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Mathematical Modelling of Infectious Diseases - Its Relevance in Time to COVID-19

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Abstract:

Infectious diseases are caused by pathogenic microorganisms such as bacteria, viruses, parasite or fungi. For example- ***viruses*** *give rise to HIV, influenza, SARS, measles and COVID-19,* ***bacteria*** *give rise to TB, anthrax, salmonella, Chlamydia and cholera, and* ***protozoa*** *give rise to malaria and trypanosomiasis (sleeping sickness). A disease can spread directly or indirectly, from one person to another by respiratory droplets (e.g. measles), via body secretions (e.g. Chlamydia), by biting tsetse flies (e.g. trypanosomiasis) or mosquitoes (e.g. malaria), or by ingestion in food or water (e.g. cholera).Depending on mode of transmission and fatality, the severity of disease is assessed. An in depth understanding of the pathogen and epidemiology of disease helps in control or eradicate it.*

Keywords: Mathematical model, Epidemic modelling, SEIR model, basic reproduction number, total population, recovery rate, recovery period.

Introduction

A **mathematical model** is an imaginary micro world consisting of entities behaving according to precisely specified rules. Mathematics provides us with a language for formulating these rules of behaviour in a concise and unambiguous way. Once a mathematical model is constructed, **mathematical analysis**, often combined with **computer simulations**, helps us to investigate the global behaviour of the model, drawing out the consequences of the assumptions that we have made. Thus, within the context of the model, we can make predictions of the future of our imaginary world and also study how these predictions change as the rules governing the entities described by the model are varied.

Thus, a mathematical model for the spread of **an infectious disease in a population** of hosts describes the transmission of the pathogen among hosts, depending on patterns of contacts among infectious and susceptible individuals, the latency period from being infected to becoming infectious, the duration of infectiousness, the extent of immunity acquired following infection, and so on. Once all of these factors are formulated in a model, we can make predictions about the number of individuals who are expected to be infected during an epidemic, the duration of the epidemic, the peak incidence, and, indeed, we can predict the entire epidemic curve, providing us with the expected number of cases at each point in time.

The importance of **Mathematical modelling** in real world problems is undisputed and recently it has emerged as a very important tool in almost all areas of engineering, applied sciences, social sciences, economy and management etc. **Alternative mechanisms** can be explored through modelling in order to understand the system. These models further may be assessed without resorting to **costly or ethically impossible experiments** (e.g. disease treatment, vaccination, atomic explosion). These Mathematical Models can be used to generate **quantitative predictions and qualitative insights** in to the systems. *Theoretical models* have their importance over empirical modes as in science we not only need to understand patterns but also to answers why those patterns arise. We are more into causation than correlation!

Control interventions and Motivation:

Human behaviour changes due to information about the presence of disease and healthy individuals take preventive measures. Such individuals are artificially immune to the infection. These behavioural changes affect disease progression. This behavioural change can be induced with the help of media. Individuals can be informed about the disease spread so as to protect them. This information will be related to the infective population at any given time. The availability of treatment in general, is limited and

hence may not be available to all the infective human beings. There are various interventions, pharmaceutical and non-pharmaceutical that may be applied for control of the spread:

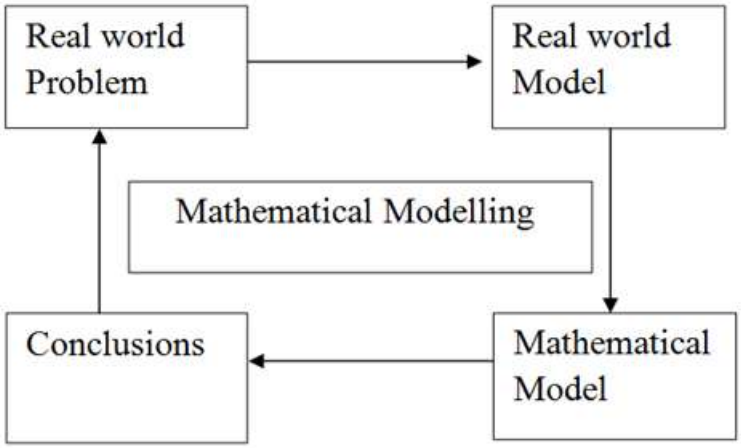
- Treatment (may be available to all, but mostly limited)
- Vaccination
- Screening
- Isolation and quarantine and social distancing
- Awareness or information induced behavioural change

Some Major Challenges:

- Choosing suitable intervention during an outbreak is still challenging: **(Prevention vs. Treatment)**
- There is trade-off among the available control interventions **(pharmaceutical vs. non pharmaceutical)** for their implementation during the epidemic outbreak.
- Quantifying the combination of suitable control policies which minimize economic burden as well as disease burden.
- Validation of results of theoretical models with data or pattern.
- Determination and implementation of suitable control policies.

Objective:

- To develop a mathematical model this accounts for the effect of individual's behavioural response (i.e. Non pharmaceutical control intervention) and **limited treatment** (i.e. pharmaceutical control intervention).
- To understand the effect of treatment and behavioural response on the dynamics of disease.
- To quantify a suitable combination of control policies that **minimizes** economic burden as well as disease burden.
- To determine and minimize the **"pre-defined cost".**



Basic Model Framework (SEIR model)

There are various models proposed to study and predict the COVID-19 status in India. Every model has its merit and demerit and on should not read too much from them as scenario is very dynamic.

In general, the spread of an infectious disease depends upon the population, the mode of transmission of disease and features of pathogen.

The ***SEIR model*** is a simple mathematical model of epidemics. An epidemic is when the number of people infected with a disease is increasing in a population. S, E, I, and R stand for:

S – *susceptible* - These are people that are not infected with the disease yet. However, they are not immune to it either and so they can become infected with the disease in the future.

E - *Infected/Exposed* – Once the pathogen of the disease is transmitted to a susceptible host, it becomes infected with micro-parasites. In certain cases the level of pathogen in the early phase may remain low enough to infect another susceptible.

Such an individual though infected cannot infect others.

I - *infected or infectious* - These are people that are infected with the disease and can transmit the disease to susceptible people.

R – *recovered* – These are people that are infected from the disease and are immune, so they can no longer be infected with the disease.

Depending upon the level of pathogen, the population, Total population (N_o), in general can be classified as :

- Susceptible population (healthy population prone to infection)-*S*
- Infected (or exposed)/Latent Population-*E*
- Infective population-*I*
- Removed or Immune population-*R*

So that $N_o = S+E+I+R$

S (Susceptible)⟶ E (Exposed)⟶ I (In

If β = average number of contact between susceptible and infective which leads to new infection per unit time per susceptible per infective, then

$$S(t+\Delta t) = S(t) - \beta S(t)I(t)\Delta t$$

$$I(t+\Delta t) = I(t) - \beta S(t)I(t)\Delta t$$

This leads to :

$$\frac{dS(t)}{dt} = -\beta S(t)I(t)$$

$$\frac{dI(t)}{dt} = \beta S(t)I(t)$$

In this model, It is assumed that the whole population is divided into two subclasses-susceptible and infective; and if one is infected then it remains in that class.

As total population is constant, we may write , the above as :

$$\frac{dI}{dt} = \beta(N_o - I)I$$

Here N_o is total population.

However, it may not be the case, always, as the infected person may recover. However, the recovery may not provide immunity to the disease.

This leads to following modification

$$\frac{dS(t)}{dt} = -\beta S(t)I(t) + \gamma I(t)$$

$$\frac{dI(t)}{dt} = \beta S(t)I(t) - \gamma I(t)$$

Here γ is recovery rate. This is reciprocal to time spent by infected individual in during its infection and is also known as ***recovery period.***

Here it should be noted that

$$\frac{dI}{dt} > 0, \quad if \frac{\beta S}{\gamma} > 1$$

and

$$\frac{dI}{dt} < 0, \quad if \frac{\beta S}{\gamma} < 1$$

In the beginning, this threshold is called as **Basic reproduction number R_o .**

Thus we define

$$R_o = \frac{\beta N_o}{\gamma}$$

The *basic reproduction number (*denoted by R_0*)* is a measure of how transferable a disease is. It is the average number of people that a single infectious person will infect over the course of their infection. This quantity determines whether the infection will spread exponentially, die out, or remain constant**:** **if $R_0 > 1$,** then each person on average infects more than one other person so the disease will spread; **if $R_0 < 1$,** then each person infects fewer than one person on average so the disease will die out; and **if $R_0 = 1$,** then each person will infect on average

exactly one other person, so the disease will become ***endemic:*** it will move throughout the population but not increase or decrease.

The basic reproduction number can be computed as a ratio of known rates over time: if an infectious individual contacts β other people per unit time, if all of those people are assumed to contract the disease, and if the disease has a mean infectious period of 1/γ, then the basic reproduction number is just $R_0 = \beta/\gamma$. Some diseases have multiple possible latency periods, in which case the reproduction number for the disease overall is the sum of the reproduction number for each transition time into the disease. For example, **Blower et al.[1] model** two forms of tuberculosis infection: in the fast case, the symptoms show up immediately after exposure; in the slow case, the symptoms develop years after the initial exposure (endogenous reactivation). The overall reproduction number is the sum of the two forms of contraction: $R_0 = R_0^{\text{FAST}} + R_0^{\text{SLOW}}$.

The epidemiological definition of ***basis reproduction number*** is the average number of secondary cases produced by one infected individual introduced into a population of susceptible individuals.

$R_o = \frac{\beta N_o}{\gamma}$ = Total number of infections generated by an infective individual in its infectivity period.

Further modification to these models can be done by considering a disease where recovery offers permanent immunity. This leads to recovered individuals moving to a separate removed or recovered class. In addition, we also consider the demographic effects such as birth rates and death rates in population as well as disease related death rates.

These modification leads to the following model.

$$\frac{dS}{dt} = \Lambda - \beta SI - \mu S$$

$$\frac{dI}{dt} = \beta SI - (\mu + \delta + \gamma)I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

With initial conditions as $S(0) > 0$, $I(0) > 0$, $and\ R(0) \geq 0$.

Consider the example of SEIR model :

$$\frac{dS}{dt} = \Lambda - \beta SI - \mu S \quad \frac{dE}{dt} = \beta SI - (\mu + \kappa)E$$

$$\frac{dI}{dt} = \kappa E - (\mu + \gamma)I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

Disease Free Equilibrium Point (DFE) : $(\frac{\Lambda}{\mu}, 0, 0, 0)$.

Computation of R_0 for SEIR Model

The characteristic equation of the linearized matrix (around DFE) corresponding to the SEIR model system is given as

$$(\lambda + \mu)^2\left((\lambda^2 + (2\mu + \kappa + \gamma)\right)\lambda + \left((\mu + \kappa)(\mu + \gamma) - \frac{\kappa\beta\Lambda}{\mu}\right) = 0$$

Thus all roots of above equation will be with negative real parts (implying stability of DFE) if

$$(\mu + \kappa)(\mu + \gamma) - \frac{\kappa\beta\Lambda}{\mu} > 0$$

$$\Rightarrow \boldsymbol{R_0} = \frac{\boldsymbol{\kappa\beta\Lambda}}{\mu(\mu + \boldsymbol{\kappa})(\mu + \boldsymbol{\gamma})} < 1$$

So, disease will be eradicated if $\boldsymbol{R_0 < 1}$.

Thus $\boldsymbol{R_0}$ plays very crucial role in disease eradication.

This can be interpreted as following :

$$\boldsymbol{R_0} = \boldsymbol{\beta}.\frac{\boldsymbol{\Lambda}}{\mu}.\frac{\boldsymbol{\kappa}}{(\mu + \boldsymbol{\kappa})}.\frac{\mathbf{1}}{(\mu + \boldsymbol{\gamma})}$$

Which is *number of new infection from an infected individual in its survival time period (infectivity period) that survived through latency* and in other words **basic reproduction number.**

Conclusion :

- Mathematical modelling of infectious diseases is a continuous process. No model can be perfect. All models are dependent on assumptions.
- The further addition of compartments is possible depending on disease and controls. For example, one may consider vaccinated class, quarantine class, isolation class, hospitalized class and so on.
- A very clear understanding about system help in framing a proper model.
- One must be careful while making any prediction from the model. As assumptions may change so may result.
- The modellers must act responsibly. A model prediction should not cause panic. Always be sure to mention the worst case/best case scenario.
- The control of disease also depends on various factors such as availability of resources.

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