MATHEMATICAL MODELING OF INFECTIOUS DISEASES.

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Mathematical Modeling Of Infectious Diseases.

Introduction

The words "diseases", "infection", and "outbreak" can be heard almost everywhere ever since the Covid 19 pandemic has hit the world. Medical experts and researchers around the globe, are working to limit the spread of the virus and to find a cure for this disease. The way this or other diseases' spread is an ongoing concern, and it is apparent that there is still much more that we do not realize about the dynamics of the infectious diseases. Our understanding of infectious diseases and how they spread can impact each of our lives.

The team of experts and researchers who are currently working on understanding the dynamics of Covid19 or any other infectious diseases, not only consist of doctors, or medical experts but also consist of mathematicians and engineers. Researchers from different disciplines have come together to use the mathematical modeling and computer software to tackle the infectious diseases. Mathematicians are the unsung heroes who are also helping us overcome a global pandemic. Mathematical modeling or mathematics, in general, helps the scientists in understanding the dynamics of any infectious disease, modelers collect the data of current outbreak and previous outbreaks to predict who is most vulnerable, who may get infected, how to limit the disease and how fast will this disease spread, etc. etc. When a mathematical model is built, mathematical analysis is joint with the computer simulations, which aids the researchers in investigating the behavior of the model.

Mathematics is very useful in identifying the patterns of how a virus spreads and in finding the underlying structures to help prevent and design strategies to govern the outbreaks. The Centre for disease control and prevention (CDC) reported that they used mathematical modeling techniques to respond to the 2019's pandemic. (Prevention, 2020). CDC reported using mathematical modeling during the decision phase, planning phase, resource provision phase, and in the implementation of the social distancing, etc. during Covid 19.

How a Mathematical Model Helps in Understanding Infectious Diseases Transmission

Let us consider an example of a mathematical model, which is designed to examine the spread of a disease in a population of masses. This particular model is designed to read the patterns of human contacts, the period from coming in contact with the virus to becoming infectious, the length of sickness from the infection and immunity, etc. Once all of these factors are expressed in a model; the Scientist can make the following predictions:

- Total number of individuals who are expected to be infected during an outbreak.
- Total epidemic duration.
- When will the peak period starts.
- Expected number of deaths etc.

Types of Epidemic Modeling

The two types of epidemic modeling, are:

- Stochastic modeling, and
- Deterministic modeling.

A stochastic model is used for estimating the probability distributions of outcomes. This model depends on random variations (unknown change in hereditary traits). Deterministic mathematical models are used when dealing with huge populations. In this model, the population is categorized into different subgroups and each subgroup represents a different stage of the disease outbreak.

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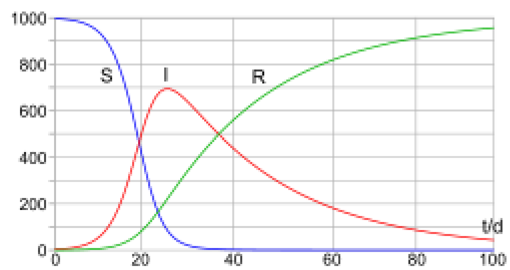
The SIR Model

The SIR model (Kermack & McKendrick, 1927) was developed in the year 1927. In this model, a fixed population is considered which is divided into three different compartments i.e. susceptible ($S(t)$), infected ($I(t)$), and recovered ($R(t)$). Image below shows the SIR model graph (Source Internet).



S (0) =997, I (0) =3, R (0) =0 rates for infection β=0.4 and for recovery γ=0.04

Susceptible (S) represents the individuals that are not yet infected with the disease at the given time (t). Infected (I) represents the individuals who are infected with the infectious disease and tend to spread it to the population of people categorized under the susceptible compartment. Recovered (R) represents the individuals who, after being infected, recovered from the disease. Recovered not only contains individuals who were able to successfully recover from the infection but also individuals who died from it as well as the individuals who cannot get infected again or transmit the disease.

Fixed population: $N = S(t) + I\ (t) + R(t)$

Mathematical Description of the SIR Model

Consider,

σ = number of individuals that can be infected per unit time by an infected patient

η = number of individuals that one person comes in contact with per unit time

τ = number of total contacts with vulnerable people

p = probability of infecting a vulnerable individual with whom an already infected patient is in contact with

β = number of individuals infected by an already infectious person (suppose that all people in patients contact are vulnerable)

The equation below is the mathematical description of the SIR model defined in the ordinary differential equation (ODE) form.

$$\tau = \frac{\eta S}{N} \ (\boldsymbol{eq}\ \mathbf{1})$$

$$\sigma = \tau * p \ (\boldsymbol{eq}\ \mathbf{2})$$

$$\sigma = \frac{\eta S}{N} * p \ (\boldsymbol{eq}\ \mathbf{3})$$

$$\beta = \eta * p \ (\boldsymbol{eq}\ \mathbf{4})$$

Let’s replace (eq.4) into (eq.3) to find (eq.5)

Let γ be the probability that a person may recover at a time (t) (from I to R compartment).

$$\frac{dS(t)}{dt} = -\beta \frac{S(t)I(t)}{N} \ (\boldsymbol{eq}\ \mathbf{5})$$

$$\frac{dI(t)}{dt} = \beta \frac{S(t)I(t)}{N} - \gamma I \ (\boldsymbol{eq}\ \mathbf{6})$$

$$\frac{dR(t)}{dt} = \gamma I(t) \ (\boldsymbol{eq}\ \mathbf{7})$$

Variations of SIR Model

There are many variations of the SIR model, some of which are listed below:

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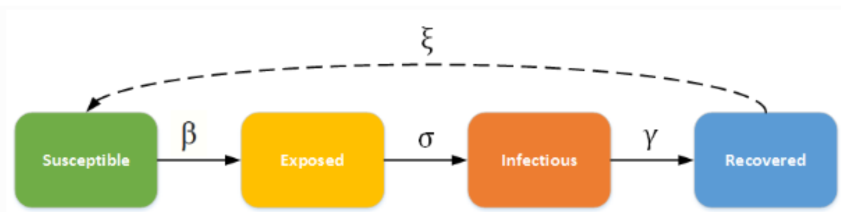
- The SIS model.
- The SIRD model.
- The MSIR model etc.

SIS model (Parshani, Carmi, & Havlin, 2010) includes the births and death, and it considers the case where there is no immunity after recovery. SIRS model is designed for scenarios where immunity only lasts for a very short period. MSIR model deals with the infants that can be born with an immunity to the infectious diseases.

The SEIR or SEIRS Model



SEIR - SEIRS model

Many infectious diseases have a hidden or latent period. That means, an individual is infected during this phase but the symptoms take quite long to occur. People going through the latent phase of the disease are not infectious. The SEIR model is designed for such diseases. SEIR stands for susceptible (S), exposed (E), infectious (I), and recovered (R). According to this mathematical model, each individual who gets the virus stays in the exposed (E) state of the model. In this stage virus of an infectious disease is supposed to be in an incubation state and it does not transmit to anyone else.

Mathematical Description of SEIR

Consider total pollution is N and $N = S + \mathrm{E} + I \ + R$ and if SEIR is written for a closed population without births or deaths i.e. SEIR without any important dynamics then:

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$$\frac{dS}{dt} = -\frac{\beta SI}{N}\ (\boldsymbol{eq\ 1})$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - \sigma E\ (\boldsymbol{eq\ 2})$$

$$\frac{dI}{dt} = \sigma E - \gamma I\ (\boldsymbol{eq\ 3})$$

$$\frac{dR}{dt} = \gamma I\ (\boldsymbol{eq\ 4})$$

In the SIR model, supporting dynamics like birth and death can stand an epidemic or allow infectious diseases to spread. The mathematical model of SEIR with vital dynamics is written as,

μ = birth dates

v = death rates,

$$\frac{dS}{dt} = \mu N - vS - \frac{\beta SI}{N}\ (\boldsymbol{eq\ 1})$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - vE - \sigma E(\boldsymbol{eq\ 2})$$

$$\frac{dI}{dt} = \sigma E - \gamma I - vI(\boldsymbol{eq\ 3})$$

$$\frac{dR}{dt} = \gamma I - vR\ (\boldsymbol{eq\ 4})$$

SEIRS or susceptible (S), exposed (E), infectious (I), recovered (R), and susceptible (S) model is used to let recovered patients to return to a vulnerable state.

Mathematical Description of SEIRS

ξ= rate of recovered individuals returned to the vulnerable or susceptible state due to the loss of immunity.

$$\frac{dS}{dt} = -\frac{\beta SI}{N} + \xi R - vS \; (\boldsymbol{eq\ 1})$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - \sigma E \; (\boldsymbol{eq\ 2})$$

$$\frac{dI}{dt} = \sigma E - \gamma I \; (\boldsymbol{eq\ 3})$$

$$\frac{dR}{dt} = \gamma I - \xi R \; (\boldsymbol{eq\ 4})$$

Vaccination Modeling

Vaccines are the best preventive tool in reducing mortality and illness rates among the population. However, health authorities find the implementation of vaccination policies challenging. To evaluate the various vaccination policies; modeling has become an integral part of the whole process (JA Bogaards, 2011). On the other hand, measuring the effectiveness of a vaccination program is also challenging and costly, which further raises the need for studies based on the whole population (Not feasible either). In this scenario, mathematical modeling creates a way out in measuring the effectiveness of indirect protection given through immunization. Two vaccines for rotavirus and HPV (Human Papilloma Virus) have been recently introduced to cater to diarrhea and cancer problems (C de Martel, 2012). Both vaccination programs have been implemented by many countries. Different transmission models have been constructed in order to attain a vast epidemiological effect and to understand the effects of the applied vaccination (C Atchison, 2010). To understand, HPV vaccination programs are taken as an example to understand the effectiveness of the immunization program. HPV leads to different complex issues, because it involves differences in sex outcomes, sexual transmissions, and adolescent vaccination. Different models have been studied in order to find out the optimal solution against HPV (IA Korostil, 2013).

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The models provided a better understanding of the effectiveness among vaccination models due to variation in various biological processes including virus stains, immunity, immunity, etc. Furthermore, modeling gave very informative insights regarding the questions, such as: the ages of target vaccination done of the key issues in HPV vaccination and catch-up policy related to the vaccination program.

Mass Vaccination Mathematics

It is a fact that diseases can no longer exist in the population if the number of individuals immune, exceeds the herd of immunity level. This means if a vaccination works and the number of the immune people increases then an infectious disease can be eliminated. For example: since the vaccination of smallpox was invented; the disease is now in control. Currently, polio vaccine drives are running under the WHO’s supervision to eliminate this disease. Scientists use mathematical modeling to calculate the critical immunization threshold, which indicates the smallest amount of the population that must be immunized at birth to eliminate a certain infection, completely.

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