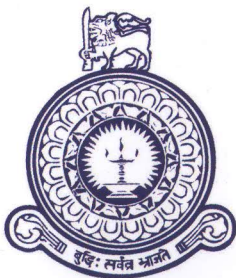


Proceedings of the International Conference on Computational Modelling and Simulation 2017

17–19 May
Colombo, Sri Lanka

*“Computational and Simulation Perspectives:
Looking ahead and moving across boundaries”*



Faculty of Science,
University of Colombo,
Colombo, Sri Lanka.



Proceedings of the International Conference on Computational Modelling and Simulation

Published by *Faculty of Science, University of Colombo*

ISBN : 978-955-703-011-1

Cover : T. Indika Sanjeeva

Printed by : S & S Printers, Jayantha Weerasekara Mawatha, Colombo 10, Sri Lanka

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

RGUI Meththananda^{1*}, NC Ganegoda² and SSN Perera³

¹ Department of Spatial Sciences, General Sir John Kotelawala Defence University, Southern Campus, Sri Lanka

² Department of Mathematics, University of Sri Jayewardenepura, Nugegoda, Sri Lanka

³ Department of Mathematics, University of Colombo, Colombo 3, Sri Lanka

*umameththananda@gmail.com

Abstract

Nowadays the world has to deal with a large number of diseases which challenge public health. Most of these diseases are preventable based on interventions placed at various levels of the transmission of the disease. One such attempt by modern researchers is to construct mathematical models of disease transmission and find solutions to control these diseases. In the basic context, the rates of change of the susceptible, infected and immune populations describe the way of disease transmission regardless of proper quantification of the phenomena associated with accumulations such as history of infection, immune response, burden of the disease and effect of prolonged treatments. In that perspective, this study conveys a feeling for modeling in terms of integrals to cater to 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 Riemann integration to cater to a higher degree of discreteness and structural refinements to incorporate the increasing complexity of the 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 inverse operation of differentiation. This paper focuses on integral equations, where the unknown function appears inside a definite integral. This category of equations although not familiar among applied mathematicians compared to differential equations, has vast potential in both applications and theoretical development. The general form of an integral equation in $u(x)$ is defined by

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

Here h , f and b are functions of the 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 Volterra integral equations and those with fixed limits of integration called Fredholm integral equations [6]. The function $K(x,t)$ appearing within the integral is called the Kernel, which is the main structural entity in both the 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 rates of change of the susceptible, infected and immune populations. In natural circumstances, the history of the infection, immune response, burden of the disease and the effect of prolonged treatment are some aspects to be considered in modeling disease transmission. The above phenomena of accumulation types needs to be encountered in a model to have effective preventive measures on disease transmission. These phenomena can be modeled using integral equations. The 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 by considering the characteristics of accumulations, the

kernel plays a vital role since both modeling and solving processes depend 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 the 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 a 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].

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

$$\mathcal{L}\{u(x)\} = \mathcal{L}\{f(x)\} + \mathcal{L}\{K(x)\}\mathcal{L}\{u(x)\}$$

The 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 the integration, the degenerated kernel reduces the Fredholm integral equation to a system of linear equations as

$$c_k = \int_a^b m_k(t)u(t)dt$$

$$u(x) = f(x) + \sum_{k=1}^n c_k l_k(x).$$

The method of successive approximation is another approach which can be used in the presence of a resolvent kernel. Numerical techniques based on the trapezoidal rule and Simpson's rule are also extremely useful in solving highly complicated problems [2].

IV. STRUCTURING THE INTEGRAL

Since there is a potential structural refinement by integral calculus for 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 an infected population

or the 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 a natural context such as effect of immune response or prolonged treatment. Applicability of the 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].

$$\frac{dM}{dt} = \mu L - (\delta + I)M$$

$$I = \frac{\alpha E^2}{\beta + E^2}, \quad E = \int_{t-\tau}^t L(t')dt'$$

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 is a possibility of expressing M as an easier explicit formula. This is due to the existence of a difference kernel which enables solving the integral equation by applying Laplace transforms for convolution.

Case II: Replacing Riemann integration by Lebesgue integration would be applicable, since approaching accumulation of quantities related to disease transmission incorporates with it 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 for in its structure.

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

As quantities brought by $u(t)$ incorporate a quality of discreteness, Lebesgue integration along with the almost everywhere principle would be preferred over Riemann 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 the infection, which is responsible for the immune response. On the other hand, quick losses in observations would not harm the continuous immune response as shown below in FIG. 1 [5]. Here N represents an observational measure on disease taken via blood sampling.

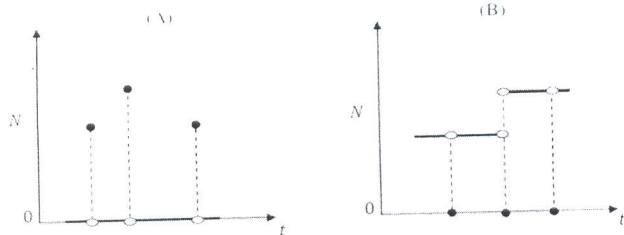


FIG. 1 (A) - Almost everywhere zero and (B) - almost everywhere non-zero

Case III: In modeling disease transmission, the corresponding populations would depend on environmental factors such as climate support for the infection. For some diseases, this environmental factor may have seasonal effects to be concerned with, such as the increase in the spread of dengue fever over rainy seasons. Considering these factors, there is an observable structural refinement to 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 gives 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 the dengue virus, the term $l(\tau)$ heavily depends on rainfall. In favorable conditions $l(\tau)$ would be set to even 1, and a structural refinement 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 general phenomena in disease transmission via integral equations. Solving

aspects may encourage having some integral structures such as the convolution theorem in the Laplace transform which allows the incorporation of lags and delays. Furthermore, such structures can be used as alternatives to complicated differential equations in some scenarios.

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

Structural refinements to integrals can be carried out to cater to 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 a probability function is incorporated.

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

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