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Infectious Diseases Modeling: An Epidemic model (SIR Model)

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***Abstract*- This article try to give a basic understanding of Infectious diseases and the model as SIR with different situational applications based on mathematical and statistical formulae. The importance of Infectious disease is more in this day, to analysis and determines the various unknowns and prediction in feature. This article covers the basic and necessary contents and equations in using model as SIR model. The SIR model labels these three compartments S = number susceptible, I = number infectious, and R =number recovered (immune). This is a good and simple model for many infectious diseases. In this article, the methodology is explained based on approximate solutions by numerical methods in SIR model. The infective population at some time t is larger than the initial number, and it might be an epidemic. The $I_0 > 0$ then state this observation in terms of S_0. If $S_0 < \beta/r \equiv \rho$ then the infective population decreases initially and if $S_0 > \beta/r \equiv \rho$ then the infective population increases initially.**

***Index terms*- Infectious Diseases, Modeling , SIR model, Endemic , Epidemic**

I.INTRODUCTION

Infectious diseases have a substantial impact on society of human being, it affect the public health, healthcare, economic and society. Any infectious diseases must be control and prevent the emergence, expansion or resurgence of pathogens warrants continuous evaluation using different methods.

Infection may be defined as the invasion or one organism by a small infecting organism. To get spread of infection there will be a Host. Here hosts may some living things such as animals, humans etc.,. If there is a spread of such infection becomes a disease. Infectious diseases are an important cause of death of living organism. Now days there are more death happening in Human community. For instance, one of the most popular disease under infectious is HIV/AIDS. In recent scenario, COVID 19 is an infectious disease. To study this type of Infectious diseases, there will be several methodologies in analysis of such diseases under the clinical or lab area. In other way is modeling these diseases by using statistical and mathematical concepts and predict their various functionalities with respect to transmission, spread, and distribution and so on.

Here in this article, it is going to be considering about the mathematical and statistical model. By using this model one may study the nature of these diseases and apply some optimal control strategies against new or emergent infection such as COVID-19. Mathematical and statistical model are being increasingly used to find the transmission of infection and it is possible to evaluate the potential impact of control programs in reducing morbidity and mortality. A disease model is an animal or cells displaying all or some of the pathological processes that are observed in the actual human or animal diseases. This disease models are used to understand the disease develops and testing potential treatment approaches.

In clinical or medical term these models are classified as epidemical models. Epidemics of infectious diseases are not new to the world. The morbidity and mortality of infectious diseases profoundly shaped politics, culture and economic of the spread.

There are some terms that are used in this infectious disease tasks such as epidemic, pandemic, endemic, epicenter. There terms were explained as:

An epidemic disease is one affecting many persons at the same time and spreading from one person to another in a locality where the disease is not permanently prevalent otherwise the diseases occurring at the level of a region or country. The meaning of Epidemic is “A temporary prevalence of disease”.

A pandemic disease is one affecting many persons at the same time and spreading form one person to another in a large area. Here the area is an entire country, continent or the whole world. The pandemic is an epidemic that has spread over a wider area otherwise a world wide spread of a new disease. The meaning of Pandemic is general and universal.

To relate these terms "Epidemic and Pandemic" as start of some diseases spread rapid within a community or region where as a pandemic is a wider spread of diseases across the countries or continents or the global.

The term endemic, is an infection in a population when that infection is constantly maintained at a baseline level in a geographic area without external inputs

The epicenter is a "Focal point, as of activity, this means more or an accelerating number of cases being confirmed there than anywhere else in the world.

2. STATISTICAL AND MATHEMATICAL MODELS IN INFECTIOUS DISEASES MODELING

The modeling of infectious diseases is a tool that has been used to study is classified into mathematical and statistical model. These are all applied with the principles of mathematical and statistical based formulas and concepts to construct a model with optimal control of diseases and prediction of the unknowns to control an epidemic. In any process of modeling there are three-stage process are 1. Observation, 2. Building a model to describe and 3. Using the model to predict future observations.

2.1 Statistical models

In infectious diseases, statistical modeling is generally of known as probabilistic or stochastic models. These models are involved with certainty. The phenomena of infectious diseases are rarely as predictable

In this probabilistic model the presence of measurement of errors and uncontrolled variability of experimental conditions are considered and controlled. A very wide part of the statistical theory is concerned with this model and most elementary statistical concepts are involved. Epidemiology is more involved with the happening of certain events in natural occurrence of diseases. Most of the time, the statistical model in infectious diseases will involve with Bernoulli and Poisson distribution.

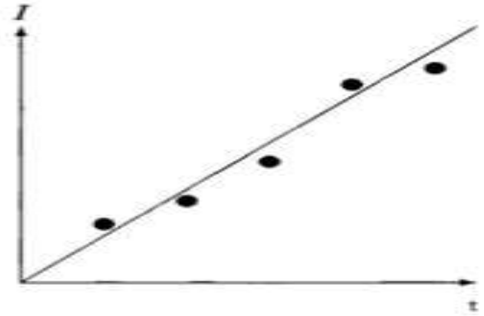

Figure 1 Experimental or observational errors.

From figure 1, the presence of measurement errors and uncontrolled variability of experimental conditions from the real data is depicted. This is an involvement of Binary data that is the response measure may take one of only two possible values and it is commonly known as Binary response. This scenario will be taken in many epidemiological studies and further there are two different types of study generate this binary response. They are (a) cohort studies with fixed follow up time and (2) Cross- sectional prevalence data. At the same there are situation to use both Classical (frequentist) or Bayesian approach.

2.2 Mathematical models

Mathematical analysis and modelling is central to infectious disease epidemiology. When dealing with large populations, as in the case of tuberculosis, deterministic or compartmental mathematical models are often used. In a deterministic model, individuals in the population are assigned to different subgroups or compartments, each representing a specific stage of the epidemic. The idea that mathematical models of infectious diseases should be confronted with real data, combined with the fact that all models are, at best, simplified representations of the real world raises the need for uncertainty quantification. Mathematical models that incorporate a dynamic risk of infection figure prominently in the study of infectious diseases epidemiology as a tool to inform public health policy.

3. SIR MODEL

Infectious diseases are a major cause of death worldwide and have in the past killed more human subjects. At that time, there is a necessity to control the diseases in various measurements, the mathematical modelling are also used to control and predict the disease in future. This modeling of infectious diseases was devised in 1760 by Bernoulli. There are various models involving in the control and prediction of infectious diseases, one of the models is SIR. The SIR model is a simple epidemic model of infectious diseases in a large population. This model was devised by Kermack and McKendric in the year of 1927.

In SIR, S stands for susceptible, I stands for infected and R stands for Recovered. Hence this SIR model has three classes or components as susceptible individuals are uninfected and susceptible to the diseases (S), infected individuals are infected and can infect susceptible (I) and finally recovered individuals have recovered from the infection and are immune to the re-infection (R). This component R is sometimes replaced as Removed and it includes cured and died. Still the day this model is used to modelling epidemics of infectious diseases.

The SIR model used to track the number of susceptible, infected and recovered individuals during an epidemic with the help of mathematical differential equations. The assumption made in this model is the given or studying population consists of three types of human subjects or individuals , whose number are denotes by S,I and R and also the function of the time (t) change according to a system of equations (differential). Again this model assumes a time scale short enough with birth and death can be neglected. Addition to this, some points are added that the removed cases may or may not have disease, but they cannot become infected and transmit the disease to others. They may have immune power either natural or unnatural way or might have diseases but are incapable of transmitting the diseases or they might die without getting cure and not transmitting the diseases.

Figure 2: a. The Scheme of the basic model for SIR

Figure 2 b. the rate of infectivity and rate of recovery

Figure 2: Scheme of SIR

In figure 2, is a scheme of SIR, Figure 2a is the basic scheme of SIR model is displayed, boxes are the components and arrows indicate the direction of the travel. This above model is without any rate of occurrence, when the rate involves the model is shown in Figure 2b.

The SIR model is simple and easy to use by involving differential equations as a deterministic model as an assumption of non-randomness and the starting conditions give the same results and the other case of continuous time that is non discrete time. The analogous to this model is that the infected and susceptible individuals occur at rate proportional to their respective observations in the population. The rate of infection is defined by βSI, this will be occurred between Susceptible and infected and the term β is a parameter of infectivity. Infected individuals are assumed to recover with a constant probability at any time (t) this gives a recovery rate r and the overall recovery rate is rI and this happened between infected and recovered.

3.1 Assumptions

1. The population is fixed.
2. After recovery, immunity is conferred
3. The gain in the infective component is at a rate proportional to the number of infective and susceptible, βSI , β> 0. Susceptible are lost at the same rate.
4. The rate of recover to the removed class is proportional to the number of infective, rI, r>0
5. The incubation period is shot enough to be negligible.
6. The various groups are uniformly mixed

From the figure 2, the scheme of SIR can be translated into a set of differential equations:

$$\left.\begin{aligned} dS/dt &= -\beta SI \\ dI/dt &= \beta SI - rI \\ dR/dt &= -rI \end{aligned}\right] - \text{---------} \quad (1)$$

Using this SIR model, it will involve with a mild, short lived epidemic. In this model changes are occurred continuously in the time, rather than in discrete steps. The above equation in (1) is a set of nonlinear , ordinary differential equations for this disease model. The size of the population N is equivalent to (S+I+R) is the initial population size. Within initial conditions, $S(0) = S_0 > 0$, $I(0)= I_0 > 0$ and $R(0) = 0$. The parameter β has units of one over time per individual, but the parameter r has units of one over time. These parameters used to characterize the disease.

There are various approaches one can take to understanding the predictions of this model and the behavior of its solutions. Kermack and McKendrick derived an approximate result for the removal rate, dR/dt in terms of a hyperbolic secant function. These methods are considered as standard tools in the analysis of ordinary differential equations.

3.2 Approximate solutions by numerical methods in SIR model

In any model it is very serious issue to finding the parameter that are involved in any field. To understand the predictions of this model and the behavior of its results are important to interpret. Thus the primary question is that the value of β, r, S_0 and I_0 will be an epidemic. At first the $I(t) > I_0$ for some t and t>0. In this condition, the infective population at some time t is larger than the initial number, and it might be an epidemic.

The derivative of I initially is $\frac{dI}{dt}|t = 0 = I_0$ $(\beta S_0$ - r) ----- (2)

If the infective population increases initially if I_0 $(\beta S_0$ - r) > 0 and the infective population decreases initially if I_0 $(\beta S_0$ - r) < 0. Since $I_0 > 0$ then state this observation in terms of S_0. If $S_0 < \beta/r \equiv \rho$ then the infective population decreases initially and if $S_0 > \beta/r \equiv \rho$ then the infective population increases initially. It is also to be noted that $\frac{dS}{dt} < 0$. Thus the susceptible population always decreases. In a particular susceptible population $S(t) < S_0$, then the conclusion that if $S_0 < \rho$ then $S(t) < \rho$ for all time. Thus, $\frac{dI}{dt} \leq 0$ for all time, in which the case $I(t) < I_0$ and the infection dies out that is there is no epidemic.

On the other hand, if $S_0 > \rho$ then I(t) increases initially and there exist a chance of epidemic. These observations describe a threshold phenomenon. Let $S_c = \rho = r/\beta$ the critical value of the susceptible population. If the initial susceptible population is larger than this value, $S_0 > S_c$ then there is an epidemic otherwise not. The population that is from susceptible must be large enough for an epidemic to occur.

As the role of explaining threshold to a better manner, the ratio $\rho = \frac{r}{\beta}$ is sometimes known as a relative removal ration and the contact ratio is $\sigma = \frac{1}{\rho} = \frac{\beta}{r}$ and the quantity β has the units of 1/ time and it gives the removal rate from the infective components. The average period of infectivity is 1/r and the ratio β /r is the fraction of the population that comes into contact with an infective individual during the period of infectiousness. The important and basic measure is the reproductive rate of the infection R_0 and the reproductive rate of infection (R_0) = $\frac{\beta S0}{r}$. The basic $R_{0\ is}$ the number per unit time of secondary infections produced by one primary infection in a complete susceptible population. If R0 >1 then an epidemic will occur. In case of $R_0 > 1$ is implies that more than one secondary infection from a primary infection.

As mentioned earlier, the size of population or total population is N then N= S+I+R is constant and it is equal to the initial time the R=0 then the N (Initial time) = S +I, this means that the recovery is zero and it will be get eliminated so that the model become with two equations and two unknowns as S and I with respect to time (t).

5. CONCLUSION

The idea behind compartmental models is to divide the host population into a set of distinct classes, with respect to its epidemiological status. Epidemiology is essential a population biology discipline concerned with public health. Epidemiology is heavily influenced by mathematical theory. Any model is a caricature of reality as represented by empirical data. One simple model is SIR formalism which classifies individuals as S = number susceptible, I = number infectious, and R = number recovered (immune). This is a good and simple model for many infectious diseases.

In this article, the methodology is explained based on approximate solutions by numerical methods in SIR model. The infective population at some time t is larger than the initial number, and it might be an epidemic. The $I_0 > 0$ then state this observation in terms of S_0. If $S_0 < \beta/r \equiv \rho$ then the infective population decreases initially and if $S_0 > \beta/r \equiv \rho$ then the infective population increases initially.

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