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Compartmental Analysis of Influenza A (H1N1) Virus using Induced SEIR Model

Harpreet Kaur[1], Atendra Singh Yadav[2]

[1,2]Department of Mathematics, Guru Kashi University, Talwandi Sabo, Punjab, India
Emails ID: toorharpreet1286@gmail.com , drasyadavmathematics@gmail.com

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ABSTRACT

Influenza A (H1N1) is highly contagious infectious disease. H1N1 has played a vital role in influenza pandemics from the deadly 1918 Spanish flu to milder but widespread 2009 swine flu pandemic. The 2009 H1N1 strain replaced older seasonal H1N1 strains and still circulate in current scenario. The improved induced SEIR mathematical model used to monitor H1N1 mutations to detect potential new pandemic threats through basic reproduction number, stability of the model. Also, MATLAB software used to represent the result graphically. The trends of several parts of the population that are suspectable, exposed, infectious, and recovered are examined based on the numerical solutions.

Keywords: *Mathematical Modelling, SIR and SEIR Model, Jacobian Matrix, H1N1 Virus.*

1. INTRODUCTION

The word "influenza" originates from the Italian word "influence," and it was first used in 1357 AD because people thought the illness was brought on by supernatural forces. The World Health Organization (WHO) raised the level (Level 6) of pandemic alert and proclaimed anemergency of international public health emergency in response to the 2009 H1N1 (swine flu) outbreak, classifying it as a serious global health hazard. An epidemic appeared impending in India as the number of verified H1N1 cases and associated mortality increased [Mir S.A., 2009]. Given the quick transmission, especially among school-aged children in May 2009, the early outbreak in Japan had an estimated basic reproduction number(R_0) of 2.0 to 2.6 [Nishiura H. et al., 2010]. Epidemic forecasting and policymaking heavily rely on mathematical modeling, especially when employing the basic reproduction number(R_0). To avoid misunderstandings or improper use of model predictions, it is crucial to explain key epidemiological ideas in a clear and concise manner to a non-expert audience. Developing effective immunization and treatment programs to stop the spread of disease requires the application of optimal control techniques using a normalized SEIR model [De Pinho et al., 2018]. Using the non-linear least squares method, this work focuses on numerical simulations, theoretical modeling, and mathematical analysis of H1N1 viral transmission. Furthermore, important factors influencing the transmission of disease are identified using local and global sensitivity studies. The paper provides a numerical solution utilizing a suitable computational technique and further investigates the existence and uniqueness of an optimal control approach [Md Kamrujjaman et al., 2024]. Additionally, the SIR model in Europe is used to analyze how contact rates and population density affect the dynamics of influenza A (H1N1) and COVID-19 transmission [Peker Dobie A. et al., 2024].

2. IMPROVED MATHEMATICAL MODEL:

Determine how the compartments relate to one another by applying differential equations. Parameters such as the incubation period, mortality rate, recovery rate, and transmission rate control the flow between compartments.

2.1. Base Model: SIR (Susceptible-Infectious-Recovered) Model

The SIR model is basic compartmental model, suitable for infectious diseases where recovered individuals gain immunity. According to Kermack and McKendrick (1927), the governing equations are:

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

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

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

Where β and γ are the transmission rate and recovery rate respectively.

2.2. Induced SEIR (Susceptible-Exposed-Infectious-Recovered) Model

The induced SEIR model is given below, where compartments to account for disease-induced mortality. The structural SEIR model is a mathematical model that includes discrete compartments for the analysis of the Influenza A (H1N1) virus. These compartments include the Susceptible S(t) group, Exposed E(t) group, Infected I(t) group, and Recovered R(t) group.

The equations of the model are given below:

$$\frac{dS}{dt} = \Lambda - \beta SE - \mu S - \omega S \qquad (1)$$

$$\frac{dE}{dt} = \beta SE - \sigma E - \mu E \qquad (2)$$

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

$$\frac{dR}{dt} = \gamma I - \mu R + \omega S \qquad (4)$$

With initial conditions,

$$S(t) = S_0 \geq 0, E(t) = E_0 \geq 0, I(t) = I_0 \geq 0, R(t) = R_0 \geq 0 \qquad (5)$$

Also, $\beta > 0, \gamma > 0, \sigma > 0, \omega > 0, \mu > 0$ and $S + E + I + R = N$

Table 1: Definition of Variable

S. No.	Symbol	Definition
1	S	Susceptible Class who can contact the disease.
2	E	Exposed Class who can transmit the disease.
3	I	Infectious Class who can transmit the disease.
4	R	Recovered Class who have gained immunity or are no longer infectious.

Table 2: Definition and values of Parameters

S. No.	Symbol	Definition	Numerical Values [Reference]
1	S(0)	Initial count of susceptible Class.	20414 [4]
2	E(0)	Initial count of exposed Class.	12651 [4]
3	I(0)	Initial count of infectious Class.	12651 [4]
4	R(0)	Initial count of recovered Class.	12347 [4]
5	Λ	Birth rate	16.27
6	β	Transmission rate	0.00274
7	σ	Exposed rate	0.2
8	γ	Recovery rate	0.4
8	μ	mortality rate	0.1
9	ω	Proportion of vaccinated population	0.2

Table 3: Numerical Data on H1N1 [4]

S.No.	State	Cases of H1N1	Deaths
1	Delhi	3141	--

2	Punjab	--	48
3	Haryana	--	26
4	Kerala	2846	61
5	Maharashtra	2027	71
6	Gujrat	1711	55
7	Tamil Nadu	1777	--
8	Rajasthan	1149	--
9	Chhattisgarh	--	43
	Total	12651	304

3. ANALYSIS OF MODEL

The characteristics equation of the given system is given by $|J-\lambda I|=0$;

$$|J-\lambda I| = \begin{vmatrix} -\beta E-\mu-\omega-\lambda & -\beta S & 0 & 0 \\ \beta E & -\beta S-\sigma-\mu-\lambda & 0 & 0 \\ 0 & \sigma & -\gamma-\mu-\lambda & 0 \\ \omega & 0 & \gamma & -\mu-\lambda \end{vmatrix} = 0$$

$$(\mu+\lambda)(\gamma+\mu+\lambda)[\lambda^2+\lambda(\beta E+\mu+\omega-\beta S+\sigma+\mu)+(\sigma\beta E+\mu\beta E+\sigma\omega-\mu\beta S-\omega\beta S+\mu\sigma+\omega\mu+\mu^2)]=0$$

Which implies, $\lambda_1=-\mu, \lambda_2=-(\gamma+\mu)$ and

$$\lambda_{3,4}=\frac{-(\beta E+\mu+\omega-\beta S+\sigma+\mu)\pm\sqrt{(\beta E+\mu+\omega-\beta S+\sigma+\mu)^2-4(\sigma\beta E+\mu\beta E+\sigma\omega-\mu\beta S-\omega\beta S+\mu\sigma+\omega\mu+\mu^2)}}{2} \quad (6)$$

As all eigen values are zero and negative. So, the system is determined to stable.

3.1 Stability Analysis

i. **Disease-free equilibrium:** The disease-free equilibrium (DEE) of an infectious disease model signifies the state, where H1N1 infection is fully absent from the human population.

At equilibrium, the model satisfying the following conditions:

$$\frac{dS}{dt}=0, \frac{dE}{dt}=0, \frac{dI}{dt}=0, \frac{dR}{dt}=0.$$

The disease-free equilibrium occurs, if no infection remains that is number of exposed cases also will be zero, $E=0$ & $I=0$.

$$\frac{dS}{dt}=0 \; gives \; S(t)=S_0=\frac{\Lambda}{\mu+\omega}$$

$$\frac{dE}{dt}=0 \; gives \; E(t)=0, always \; true.$$

$$\frac{dI}{dt}=0 \; gives \; I(t)=0, always \; true.$$

$$\frac{dR}{dt}=0 \; gives \; R(t)=\frac{\omega S_0}{\mu}$$

Thus, the disease-free equilibrium (DEE) is $(S^*, E^*, I^*, R^*)=(S_0, 0, 0, R_0)$.

The disease-free equilibrium (DEE) is locally stable if $R_0<1$, otherwise unstable if $R_0>1$.

ii. **Basic reproduction number (R_0):** The basic reproduction number (R_0) for H1N1 is a main epidemiological indicator that shows the average number of secondary infections caused by a single sick individual in the susceptible community. Mathematically, we have

$$R_0=\frac{\beta S}{\gamma}=\frac{\beta}{\sigma+\mu}$$

Basic reproduction number $R_0 = \beta * D = 0.00274 * 7 = 0.01918 < 1$.

iii. **Herd Immunity Threshold (H_T):**

It is the proportion of a population that must be immune to an infectious disease to prevent its spread. It is given by the following formula,

$$H_T = 1 - \frac{1}{R_0}$$

Where R_0 is the basic reproduction number, demonstrating the average number of secondary infections that one infected person can produce in a community that is completely susceptible. If immunity in the population exceeds H_T, the disease spread declines. Generally, R_0 for H1N1 is lies between 1.4 to 1.6 and corresponding to R_0, the value of $H_T = 29 - 38$ %.

iv. **Force of Infection:**

The rate of infection per unit of time for a vulnerable individual is known as the force of infection. Mathematically, it can be giving by

$$Force\ of\ infection = \frac{Total\ infected\ individuals}{n * t}$$

$$Force\ of\ infection = \frac{12651}{1{,}450{,}935{,}791 * 365}$$

$$Force\ of\ infection = 0.00000002388$$

$$\beta = \frac{Force\ of\ infection}{S/_N} = \frac{1{,}450{,}935{,}791 * 0.00000002388}{12651} = 0.00274$$

3.2 SEIR Model Analysis:

In order to evaluate every stage for the induced SEIR model using real numerical data of 2024 for India. The following current situation are presented graphically for H1N1 as below.

Graphical Analysis

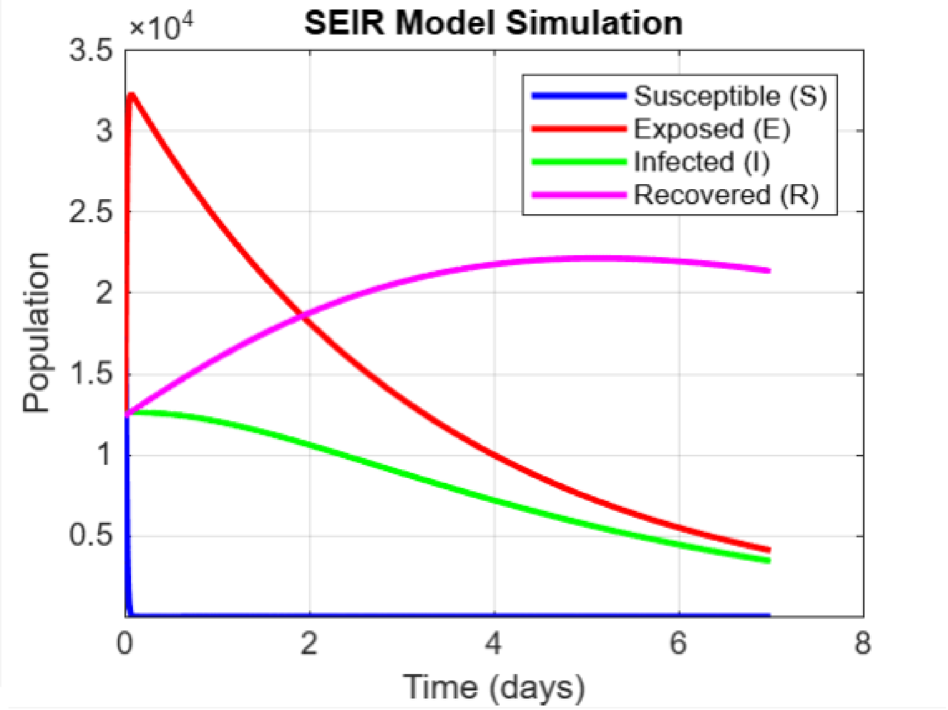

Figure 1: Induced SEIR Model. This graph is a combine representation of H1N1 virus for the year 2014.

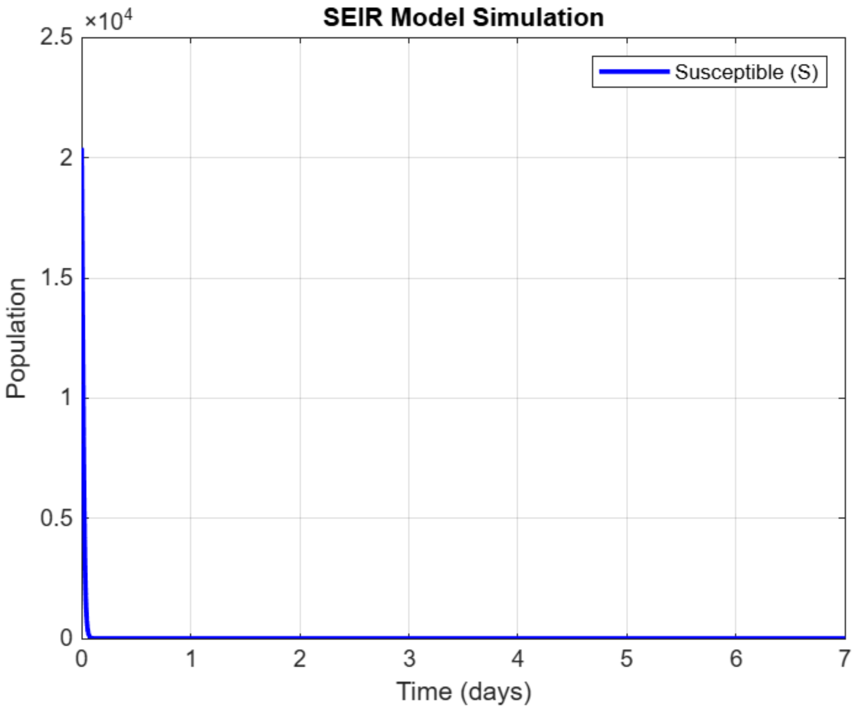

Figure 2: Induced SEIR Model for S, shows the compartment S decreases.

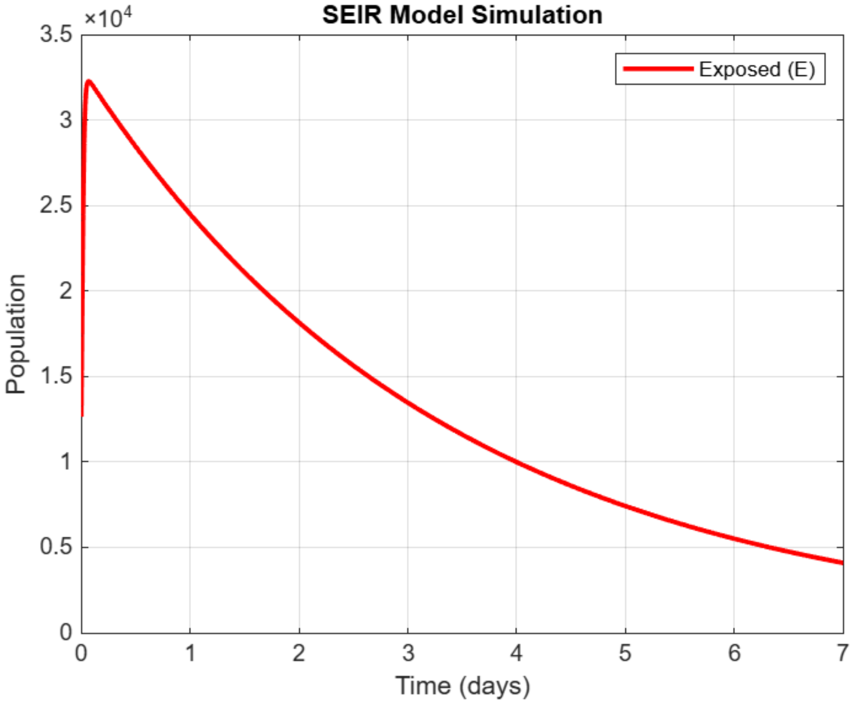

Figure 3: Induced SEIR Model for E, shows the compartment E increases initially and after treatment it decreases with respect to time.

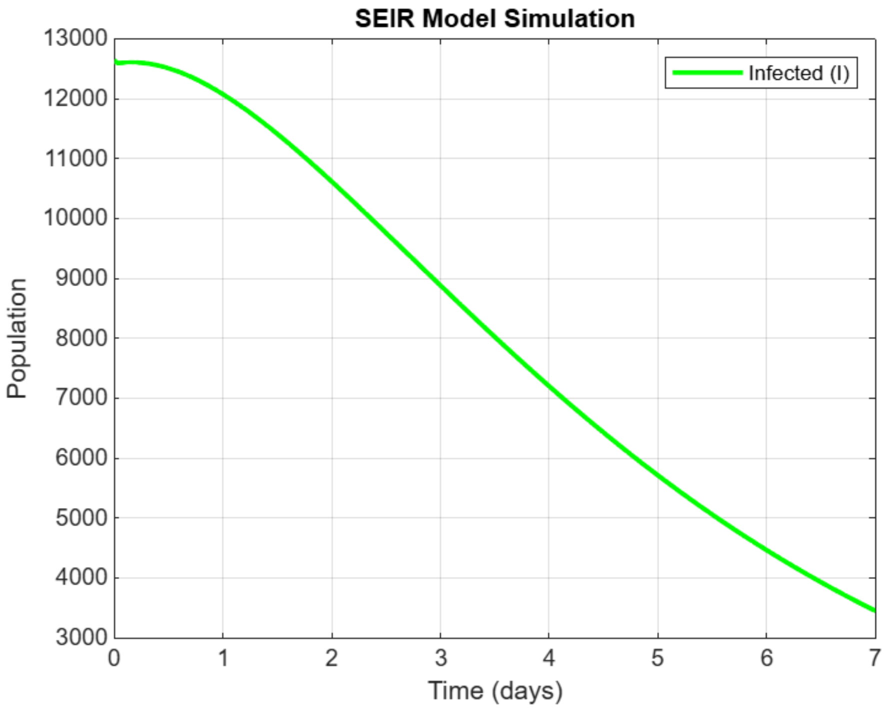

Figure 4: Induced SEIR Model for I, shows the compartment I means infection decreases with respect to time due to increasing the immunity of the patient

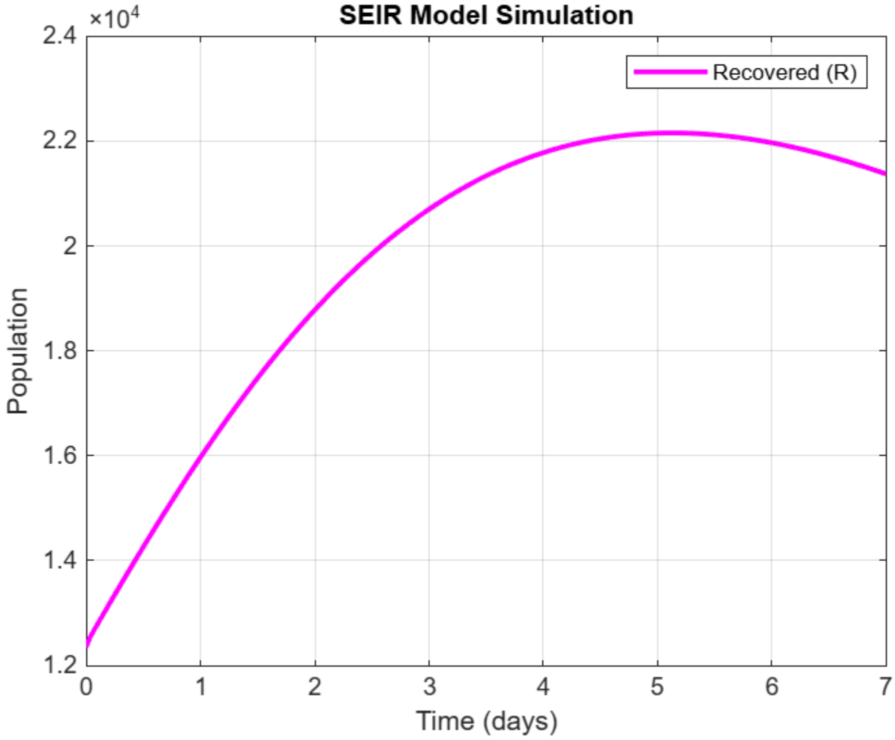

Figure 5: Induced SEIR Model for R, shows the compartment R that is recovery of the number of confirmed cases increases with respect to time.

4. DISCUSSION

Influenza A (H1N1) is a highly contagious infectious disease that has significantly contributed to past influenza pandemic, from the devastating 1918 Spanish flu to the widespread but comparatively milder 2009 swine flu pandemic. The 2009 H1N1 strain has since replaced earlier seasonal strains and continues to circulate globally. This study utilizes an improved SEIR mathematical model to monitor H1N1 mutations and assess potential pandemic threads by analysing key epidemiological indicators such as the basic reproduction number and model stability. MATLAB is employed to study graphical representation of each stage as suspectable, exposed, infected and recovered, based on numerical data. this work underscores the relevance of the role of deterministic modelling in epidemiology. By examining some parameters such as the basic reproduction number, equilibrium points, transmission rate and force of infection, the study contributes to a deeper understanding of the disease progression.

5. CONCLUSION

H1N1 influenza is highly infectious disease and it can spread easily and quickly from infected person or through contact with H1N1 virus. This study highlights on awareness of historical history of epidemic diseases and deterministic modelling used in epidemiology to improve our health system. Many mathematical models have been studied on epidemic diseases. This work focuses on many important factors, which is related to analysis each stage of H1N1 influenza disease like the concept of basic reproduction number, equilibrium point, transmission rate and force of infection.

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