Mathematical structures for integrals to enhance the applicability of integral equations in modeling disease transmission: A preliminary study

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Abstract

Nowadays world have to deal with large number of diseases which are challenging public health. Anyhow these diseases are preventable based on interventions placed on various levels of transmission of the disease. One such attempt by the modern day researchers is to incorporate the disease transmission into a mathematical model and find a solution to control these diseases. In the basic context, rate of change of susceptible, infected and immune population describes the way of disease transmission regardless of proper quantification of phenomena associated with accumulations such as history of infection, immune response, burden of a disease and effect of prolonged treatments. In that perspective this study conveys a feeling for modeling in terms of integrals to cater the accumulations mentioned above along with integral equations. The study expresses several possible alterations and refinements to enhance the applicability of integral equations. In three cases, we present an easier way of incorporating an accumulation subject to time lag, manipulating Lebesgue integration instead of Reimann integration to cater higher degree of discreteness and structural refinements to incorporate increasing complexity of phenomena.

Keywords: accumulations, integral equations, disease transmission, mathematical modelling

I. INTRODUCTION TO INTEGRAL EQUATIONS

Differential calculus and Integral calculus are two concepts tied together by the Fundamental Theorem of Calculus where integration is regarded as the opposite operation of differentiation. This paper focuses on integral equations, where the unknown function appears inside a definite integral. This category of equations is not familiar among applied mathematicians compared to differential equations, however has a vast potential in both applications and theoretical development. The general form of an integral equation in u(x) is defined by

$$h(x)u(x) = f(x) + \int_a^{b(x)} K(x,t)u(t)dt.$$

 $h(x)u(x) = f(x) + f_a$ h(x,t)u(t)ut. Here *h*, *f* and *b* are functions of independent variable *x*. K(x, t) represents the way of incorporating the effect of u(x) in the integral.

It has been observed that these integral equations fall under two main categories: those with variable limits of integration called as Volterra integral equations and those with fixed limits of integration called as Fredholm integral equations [6]. The function K(x, t) appears within the integral is called the Kernel, which is the main structural entity in both modeling and solving process of integral equations.

II. INTEGRAL EQUATIONS AND DISEASE TRANSMISSION

Health officials, scientists and researchers have an important role to play in the control of diseases by applying effective and efficient management, prevention and control measures. Thus, mathematical modeling of disease transmission has gained a lot of interest in scientific research.

The classic models in disease transmission deal with the rate of change of susceptible, infected and immune population. In the natural circumstance, history of infection, immune response, burden of a disease and effect of prolonged treatments are some aspects to be considered in modeling disease transmission. The above phenomena of accumulation type need to be encountered in a model to have effective measures on disease transmission. These phenomena can be modeled using integral equations. Current study is conducted to discover new approaches to enhance the applicability of integral equations in the modeling process of disease transmission.

III. SOLVING APPROACHES

In modeling the transmission of diseases considering characteristics on accumulations, kernel will hold a vital

role since the modeling and solving process depends on the structure of the kernel.

Among the solving techniques of integral equations, Laplace transform shows a definite advantage on a particular kernel type called difference kernel. In a difference kernel, K(x, t) depends only on the difference (x - t). i.e. K(x, t) = K(x - t)

Volterra integral equations with difference kernel such as

$$u(x) = f(x) + \int_{a}^{x} K(x-t)u(t)dt$$

can be easily solved using the Laplace transform method, since the following convolution property is easily applicable [8].

$$\mathcal{L}\{u(x)\} = \mathcal{L}\left\{f(x) + \int_{a}^{x} K(x-t)u(t)dt\right\}$$
$$\mathcal{L}\{u(x)\} = \mathcal{L}\{f(x)\} + \mathcal{L}\{K(x)\}\mathcal{L}\{u(x)\}$$

Method of series technique is possible in solving the Fredholm integral equations with degenerated kernel where $K(x, t) = \sum_{k=1}^{n} l_k(x)m_k(t)$.

$$u(x) = f(x) + \int_{a}^{b} K(x,t)u(t)dt$$
$$u(x) = f(x) + \int_{a}^{b} \sum_{k=1}^{n} l_{k}(x)m_{k}(t)u(t)dt$$

After exchanging the summation with integration, degenerated kernel reduces the Fredholm integral equation to system of linear equations as

$$c_k = \int_a^b m_k(t)u(t)dt$$
$$u(x) = f(x) + \sum_{k=1}^n c_k \ l_k(x)$$

Method of successive approximation is another approach which can be used in the presence of resolvent kernel. Numerical techniques based on trapezoidal rule, Simpson's rule will also be of extremely useful to solve the highly complicated problems [2].

IV. STRUCTURING THE INTEGRAL

Since there is a potential structural refinement by integral calculus for the disease transmission, this study can be carried out in several perspectives.

Case I: Possible incorporation for a population subjected to disease transmission can be observed in the following equation [6].

$$n(t) = n_0(t) + k \int_0^t f(t-\tau)n(\tau)d\tau$$

This is a model for forecasting a certain population n(t) which can be either the evolution of infected population or breeding of infective agents such as parasites. Here $n_0(t)$ is the initial population, k is a constant and $f(t - \tau)$ is the survival function which can be incorporated with the natural context such as effect of immune response and prolonged treatment. Applicability of above structure is extremely useful since immune response occurs with a particular time lag which can be modeled via a function like $f(t - \tau)$.

A certain model of population dynamics of acquired immunity to parasite infection reveals the rate of change in mean worm burden (M) (i.e. proportion of adult worms per host) as follows [7].

$$\frac{dM}{dt} = \mu L - (\delta + I)M$$
$$I = \frac{\alpha E^2}{\beta + E^2}, \quad E = \int_{t-T}^{T} L(t')dt'$$

Here *I* is the cumulative effect of increased mortality of the worms by immune response and L(t) is the mean number of tissue dwelling larvae in a host at time *t*. Considering the earlier population model for n(t) in this same situation, there will be a possibility of expressing *M* as an easier explicit formula. This is due to the existence of a difference kernel which enables to solve the integral equation by applying Laplace transforms for convolution.

Case II: Replacing Riemann integration by Lebesgue integration would be applicable, since in approaching accumulation of quantities related to disease transmission incorporates with a certain quality of discreteness. In most of the situations such as quantifying the risk of a disease, the present state relates to the accumulation of what has happened to it previously [6]. The following integral equation in u(t), conveys the same context where accumulation of previous states has been accounted in its structure.

$$u(t) = \int_0^t K(t,\tau)u(\tau)d\tau$$

As quantities brought by u(t) incorporates with a quality of discreteness, Lebesgue integration along with the almost everywhere principle would be preferred over Reimann integration. In a particular situation of quantifying the risk via blood sampling, each observation could indicate temporal changes. Sometimes such indications have no contribution to the history of infection, which is responsible for the immune response. On the other hand, quick losses in observations would not harm to the continuous immune response as shown below in FIG 1 [5]. Here *N* represents an observational measure on disease taken via blood sampling.



III: Case In modeling disease transmission, corresponding populations would depend on environmental factors such as climate support for the infection. In some diseases this environmental factor may have the seasonal effect to be concerned such as the spread of dengue fever changes over rainy season. Considering these factors, there is an observable structural refinement for prevailing models. For instance, in the following Lotka's integral equation, probability that a female lives to a certain age τ given by $l(\tau)$ and the probability that she will give birth to a female given by $m(\tau)$ are incorporated in modeling the birth rate of a population (b(t)) [6]. Here g(t) has a measure on females already born.

$$b(t) = g(t) + \int_{\alpha}^{\beta} b(t-\tau) l(\tau) m(\tau) d\tau$$

In this type of a model for mosquitoes transmitting dengue virus, term $l(\tau)$ heavily depends on rainfall. In favorable conditions $l(\tau)$ would be set to even 1 and a structural refinements can be carried out for other degrees of favorability. Complexity of $l(\tau)$ would be increased when more and more climatic factors such as temperature, humidity etc. are involved subject to the availability of data.

V. CONCLUDING REMARKS

It is possible to model most of the general phenomena in disease transmission via integral equations. Solving aspects may encourage having some integral structures, such as convolution theorem in Laplace transform allows to incorporate lags and delays. Furthermore, such structures can be used as alternative to complicated differential equations in some scenarios.

Often in modeling with integral equations, continuous functions are expected allowing Reimann integration to occur. However, some phenomena are there with higher degree of discreteness, where the Lebesgue integration is preferred. Such structures are facilitated mainly by almost everywhere principle.

Structural refinements to integrals can be carried out to cater the complexity of a phenomena. Usually it occurs in disease transmission modeling due to the heterogeneity in influencing factors such as climatic conditions. In those situations, weight on quantified variables via probability function is incorporated.

Applicability of integral equations can be enhanced through structuring integrals in different ways. It ranges over catering many phenomena that accumulations are involved in disease transmission.

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