Compartmental Epidemiological Models and Their Associated Incidence Rate

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Abstract

Compartmental models in epidemiology are used to construct mathematical models reflecting the dynamic properties of infectious diseases, analyze the dynamic behavior of the model so formed, and perform some simulations. The research results help to predict the growth of infectious diseases, determine the key factors of their spread, and seek the optimum strategies for preventing and controlling their spread. This paper focuses on different compartmental models used in epidemiology. Different disease transmission rates applied to these models are mentioned. Different incident rates bilinear (βSI), saturated($\frac{\beta SI}{1+\alpha I}$), nonlinear ($\beta SI^p$), and standard Incidence ($\frac{\beta SI}{N}$) have been comparatively studied

Keywords: Compartmental model, transmission rate, nonlinear incidence.

Introduction

Historical Background

Epidemic dynamics is an important method of studying the spread of infectious diseases. It is based on the specific property of population growth, the spread rule of infectious disease, and the related social factors, etc. Communicable diseases have been a great challenge to humankind since the beginning of human history. At present, we still have a deal with infectious diseases like measles, AIDS, Plague, Malaria, T.B., Dengue, SARI, and COVID-19. Millions of people die annually from these diseases, and billions of others are infected. These diseases will soon be eliminated with the improvement in medical science care and the awareness process. Communicable diseases caused by various microbes, pathogens or microorganisms have been a threat to public health (Martcheva, 2015). They are caused by pathogens and can be easily transmitted from one infected person to another non-infected person. The most common examples are influenza or flu, measles, rubella, HIV, mumps, malaria, and smallpox (Brauer et al., 2012; Waltman, 2013). The emergence and reemergence of infectious diseases have become a significant worldwide problem. So, a Proper understanding of disease transmission dynamics caused by existing and new pathogens facilitates devising prevention tools (Foppa, 2016; Dym, 2004). Prevention tools against the transmission of disease need to be developed. The implementation and proper use of these sophisticated tools against microbes is another challenge. This article addresses some theoretical frameworks and intends to provide some basic information about the infection mechanisms of microbes,

their orientation, control mechanisms and the role of mathematical models in epidemiology (Murray, 2001; Banerjee, 2021).

Most infectious disease dynamic models are based on the compartment structure of the disease. First provided by Kermack and McKendrick in 1927, the compartment structures for dynamic models were developed by numerous other bio-mathematicians in 1932 onwards. Those who recover from viral diseases such as influenza, measles, swine flu, and chikungunya develop immunity to the same virus. The SIR model can be used to describe these illnesses. Furthermore, those who recover from bacterial illnesses such as gonorrhoea, the bubonic plague, tuberculosis, syphilis, etc., do not develop immunity and are susceptible to re-infection. The SIS model can be used to investigate the dynamics of these illnesses.

The main objective of this paper is to overview of compartmental epidemiological models that incorporate different forms of incidence rates.

Importance of Compartmental Models in Epidemiology

Compartmental models are fundamental in epidemiology because they provide a simplified yet powerful framework for understanding how diseases spread in populations. Their importance lies in the following key aspects:

1) Simplification of the complex system: Compartmental models divide a population into groups (compartments) based on disease status, such as susceptible (S), infected (I), recovered (R). This abstraction allows researchers to study the dynamics of disease transmission without needing to track every individual.
2) Predicting disease spread: These models help forecast future outbreaks, estimate the peak of infections, and predict how long an epidemic might last by modelling transitions between compartments using differential equations.
3) Evaluating control strategies: Compartmental models are crucial for simulating interventions such as vaccination programs, quarantine and isolation, social distancing, treatment or antiviral use. They help to determine the effectiveness and optimal timing of these interventions.
4) Estimating epidemiological parameters: They enable estimation of key parameters like basic reproduction number, infection and recovery rates, and herd immunity thresholds. These estimates inform public health decisions.
5) Flexibility and extendibility: Models can be adapted to include: Age structure, spatial effects, latent periods (e.g., SEIR models), behavior change, reinfection or waning immunity.
6) Guiding policy and public health decisions: Governments and health agencies use compartmental models for Planning resource allocation (e.g., hospital beds, vaccines), implementing timely interventions and communicating risks to the public.

Fundamental Forms of Compartmental Models

Compartmental models are mathematical frameworks used in epidemiology to describe the spread of infectious diseases within a population. These models divide the population into different compartments *like susceptible (S), exposed (E), infected (I), recovered (R) and immune (M or P or Y)* based on disease status and describe transitions between these compartments using differential equations. *P*arameters β and γ are used to represent transmission rate and recovery rates. These compartmental models predict outbreaks, evaluate control measures (e.g., vaccination, quarantine), and estimate the basic reproduction number (R_0). Age-structured models **(**Consider different transmission rates based on age groups**), s**patial models **(**incorporate geographic spread), and stochastic models **(**include random variations to capture uncertainty in disease spread) are some extended forms of these models.

Models Without Latent Periods

In these models, the infected individuals become infectious immediately (Martcheva, 2015). These models are as follows:

1. **SI Model:** In this model, the infectives cannot recover from the infection. It is represented in Diagram 2. The model equations are:

Figure 2: SI model

$$\frac{dS}{dt} = -\beta SI, \text{ and } \frac{dI}{dt} = \beta SI$$

2. **SIS Model:** In this model, the infected individuals are recovered but gain no immunity from infection. It is a represented diagram. 3. The model equations are:

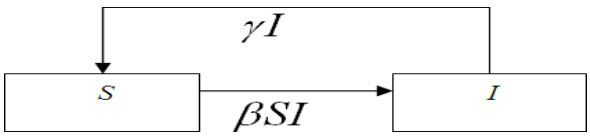

Figure 3: SIS model

$$\frac{dS}{dt} = -\beta SI + \gamma I, \text{ and } \frac{dI}{dt} = \beta SI - \gamma I.$$

3. **SIR Model:** In this model, the infectives obtain permanent immunity to the disease after recovering from infection. It is represented by diagram 4.

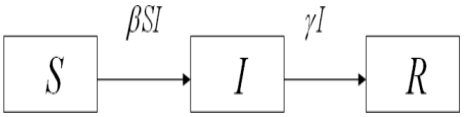

Figure 4: SIR model

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

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

$$= BI(S - \rho) \text{ where } \rho = \frac{\gamma}{\beta}$$

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

4. **SIRS Model:** In this model, the recovered individuals may have only temporary immunity after they recover from infection. Diagram 5 represents this model.

   The model equations are:

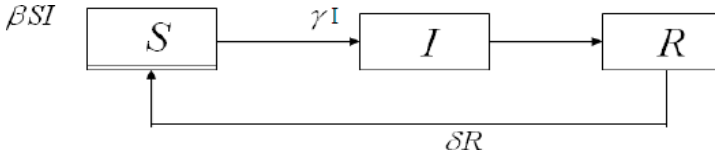

Figure 5: SIRS model

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

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

$$\beta I(S - \rho), \text{ where } \rho = \frac{\gamma}{\beta}$$

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

5. **SIRI Model:** In this model, the infective individuals cannot obtain permanent immunity to the disease when they recover from infection. Diagram 6 represents in model: The model

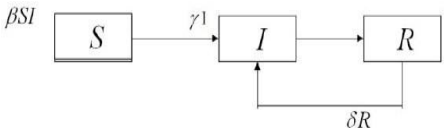

Figure 6: SIRI model

equations are:

$$\frac{dS}{dt} = -\beta SI\ , \frac{dI}{dt} = \beta SI - \gamma I + \delta R = \beta I(S - \rho) + \delta R, \text{ where } \rho = \frac{\gamma}{\beta}, \text{ and } \frac{dR}{dt} = \gamma I - \delta R.$$

6. **MSIR Model:** Babies are not born into the susceptible compartment for many illnesses, such as measles, but are instead immune to the illness for the first several months of their lives because of maternal antibodies (either through the placenta or through colostrum). This can be shown by including an M class (for maternally derived immunity) at the beginning of the model. It is represented by diagram 7.

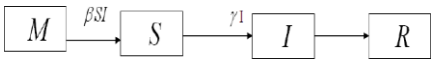

Figure 7: MSIR model

Models with Latent Periods

There is often a considerable period during which the affected person is infected but not yet contagious for many serious infections. In the course of this latent time, the person is in the exposed compartment (E) (Martcheva, 2015). The following are these models:

1. **SEI Model:** This model is represented by Diagram 8

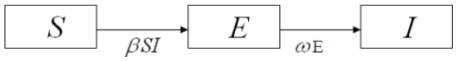

Figure 8: SEI model

2. **SEIR Model:** In this model, the population is broken into four compartments: susceptible, exposed, infectious and recovered. This model is represented by Diagram 9.

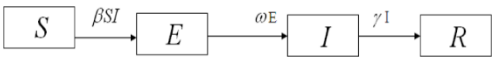

Figure 9: SEIR model

3. **SEIS Model:** In this model, the population is broken into four compartments: susceptible, exposed, and infectious again susceptible. Diagram 10 represents this model.

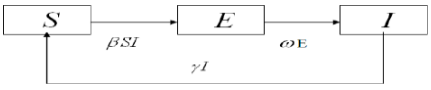

Figure 10: SEIS model

4. **SEIRS Model:** The population is divided into five compartments in this model: susceptible, exposed, infectious, recovered, and susceptible again. The representation of this model is Diagram 11

5. **MSEIR Model:** The MSEIR model is used for epidemiological classes in cases of disease where the factors of latency period and passive immunity are present. Diagram 12 serves as a representation of this model.

   where M is births and passive immunity.

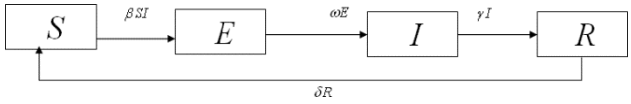

Figure 11: SEIRS model

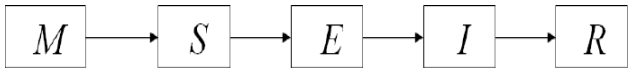

Figure 12: SEIRS model

Different Disease Transmission Rates

Infectious diseases can be transmitted by direct contact. The contact rate of infection, represented by P(N), is the number of people contacted by an infectious per unit of time. Depending on the population as a whole, N. The persons may become infected if they come into contact with an infectious susceptible. Assume that there is a β_0 probability of infection for every contact. Subsequently, the function β0N is referred to as an adequate contact rate, denoting the degree of infection caused by the infectious agents and typically reliant on the bacterial or viral toxicity and environmental conditions.

The average rate at which susceptible individuals come into contact with infected persons per unit of time is known as the contact rate, and it is commonly represented by the symbol β.

$$\beta = \text{contact rate} \times \beta_0.$$

For example, if an average individual has 10 contacts per day and the probability of disease transmission per contact is 0.2 (20%), then β =10 contacts/day × 0.2 transmission/contact = 2

This means that each susceptible individual is effectively exposed to the infection at a rate of 2 contacts per day.

To determine the unit of β, we need to consider the units of its components: the average number of contacts per susceptible individual per unit of time and the probability of disease transmission per contact. The unit of β will be a combination of these units. An average number of contacts per susceptible individual per unit time has units of “contacts” per “unit time” (e.g., contacts per day, contacts per week), and the

probability of disease transmission per contact is a dimensionless quantity, as it represents a probability or a ratio. To obtain the unit of β, we multiply the units of the average number of contacts per susceptible individual per unit of time by the dimensionless unit of the probability of disease transmission per contact.

Force of Infection

The force of infection (often denoted by λ is a crucial concept in the mathematical modelling of infectious diseases. It quantifies the rate at which susceptible individuals become infected. Essentially, it measures the risk of infection for a susceptible person per unit of time, based on the current epidemiological conditions.

It represents the rate at which susceptible individuals become infected per unit of time. It can be approximated as: The force of infection $= \frac{Total\ Infected\ individuals}{n \times T}$ where T is period (1 year = 365 days).

The effective daily transmission rate (β) in the population is given by

$$\beta = \frac{force\ of\ infection}{\frac{S}{N}}$$

Assuming the initial number of susceptible individuals S is approximately the total population N, ($S(t) \to N$), especially at the beginning of the outbreak:

Bilinear incidence

If the contact rate is proportional to the total population size, i.e. $P(N) = kN$, then the incidence βIS, where $\beta = \beta_0 k$, is called the transmission coefficient. This type of incidence is called a bilinear incidence or a simple mass action incidence. The transmission rate β is often assumed to be proportional to the product of the susceptible and infectious populations. It is called "bilinear" because it is a product of two linear terms: S and I. Bilinear incidence models are used in epidemiology to study the dynamics of various infectious diseases, including influenza, HIV/AIDS, and sexually transmitted infections. Most of the standard epidemiological models used a bilinear incidence rate. In this incidence rate, it is assumed that the population is homogeneously mixed and is normally used for airborne diseases. However, in case of a large number of susceptible or population is not homogeneously mixed (i.e. heterogeneous mixing), it is not realistic to consider the bilinear incidence rate due to the number of susceptible with which every infective contact is limited within a definite time. It allows researchers to explore how changes in the size of the susceptible and infectious populations affect the spread of the disease over time and to evaluate the potential impact of interventions such as vaccination or behavior change campaigns.

Standard Incidence

If the contact rate is constant, i.e. $P(N) = k$, then the incidence $\beta \frac{SI}{N}$, where $\beta = \beta_0 k$ is called the standard incidence. If S, I, and N are several susceptible, infectious, and total populations at time t, respectively, then $\frac{S}{N}$ and $\frac{I}{N}$ represent the susceptible and infectious fractions, respectively.

If β is the average number of adequate contacts of a single susceptible with other members of the population per unit time, then $\frac{\beta\, I}{N}\beta$ is the average number of contacts with infectives per unit time of a single susceptible and $\beta \frac{I}{N}\, S$, that is, $\frac{\beta IS}{N}$ is the number of new cases per unit of time due to the S susceptible. Thus, $\frac{\beta IS}{N}$ is the rate at which the susceptible population becomes infected. This form of horizontal incidence is called the standard incidence (proportionate mixing incidence) because it is formulated from the basic principles. The standard incidence rate adjusts the bilinear form by normalizing it for the total population N (usually the sum of susceptible, infected, and recovered individuals). This Incidence rate $\beta S \frac{I}{N}$ is useful in models where the population size is large and possibly variable.

Saturated Incidence Rate

Saturated incidence rates are used in epidemic models when the transmission rate of the disease does not increase indefinitely with the number of infected individuals but instead levels off or saturates as infection levels rise. This can reflect real-world constraints such as limitations on the number of effective contacts due to behavioral changes, healthcare capacity, or other social factors. Saturated incidence rates are often represented using Michaelis-Menten kinetics, also known as the Holling type II functional response in ecological models. They are used to model scenarios where the incidence rate plateaus as the number of infected individuals becomes large, preventing the unrealistic assumption of unlimited growth in infection rate. The most commonly used saturated incidence rates are $\frac{\beta SI}{1+\alpha S}$ and $\frac{\beta SI}{1+\alpha I}$.

Nonlinear Incidence Rate

Nonlinear incidence rates in epidemiological models like the SIR and SIS models extend beyond the simple bilinear form and capture more complex interactions in disease transmission. These nonlinear rates can better represent various real-world scenarios where the rate of new infections does not increase proportionally with the number of susceptible and infected individuals. Liu et al. (1986, 1987) introduced a non-linear incidence rate of the form $\beta I^p S^q$, which shows a much wider range of dynamic behaviors than do those with a bilinear incidence rate βIS. These behaviours are determined mainly by p and β, and secondly by q. For these models, there may exist multiple equilibria in the feasible region, and thus the model becomes more general and informative. For more application of this incidence rate, one can

refer to (Dubey et al., 2015; Grigorieva et al., 2016; Wang et al., 2021). Different types of nonlinear incidence rates commonly used in SIR and SIS models are $\frac{\beta SI}{1+\alpha I}$, $\frac{\beta SI}{1+\alpha S}$, $\frac{\beta SI}{1+\alpha S+\gamma I}$, $\frac{\beta SI}{1+\alpha(S+I)}$.

Nonlinear incidence rates in SIR and SIS models provide a richer framework for modelling disease dynamics by incorporating more realistic factors such as saturation effects, population interactions, and behavioral responses. They allow for more accurate predictions and better insights into the spread and control of infectious diseases compared to simple bilinear models.

Non-monotonic Incidence Rate

A non-monotonic incidence rate in epidemiological models like the SIR or SIS models captures the complex dynamics where the rate of new infections does not simply increase or decrease with the number of susceptible or infected individuals but can also exhibit peaks and troughs. This can model phenomena where the infection rate might increase up to a certain point and then decrease, reflecting various real-world scenarios such as behavioral changes, resource limitations, or public health interventions. Capasso & Serio (1978) proposed a non-monotonic incidence rate $g(I)S = \frac{\beta IS}{1+\alpha I^2}$ in which g(I) is non-monotonic, that is, g(I) increases when I is small and decreases when I gets large. In this incidence rate, βI measures the force of infection, and $\frac{1}{1+\alpha I^2}$ describes the psychological or inhibitory effect from the behavioural change of the susceptibles when the number of infectives gets large. This is important because the number of effective contacts between infectives and susceptibles decreases at high infective levels due to the quarantine of infectives or due to the protective measures by the susceptible.

The general incidence rate $g(I).S = \frac{\beta I^P}{1+\alpha I^q}$ was given by Liu et al. (1986) and used by many authors (Moghadas & Gumel, 2002; Alexander & Moghadas, 2004; Khan et al., 2015). Logistic Incidence Rate ($\beta SI(1-\frac{I}{K})$), Oscillatory Incidence Rate ($\beta SI\ Sin(\omega I)$), Threshold-Based Incidence Rate ($\beta\ SI\frac{A}{B+I^2}$), Holling Type III Functional Response ($\frac{\beta SI^2}{1+\alpha I^2}$), General Polynomial Form ($\beta SI\left(1-\frac{I}{K}\right)^n$) are some of the other monotonic incident rates.

Non-monotonic incidence rates in SIR and SIS models offer a powerful tool for capturing the complex dynamics of disease spread. They reflect realistic scenarios where infection rates can increase up to a point and then decrease, exhibiting peaks and troughs due to various internal and external factors. These models are crucial for accurately predicting and managing epidemic behaviors in complex environments.

Apart from the above-discussed incidence rates, several incident rates are investigated by researchers and provide detailed qualitative analyses of the models. In the case of the Yoga awareness model, the disease

transmission rate can be considered as $\beta e^{-cM} SI$, where M is the Yoga awareness infected mass and c is constant (Bhatta, 2024).

Discussion of Key Study

Different compartmental models have been used in epidemiology because different diseases and public health questions require models with different levels of complexity and realism. Each compartmental model captures specific aspects of disease transmission, progression, and control strategies.

The SIR model is used for diseases where recovery gives long-term immunity (e.g., measles, COVID-19 in some cases). The SEIR model adds an exposed (latent) class for diseases with an incubation period (e.g., Ebola, COVID-19). The SIS model is used for diseases with no lasting immunity where recovered individuals become susceptible again (e.g., gonorrhea). The SEIRS model accounts for waning immunity, where recovered people may lose immunity and become susceptible again.

The **bilinear, saturated, standard, and nonlinear incident rates** are important in mathematical modelling, especially in epidemiology and population dynamics. Each of these incident rates describes how a disease spreads based on the interaction between susceptible and infected individuals. Bilinear is basic and commonly used in SIR models. It assumes direct proportionality between susceptible (S) and infected (I) and has no saturation effect. Saturated incident rate accounts for behavioral or medical constraints limiting infection spread. Saturation occurs when infected individuals increase, and is suitable for modelling diseases with limited healthcare or contact. The standard rate is used in models with heterogeneous populations. It is a generalization of the bilinear model. A non-linear rate is applied in complex epidemiological models.

Conclusion

Various compartmental epidemic models have been studied. The mathematical modelling of different infectious diseases is mentioned. Different compartmental models are used to ensure that the model closely reflects the biological, social, and environmental realities of the disease being studied, thereby improving understanding, prediction, and control of epidemics.

This work also highlights the important relationship between different incident rates. Bilinear incident rate is used in basic SIR/SEIR models. Saturated incident rate is applied for diseases like COVID-19 with behavioral constraints and it is more realistic under high infection loads and limits explosive outbreaks. It captures more realistic contact saturation. Non-linear incident rates are used for great propagator situations and vector-borne diseases. It captures nonlinear infection dynamics (e.g. clustering). Standard incident rates are used when the total population varies and are normalized by total population size.

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