

# A Review on Modeling of Epidemics Spreading in Social Interactions

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**Abstract**— Epidemic diseases spread is one of the major problem related to our health and it increases as our involvement in society increases. The way people interact with each other are the key factors that impact on epidemics spreading. The standard epidemic model is SIR model stands for susceptible-infected-recovered model which was found years ago and used for various disease spread control. Traditional models which are used by some modifications in susceptible-infected-recovered (SIR) model ignore the crowding effect and thus has some unrealistic assumption. In this paper, a novel model called improved SIR model is explained which will give the better realistic simulation results by considering crowding or protection effect. The model can be used to prevent and control the spreading of infectious diseases like malaria, swine flue, chicken pox etc. by understanding different parameters related to them such as rate of infection, rate of recovery, contact rate, epidemic threshold etc. The efficiency of this model can be analyze in a social sub-networks like school, classroom, hostel etc. with some potential immunization strategies, such as random set(RS) immunization, dominating set(DS) immunization, and high degree set(HS) immunization.

**Index Terms**— SIR epidemic model, social contact network, epidemic outbreak, immunization strategies, crowding effect

## I. INTRODUCTION

Study of epidemics has always been a topic where biological issues mix with the social ones. Many diseases spread through human contacts with infective individuals. The pattern of these diseases causing contacts forms a network.

Social contact networks are social networks made up of set of individuals or interpersonal contact between them. The contacts can be online interactions or face to face interactions. The paper describes the epidemic models on social contact networks, in which the links between persons are face to face interactions which may lead to infection among them. The modeling of infectious diseases is a tool which has been used to study the mechanisms by which disease spreads.

Studying the epidemic models help the people to know the dynamics of epidemics on social network and help them to mitigate the disease when epidemic outbreaks. There are two type of epidemic models viz. stochastic and deterministic models. Stochastic models depend on the

variation by risk of exposure, disease and other illness dynamics and mostly used in small population. In deterministic models population is divided into small subgroups or compartments, each representing specific stage of epidemics and model is formulated by differential equations.

The standard epidemic model i.e susceptible-infected-recovery (SIR) model is widely used because of its usability and simplification. The SIR model can be used to analyze the number of individuals in three compartments which are susceptible, infected and recovered. But in a community with single epidemic source, the epidemic may never outbreak to a significant number of individuals although the SIR model would predict significant number of infected individuals. Therefore, here proposed the stochastic models to estimate the epidemic parameters. Here considered, the real social contact networks exhibit heterogeneous properties rather than homogeneous properties on which the standard SIR model is based. The Barabasi-Albert (BA) model is used to generate such artificial social contact network.

## A. Epidemics

Epidemics are defined as outbreaks that affect non-zero fraction of the population in the limit of large system size. When talking about epidemic disease first thing in mind is about contagious diseases like- influenza, measles and sexually transmitted diseases, which spread from person to person. In extreme cases a single disease outbreak can have significant effect on whole civilization.

## B. Standard Epidemic Model

SIR is the standard epidemic model which was firstly invented in 1927 by W. O. Kermack and A. G. Mckendrick and has played a major role in mathematical epidemiology. In this epidemic model the population is partitioned into three disjoint groups of susceptible S, infected I and recovered R with numbers s, i and r respectively. The model is used by one would like to determine the parameters to control or prevent the epidemics. The total population is given as,

$$n = s + i + r \dots\dots\dots(1)$$

the SIR model is appropriate to use under following assumptions,

- 1) Population is fixed
- 2) The only way a person can leave a susceptible group is to become infected. The only way a person can leave infected group is to recover from the disease. Once a person has recovered, the person received immunity.

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- 3) The susceptible are those who are not infected and not immune, the infectives are those who are infected and can transmit the disease, and recovered are those who have been infected and are immune. Here, assume that recovered are permanently immune,
- 4) Age, sex, social status and race do not affect the probability of being infected.
- 5) There is no inherited immunity
- 6) The member of population mix homogeneously

C. Differential Equations And Parameters Of The Model

The basic differential equations are as follows,

$$ds/dt = -\alpha si, \dots\dots\dots(2)$$

$$di/dt = \alpha si - \beta i, \dots\dots\dots(3)$$

$$dr/dt = \beta i \dots\dots\dots(4)$$

the above equations describe the transition of individuals from S to I to R.  $\alpha$  and  $\beta$  are the parameters called as transmissivity and recovery rate. The parameter  $\alpha$  is determined by both encounter frequency and the efficiency with which disease transmit per encounter. The interpretation and estimation of  $\beta$  is more easy as,  $\beta^{-1}$  is the average duration of the infection.

II. LITERATURE REVIEW

For a person to get infected by some disease is a vital problem as it is a health related issue, there must be some method to control such epidemic disease spreading so that people will become aware of that and can protect themselves from getting infected. Many approaches have recently been proposed to model the spread of epidemics in social contact network.

Teri Johnson proposed a SIR model for the mathematical modeling of the diseases with an example of the infectious disease Varicella, commonly known as Chicken Pox. But this model does not work with all diseases. This model helps to explain the change in the number of people needing medical attention during epidemic. The model considered lots of assumptions to model the epidemic spread successfully.[1]

Tian Gao, designed a system to implement stochastic algorithm on an FPGA system to accelerate a biological simulation. The proposed model SIR which shows the epidemic spreading using FPGA( Field Programmable Gate Array). In this paper, Tian Gao compared the SIR model effectiveness by simulation only and by hardware i.e using FPGA. Showing that modeling of epidemic spreading is much faster by using FPGA technology rather than simulation. The system is very effective, faster and flexible with any number of the population.[2]

As in recent years, individual based epidemic simulations on synthetic social contact networks have been used in supporting public health epidemiology. Such models are also useful in understanding the disease spread through a small

subset of the population. In order to check the epidemic disease spread, it is necessary to divide the people into small groups called as social sub-networks is given by H. Xia, M. V. Marathe and H. S. Mortveit by giving certain examples like illustrating multilevel refinement and analysis technique for embedding detailed high school network. This makes the epidemic simulation easy.[3]

Many large networks follow the scale free power law distribution this helps in finding the new vertices connected to the existing one to find the network expanding continuously. It is given by Albert- Laszlo Barabasi and Reka Albert and have also given the report on existence of high degree of self-organization characterizing the large scale properties of complex networks.[4]

III. PROPOSED EPIDEMIC MODEL

For the epidemic diseases spreading among people in society, various parameters are responsible such as environmental conditions, individual people immunity, contact rate between people, recovery rate, epidemic threshold, etc... if any of these changes within particular time then it is difficult to model the epidemic spread. The SIR model is the standard epidemic model based on the different differential equations. Till now this was the only model used to understand the epidemic spread of different diseases among the social networks. But this model is not that much effective as it is based on the assumption that the each person in society has the homogeneous connections i.e equal probability to contact with any other people in society, but in real network it is not.

So here, proposed a improved SIR model called ISIR which is based on the real heterogeneous connections among people and considers that the infection rate is not a fixed value, but a function of number of infected individuals  $\lambda = \beta(I)$ .  $\beta$  is the contact rate. Considering both the deterministic and stochastic models in scale free social network. Proposed model also tries to simulate epidemics on artificial as well as real social contact network. The artificial network generated by BA (Barabasi Albert) generator with different parameters. To study the infection, here used the q-influence model. The model shows that if A is the reference node with n infected neighbors at time t each one having fixed probability of q will infect each others, then the probability of reference node will get infected at the next time by its n infected neighbors is given as,

$$P = 1 - (1 - q)^n \dots\dots\dots(5)$$

The proposed model is used to examine the immunization methods to control the epidemics on social contact networks using four epidemic control methods, which are random set immunization(RS), dominating set immunization(DS), high degree set immunization(HS) and critical node set immunization(CS). Having following stages,

1. Collection of dataset
2. Application of pre-processing techniques to remove unwanted entries
3. Development of genetic algorithm to mode disease spreading

4. Taking input from the user about environmental conditions around them
5. Comparing these environmental conditions with the model, in order to get the prediction details about the disease.

The genetic algorithm for designing the model is shown in fig. 1

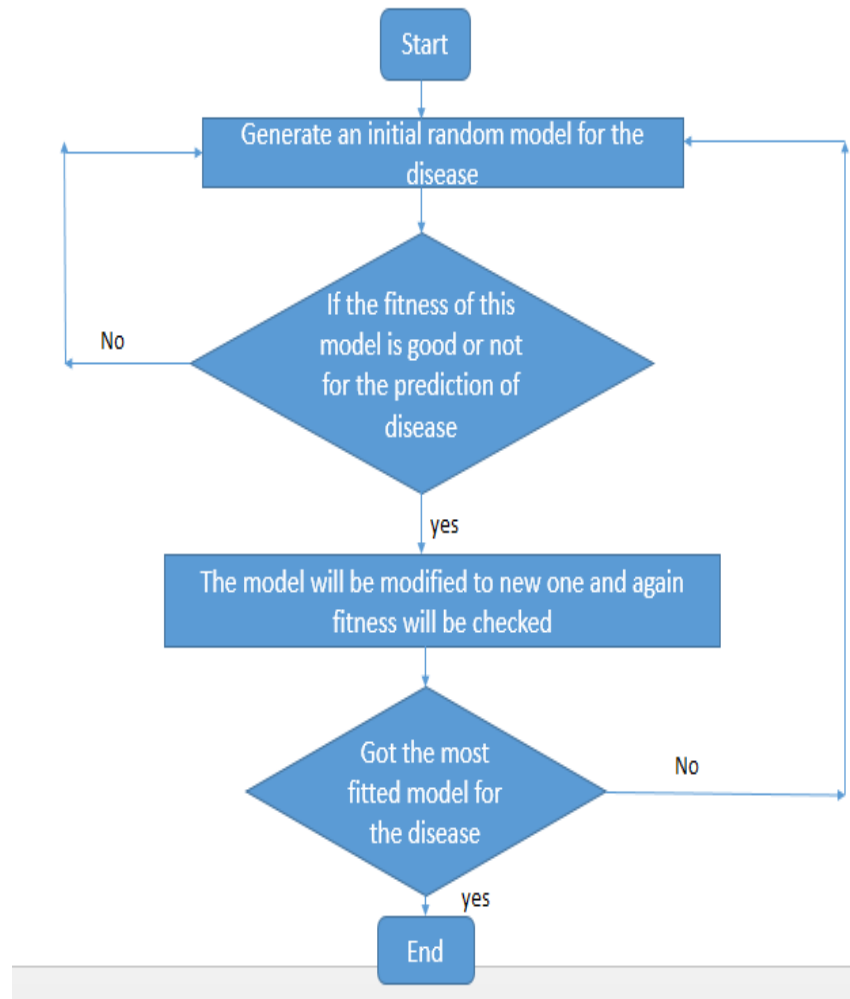


Fig.1 Genetic Algorithm for model design

#### IV. CONCLUSION

The paper explains, how the standard epidemic model works to recognize the people who are susceptible, infected and recovered from certain infectious disease. The proposed model provides the improved SIR model for epidemic control in a social contact network by considering some realistic assumptions like the real heterogeneous contact networks and also explained immunization strategies. It also can be used to analyze the epidemic dynamics, understand the epidemic disease spread and optimize control strategies for it by analyzing the performance of it in a simulation.

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