

# Some Mathematical Models for Epidemiology

Vinod Kumar and Deepak Kumar

Department of Mathematics, Manav Rachna International University Faridabad, India

**Abstract**—This work is describing the role of dynamic compartmental modelling and their conceptual aspects in epidemiology. The work emphasizes an understanding of different mathematical models applied to the population dynamics of infectious diseases. Also, we are mainly discussing the future aspects of governing equations for different infectious diseases.

**Index Terms**— Mathematical Modelling, Compartmental Model, Epidemiology.

## 1 INTRODUCTION AND BRIEF HISTORY OF MATHEMATICAL MODELLING IN EPIDEMIOLOGY

In India, the drastic effects of epidemic disease were remarkable in the field of epidemiology, for example, the "Bubonic Plague" is one of them, which caused by the bacterium *Yersinia pestis*, devastated population in Europe from the 14<sup>th</sup>-16<sup>th</sup> centuries, killing between one-half to one-third of the entire population (Langer 1970) and according to WHO reports 1000-3000 cases of bubonic plague every year [1]. The history of mathematical modelling on communicable and non-communicable diseases has been shown a great concern of human kind. The dynamic models for infectious diseases are mostly based on their compartmental structure. The compartmental structures for well-recognized SIR (Susceptible (S)-Infective (I)-Recovered (R)) on infectious diseases for example influenza, swine flu, plague, HIV/AIDS, malaria etc. are firstly given by Kermack and Mc Kendrick in 1927 and are developed by many other bi-mathematicians in 1932 [2, 8, 13, 16, 17]. Analysis of numerical simulation of swine flu in mathematical transmission model and explain the approach of controlling form such infectious diseases [3, 4, 11]. Mathematical models for the infectious diseases in populations have been analysed and applied to infectious diseases for developing vaccination policies. Threshold theorems involving the basic reproduction number  $R_0$  and these numbers are reviewed for define the epidemic models [7, 9, 14]. Dynamic of compartmental model for epidemic is an important method of analysing the effect of infectious disease. It is based on the specific property of population growth with structure, to define spread rule of infection disease, and the related factors etc. To construct mathematical models which analysis these factors numerically and define the behaviour of various parameters. This research is helpful to predict the

growth of infectious disease, to determine the key factors of the spread of infectious disease and to seek the optimum strategies of preventing and controlling the spread of infection diseases [5, 10,12].

The dynamic models on epidemic diseases play the important role of studying the spread of infection disease. These are based on compartmental structures of population growth, spread rule of infectious disease, and the related social factors etc. and which are given by Kermack and Mc Kendrick and many others mathematicians. A various types of mathematical models have been used in mathematical epidemiology. By modifying the basic SIR model, we have obtained proposed infectious diseases compartmental ODE-models for further development in the future epidemiology.

## 2 MATHEMATICAL MODELS

In this work we define the differential equations based models and using parameters as follows:

Susceptible Class (S), Infective Class (I), Recovered Class (R), infected with influenza ( $I_1$ ), recovered from influenza (T), infected with secondary pneumonia ( $I_2$ ), transmission rate of influenza ( $\beta_1$ ), recovery rate of influenza ( $\gamma_1$ ), rate at which an individual loses susceptibility ( $\sigma$ ), rate of re-susceptible ( $\delta$ ), transmission rate of infection ( $\beta$ ), excess death rate due to infection (d),transmission rate of bacterial infection( $\beta_2$ ), recovery rate of bacterial infection ( $\gamma_2$ ), excess death rate due to bacterial infection( $d_2$ ), vaccination rate( $v$ ).

### 2.1 Basic forms of compartmental models for various type of disease

(1) SIR Model:

The base model, when the infective gain permanent immunity to the disease after recovering from infection. It is given by following diagram:



The governing equations are as follows:

$$\frac{dS}{dt} = -\beta SI$$

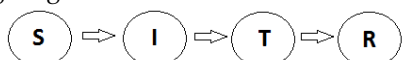
$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

(2) SITR Model:

The compartment model (SITR) is a system of differential equations, which are designed for the susceptible to infection (S), infection (I), Treatment (T), completely recovered from infection(R).

Compartment model for epidemic disease is given by following diagram:



Susceptible Class, S: Susceptible to infection,  $\beta$  transmission rate,

$$\frac{dS}{dt} = -\beta SI$$

Infective Class, I: Infection I,  $\gamma$  rate of selection treatment, d death rate due to infection,

$$\frac{dI}{dt} = \beta SI - \gamma I - dI$$

Treatment Class, T: Treatment for infection,  $\sigma$  removal rate from infection due to treatment,

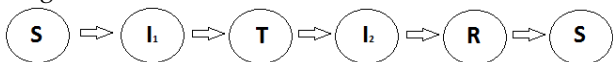
$$\frac{dT}{dt} = \gamma I - \sigma T$$

Removed Class, R: Completely removal from infection,

$$\frac{dR}{dt} = \sigma T$$

(3) SI<sub>1</sub>TI<sub>2</sub>RS Model:

In these models the infected individuals becomes infectious immediately. It is given by following diagram:



The governing equations of the model are as follows:

$$\frac{dS}{dt} = -\beta_1 S_1 I_1 + \delta R$$

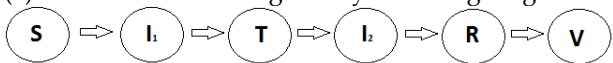
$$\frac{dI_1}{dt} = \beta_1 S_1 I_1 - \gamma_1 I_1$$

$$\frac{dT}{dt} = \gamma_1 I_1 - (\sigma + \beta_2 I_2) T$$

$$\frac{dI_2}{dt} = \beta_2 I_2 S - (\gamma_2 + d_2) I_2$$

$$\frac{dR}{dt} = \gamma_2 I_2 + \sigma T - \delta R$$

(4) SI<sub>1</sub>TI<sub>2</sub>RVMModel:It is given by following diagram:



The governing equations of the model are as follows:

$$\frac{dS}{dt} = -\beta_1 S_1 I_1 - \alpha$$

$$\frac{dI_1}{dt} = \beta_1 S_1 I_1 - \gamma_1 I_1$$

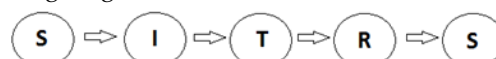
$$\frac{dT}{dt} = \gamma_1 I_1 - (\sigma + \beta_2 I_2) T$$

$$\frac{dI_2}{dt} = \beta_2 I_2 S - (\gamma_2 + d_2) I_2$$

$$\frac{dR}{dt} = \gamma_2 I_2 + \sigma T$$

$$\frac{dV}{dt} = \alpha$$

(5) Mathematical Model on Influenza: It is given by following diagram:



The governing equations of the model are a follow: -

$$\frac{dS}{dt} = -\beta SI + \delta R$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dT}{dt} = \gamma I - (\sigma + d)T$$

$$\frac{dR}{dt} = \sigma T - \delta R$$

### 3 DISCUSSION

The result of this research will be helpful to predict the growth of infectious disease, to determine the key factors of the spread of infectious disease and to seek the optimum strategies of preventing and controlling the spread of infectious diseases. This modified SIR model can possibly allow decision makers to make a better informed decision on the impact of future epidemic, endemic or pandemic stage and to determine the appropriate interventions for limiting these deadly complications [6]. Our investigation is focusing on future work of epidemiology survey and analysis numerically with the help of MATLAB. This study also provides the considerable role of correlation of mathematical modelling and dynamical aspects of some specific epidemic diseases.

### References

- [1] M.K. Keeling and C.A. Gilligan (2000): Bubonic Plague. TheRoyal Society.
- [2] Murray J D (2002) Mathematical Biology. New York: Springer Verlag.
- [3] Prasenjit Das (2014): Stability Analysis of Swine Flu Transmission - A Mathematical Approach. Computational and Mathematical Biology, Issue 3(1).
- [4] Mark Lawley (2010): An Optimal Control Theory Approach to Non- Pharmaceutical Interventions. BMC Infectious Diseases.

- [5] Fred Brauer (2008): Some Mathematical Background for Mathematical Epidemiology.
- [6] Kayla Henneman, Dan Van Peurse, Victor C. Huber (2013): Mathematical modeling of influenza and a secondary bacterial infection. WSEAS TRANSACTIONS on BIOLOGY and BIOMEDICINE, Issue 1, Volume 10,
- [7] James Holland Jones (2007): Notes on  $R_0$ . Department of Anthropological Sciences Stanford University.
- [8] Renato Casagrandi (2006): The SIRC model and influenza A. Elsevier - Mathematical Biosciences 200, 152–169.
- [9] C.W.Brown: Algorithmic Methods for Computing Threshold Conditions in Epidemic Modelling. Available at <http://www.cs.usna.edu/~qepcad/SLFQ/Home.html>.
- [10] Frank G. Ball (1991): Dynamic Population Epidemic Models. Mathematical Biosciences 107:299-324.
- [11] Meghna R. Sebastian (2009): Swine Origin Influenza (Swine Flu). Indian Journal of Pediatrics, Volume 76—August, pp: 833-841.
- [12] Michael Hohle (2005): Inference in disease transmission experiments by using stochastic epidemic models. Appl. Statist. 54, Part 2, pp: 349–366.
- [13] Peter Palese and James F. Young (1982): Variation of Influenza A, B, and C Viruses. Science, Vol. 215.
- [14] Frank Ball and A.D. Barbour (1990): Poisson Approximation for Some Epidemic Models. Journal of Applied Probability, Vol.7, No.3, pp: 479-490.
- [15] Herbert W. Hethcote (2000): The Mathematics of Infectious Diseases. SIAM Review, Vol. 42, No. 4. pp. 599-653.
- [16] Jeffery K. Taubenberger and David M. Morens (2006): 1918 Influenza: the Mother of All Pandemics", Emerging Infectious Diseases, www.cdc.gov/eid, Vol. 12, No. 1.
- [17] M. Derouich, A. Boutayeb (2006): Dengue fever: Mathematical Modelling and Computer Simulation. Elsevier-Applied Mathematics and Computation 177, 528–544.
- [18] Vinod Kumar Bais and Deepak Kumar (2015): SITR Dynamical Model for Influenza. International Journal of Engineering Technology Science and Research, Volume 2 special issue. pp 76-79.