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Review on SEIR Model of Infectious Diseases

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Abstract: Infectious diseases pose a continuous challenge to the society worldwide. Recent global health crises, such as the COVID-19 pandemic, have helped us to understand the importance of studying infectious disease modelling. It can improve public health policy and response in epidemic situation. It also helps in taking risk mitigation measures, prompting timely interventions, and aiding preparedness for healthcare delivery systems. Here, I have focused on SEIR model of infectious diseases. Disease modelling incorporates many hurdles. It depends on various factors, some of them depends on behavioral nature of mankind, some factors depend on purely statistical interpretation. Moreover, depending upon demography, climate, economic conditions some alteration in a base model is necessary when we change the region of study. Precautionary measures taken by authority, such as, vaccination, awareness drive etc. also affects the modelling region wise. In this review, I have discussed mathematical details of an infectious disease modelling, as well as, how to simulate an infectious disease following SEIR model. Implementation of SEIR model in case of various infectious diseases and the future trend of epidemiology have also been discussed.

Key words: Disease Modelling; SEIR Model; Data Interpretation; Simulation; Future Trend.

1 Introduction

Mathematical models in epidemiology are an important tool for comprehending the future trend and taking precautionary measures to control any infectious disease. However, mimicking an infectious disease by some set of equations is really a difficult job. Firstly, spreading of an infectious disease depends upon many factors and some of them like personal hygiene and health, economic situation etc. are very hard to incorporate as a variable in a mathematical model. Secondly, effect of some factors, such as climate condition, demography, personal awareness etc. in spreading of a disease can only be studied statistically. For an effective mathematical model of an infectious disease researchers have to study a large data related with spreading of that disease to incorporate local influences in disease spreading, behavioral natures etc. in the specified model.

As epidemics and pandemics have affected human civilization from the beginning, researchers have tried to model an epidemic spreading using the tools of modern science. Most significant early models in epidemiology, known as SIR (Susceptible, Infectious, Recovered/ Immune) model, was introduced in 1927 [1]. It is also known as compartmental modelling in the literature, as it divides total populations into three different compartments named susceptible, infectious and recovered/removed/immune. It is a very simplified model and has many drawbacks [2, 3]. These have been discussed in the section (2).

Since then, many attempts have been done to make this model more realistic incorporating various demographic, socio-economic and behavioral natures in it and the result is the SEIR (Susceptible, Ex-

posed, Infectious, Recovered/ Immune) model [4, 5, 6, 7, 8]. In this case, apart from three compartments of SIR, one extra compartment named "exposed" was added. SEIR models can represent many human infectious diseases such as measles [9, 10], pox [11, 12], flu [13, 14], dengue [15, 16], tuberculosis [17], Ebola [18], malaria [19] etc. Recent impact of COVID-19 has also prompted researchers to predict its future trend of an infectious disease [20, 21, 22, 23]. The beauty of this model is that it can incorporate many socio-economic, environmental, precautionary measures by local authorities and behavioral factors which is impossible using SIR. The detailed mathematics of this model has been explained in section (3).
Now, let us briefly remember SIR modelling in the following section before going SEIR model.

2 Brief review of SIR model

As we have already discussed in the introduction, classic SIR model has three groups: susceptible S(t), infectious I(t) and recovered R(t), with a total population size N = S(t) + I(t) + R(t). Here, it is assumed that although S, I and R may vary with time but total population is constant. Classic SIR model is parameterized by the infectious period, $\frac{1}{\gamma}$ (The time duration when a person with an infectious disease can transmit the illness to others), the basic reproduction number $\mathcal{R}_0$ (The number of secondary cases for each infection in a completely susceptible environment) and the contact rate, β (the number of people an infected individual comes into contact with during their infectious period). In general, $\beta = \gamma\mathcal{R}_0$. Again, another basic assumption is that, once recovered peoples do not get affected by the same disease again.

2a. Mathematical Formulations

According to the above considerations, the basic mathematical equations which govern this model are as follows [24, 25, 26, 27, 28]:

$$\begin{aligned} S(t) + I(t) + R(t) = N \quad or \\ s(t) + i(t) + r(t) = 1 \end{aligned} \tag{1}$$

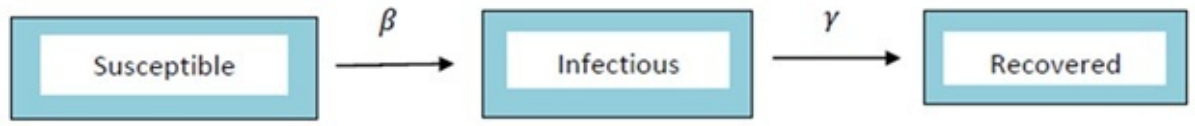

Figure 1: Schematic diagram of Classic SIR model. It has three compartments namely "Susceptible", "Infectious" and "Recovered". It is parameterized by contact rate β and infectious rate $\frac{1}{\gamma}$

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$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = \frac{ds}{dt} + \frac{di}{dt} + \frac{dr}{dt} \tag{2}$$

$$\frac{dS}{dt} = -\beta I(t) \times \frac{S(t)}{N} \tag{3}$$

$$\frac{dI}{dt} = \beta I(t) \times \frac{S(t)}{N} - \gamma I(t) \tag{4}$$

$$\frac{dR}{dt} = \gamma I(t) \tag{5}$$

Here, $s(t)$, $i(t)$ and $r(t)$ are fraction of total population belongs to susceptible, infectious and recovered compartments respectively.

2b. Equilibrium

In case of any infectious disease there exists two types of equilibrium. First one is disease-free equilibrium (DFE). It represents a state where a disease is absent

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from a population. The second one is endemic equilibrium (EE). It signifies a state where the disease is consistently present and circulating within the population but the number of infected people does not increase exponentially. If number of infected people increases exponentially, then the situation is called pandemic. The state of equilibrium is estimated by the basic reproduction number, $\mathcal{R}_0$. Here, $\mathcal{R}_0 < 1$ indicates the DFE (disease dies out) and $\mathcal{R}_0 > 1$ suggesting the EE (disease persists). In case of EE,

$$\mathcal{R}_0 \times S(t) = S_0 \tag{6}$$

From equation (3) and (5), one can derive the following expression,

$$S_t = S_0 e^{-\frac{\mathcal{R}_t}{N}(\mathcal{R}_t - \mathcal{R}_0)} \tag{7}$$

Here, $\mathcal{R}_t$ is called "real time reproduction number" and $\mathcal{R}_t = \mathcal{R}_0$ when t=0. Again, equation (4) and (6) reduces to

$$\begin{aligned} \frac{dI}{dt} &= \left(\mathcal{R}_t \frac{S(t)}{N} - 1\right)\gamma I \\ &= (\mathcal{R}_e - 1)\,\gamma I \end{aligned} \tag{8}$$

where,

$$\mathcal{R}_e = \mathcal{R}_t \frac{S(t)}{N} \tag{9}$$

$\mathcal{R}_e$ is called "real time effective reproduction number". When,$\mathcal{R}_e \geq 1$, I grows exponentially and when $\mathcal{R}_e \leq 1$, I decays exponentially. When, $\mathcal{R}_e = 1$, Temporal plot of I reaches a steady state.Considering $\gamma(t) \approx$ constant for a particular period of time (in case of endemic equilibrium), integrating equation (8), we get

$$I_t = e^{\gamma t(\mathcal{R}_e - 1)} \tag{10}$$

Equation (7) and (10) gives number of susceptible and infected people at the time of endemic equilibrium. Here we have faced the basic reproduction number ($\mathcal{R}_0$) and the effective reproduction number ($\mathcal{R}_e$). I have already discussed that $\mathcal{R}_0$ is the average number of new infections caused by a single infectious individual in a fully susceptible population during their infectious period i.e. at the beginning of the infection. On the other hand, effective reproduction number, $\mathcal{R}_e$ represents the average number of secondary cases generated by an infectious individual at time t, considering the population's current immunity and public health interventions. Unlike $\mathcal{R}_0$, $\mathcal{R}_e$ reflects changes in susceptibility, contact patterns, and other mitigation effects. Like $\mathcal{R}_0$, if $\mathcal{R}_e > 1$, the epidemic is growing; if $\mathcal{R}_e < 1$, the epidemic is shrinking. $\mathcal{R}_e$ provides a real-time picture of the transmission dynamics and is crucial for indicating public health interventions during an epidemic. $\mathcal{R}_e$ is defined by equation (9). It implies that $\mathcal{R}_e$ is directly proportional to $\mathcal{R}_0$ and the proportion of the population that is still susceptible.

2c. Simulation and Data Interpretation

Solving the equations (3), (4) and (5) for some pre-assumed β, γ and total population N one can predict the number of infectious and recovered people. β, γ will depend upon the nature of precise infectious disease and other factors. In Figure 2 (right plot), I have shown one such temporal variation of infectious and recovered people considering $= 0.0026$, $\gamma = 0.5$ and total population $N = 762$. Now comparing number of infectious people obtained from SIR model (Shown by red line in Figure 2) with actual number of infectious people obtained from observed data/survey, one can comprehend how far the model mimics the actual situation. One such comparison plot has been shown in Figure 2 (left plot). The simulation has been done using "R" programming language. This example is purely a toy model to understand the actual situation.

Classic SIR Model is very simplified model. Some of its assumptions like: homogeneous mixing of the infected and susceptible populations, susceptible become infectious without any latency, the total population is constant in time, the susceptible population decreases monotonically to-

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wards zero and the recovered population do not infect again etc. are not correct in reality. Moreover, there is very limited scope to include taking care of precautionary methods such as vaccinations, awareness campaign etc. which reduce effect of spreading of an infectious disease. Actually, SIR model can mimic a disease for short-term intervals only [29,30]. The modified form of SIR is SEIR model.In the next section, I shall elaborately discuss mathematics of SEIR model.

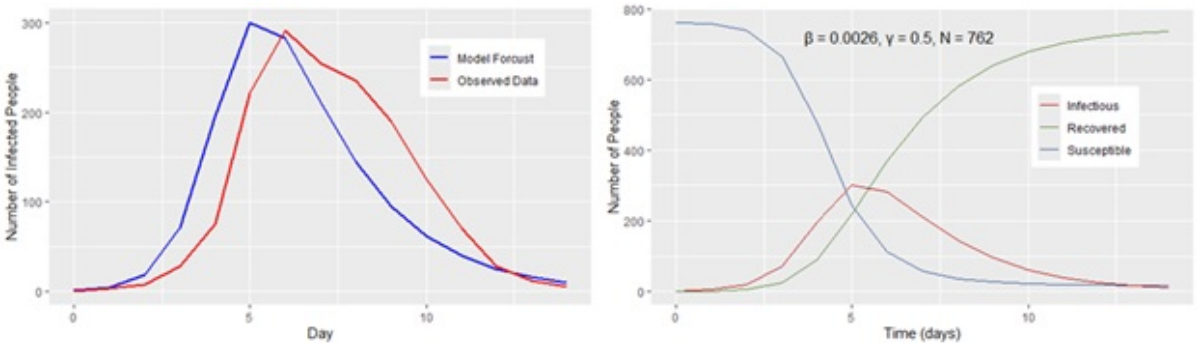

Figure 2: (left plot) Plot of susceptible, infectious and recovered people obtained from solving SIR model considering = 0.0026, $\gamma = 0.5$ and N = 762.(Right plot): Comparison of Model forecast data with observed data.

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SEIR Model

SEIR model has four compartments. The new edition "exposed" was introduced to counter the latency period of any infection. Moreover, depending upon nature of disease and local factors, mitigation measure taken, the four compartments may be interrelated with each other [31, 32, 33, 34]. As for example, for many respiratory infections, immunity after recovery is temporary and recovered individuals will lose immunity and return to S after an average protected period which one can include here [35]. Demography contributes to flows in and out of each compartment. In reality, all groups will experience background death from other causes. At the same time, in a stable population,background deaths are balanced by births into susceptible compartment.

3a. Mathematics

As I have already discussed that in SEIR model, people may impose various types of new relations among the four compartments depending upon nature of the disease, mitigation measures taken, demographic and weather conditions. Sometime some new compartments may also be added with the above four. All of them are nothing but minor modification of basic SEIR model. In this case, I shall follow the schematic diagram of SEIR model given in Figure 3 for writing mathematical equations. This particular scheme is very much convenient to describe disease like COVID-19 [36]. Here, upon being infected from the susceptible group $S(t)$, the individual will move to exposed group $E(t)$ with the transmission rate β at a rate $\beta\frac{IS}{N}$ and remain there for an average period of $\frac{1}{\nu}$ before moving to infected group $I(t)$. At the same time, for disease like COVID-19, some asymptotic people will directly move to infected group with a rate, ρ. Death due to the particular infection will cause a loss of individuals from the group $I(t)$ at a rate α and recovery of people from $I(t)$ to $R(t)$ at a rate γ. The parameter λ represents the import to the susceptible population from outside (due to birth) and δ is the background death due to other causes. In SEIR model, "susceptible $S(t)$", "exposed $E(t)$", "infected $I(t)$" and "recovered $R(t)$" denote the instantaneous size of the popu-

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lation, i.e. at any instant, if N is the total population.
So, in this model β, ρ, ν, γ, α known as transmission rate, asymptomatic transmission rate, inverse of incubation period/latency period, inverse of mean infection period and death rate due to infectious disease will purely depend upon nature of infectious disease. While birth rate, λ and death rate due to other normal causes, δ will depend on local demographic data [22, 31, 32, 36].
Now, according to preliminary assumptions of the SEIR model for this particular case,

$$S(t) + E(t) + I(t) + R(t) + \alpha I(Death \quad due \quad to \quad pandemic) = N \tag{11}$$

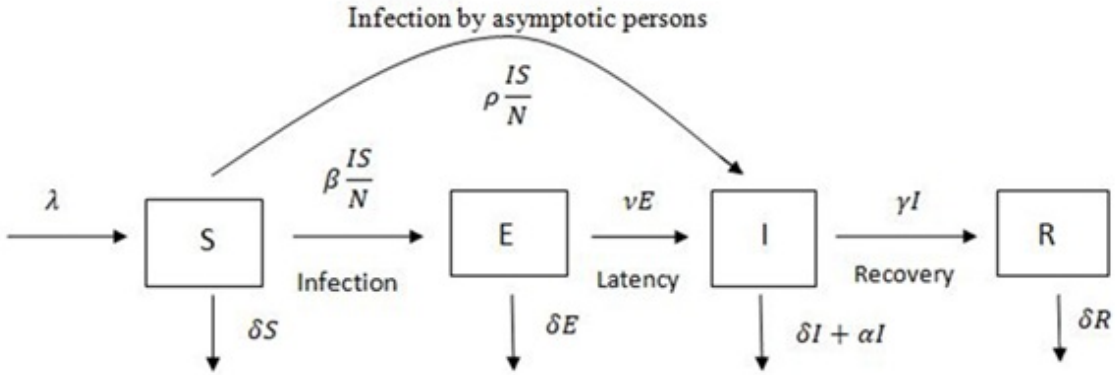

Figure 3: Schematic diagram of a typical SEIR model. It consists of four basic compartments, namely Susceptible (S), Exposed (E), Infected (I) and "Recovered (R)". Depending on the disease and its local parameters some extra compartments may be attached with specific relationship

.

$$\frac{dS}{dt} = dN - (\beta + \rho)\frac{IS}{N} - \delta S \tag{12}$$

$$\frac{dE}{dt} = \beta\frac{IS}{N} - \nu E - \delta E \tag{13}$$

$$\frac{dI}{dt} = \nu E + \rho\frac{IS}{N} - \gamma I - (\delta + \alpha)I \tag{14}$$

$$\frac{dR}{dt} = \gamma I - \delta R \tag{15}$$

Note that, if we consider $\nu \to \infty$, $\rho \to 0$, $\beta = constant$, $\delta = 0$, $\alpha = 0$ and R is removed/ recovered population, then the above model reduces to classic SIR model.

3b. Equilibrium

As we are already aware that, in case of infectious disease spreading, there are two types of equilibrium, Disease-Free Equilibrium (DFE) and endemic equilibrium (EE).

Disease-Free Equilibrium (DFE)

Let us first discuss DFE. In this case, presently there is no infectious disease, i.e., $I(t) = E(t) = R(t) = 0$ and $S(t) = N$. So, if number of total populations remains constant, then birth rate, λ should be balanced by death rate due to other causes except infectious disease, i.e. $\delta S = \delta N$. This leads to $\lambda = \delta S$, i.e.

$$(S, E, I, R) = \left(\frac{\lambda}{\delta}, 0, 0, 0\right) \tag{15a}$$

Now, I have to calculate basic reproduction number for DFE. In general,$\mathcal{R}_0$ is calculatedin the literature following next generation matrix method [37,38,39].
Let us briefly explain what is this technique. Let $x = (x_1, x_2, ..., x_n)^T$ be the number of individuals in each compartment, where the first $m \leq n$ compartments contain infected individuals. In case

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of DFE one can write,

$$\frac{dx_i}{dt} = \mathcal{F}_i(x) - \mathcal{V}_i(x) \tag{16}$$

for i = 1,2, ..., m. Here, $\mathcal{F}_i$ (x) is the rate of appearance of the new infections in compartment i, and $\mathcal{V}_i$ (x) is the rate of transitions between compartment i and other infected compartments. If

$$F = \left[\frac{\partial \mathcal{F}_i(x_0)}{\partial x_j}\right] \quad and \quad V = \left[\frac{\partial \mathcal{V}_i(x_0)}{\partial x_j}\right] \tag{17}$$

for $1 \leq i, j \leq m$. As per definition of $\mathcal{F}_i$ and $\mathcal{V}_i$, F is entry wise non-negative and V is a non-singular M-matrix [10], so V^{-1} is entry wise non-negative. Let $\psi(0)$ be the number of initially infected individuals. Then $FV^{-1}\psi(0)$ is an entrywise non-negative vector giving the expected number of new infections. Matrix FV^{-1} has (*i,j*) entry equal to the expected number of secondary infections in compartment i produced by an infected individual introduced in compartment *j*. Thus, FV^{-1} is the next generation matrix and

$$\mathcal{R}_0 = f(FV^{-1}) \tag{18}$$

where, f denotes the spectral radius. In case of our model, $n = 4$ and $x = (E,I,S,R)$. where only the first two compartments, i.e. E and I contain infected individuals. Remembering that at DFE, $S \approx N$ and following equation (16), we can write (for i = 1(E), 2(I)),

$$\mathcal{F}\left(\beta\frac{IS}{N}, \rho\frac{IS}{N}\right) \approx (\beta I, \rho I) \tag{19}$$

$$\begin{aligned} V = ((+\delta)E - E+ \\ (\gamma + \delta + \alpha)I) \end{aligned} \tag{20}$$

where *+ve* sign indicates transfer into the *i*-th component and *-ve* sign for out of it.

$$\begin{aligned} F &= \begin{pmatrix} 0 & \beta \\ 0 & \rho \end{pmatrix} \quad and \\ V &= \begin{pmatrix} v+\delta & 0 \\ -v & \gamma+\delta+\alpha \end{pmatrix}. \end{aligned} \tag{21}$$

Thus,

$$V^{-1} = \frac{A}{(v+\delta)(\gamma+\delta+\alpha)} \tag{22}$$

where,

$$A = \begin{pmatrix} \gamma+\delta+\alpha & 0 \\ v & v+\delta \end{pmatrix}$$

$$\mathcal{R}_0 = \frac{\beta v + \rho(v+\delta)}{(v+\delta)(\gamma+\delta+\alpha)} \tag{23}$$

Here one can notice that value of basic reproduction rate, $\mathcal{R}_0$ will depend on value of death rate of the infectious disease, α, transmission rate, β, asymptomatic transmission rate, ρ, inverse of incubation period/latency period, ν inverse of mean infection period, γ and the death rate due to other causes, δ.

Endemic equilibrium (EE)

We have already discussed that endemic equilibrium means disease persists in the society however infectious people do not grow following power law. Here disease persists with constant number of populations in each compartment. So, in this case following equations (12, 13, 14 and 15) one can write,

$$(\beta+\rho)\frac{I_{EE}S_{EE}}{N} = \lambda - \delta S_{EE} \tag{24}$$

$$\beta\frac{I_{EE}S_{EE}}{N} = (\nu+\delta)E_{EE} \tag{25}$$

$$\rho\frac{I_{EE}S_{EE}}{N} = (\gamma+\delta+\alpha)I_{EE} - \nu E_{EE} \tag{26}$$

$$I_{EE} = \frac{\delta}{\gamma}R_{EE} \tag{27}$$

Again, from equation (13),

$$\begin{aligned} S_{EE} + E_{EE} + I_{EE} + R_{EE} + \alpha I_{EE} \\ = N = \frac{\lambda}{\delta} \end{aligned} \tag{28}$$

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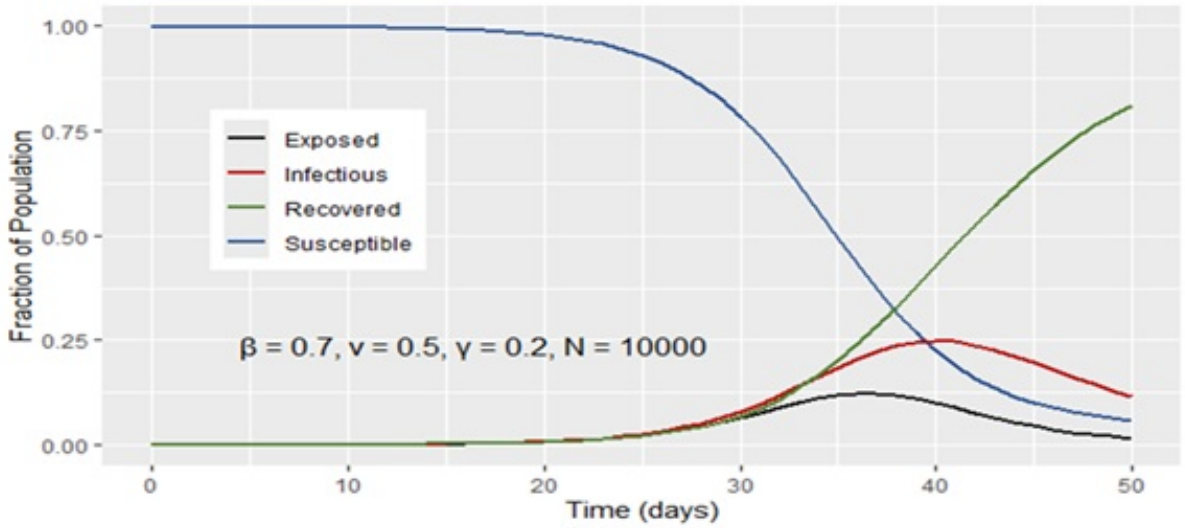

Figure 4: Simulation of infectious disease using SEIR model. Here we have chosen β=0.7, ν=0.5, γ=0.2 and total population $N = 10000$. All other parameters have been set as zero for simplicity. Four different population has been represented by different colours.

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This leads to the following solutions,

$$S_{EE} = \frac{S_0}{\mathcal{R}_0} = \frac{\lambda}{\delta \mathcal{R}_0} \tag{29}$$

$$I_{EE} = \frac{\lambda(\delta - 1)}{\delta(\alpha + 2\gamma - \alpha\delta)} \tag{30}$$

$$R_{EE} = \frac{\gamma}{\delta} I_{EE} = \frac{\gamma\lambda(\delta - 1)}{\delta^2(\alpha + 2\gamma - \alpha\delta)} \tag{31}$$

Now, one can easily calculate E_{EE} by subtracting susceptible, infectious and recovered people from the total population.

3c. Simulation

Solving equations (12), (13), (14) and (15) and considering precise values for α, β, γ, δ, λ, ν and N one can mimic a real infectious disease using SEIR model. One such simulation has been shown in Figure 4. Here I have considered α=0, β=0.7, γ=0.2, ν=0.5, λ=0, δ=0. It is a simple toy model to show how one can simulate an actual disease. Depending upon the nature of disease and other factors one has to define relations among the compartments of SEIR and necessary parameters. Then suitable estimations of the required parameters and solving differential equations which describe the model using appropriate computing technique one can mimic the disease mathematically. Here I have used **R** programming language to plot Figure 4. Now matching temporal variation of infectious and recovered people gather from survey data with the result obtained from simulation using SEIR model, one can check the effectiveness of the simulation.

4 Implementation of SEIR model

We have already discussed that SEIR models may vary in number of compartments and their interactions depending upon complexity of the infectious disease and the factors affecting it. For suitable modeling of an infectious disease, thoughtful design of these compartments is crucial. One has to keep in mind the specific problems, available data, and existing knowledge about the disease etc. Selection of estimation methods is also very much important, as different methods may rely on varied assumptions and yield different results. This may be confusing.Further, sensitivity analysis plays a vital role. Again, model validation and calibration are indispensable for ensuring the model's fidelity to real-world data.Validating models against

 https://doi.org/10.10.54280/jse.255106

historical outbreak data and calibrating them using current, real-world data makes the model relevant and accurate over time. In the introduction and at the beginning of section 3, I have given many references from the literature which informs that SEIR model has been used to mimic various infectious diseases like influenza, pox, dengue, tuberculosis etc. Over the time it has proved its effectiveness. Recently COVID-19 pandemic has hit the world and we can find various example in the literature where SEIR model has been used to predict and handle COVID-19 in various countries [22,31,36, 40-45]. Here the authors efficiently expressed COVID-19 mathematically using SEIR modelling. They have also successfully incorporated various mitigation factors such as lockdown, social distancing, vaccination etc, weather and climatic conditions etc. to study its spreading nature. It has helped the policymakers to choose suitable mitigation methods to curb COVID-19 so that our life can be saved. Not only this, it has helped to distribute vaccine in according to need basis. Thus, SEIR model has been implemented successfully to analyze and modelling of infectious diseases in the field of epidemiology.

In the next subsection I have given an estimate of SEIR variants for an infectious disease like COVID-19 in India.

Table 1: SEIR variants following section 3 for estimating COVID-19 outbreak in India

Symbol	Description	Value	Method
β	Transmission Rate	Different for different states	Assumption (depends upon various factors)
ρ	Asymptomatic Transmission Rate	Different for different states	Assumption (depends upon various factors)
$\frac{1}{\nu}$	Incubation Period	Different for different states ($\leq$ 14 days)	Based on results from previous studies [46]
$\frac{1}{\gamma}$	Mean Infection Period	$\sim$ 21 Days	Based on results from previous studies [47]
δ	Normal Death Rate before COVID period	$\sim$ 7.1 per 1000 population per year	Based on census data and World Bank Open data [48,49]
α	Death Rate due to Covid-19	Less than $\sim$ 345 per million per day	Based on results from previous studies [50]
N	Total population	1.4 Billion in 2020	Based on population data [51]
λ	Susceptible birth Rate	$\sim$17 per 1000 per year	Based on census data [48,49]

4a. SEIR variants for COVID-19 in India

To estimate the number of infected, recovered and dead people using SEIR model depicted in Section 3, one has to put the values of SEIR variants in the programming. The probable values for estimating COVID-19 situation in India been given in Table 1. Here we observe that except β and ρ all other variants depends on the nature of the infectious disease. As, transmission rate and its corresponding asymptomatic value for an infectious disease also dependent on various other factors, such as susceptible age group, social awareness, climate etc., so they have no fixed value. They also depend upon time. Mostly, β

 https://doi.org/10.10.54280/jse.255106

and ρ are estimated purely from assumption so that the number of Infected (I), "Recovered (R)" and dead people calculated from SEIR model simulation matches with the real data obtained from survey. For more information one can go through [36,52,53].

5 Future directions and emerging trends

With time we have progressed a lot in computational physics. This has taught us handling large amount of data and finding suitable outcomes by analyzing it. At the same time with the development in e-governance, large amount of data related with various infectious diseases is being uploaded for common people. As infectious disease depends upon various parameters which depends upon behavioral nature of the people, they can only be taken care of using statistical methods. This requires handling large amount of data to understand behavioral nature. This has prompted researchers to integrate SEIR models with machine learning and data-driven approaches to improve their accuracy and robustness. Using machine learning algorithms to estimate SEIR model parameters from large datasets is being turning very common now-a-days. Incorporating data-driven approaches, such as Google mobility data, to inform SEIR model parameters and improve predictions. Real-time data analytics and big data technologies offer unprecedented opportunities for infectious disease modeling. High-resolution, real-time data from sources such as social media, mobile phones, and satellite imagery allow models to become more dynamic and responsive to changing out-break conditions. By leveraging these data streams, future models can improve the timeliness and accuracy of predictions, facilitating more effective response strategies. The integration of ML and AI into infectious disease modeling enhances the potential of these real-time data sources. They can analyze complex datasets, identify patterns, and predict outbreak trends with high accuracy. They could also help analyze vast amounts of raw data collected during outbreaks, further empowering predictive capabilities and enabling the identification of mitigation techniques. Combining real-time data analytics with ML and AI methods will provide more accurate and timely insights, ultimately improving public health interventions and outcomes.
Moreover, to improve epidemiology better and realistic way, a proper coordination among expertise from epidemiology, statistics, biology, policy makers, and social sciences is very much necessary. This interdisciplinary approach can amalgam the multi-dimensional impacts of outbreaks, including direct health effects, economic disruptions, and societal changes. This is necessity of time.

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