Extrapolation Method for Numerical Solution of a Model for Endemic Infectious Diseases

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Extended Abstract

Introduction

Many infectious diseases are endemic in a population. In other words they present for several years. Suppose that the population size is constant and the population is uniform. In the SIR model the population is divided into three disjoint classes which change with time t and let $S(t)$, $I(t)$ and $R(t)$ be the fractions of the population that susceptible, infectious and removed, respectively. This model formulated as the following system of nonlinear Volterra integral equation.

$$
\begin{cases}
I(t) = I_0(t)e^{-\mu t} + \int_0^t \beta S(\tau)I(\tau)P(t-\tau)e^{-\mu(t-\tau)}d\tau, \\[2mm]
R(t) = \left[R_0 + I_0(0) - I_0(t) - \varphi\right]e^{-\mu t} + \varphi + \int_0^t S(\tau)\left[\beta I(\tau)\left(1 - P(t-\tau)\right) + \theta\right]e^{-\mu(t-\tau)}d\tau, \\[2mm]
S(t) + I(t) + R(t) = 1, \quad t > 0.
\end{cases}
$$

Where $I(t)$, $R(t)$ and $S(t)$ are unknown functions and other constants and functions are known. The susceptibles are transferred at a rate equal to βS times the number of infectives, where β is a constant. $P(t)$ is the nonincreasing probablity function of remaining infectious t units after becoming infectious, with $P(0) = 1$ and $P(\infty) = 0$ and $P(t)$ is dominated by a decaying exponential, such as gamma distributed. Since the population size is constant, the birth rate must be equal to the death rate μ. The death rate is the same for susceptibles, infectives and removed individuals. The fraction φ of newborns are immunized so that the flow rate of immunized newborns into the removed class is $\varphi\mu$. The initial susceptible and removed fractions be $S_0 > 0$ and $R_0 \geq 0$ and $I_0(t)e^{-\mu t}$ be the fraction of the population that was initially infectious and is still alive and infectious at time t.

Material and methods

We apply the Richardson extrapolation method for numerical solution of this model, so that the nonlinear system is solvable by an iterative process with a good accuracy. The algorithm of such systems completely described. This algorithm has a kind of nested structure, which cause we use the lag data in the future times, and it is the interesting section of programing of the algorithm. This algorithm is ready for programing with every program language, which we do this process by Mathematica programing software. Convergence and accuracy of the method is

illustrated by either theoretical and numerical analysis, and some benchmark sample problems. For this aim by using Laplase transform, we sketch a spectrum of sample problems. These problems have analytical solution and appropriate for comparison with numerical solutions.

Results and discussion

We solve some test examples by using present technique to demonstrate the efficiency, high accuracy and the simplicity of the present method. The main advantage of the method is the applicability of method for a large interval of time, as the algorithm shows. Numerical results shows the accuracy of the method for a long time interval.

Conclusion

The following conclusions were drawn from this research.

- The proposed algorithm is very suitable for mathematical programing.
- Many cancer problems have such structure and the method is applicable for them.
- This method has two characteristics, solve a nonlinear problem and use of previous solution in new interval. So the method is applicable for various kind of problems with little additional works.

Keywords: Extrapolation method, Infectious diseases, Susceptible class, Infective class, Removed class, Nonlinear Volterra integral system.

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