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An SEQIJR Epidemic Model: Determination of the Basic Reproduction Number and Numerical Simulation of Disease Dynamics

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ABSTRACT
The aim of this study is to construct an SEQIJR model for infectious disease transmission, determine its basic reproduction number, and perform numerical simulations to analyze the model's dynamics. The model incorporates quarantine and isolation as explicit compartments, while the basic reproduction number R_0 is derived using the next generation matrix method. Numerical simulations are carried out using hypothetical initial conditions and parameter values chosen to be consistent with the fundamental assumptions of the model. The analysis yields an explicit expression for the basic reproduction number. The simulation results provide insights into the temporal progression of the disease and show that the exposed compartment exhibits a rapid increase during the early stages of the outbreak. These findings highlight the role of quarantine and isolation in influencing disease dynamics, and the resulting model can serve as a reference for early prevention strategies in managing infectious disease transmission.

KEYWORDS
SEQIJR, Basic Reproduction Number, Next Generation Method, Disease transmission.

1. INTRODUCTION

Mathematical modeling has become an essential tool for understanding the dynamics of infectious diseases and designing effective control strategies. Compartmental models, such as SIR and SEIR, enable researchers to predict disease transmission and evaluate the impact of interventions such as quarantine and isolation. This approach is highly relevant for addressing global pandemics by utilizing epidemiological data to support evidence-based decision making [1].

Several infectious diseases, both at global and local scales, exhibit similar epidemiological patterns, such as SARS, MERS, COVID-19, and certain types of influenza. These diseases present unique challenges due to transmission by exposed individuals (asymptomatic or pre-symptomatic) and the varying effectiveness of interventions such as quarantine [2]. These characteristics require a mathematical model capable of capturing complex transmission dynamics, including the role of exposed individuals in disease spread. In addition, isolation and quarantine policies play a crucial role in reducing transmission, making it necessary to model them explicitly.

Previous studies have developed various compartmental models for infectious diseases, such as the standard SEIR model or models incorporating quarantine compartments [3]. However, many of these models do not account for the ability of exposed individuals to transmit the disease or the recovery dynamics within the exposed compartment, both of which can significantly influence the estimation of disease spread [4]. In addition, several models do not explicitly distinguish between quarantine and isolation, even though these represent different intervention strategies in controlling disease transmission.

To address these limitations, this study proposes a new compartmental model consisting of six compartments: susceptible

(S), exposed (E), quarantine (Q), infected (I), isolation (J), and recovered (R). The model assumes no migration and focuses solely on epidemiological transitions, while allowing exposed individuals to transmit the infection and recover within the latent stage. Quarantine and isolation are explicitly incorporated as key intervention mechanisms. This approach is designed to more realistically capture the transmission dynamics of infectious diseases [5].

The basic reproduction number (R_0) is a key indicator for assessing the transmission potential of a disease within a fully susceptible population. In this study, R_0 is calculated using the next generation matrix approach, which enables a systematic analysis of the contributions of the exposed and infectious compartments to overall transmission [6]. This approach provides an accurate estimate of R_0, which is essential for evaluating the effectiveness of control strategies such as quarantine and isolation.

This study has both theoretical and practical significance. Theoretically, the proposed model enriches the literature on infectious disease modeling by incorporating more detailed representations of exposed dynamics and intervention mechanisms. Practically, the findings, particularly the estimation of R_0, can provide valuable insights for policymakers in designing effective pandemic control strategies, such as optimizing quarantine and isolation measures, to reduce the impact of disease transmission on the community [7].

2. LITERATURE REVIEW

2.1 Basic Reproduction Number

The basic reproduction number R_0 represents the expected number of new infections generated by a single infectious individual in a population where all individuals are susceptible [8]. This parameter determines whether an infection can successfully invade a susceptible population. When $R_0 < 1$, the expected number of secondary infections produced by a typical infectious individual is less than one, implying that the disease cannot sustain transmission and will die out. In contrast, when $R_0 > 1$, each infectious individual generates more than one new case on average, leading to exponential growth of the infected population and the establishment of the disease within the community [9].

2.2 Ordinary Diferential Equation System

Ordinary differential equation (ODE) systems are fundamental tools for modeling time-dependent phenomena in science and engineering. A system of ODEs describes how multiple variables evolve over time, where each equation specifies the rate of change of one variable as a function of all variables in the system [10]. A general linear system of n ODEs with n unknown functions $x_1, x_2, \ldots, x_n$ can be written as:

$$\begin{aligned} a_{11}x_1 + a_{12}x_2 + \cdots + a_{1n}x_n &= b_1, \\ a_{21}x_1 + a_{22}x_2 + \cdots + a_{2n}x_n &= b_2, \\ &\vdots \\ a_{n1}x_1 + a_{n2}x_2 + \cdots + a_{nn}x_n &= b_n \end{aligned}$$

where a_{ij} denotes the coefficient multiplying the j-th variable in the i-th equation. This representation highlights the coupled nature of ODE systems, enabling the formulation of models that capture interactions among variables. Because of their well established theoretical properties, ODE systems form the mathematical foundation for many dynamic models, including compartmental models in epidemiology [11].

2.3 Next Generation Matrix

A linear ODE system can be represented through its Jacobian matrix. For the construction of the Next Generation Matrix (NGM), this matrix is decomposed into F (the transmission part, representing new infections) and V(the transition part, representing changes in state). The NGM is then computed as $K = FV^{-1}$ [12].

3. METHODOLOGY

This mathematical modeling on the spread of infectious disease is a theoretical study. The model has been constructed is SEQIJR which considering quarantine and isolation factors as model variables, the model analysis uses the generation matrix method

[13] to obtain the basic reproduction number of disease. Numerical simulation of model used hypothetical initial conditions and parameter values that are selected to be consistent with the fundamental assumptions of the model [14]. The initial values of each compartment are not derived from empirical observations but are constructed as simulation data representing plausible population states at the onset of disease transmission.

4. RESULT & DISCUSSION

4.1 SEQIJR Model Formulation

The SEQIJR model on the spread of infectious disease is divided into six compratments, namely Susceptible (S), Exposed (E), Quarantine (Q), Infected (I), Isolated (J), Recovered (R). This model assumed a closed population in which individuals cannot freely enter or leave the region. Furthermore, exposed individuals possess the ability to transmit the disease, similar to the infected individual. Quarantine is applied to exposed individuals who might recover. In addition, individuals in the isolation compartment may only exit through recovery or death. The changes that occur in each human population in the transmission for the SEQIJR model can be interpreted by **Figure 1**. Based on the diagram in **Figure 1**, the rate of change in the number of

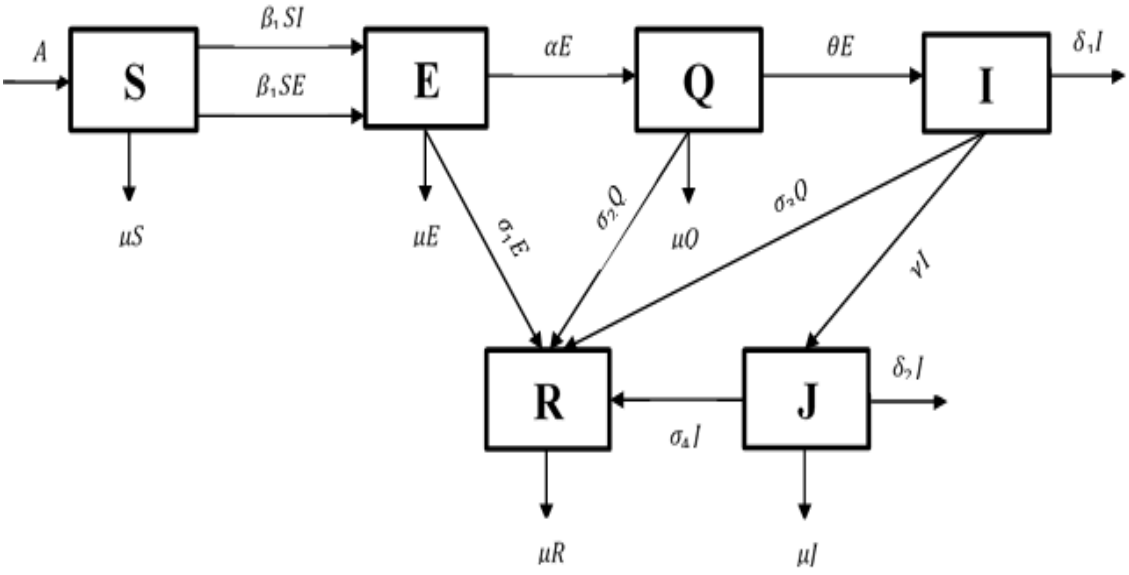

Figure 1. Compartment Diagram of SEQIJR Model

people Suspected, Exposed, Quarantine, Infected, Isolated, and Recovered over time in the SEQIJR mathematical model of the can be interpreted as follows:

$$\frac{dS}{dt} = A - S(\beta_1 I + \beta_2 E) - \mu S \tag{1}$$

$$\frac{dE}{dt} = S(\beta_1 I + \beta_2 E) - E(\alpha + \sigma_1) - \mu E \tag{2}$$

$$\frac{dQ}{dt} = \alpha E - Q(\theta + \sigma_2) - \mu Q \tag{3}$$

$$\frac{dI}{dt} = \theta Q - I(\gamma + \delta_1 + \sigma_3) - \mu I \tag{4}$$

$$\frac{dJ}{dt} = \gamma I - J(\sigma_4 + \delta_2) - \mu J \tag{5}$$

$$\frac{dR}{dt} = \sigma_1 E + \sigma_2 Q + \sigma_3 I + \sigma_4 J - \mu R \tag{6}$$

The definition of each variable and parameter is illustrated in **Table 1** as follow

Table 1. Definition of Variables/Parameters

Parameter/Variable	Definition
S	Number of suspected populations
E	Number of exposed populations
Q	Number of quarantine populations
I	Number of infected populations
J	Number of isolated populations
R	Number of recovered populations
A	The rate of birth/recruitment
β	The rate of transmission
α	The rate of quarantine
γ	The rate of isolation
θ	The rate of infection
σ	The rate of recovery
δ	The rate of disease-induced mortality
μ	The rate of natural mortality

4.2 Analysis of Free-Disease Equilibrium

To determine Equilibrium point of the model, each equation in **Equation (1) - (6)** must be equal to zero, $\frac{dS}{dt} = \frac{dE}{dt} = \frac{dQ}{dt} = \frac{dI}{dt} = \frac{dJ}{dt} = \frac{dR}{dt} = 0$. Thus obtained:

$$A - S(\beta_1 I + \beta_2 E) - \mu S = 0 \tag{7}$$
$$S(\beta_1 I + \beta_2 E) - E(\alpha + \sigma_1) - \mu E = 0 \tag{8}$$
$$\alpha E - Q(\theta + \sigma_2) - \mu Q = 0 \tag{9}$$
$$\theta Q - I(\gamma + \delta_1 + \sigma_3) - \mu I = 0 \tag{10}$$
$$\gamma I - J(\sigma_4 + \delta_2) - \mu J = 0 \tag{11}$$
$$\sigma_1 E + \sigma_2 Q + \sigma_3 I + \sigma_4 J - \mu R = 0 \tag{12}$$

Equilibrium points for disease-free are conditions where there is no spread of the disease, $S = E = I = 0$. By substituting it to **Equation (7)-(12)**, it obtained an equilibrium of free-disease:

$$E_0 = \left(\frac{A}{b},\, 0,\, 0,0,\, 0,\, 0\right)$$

4.3 Basic Reproduction Number R_0

Basic reproduction number can be determined by Next Generation Matrix. In the model, it can be seen that there are three variables involved in the transmission of disease, E, Q, and I. Therefore, determination of R_0 considers only these three corresponding equations, **Equation (2), (3)**, and (4). Let F is a vector for non-linear part of the equations and V is a vector for linear part.

$$F = \begin{bmatrix} F_1 \\ F_2 \\ F_3 \end{bmatrix} = \begin{bmatrix} \beta_1 IS + \beta_2 ES \\ 0 \\ 0 \end{bmatrix} \text{ and } V = \begin{bmatrix} V_1 \\ V_2 \\ V_3 \end{bmatrix} = \begin{bmatrix} \alpha E + \sigma_1 E + \mu E \\ -\alpha E + \theta Q + \sigma_2 Q + \mu Q \\ -\theta Q + \gamma I + \delta_1 I + \sigma_3 I + \mu I \end{bmatrix}$$

Next, the matrix F and V, each of order 3×3, are obtained from the partial derivatives of F and V with respect to E, Q, and I, followed by substitution of the free-disease equilibrium point.

$$F = \begin{bmatrix} \frac{\partial F_1}{\partial E} & \frac{\partial F_1}{\partial Q} & \frac{\partial F_1}{\partial I} \\ \frac{\partial F_2}{\partial E} & \frac{\partial F_2}{\partial Q} & \frac{\partial F_2}{\partial I} \\ \frac{\partial F_3}{\partial E} & \frac{\partial F_3}{\partial Q} & \frac{\partial F_3}{\partial I} \end{bmatrix} = \begin{bmatrix} \beta_2 S & 0 & \beta_1 S \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} = \begin{bmatrix} \frac{\beta_2 A}{\mu} & 0 & \frac{\beta_1 A}{\mu} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \tag{13}$$

and

$$V = \begin{bmatrix} \frac{\partial V_1}{\partial E} & \frac{\partial V_1}{\partial Q} & \frac{\partial V_1}{\partial I} \\ \frac{\partial V_2}{\partial E} & \frac{\partial V_2}{\partial Q} & \frac{\partial V_2}{\partial I} \\ \frac{\partial V_3}{\partial E} & \frac{\partial V_3}{\partial Q} & \frac{\partial V_3}{\partial I} \end{bmatrix} = \begin{bmatrix} \alpha+\sigma_1+\mu & 0 & 0 \\ -\alpha & \theta+\sigma_2+\mu & 0 \\ 0 & -\theta & \gamma+\delta_1+\sigma_3+\mu \end{bmatrix} \tag{14}$$

From **Equation (14)**, determinant of matrix V is obtained as follows.

$$|V| = (\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)$$

Then, cofactor and adjoint of matrix V is obtained as follows respectively.

$$\begin{bmatrix} (\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu) & \alpha(\gamma+\delta_1+\sigma_3+\mu) & \alpha\theta \\ 0 & (\alpha+\sigma_1+\mu)(\gamma+\delta_1+\sigma_3+\mu) & \theta(\alpha+\sigma_1+\mu) \\ 0 & 0 & (\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu) \end{bmatrix}$$

and

$$\begin{bmatrix} (\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu) & 0 & 0 \\ \alpha(\gamma+\delta_1+\sigma_3+\mu) & (\alpha+\sigma_1+\mu)(\gamma+\delta_1+\sigma_3+\mu) & 0 \\ \alpha\theta & \theta(\alpha+\sigma_1+\mu) & (\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu) \end{bmatrix}$$

Thus,

$$V^{-1} = \frac{1}{(\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)} \begin{bmatrix} (\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu) & 0 & 0 \\ \alpha(\gamma+\delta_1+\sigma_3+\mu) & (\alpha+\sigma_1+\mu)(\gamma+\delta_1+\sigma_3+\mu) & 0 \\ \alpha\theta & \theta(\alpha+\sigma_1+\mu) & (\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu) \end{bmatrix}$$

$$= \begin{bmatrix} \frac{1}{\alpha+\sigma_1+\mu} & 0 & 0 \\ \frac{\alpha}{(\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu)} & \frac{1}{\theta+\sigma_2+\mu} & 0 \\ \frac{\alpha\theta}{(\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)} & \frac{\theta}{(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)} & \frac{1}{\gamma+\delta_1+\sigma_3+\mu} \end{bmatrix} \tag{15}$$

Next, the form of the next generation matrix that serves as the basis for determining the value of R_0 is obtained through the operation:

$$K = F.V^{-1} \tag{16}$$

By substituting **Equation** (13) and (15) to **Equation** (16), the following matrix is obtained.

$$K = \begin{bmatrix} \frac{\beta_2 A}{\mu} & 0 & \frac{\beta_1 A}{\mu} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{\alpha+\sigma_1+\mu} & 0 & 0 \\ \frac{\alpha}{(\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu)} & \frac{1}{(\theta+\sigma_2+\mu)} & 0 \\ \frac{\alpha\theta}{(\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)} & \frac{\theta}{(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)} & \frac{1}{(\gamma+\delta_1+\sigma_3+\mu)} \end{bmatrix}$$

$$= \begin{bmatrix} \frac{\beta_2 A}{\mu(\alpha+\sigma_1+\mu)} + \frac{\beta_1 A\alpha\theta}{\mu(\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)} & \frac{\beta_1 A\theta}{\mu(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)} & \frac{\beta_1 A}{\mu(\gamma+\delta_1+\sigma_3+\mu)} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

From this matrix, the characteristic equation can be determined as follow.

$$det\,(C-\lambda I) = 0 \tag{17}$$

$$\begin{bmatrix} \frac{\beta_2 A}{\mu(\alpha+\sigma_1+\mu)} + \frac{\beta_1 A\alpha\theta}{\mu(\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)} - \lambda & \frac{\beta_1 A\theta}{\mu(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)} & \frac{\beta_1 A}{\mu(\gamma+\delta_1+\sigma_3+\mu)} \\ 0 & -\lambda & 0 \\ 0 & 0 & -\lambda \end{bmatrix} = 0$$

$$\left(\frac{\beta_2 A}{\mu(\alpha+\sigma_1+\mu)} + \frac{\beta_1 A\alpha\theta}{\mu(\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)} - \lambda \right) \lambda^2 = 0$$

Eigenvalues from **Equation** (17) is found as follows:

$$\lambda_{1,2} = 0,\ \lambda_3 = \frac{\beta_2 A}{\mu\,(\alpha+\sigma_1+\mu)} + \frac{\beta_1 A\alpha\theta}{\mu\,(\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)}$$

Since R_0 is the greatest eigenvalue of the characteristic equation, the basic reproduction number is found.

$$R_0 = \frac{\beta_2 A}{\mu\,(\alpha+\sigma_1+\mu)} + \frac{\beta_1 A\alpha\theta}{\mu\,(\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)}$$

4.4 Numerical Simulation

The parameter and initial values used to obtain numerical simulation in this model are presented in **Table 2**. Based on the

Table 2. Initial Value of Variable

Variables	Value
N	9 526 285
S	9 225 747
E	11 561
Q	1 021
I	145 229
J	328
R	142 399

Table 3. Definition of Parameter

Parameter	Value
A	0.006
μ	0.002
β_1	0.143
β_2	0.864
α	0.088
θ	0.015
γ	0.015
δ_1	0.0173
δ_2	0.0172
σ_1	0.031
σ_2	0.032
σ_3	0.034
σ_4	0.039

parameter and variable, the simulation of the model with basic reproduction number

$$R_0 = \frac{\beta_2 A}{\mu\,(\alpha+\sigma_1+\mu)} + \frac{\beta_1 A\alpha\theta}{\mu\,(\alpha+\sigma_1+\mu)(\theta+\sigma_2+\mu)(\gamma+\delta_1+\sigma_3+\mu)}$$

is presented in **Figure 2**. The numerical simulation results of the SEQIJR model reveal disease transmission dynamics consistent with the characteristics of infectious diseases. Based on the parameter values used, the exposed compartment (E) exhibits a rapid increase in population at the early stage of the outbreak and reaches its peak on day 10, with approximately 5,666,327 individuals. This phenomenon can be explained by the structure of the model, in which susceptible individuals (S) who are exposed to the disease do not immediately enter the infectious compartment (I), but instead pass through the exposed stage

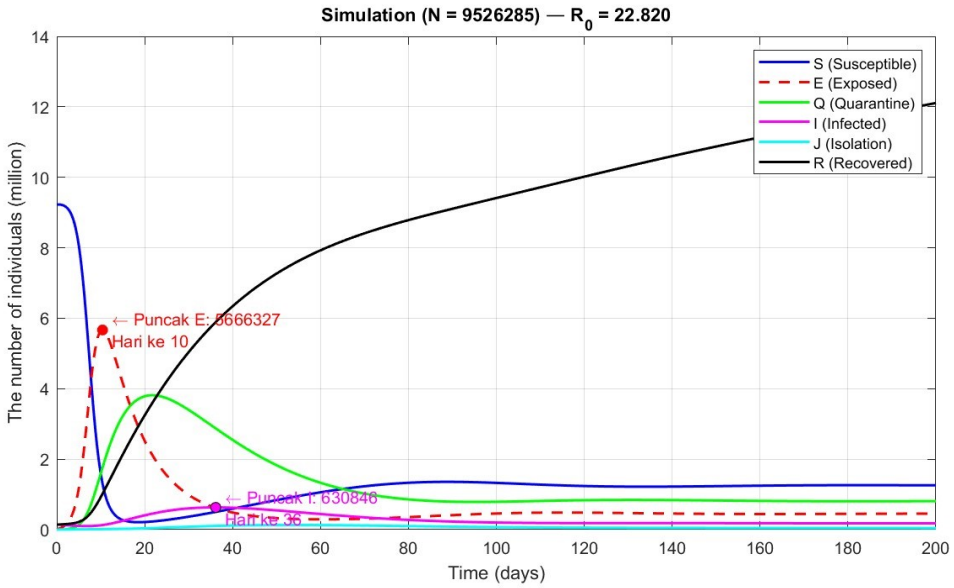

Figure 2. Numerical Simulation of SEQIJR Model

(E). The relatively high transmission rate from S to E leads to rapid accumulation in the exposed compartment. Moreover, the duration of the exposed period, due to the small total exit rate from E ($\alpha + \sigma_1 + \mu$), results in a longer residence time within the compartment, causing its peak to be substantially larger than that of other compartments.

In contrast to E, the infectious compartment (I) reaches its peak later, on day 36, with approximately 630,846 individuals. The significantly smaller peak of I compared to E indicates that most individuals in the exposed stage do not directly progress to the infectious stage. This aligns with the model structure, in which individuals in E may transition to the quarantine compartment (Q) or directly recover into R without becoming infectious. Additionally, the infectious compartment has a relatively large total exit rate, through recovery, disease-induced mortality, and isolation ($\gamma + \delta_1 + \sigma_3 + \mu$), resulting in a shorter infectious period. The combination of high exit rates and alternative pathways from E to Q or R contributes to the smaller infectious peak relative to the exposed peak.

The simulation also shows that the recovered compartment (R) increases monotonically throughout the simulation period. This behavior arises from the model structure, in which individuals from all infected compartments (E, Q, I, and J) transition into R through their respective recovery rates ($\sigma_1, \sigma_2, \sigma_3, \sigma_4$). Since there is no outflow from R other than natural mortality, the total population in this compartment continues to grow. This condition reflects a disease with a high recovery rate relative to disease-induced mortality.

The susceptible compartment (S) experiences a sharp decline during the early outbreak phase due to high infection pressure from contacts with exposed and infectious individuals. After reaching its minimum, S gradually increases as the recruitment rate A replenishes the susceptible population once the transmission pressure decreases.

Overall, the epidemiological patterns produced by the simulation depict an outbreak with an explosive initial phase, characterized by a large exposed peak followed by a smaller but delayed infectious peak. Furthermore, the dominant flow into the recovered compartment suggests the effectiveness of recovery mechanisms through medical treatment, isolation, and immune response. These findings also highlight that the presence of quarantine (Q) and isolation (J) compartments significantly contribute to reducing the infectious peak, making them potentially effective control strategies.

The constructed model further demonstrates high sensitivity to the transmission parameters β_1 and β_2, which directly influence the basic reproduction number R_0. Therefore, interventions aimed at reducing contact between susceptible individuals and exposed/infectious groups constitute the most effective approach to suppress disease transmission. The implementation of measures such as social activity restrictions, increased quarantine compliance, and effective medical isolation can theoretically reduce R_0 to below 1, thereby enabling the outbreak to be controlled and eventually die out naturally.

5. CONCLUSION

Based on the results of this study, it can be concluded that the SEQIJR model is a useful framework for representing the transmission dynamics of specific infectious diseases. The model analysis provides a clear formulation and interpretation of the basic reproduction number, offering insight into the conditions under which an outbreak may occur. Furthermore, the numerical simulations illustrate the predicted progression of disease cases and demonstrate that quarantine and isolation interventions can effectively reduce and delay disease transmission. Overall, the findings of this research can serve as a scientific basis for early prevention strategies in managing the spread of infectious diseases.

REFERENCES

[1] N. Ferguson, d. Laydon, g. Nedjati Gilani, N. Imai, k. Ainslie, m. Baguelin, s. Bhatia, a. Boonyasiri, z. Cucunuba Perez, g. Cuomo-Dannenburg, a. Dighe, i. Dorigatti, h. Fu, k. Gaythorpe, w. Green, a. Hamlet, w. Hinsley, l. Okell, S. van Elsland, h. Thompson, r. Verity, e. Volz, h. Wang, Y. Wang, p. Walker, C. Walters, p. Winskill, c. Whittaker, c. Donnelly, s. Riley, and a. Ghani, "Report 9: Impact of non-pharmaceutical interventions (NPIs) to reduce COVID19 mortality and healthcare demand," Mar. 2020, publisher: Imperial College London.

[2] R. Li, S. Pei, B. Chen, Y. Song, T. Zhang, W. Yang, and J. Shaman, "Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV-2)," *Science*, vol. 368, no. 6490, pp. 489–493, May 2020.

[3] A. J. Kucharski, T. W. Russell, C. Diamond, Y. Liu, J. Edmunds, S. Funk, R. M. Eggo, F. Sun, M. Jit, J. D. Munday, N. Davies, A. Gimma, K. Van Zandvoort, H. Gibbs, J. Hellewell, C. I. Jarvis, S. Clifford, B. J. Quilty, N. I. Bosse, S. Abbott, P. Klepac, and S. Flasche, "Early dynamics of transmission and control of COVID-19: a mathematical modelling study," *The Lancet Infectious Diseases*, vol. 20, no. 5, pp. 553–558, May 2020.

[4] G. Giordano, F. Blanchini, R. Bruno, P. Colaneri, A. Di Filippo, A. Di Matteo, and M. Colaneri, "Modelling the COVID-19 epidemic and implementation of population-wide interventions in Italy," *Nat Med*, vol. 26, no. 6, pp. 855–860, Jun. 2020.

[5] C. N. Ngonghala, E. Iboi, S. Eikenberry, M. Scotch, C. R. MacIntyre, M. H. Bonds, and A. B. Gumel, "Mathematical assessment of the impact of non-pharmaceutical interventions on curtailing the 2019 novel Coronavirus," *Mathematical Biosciences*, vol. 325, Jul. 2020.

[6] P. Van Den Driessche, "Reproduction numbers of infectious disease models," *Infectious Disease Modelling*, vol. 2, no. 3, pp. 288–303, Aug. 2017.

[7] S. E. Eikenberry, M. Mancuso, E. Iboi, T. Phan, K. Eikenberry, Y. Kuang, E. Kostelich, and A. B. Gumel, "To mask or not to mask: Modeling the potential for face mask use by the general public to curtail the COVID-19 pandemic," *Infectious Disease Modelling*, vol. 5, pp. 293–308, 2020.

[8] K. Dietz, "The estimation of the basic reproduction number for infectious diseases," *Stat Methods Med Res*, vol. 2, no. 1, pp. 23–41, Mar. 1993.

[9] P. Van Den Driessche and J. Watmough, "Further Notes on the Basic Reproduction Number," in *Mathematical Epidemiology*, J. M. Morel, F. Takens, B. Teissier, F. Brauer, P. Van Den Driessche, and J. Wu, Eds. Berlin, Heidelberg: Springer Berlin Heidelberg, 2008, vol. 1945, pp. 159–178, series Title: Lecture Notes in Mathematics.

[10] B. Denis, "An Overview of Numerical and Analytical Methods for solving Ordinary Differential Equations," 2020, version Number: 1. [Online]. Available: https://arxiv.org/abs/2012.07558

[11] P. Dawkins, "Paul's Online Math Notes: Systems of Differential Equations," 2007.

[12] O. Diekmann, J. A. P. Heesterbeek, and M. G. Roberts, "The construction of next-generation matrices for compartmental epidemic models," *J. R. Soc. Interface.*, vol. 7, no. 47, pp. 873–885, Jun. 2010.

[13] M. G. Roberts and J. A. P. Heesterbeek, “Characterizing the next-generation matrix and basic reproduction number in ecological epidemiology,” *J. Math. Biol.*, vol. 66, no. 4-5, pp. 1045–1064, Mar. 2013.

[14] H. W. Hethcote, “The Mathematics of Infectious Diseases,” *SIAM Rev.*, vol. 42, no. 4, pp. 599–653, Jan. 2000.