K} \right) M.
\]

\[
\dot{I} = q \tilde{E} V.
\]

To estimate the parameters of the model we can use time series fitting methods (Hilborn & Walters, 1992) but these required a very strong assumption regarding the behaviour of error structure. Here, the study used Schnute (1977) method for some additional benefits for estimating parameters. Study uses identification and effort information to predict the identification per unit of effort.

We already define the identification function as \( I = q \dot{X} \), thus identification per unit of efforts becomes
\[
\frac{\dot{I}}{E} = q \dot{X} = V.
\]

Thus, we get
\[
X = \frac{V}{q}.
\]

The net rate of growth of infection which is \( \dot{X} = rX \left( 1 - \frac{X}{K} \right) M - qXE \) can also expressed in terms of \( V \).
\[
\dot{V} = rV \left( 1 - \frac{V}{qK} \right) M - qVE.
\]

Thus,
\[
\frac{\dot{V}}{V} = r \left( 1 - \frac{V}{qK} \right) M - qE.
\]

Integrating this equation over the interval \( t \) to \( t + 1 \)
\[
\ln \left( \frac{V_{t+1}}{V_t} \right) = rM - qE - \frac{\mu M}{qK} V_t.
\] (10)

Here, \( E \) is the effort rate of identification, which can be supplemented by number of test per day \( (T_i) \) since we assume and \( V \) is the identification per unit of effort. Here, the integration over some time periods means averaging over the time periods and that is normally one year or month. Let us consider \( V_0 \) is the initial identification per unit effort at the commencement of the period. Now, in equation (10) the parameter \( M \) has no importance when we consider the case of a single country. In case of cross country reference \( M \) may be a significant/insignificant parameter. Here, in our study we consider with the data set of a specific country, so we assume \( M = 1 \). Thus from equation (10) we can estimate the parameter \( r, q \) and \( K \) through linear regression of \( \ln \left( \frac{V_{t+1}}{V_t} \right) \) on \( E_1 \) and \( V_1 \). But this create another data based problem, like SARS-CoV-2 data as maintained by the country level, and study can modified them in the form of \( E \) and \( V \), but not in the form of \( V_{t+1} \) and \( V_t \). The variable like \( V_{t+1} \) and \( V_t \) involves data at instantaneous time point of commencement. This is a serious data issue. To solve such data problem, the study follows the method adopted by Schnute (1977). Schnute undertakes that \( V_{t+1} \) can be approximated by
\[
V_{t+1} = \frac{1}{2} (V_t + V_{t-1})
\]

Thus the identification per unit of test for each day \( t \) is equal to the average of the \( V_t \) and \( V_{t-1} \). Hence, the equation (10) becomes
\[
\ln \left( \frac{V_{t+1} + V_t}{V_t + V_{t-1}} \right) = r - qE - \frac{r}{qK} V_t.
\] (11)

But the functional significance of the equation (11) is weak because here we are going to predict \( V_{t+1} \) without having any information on \( E_{t+1} \), which is also against the construction of our model. Rather we can make an assumption that identification per unit effort of any day \( t \) is approximately equal to the identification per unit of effort for the just preceding day \((t-1)\). That means \( V_{t-1} \rightarrow V_t \) and \( V_t \rightarrow V_{t-1} \). Considering such assumption propounded by Schnute, the equation (11) can be written as
\[
\ln \left( \frac{V_t}{V_{t-1}} \right) = r - qE - \frac{r}{qK} V_t.
\] (12)

The basic improvement over equation (10) made by equation (12) is that, equation (10) express the dependent variable is an index of change in relative identification of infection over a broad spectrum like year or month. But in case of disease like SARS-CoV-2, index of change in relative identification of infection over a single unit of time like hour or day. Time averaged regressors may be another kind of solution under such case.

Conclusion

Present study trying to illustrate the identification of infected under two frames like discrete and continuous set. The importance of effort for the identification under each process can be replaced by variables like test. Thus, number test per day is the most significant variable to overcome the disease. Considering the rate of test both the model established that identification is not a linear function rather a quadratic function of tests. Considering the test variable, the study tries to capture the net benefit function and optimization of the net benefit is serving us to identify the carriers under both the discrete and continuous setup. Present study does not deal with any numerical application of the derived model, but the results of the models can be verified by using ridge regression techniques applied through R-studio or Python language.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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