Fixed Point Method for Infectious Diseases

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Abstract: Fixed point method for solving one dimensional problem has been well studied. Here we consider two dimensional fixed point method and apply it to solve the SIR model which is a system of nonlinear integral equations. It is used to describe endemic infectious diseases for which infection confers permanent immunity.

Key–Words: Volterra integral equation, Fixed point method, Infectious diseases, Contraction, SIR model.

1 Introduction

Many mathematical models have been developed to describe the dynamics of infectious diseases. The Kermack-McKendrick (or SIR) model is perhaps the most well-known epidemiological model [1]. It divides the population into three separate compartments relating to the infectious disease dynamics and then uses a system of ordinary differential equations to track how individuals move between them. More precisely, a typical subdivision consists of susceptibles S, infectives I, and a third, removed class R of individuals who can no longer contract the disease because they have recovered with immunity, have been placed in isolation, or have died. If the disease confers a temporary immunity on its victims, individuals can be moved from the third class to the first. Here we adopt the technique of the Kermack-McKendrick model (with some modifications), but take another approach to the underlying mathematics. In particular, we include terms that account for birth and natural death of individuals and incorporate the vaccination of newborns and susceptible individuals. As an example, measles is a serious childhood disease that can lead to many complications and even death [3]. Because of a major outbreak in 1989-1991, the United States changed to a two-dose measles vaccination program. As a result, the basic reproduction number R_0 in the SIR model now appears to be below 1 throughout the United States; so that measles is no longer considered to be endemic there. Using this framework, we build a system of integral equations to describe the disease dynamics that are adapted from Hethcote & Tudor [4]. We then employ a fixed point method to establish the existence of a stable equilibrium. In section 2, we will recall some preliminary backgrounds followed by introducing notations in section 3. We describe our model in section 4 and provide the main result in section 5. Several discussions and conclusion are presented in section 6.

2 Preliminary Backgrounds

In this section, we recall some basic concepts of integral equations and fixed point theorem which are described in the following two subsections.

2.1 Integral Equations

An integral equation is an equation in which the unknown function u(t) appears under an integral sign. A general example of the Volterra integral equation in u(t) is:

$$(Tu)(t) = f(t) + \int_0^t K(t, x, u(x))dx \qquad (1)$$

where $K(t, x, u(x))$ is called the kernel of the integral equation and is continuous with respect to t, x and u(x) on the domain D such that $0 < t < b, a < x < t$ and u(x) is bounded, i.e. $c < u(x) < d$ for some constants a, b, c and d, $f(x)$ is continuous on [0,t] and bounded, namely, $m_1 < f(x) < m_2$ and $K(t, x, u(x))$ is Lipschitz with respect to u(x), i.e., if there is a positive constant L such that:

$$|K(t, x, B(x)) - K(t, x, A(x))| = L|B(x) - A(x)| \qquad (2)$$

for $(t, x, B(x))$ and $(t, x, A(x))$ in the domain of K. When $Tu = 0$ it is called a Volterra equation of the first kind and is called a Volterra equation of the second kind when $Tu = u$. When $f(x) = 0$, then it is called homogeneous [2]. In what follows, we will use integral equations to describe our model.

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2.2 Fixed Point Method

Let V be a Banach space with the norm $|.|_V$, and let W be a subset of V. Consider the operator $T : W \to V$ defined on W. We say an operator is contractive with contractivity $a \in [0,1)$ if:

$$|T(x) - T(y)|_V \leq a|x - y|_V, x, y \in W \quad (3)$$

Theorem 1 [5] *Assume that W is a nonempty closed set in V and $T : W \to W$ is a contractive mapping with contractivity constant $0 < a < 1$. Then there exists a unique $x^* \in W$ such that:*

$$T(x^*) = x^* \quad (4)$$

Moreover for any $x_0 \in W$, the sequence $x_n \in W$ defined by:

$$x_{n+1} = T(x_n) \quad (5)$$

converges to x^*.

In what follows we will consider $W = R^2$, the integral equation:

$$X(t) = G(t) + \int_0^t K(t,x)H(x,X(x))dx \quad (6)$$

for all $t \in I = [a,b]$ and assume that $G \in C[a,b]$ and $K \in L^2([a,b] \times [a,b])$. Define the operator T as:

$$(TX)(t) = G(t) + \int_0^t K(t,x)H(x,X(x))dx \quad (7)$$

Notice then that the solution of the above integral equation (6) can be obtained using the operator T. In fact, we will use this operator to define iterations and establish the existence of an equilibrium for our model for infectious disease.

3 Notations

In what follows, we will use the following notations.

$S(t)$: The fraction of the population that is susceptible

$I(t)$: The fraction of the population that is infectious

$I_0(t)$: Function describing the initial infectious population

$R(t)$: The fraction of the population that is removed

β: Average number of contacts (sufficient for transmission) between individuals in the population

μ: The rate of natural death

$P(t)$: The probability of remaining infectious t units after becoming infectious

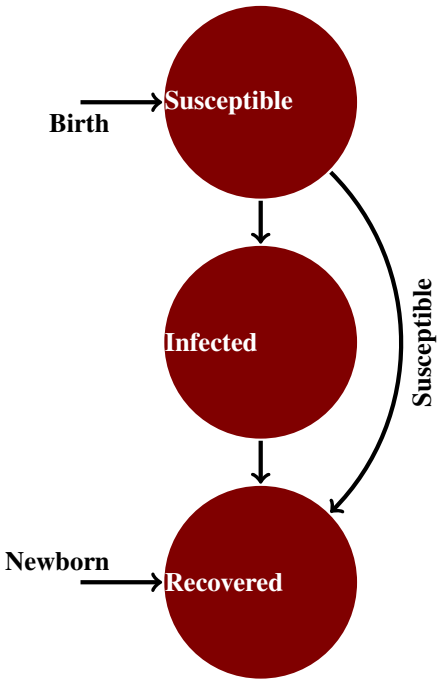
$Q(T)$: The probability of being alive at time $t_0 + T$, given that an individual is alive at time t_0

ρ: Rate of newborn immunization

θ: Rate of susceptible immunization

4 Model

In this section, we formulate a general idea for developing the model by showing the following simple diagram followed by detailed discussions.



Following the framework of the Kermack-McKendrick (or SIR) model, we divide the population into three separate compartments that relate to an individual's exposure to the disease. One compartment corresponds to those who are not currently infected by the disease but are susceptible to being infected at some time in the future. The second compartment contains the fraction of the population that is currently infectious and capable of spreading the disease, and the final compartment corresponds to those who are removed from the disease dynamics (either as a result of recovery or immunization).

We also make the following assumptions:

(i) Contact between individuals in the population occurs at a constant rate, and such contact is sufficient to transmit the disease.

(ii) The probability of remaining infectious follows a non-increasing function P(t) such that:

$P(0) = 1$ and $lim_{t\to\infty}P(t) = 0$.

(iii) If an individual is alive at time t_0, then the conditional probability of him or her being alive at time t_{0+t} is independent of age and may be modeled using the following function:

$$Q(t) = e^{-\mu t} \quad (8)$$

(iv) Infection is not passed from mothers to their newborns.

(v) Both newborns and susceptible individuals in the population are successfully immunized at constant rates.

(vi) The total population remains constant.

Hence we illustrate the model in the above diagram at the beginning of this section.

Let's now consider the dynamics happening in the Infectious compartment. In general, we have:

$$\begin{aligned}&(Infectious\ at\ Time\ t)\\&=(Total\ Infectious\ at\ t=0)\\&\times Pr(Still\ Being\ Alive)\\&+\int_0^t Pr(Becoming\ Infected)\\&\times Pr(Still\ Being\ Infected)\\&\times Pr(Still\ Being\ Alive)dx\end{aligned}$$

so that mathematically:

$$I(t)=I_0(t)e^{-\mu t}+\int_0^t \beta S(x)I(x)P(t-x)e^{-\mu(t-x)}dx \tag{9}$$

Similarly in the Removed compartment:

$$\begin{aligned}&(Removed\ at\ Timet)=(Total\ Removed\ at\ t=0)\\&\times Pr(Still\ Being\ Alive)\\&+[Removed\ from\ Infected\ at\ t=0]\\&\times Pr(Still\ Being\ Alive)+(Immunized\ Newborns)\\&+\int_0^t Pr(Becoming\ Infected)\times Pr(Recovering)\\&\times Pr(Still\ Being\ Alive)dx\\&+\int_0^t (Immunized\ Susceptibles)\\&\times Pr(Still\ Being\ Alive)dx\end{aligned}$$

so that we have:

$$\begin{aligned}R(t)&=R_0e^{-\mu t}+[I_0(0)-I_0(t)]e^{-\mu t}+\phi(1-e^{-\mu t})\\&+\int_0^t \beta S(x)I(x)[1-P(t-x)]e^{-\mu(t-x)}dx\\&+\int_0^t \theta S(x)e^{-\mu(t-x)}dx\end{aligned} \tag{10}$$

Finally since the population is assumed constant, our third equation is given by:

$$S(t)+I(t)+R(t)=1 \tag{11}$$

which may be solved for S(t) if so desired.

5 Main Theorem

Let X_0 (t) be the initial function. We define the fixed point iteration:

$$\begin{aligned}X_{n+1}(t)&=(TX_n)(t)\\&=G(t)+\int_0^t K(t,s)H(s,X_n(s))ds\end{aligned} \tag{12}$$

for $t\in[a,b]$ and integers $n=0$. The above model can be expressed in terms of the operator T if:

$$X(t)=[I(t)\ \ R(t)]^t \tag{13}$$

so that:

$$T_1(X(t))=G_1(t)+\int_0^t K_1(t,s)H(s,X(s))ds, \tag{14}$$

$$\begin{aligned}T_2(X(t))&=G_2(t)+\int_0^t (K_{21}(t,s)H_{21}(s,X(s))\\&+K_{22}(t,s)H_{22}(s,X(s)))ds\end{aligned} \tag{15}$$

where:

$$G_1(t)=I_0(t)e^{-\mu t}$$

$$K_1(t,s)=\beta P(t-s)e^{-\mu(t-s)}$$

$$H_1(t,X(t))=(1-I(t)-R(t))I(t)$$

$$G_2(t)=R_0e^{-\mu t}+[I_0(0)-I_0(t)]e^{-\mu t}+\phi(1-e^{-\mu t})$$

$$K_{21}(t,s)=\beta(1-P(t-s))e^{-\mu(t-s)}$$

$$H_{21}(t,X(t))=(1-I(t)-R(t))I(t)$$

$$K_{22}(t,s)=\theta e^{-\mu(t-t)}$$

$$H_{22}(t,X(t))=1-I(t)-R(t)$$

Theorem 2 *Consider the operator T with two components (14), and (15) and assume* $G\in C[a,b], K_i\in L^2([a,b]\times[a,b])$*, and* H_{ij} *satisfy a uniform Lipschitz condition with respect to its second argument. Then T has a unique fixed point in* $C[a,b]$*. Moreover, this iterative method (12) converges for any initial function* $X_0\in C[a,b]$*.*

We will provide proof of this theorem in a future paper.

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6 Conclusion

We have applied a fixed point method to solve the SIR model. It is possible to use the same idea to solve the SEIR model which is similar to the SIR model except that a class of exposed individuals is considered. Also, the fraction of the population that was initially exposed is still alive at some time. Our proof is different from standard methods; we use an iteration method which will give rise to the unique solution.

REFERENCES

[1] Linda JS Allen, Fred Brauer, Pauline Van den Driessche, and Jianhong Wu. Mathematical epidemiology. Springer, 2008.

[2] Kendall E Atkinson et al. A survey of numerical methods for solving non-linear integral equations. Journal of integral equations and applications, 4(1):15-46, 1992.

[3] Herbert W Hethcote. The mathematics of infectious diseases. SIAM review, 42(4):599-653, 2000.

[4] Herbert W Hethcote and David W Tudor. Integral equation models for endemic infectious diseases. Journal of mathematical biology, 9(1):37-47, 1980.

[5] Khosrow Maleknejad and Parvin Torabi. Application of fixed point method for solving nonlinear Volterra-Hammerstein integral equation. University Politehnica of Bucharest Scientific Bulletin, Series A: Applied Mathematics and Physics, 74(1):45-56, 2012.