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EPIDEMIC SEIQRV MATHEMATICAL MODEL AND STABILITY ANALYSIS OF COVID-19 TRANSMISSION DYNAMICS OF CORONAVIRUS†

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Abstract. In this study, we propose a dynamic SEIQRV mathematical model and examine it to comprehend the dynamics of COVID-19 pandemic transmission in the Coimbatore district of Tamil Nadu. Positiveness and boundedness, which are the fundamental principles of this model, have been examined and found to be reliable. The reproduction number was calculated in order to predict whether the disease would spread further. Existing arrangements of infection-free, steady states are asymptotically stable both locally and globally when $R_0 < 1$. The consistent state arrangements that are present in diseases are also locally steady when $R_0 < 1$ and globally steady when $R_0 > 1$. Finally, the numerical data confirms our theoretical study.

AMS Mathematics Subject Classification : 34D20, 65P40.
Key words and phrases : Omicron, steady states, reproduction number, stability.

1. Introduction

Direct contact with an infected object or breathing in aerosols from an infected person are both effective ways to spread COVID-19 from one person to another. The viral coronavirus SARSCoV-2, which has emerged as a highly infectious virus that targets the human respiratory system, causes Coronavirus Disease 2019 (COVID-19). The Omicron variant, also known as B.1.1.529 SARS-Cov-2 variants, spreads more quickly than the actual coronavirus infection. Individuals infected with the Omicron variant may display signs and symptoms similar to those seen with previous variants. The virus may cause lenient diseases, according to basic information, but some people may still develop serious

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sickness and need confinement as a result of exposure to this variation. Governments have been setting up a variety of control measures to effectively stop the spread of COVID-19, including strict, essential lockdowns and encouraging people to keep an adequate distance between one another, stay away from congested occurrences, set a limit on the number of people in any gathering, and wear face masks in public. The best public health measures for preventing COVID-19 and lowering the possibility of new variants emerging continue to be vaccination and quarantine. People who have received their COVID-19 vaccinations in a timely manner and are exposed to the virus have a lower risk of developing a serious illness than people who have not received the vaccine and are exposed to the virus. Researchers have been compelled to rethink models that contributed to India's understanding of COVID-19 and response to the outbreak in light of the highly contagious Omicron variant.

Establishing successful techniques to control an infectious disease's spread in a population requires an awareness of the dynamics of the disease. The dynamics of some specific infectious disease types are being studied using recent mathematical models. The basic principle of basic deterministic models is the compartmentalization of the population. For COVID-19, some authors proposed models without the vaccination compartment. Byul et.al.[6] presented a model that examined the impact of various prevention and reduction approaches for COVID-19 spread, including the use of early medical measures and isolation from society. Daniel [12] proposed a mathematical model that outlined the mechanisms for propagation in the dynamics of infection and the effect of the natural reservoir on the transmission of the disease among people as well. Pakwan et. al. [26], carried out studies regarding a model of a vaccine class that produced excellent vaccine results and helped to understand how to prevent the COVID-19 pandemic. For the purpose of to put an end to the COVID-19 outbreak in India, Biswas et. al.[28], researched strategies for prevention using an empirical compartmental model for the Indian scenario. Tyagi's model SEIQR [30], which he has proposed, was essential in directing crucial choices and measures to avoid during the pandemic. Several researchers have created mathematical models with a compartment for vaccinations but none for quarantine. In order to allow for the proper vaccination of susceptible individuals in the host population after a sick person recovers from a disease, Oke et. al. [25], proposed the SIRV model, which excludes Quarantine. The Maski et.al [24], proposed SIIR model had the benefit of being able to explicitly handle asymptomatic people, who are often hard to find in the real world. Rao et. al. [27], investigated how vaccination and treatment efforts impacted the spread of disease when there were delays in treatment.

As studied by Chatzarakis et. al.,[7], the vaccine and quarantine classes are remembered for the model definition of an exemplary model, which enables the provision of suitable antibodies to the recovered and defenceless individuals in the host population when a washed-out individual recovers from an illness. The transmission power of disease is frequently referred to as the rate at which people

are infected per unit time when a sick person comes into contact with a susceptible person while they are ill. From the disease-present consistent state to the infection-absent consistent state, asymptotic strong characteristics change. We developed an Omicron variant model with a variable size populations from papers ([2],[4],[9],[11],[15],[16],[18],[19],[20],[22],[23], [29]) in this paper. In this study, we divided the population into six compartments and proposed the SEIQRV model. Computational simulations were run at the conclusion of the study to validate and support our theoretical conclusions drawn from the COVID-19 data. In section 2, we formulated the SEIQRV model for the COVID-19 disease. In section 3, the positiveness, boundedness, existence and uniqueness of solutions of the SEIQRV model is examined and derived. In section 4, we discussed stability of the proposed model. In section 5, we have verified our theoretical findings with the numerical simulation of the real data of Omicron from Coimbatore of Tamil Nadu.

2. Model Formulation

The entire population N(t) is divided into sub-populations of state factors of persons who are Susceptible people S(t), Exposed people $E(t)$, Infected people $I(t)$, Quarentined people $Q(t)$, Recovered people $R(t)$, and Vaccinated people $V(t)$. Throughout this paper, we are going to use the notions which are given in the table 1.

Table 1. Parameters and their descriptions

Parameters	Descriptions	Values	Sources
P	Rate at which humans are recruited into the population	5	[9], [10]
ζ_1	The regular demise rate pertinent to all compartments	0.09	[9], [10]
ζ_2	Powerful irresistible contact rate between the susceptible and infected person	0.1679	[9], [10]
ζ_3	The rate at which the recovered compartment loses its immunities to treatment	0.0333	[9], [10]
ζ_4	The rate at which the vaccinated compartment loses its immunities to susceptible	0.0059	[9], [10]
ζ_5	Rate at which exposed people move to isolated class	0.3169	[9], [10]
ζ_6	Rate at which a specific part of exposed people move to infected class	0.1858	[9], [10]
ζ_7	The demise rate instigated by contaminations of infected people	0.0002	[9], [10]
ζ_8	The regular recovery rates because of different components	0.1981	[9], [10]
ζ_9	The treatment rate of the infected class	0.5864	
ζ_{10}	Contact rate between infected and recovered classes	0.0505	[9], [10]
ζ_{11}	Rate at which a specific part of isolated people gets vaccination	0.1695	[9], [10]
ζ_{12}	Rate at which a specific part of recovered people receives vaccination	0.0197	[9], [10]

Accompanying suspicions are made in the model development that, (i) Birth and passing rate is specific. (ii) Vaccine misfortunes its power prompting melting

away in people after some time. (iii) Isolated individuals can get vaccine. By the assumptions made, the system of equations of the model is formulated as

$$\begin{aligned}
\frac{dS}{dt} &= P - \zeta_1 S - \zeta_2 SI + \zeta_3 R + \zeta_4 V \\
\frac{dE}{dt} &= \zeta_2 SI - (\zeta_1 + \zeta_5 + \zeta_6)E, \\
\frac{dI}{dt} &= \zeta_6 E - (\zeta_1 + \zeta_7 + \zeta_8 + \zeta_9)I, \\
\frac{dQ}{dt} &= \zeta_5 E + \zeta_9 I - (\zeta_{10} + \zeta_{11} + \zeta_1)Q, \\
\frac{dR}{dt} &= \zeta_8 I + \zeta_{10} Q - (\zeta_1 + \zeta_3 + \zeta_{12})R, \\
\frac{dV}{dt} &= \zeta_{11} Q + \zeta_{12} R - (\zeta_1 + \zeta_4)V
\end{aligned} \tag{1}$$

Subject to initial conditions: $S(0) = S_0, E(0) = E_0, I(0) = I_0, Q(0) = Q_0, R(0) = R_0^0, V(0) = V_0$.

Remark 2.1. The system of equations can be written as

$$\begin{aligned}
\frac{dS}{dt} &= P - \zeta_1 S - \zeta_2 SI + \zeta_3 R + \zeta_4 V \\
\frac{dE}{dt} &= \zeta_2 SI - (\zeta_{22})E, \\
\frac{dI}{dt} &= \zeta_6 E - (\zeta_{33})I, \\
\frac{dQ}{dt} &= kE + \zeta_9 I - (\zeta_{44})Q, \\
\frac{dR}{dt} &= \zeta_8 I + \zeta_{10} Q - (\zeta_{55})R, \\
\frac{dV}{dt} &= \zeta_{11} Q + \zeta_{12} R - (\zeta_{66})V
\end{aligned} \tag{2}$$

(3)

where $\zeta_{22} = \zeta_1 + \zeta_5 + \zeta_6$, $\zeta_{33} = \zeta_1 + \zeta_7 + \zeta_8 + \zeta_9$, $\zeta_{44} = \zeta_{10} + \zeta_{11} + \zeta_1$, $\xi_4 = \zeta_1$, $\zeta_{55} = \zeta_1 + \zeta_3 + \zeta_{12}$ and $\zeta_{66} = \zeta_1 + \zeta_4$.

3. Qualitative Analysis of the SEIQRV Model

In this section the positivity, boundedness, existence, and uniqueness of the solution of the proposed model is discussed.

Theorem 3.1. [13] *Let Δ be a region $|t-t_0| \leq a$, $|x-x_0| \leq b$, $x = (x_1, x_2, \ldots, x_n)$, $x_0 = (x_{10}, x_{20}, \ldots, x_{n0})$, and $a, b > 0$. Also, suppose the Lipschitzian condition $|f(t,x) - f(t,x_0)| \leq K|x - x_0|$ is satisfied by $f(t,x)$, whenever (t,x) and (t,x_0) are in Δ, where $K > 0$. A vector solution $x(t)$ of the system in the interval $|t - t_0| \leq \delta$ exists, such that $\delta > 0$ which is unique and continuous.*

Theorem 3.2. *If S(0), E(0), I(0), Q(0) R(0), V(0) are positive and bounded, then S(t), E(t), I(t),Q(t), R(t), V(t) are also positive and bounded for all $t > 0$.*

Proof. Let Δ be the region $0 \leq \zeta_7 \leq R$. We have to prove that the partial derivatives of (1) are continuous and bounded in Δ.

Let $H_1 = \frac{dS}{dt}, H_2 = \frac{dE}{dt}, H_3 = \frac{dI}{dt}, H_4 = \frac{dQ}{dt}$, $H_5 = \frac{dR}{dt}, H_6 = \frac{dV}{dt}$

Now $|\frac{\partial H_1}{\partial S}| = |-\zeta_1 - \zeta_2 I| < \infty, |\frac{\partial H_1}{\partial E}| = |0| < \infty, |\frac{\partial H_1}{\partial I}| = |-\zeta_2 S| < \infty, |\frac{\partial H_1}{\partial Q}| = |0| < \infty$, $|\frac{\partial H_1}{\partial R}| = |\zeta_3| < \infty, |\frac{\partial H_1}{\partial V}| = |\zeta_4| < \infty$.

Similarly the partial derivatives of (1) exist for all variables, which are finite and bounded.

Adding all the equations of the system in (1), we get

$$\frac{dN}{dt} = P - (S + E + I + Q + R + V)\zeta_1 - \zeta_7 I \tag{4}$$

and in the infection free state we have $\dot{N} = P - N\zeta_1$. Thus

$$N(t) = \lim_{t \to \infty} \Big(\frac{P}{\zeta_1} + Ce^{-\zeta_1 t} \Big) = \frac{P}{\zeta_1}, \tag{5}$$

which means that

$$\lim_{t \to \infty} sup N(t) \leq \frac{P}{\zeta_1}. \tag{6}$$

Then it follows the positivity for all t>0. □

The system (1) is found static, i.e. the solutions of time independent are obtained. The steady state solutions in the infection free state, when $I = 0$ is given by

$$\begin{aligned} E_q^0 &= (S^0, E^0, I^0, Q^0, R^0, V^0) \\ &= \big(\frac{P}{\zeta_1}, 0, 0, 0, 0, 0, 0\big). \end{aligned} \tag{7}$$

Also, when infection is persistent the steady state solutions, i.e., $I \neq 0$ is given by

$$E_q^* = (S^*, E^*, I^*, Q^*, R^*, V^*) \tag{8}$$

$$\begin{aligned} = \Big(& \frac{\zeta_{22}\zeta_{33}}{\zeta_2\zeta_6}, \frac{\zeta_{33}(P - \zeta_1 S^*)}{\zeta_6(\zeta_2 S^* - \zeta_3 B - \zeta_4 C)}, \frac{P - \zeta_1 S^*}{\zeta_2 S^* - \zeta_3 B - \zeta_4 C}, \\ & \frac{\zeta_5\zeta_{33} + \zeta_6\zeta_9}{\zeta_6\zeta_{44}} \big(\frac{P - \zeta_1 S^*}{\zeta_2 S^* - \zeta_3 B - \zeta_4 C}\big), \\ & \frac{\zeta_8\zeta_{22}\zeta_{44} + \zeta_2\zeta_5\zeta_{10} S^* + \zeta_9\zeta_{22}}{\zeta_{22}\zeta_{44}\zeta_{55}} \big(\frac{P - \zeta_1 S^*}{\zeta_2 S^* - \zeta_3 B - \zeta_4 C}\big), \\ & \frac{\zeta_{11} A + \zeta_{12} B}{\zeta_{66}} \big(\frac{P - \zeta_1 S^*}{\zeta_2 S^* - \zeta_3 B - \zeta_4 C}\big) \Big) \end{aligned} \tag{9}$$

where

$$A = \frac{\zeta_5\zeta_{33} + \zeta_6\zeta_9}{\zeta_6\zeta_{44}}$$

$$B = \frac{\zeta_8\zeta_{22}\zeta_{44} + \zeta_2\zeta_5\zeta_{10}S^* + \zeta_9\zeta_{22}}{\zeta_{22}\zeta_{44}\zeta_{55}}$$
$$C = \frac{\zeta_{11}A + \zeta_{12}B}{\zeta_{66}}$$

The next-generation matrix method is used to calculate the reproduction number (Theorem 3.3). In earlier research on infectious disease models, determining the basic reproduction number provided insight into the stability of the system in terms of the presence or absence of disease. The reproduction number refers to the number of subsequent cases that are brought into a population that is completely susceptible by an initial case ([14],[31]).

Theorem 3.3. *Define* $Ys = \{y = 0|y_i, i = 1, 2, 3, \dots\}$. *Let* $G_i(y)$ *be the pace of new clinical indications of illness manifestations in compartment i, likewise, let* V_i^+ *be the pace at which people move into compartment i through different means and* V_i^- *be the rate at which people move out of compartment i. Then* ${y^1}_i = g_i(y) = G_i(y) - V_i(y)$, *i = 1,2,3,... and* $V_i(y) = V_i^- - V_i^+$, *where G is a positive matrix and V is a non singular matrix.*

From the model formulation (1) corresponding with our statement, we have

$$G = \begin{pmatrix} 0 & \zeta_2 S & 0 \\ 0 & 0 & 0 \\ 0 & \zeta_9 & 0 \end{pmatrix}$$
$$V = \begin{pmatrix} \zeta_{33} & 0 & 0 \\ -\zeta_6 & \zeta_{44} & 0 \\ -\zeta_5 & 0 & \zeta_{55} \end{pmatrix}$$
$$V^{-1} = \begin{pmatrix} \frac{1}{\zeta_{33}} & 0 & 0 \\ \frac{\zeta_6}{\zeta_{33}\zeta_{44}} & \frac{1}{\zeta_{44}} & 0 \\ \frac{\zeta_5}{\zeta_{33}\zeta_{55}} & 0 & \frac{1}{\zeta_{55}} \end{pmatrix}$$

and

$$GV^{-1} = \begin{pmatrix} \frac{\zeta_2 S\zeta_6}{\zeta_{22}\zeta_{33}} & \frac{\zeta_2 S}{\zeta_{33}} & 0 \\ 0 & 0 & 0 \\ \frac{\zeta_9\zeta_2 S\zeta_6}{\zeta_{22}\zeta_{33}} & \frac{\zeta_9}{\zeta_{33}} & 0 \end{pmatrix},$$

Hence, R_0 is the largest eigenvalue such that

$$R_0 = (GV^{-1}) = \frac{P\zeta_2\zeta_6}{\zeta_1(\zeta_1 + \zeta_5 + \zeta_6)(\zeta_1 + \zeta_7 + \zeta_8 + \zeta_9)}. \tag{10}$$

4. Stability Analysis of the SEIQRV Model

In this section, the stability of the solutions of the proposed model is analysed and discussed briefly.

Theorem 4.1. *The infection free consistent state E^0 is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.*

Proof. The Jacobian matrix of (1) at infection free steady state solution is given by

$$J(E_q^0) = \begin{pmatrix} -\zeta_1 & 0 & -\zeta_2 S & 0 & \zeta_3 & \zeta_4 \\ 0 & -\zeta_{22} & \zeta_2 S & 0 & 0 & 0 \\ 0 & \zeta_6 & \zeta_{33} & 0 & 0 & 0 \\ 0 & \zeta_5 & \zeta_9 & -\zeta_{44} & 0 & 0 \\ 0 & 0 & \zeta_8 & \zeta_{10} & -\zeta_{55} & 0 \\ 0 & 0 & 0 & \zeta_{11} & \zeta_{12} & -\zeta_{66} \end{pmatrix}.$$

The characteristic polynomial is
$(\lambda+\zeta_1)(\lambda+\frac{1}{2}\big(\zeta_{22}+\zeta_{33}+\sqrt{\zeta_{22}^2+4\zeta_2 S\zeta_6-2\zeta_{22}\zeta_{33}+\zeta_{33}^2}\big))(\lambda+\frac{1}{2}\big(\zeta_{22}+\zeta_{33}-\sqrt{\zeta_{22}^2+4\zeta_2 S\zeta_6-2\zeta_{22}\zeta_{33}+\zeta_{33}^2}\big))(\lambda+\zeta_{44})(\lambda+\zeta_{55})(\lambda+\zeta_{66})$.
The given system (1) is stable when
$-\zeta_{22}-\zeta_{33}+\sqrt{\zeta_{22}^2+4\zeta_2 S\zeta_6-2\zeta_{22}\zeta_{33}+\zeta_{33}^2}<0$
or $\sqrt{\zeta_{22}^2+4\zeta_2 S\zeta_6-2\zeta_{22}\zeta_{33}+\zeta_{33}^2}<(\zeta_{22}+\zeta_{33})$
or $\zeta_{22}^2+4\zeta_2 S\zeta_6-2\zeta_{22}\zeta_{33}+\zeta_{33}^2<(\zeta_{22}+\zeta_{33})^2$
or $\zeta_2 P\zeta_6<\zeta_{22}\zeta_{33}$ i.e., $\frac{\zeta_2 P\zeta_6}{\zeta_1\zeta_{22}\zeta_{33}}<1$
That is $R_0 < 1$. Clearly infection free steady state E^0 is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$. □

Investigating the global aspects of a pestilence model framework is challenging because there are no known numerical approaches for developing Lyapunov capabilities for epidemic models. Having an organised course to take is a good way to make Lyapunov function. It can be acquired using a nonlinear Lyapunov capacity of the Goh-Volterra kind or an ordered technique for direct Lyapunov capacity([3], [32]).

Theorem 4.2. *The disease free consistent state arrangements of (2) is globally asymptotically stable if $R_0 < 1$.*

Proof. We consider the Lyapunov function $G(S, E, I, Q, R, V) : \mathbb{R}^6 \to \mathbb{R}^+$ defined as G(S, E, I, Q, R, V)=γ I.

Differentiating the above function with respect to time, we get

$$\dot{G} = \gamma\dot{I} = \gamma\Big(\zeta_6 - \zeta_{33}\Big)I \leq \gamma\Big(\zeta_2 S\zeta_6 - \zeta_{22}\zeta_{33}\Big)I.$$

Taking $\gamma = \frac{1}{\zeta_{22}\zeta_{33}}$, then $\dot{G} = (\frac{\zeta_2 S\zeta_6}{\zeta_{22}\zeta_{33}} - 1)I$.
$\dot{G} = 0$, when I=0, and therefore $S \to \frac{P}{\zeta_1}, N \to \frac{P}{\zeta_1}$ as $t \to \infty$.

Hence $\{(S, E, I, Q, R, V) \in \Omega | \dot{G} \leq 0\}$ is the singleton set E^0. Thus from the La-Salle invariance rule [21], when $R_0 < 1$, the worldwide dependability of disease free consistent state is globally asymptotically steady. □

Theorem 4.3. *The disease persistent consistent state arrangements E^* of (2) is locally asymptotically stable if $R_0 < 1$.*

Proof. Consider Jacobian matrix of (1) at infection persistent steady state solution

$$J(E_q^*) = \begin{pmatrix} -\zeta_1 - \zeta_2 I & 0 & -\zeta_2 S & 0 & \zeta_3 & \zeta_4 \\ \zeta_2 I & -\zeta_{22} & \zeta_2 S & 0 & 0 & 0 \\ 0 & \zeta_6 & \zeta_{33} & 0 & 0 & 0 \\ 0 & \zeta_5 & \zeta_9 & -\zeta_{44} & 0 & 0 \\ 0 & 0 & \zeta_8 & \zeta_{10} & -\zeta_{55} & 0 \\ 0 & 0 & 0 & \zeta_{11} & \zeta_{12} & -\zeta_{66} \end{pmatrix}.$$

The characteristic polynomial is

$b_1\lambda^6 + b_2\lambda^5 + b_3\lambda^4 + b_4\lambda^3 + b_5\lambda^2 + b_6\lambda + b_7,$

where

$$\begin{aligned}
b_1 &= 1 \\
b_2 &= \zeta_1 + \zeta_{44} + \zeta_{22} + \zeta_{33} + \zeta_2 I^* + \zeta_{55} + \zeta_{66} \\
b_3 &= \zeta_1\zeta_{44} + \zeta_1\zeta_{22} + \zeta_{44}\zeta_{22} + \zeta_1\zeta_{33} + \zeta_{44}\zeta_{33} + \zeta_{44}\zeta_2 I^* + \zeta_{22}\zeta_2 I^* \\
&\quad + \zeta_{33}\zeta_2 I^* + \zeta_1\zeta_{55} + \zeta_{44}\zeta_{55} + \zeta_{22}\zeta_{55} + \zeta_{33}\zeta_{55} + \zeta_2 I^*\zeta_{55} + \zeta_1\zeta_{66} \\
&\quad + \zeta_{44}\zeta_{66} + \zeta_{22}\zeta_{66} + \zeta_{33}\zeta_{66} + \zeta_2 I^*\zeta_{66} + \zeta_{55}\zeta_{66} \\
b_4 &= \zeta_1\zeta_{44}\zeta_{22} + \zeta_1\zeta_{44}\zeta_{33} + \zeta_{44}\zeta_{22}\zeta_2 I^* + \zeta_{44}\zeta_{33}\zeta_2 I^* + \zeta_{22}\zeta_{33}\zeta_2 I^* \\
&\quad + \zeta_1\zeta_{44}\zeta_{55} + \zeta_1\zeta_{22}\zeta_{55} + \zeta_{44}\zeta_{22}\zeta_{55} + \zeta_1\zeta_{33}\zeta_{55} + \zeta_{44}\zeta_{33}\zeta_{55} \\
&\quad + \zeta_{44}\zeta_2 I^*\zeta_{55} + \zeta_{22}\zeta_2 I^*\zeta_{55} + \zeta_{33}\zeta_2 I^*\zeta_{55} + \zeta_1\zeta_{44}\zeta_{66} + \zeta_1\zeta_{22}\zeta_{66} \\
&\quad + \zeta_{44}\zeta_{22}\zeta_{66} + \zeta_1\zeta_{33}\zeta_{66} + \zeta_{44}\zeta_{33}\zeta_{66} + \zeta_{44}\zeta_2 I^*\zeta_{66} + \zeta_{22}\zeta_2 I^*\zeta_{66} \\
&\quad + \zeta_{33}\zeta_2 I^*\zeta_{66} + \zeta_1\zeta_{55}\zeta_{66} + \zeta_{44}\zeta_{55}\zeta_{66} + \zeta_{22}\zeta_{55}\zeta_{66} + \zeta_{33}\zeta_{55}\zeta_{66} \\
&\quad + \zeta_2 I^*\zeta_{55}\zeta_{66} \\
b_5 &= \zeta_1\zeta_{44}\zeta_{22}\zeta_{55} + \zeta_1\zeta_{44}\zeta_{33}\zeta_{55} + \zeta_1\zeta_{44}\zeta_{22}\zeta_{66} + \zeta_1\zeta_{44}\zeta_{33}\zeta_{66} \\
&\quad + \zeta_1\zeta_{44}\zeta_{55}\zeta_{66} + \zeta_1\zeta_{22}\zeta_{55}\zeta_{66} + \zeta_{44}\zeta_{22}\zeta_{55}\zeta_{66} + \zeta_1\zeta_{33}\zeta_{55}\zeta_{66} \\
&\quad + \zeta_{44}\zeta_{33}\zeta_{55}\zeta_{66} + \zeta_2 I^*[\zeta_{44}\zeta_{22}\zeta_{33} + \zeta_{22}\zeta_{33}\zeta_{55} + \zeta_{44}\zeta_{22}\zeta_{55} \\
&\quad + \zeta_{44}\zeta_{22}\zeta_{66} + \zeta_{44}\zeta_{55}\zeta_{66} + \zeta_{22}\zeta_{55}\zeta_{66} + \zeta_{44}\zeta_{33}\zeta_{66} + \zeta_{22}\zeta_{33}\zeta_{66} \\
&\quad + \zeta_{44}\zeta_{33}\zeta_{55} + \zeta_{33}\zeta_{55}\zeta_{66}] - \zeta_3\zeta_5\zeta_{10} - \zeta_3\zeta_6\zeta_8 - \zeta_4\zeta_5\zeta_{11}] \\
b_6 &= \zeta_1\zeta_{44}\zeta_{22}\zeta_{55}\zeta_{66} + \zeta_1\zeta_{44}\zeta_{33}\zeta_{55}\zeta_{66} + \zeta_2 I^*[\zeta_{44}\zeta_{22}\zeta_{33}\zeta_{55} \\
&\quad + \zeta_{44}\zeta_{22}\zeta_{33}\zeta_{66} + \zeta_{44}\zeta_{22}\zeta_{55}\zeta_{66} + \zeta_{44}\zeta_{33}\zeta_{55}\zeta_{66} + \zeta_{22}\zeta_{33}\zeta_{55}\zeta_{66} \\
&\quad - \zeta_{44}\zeta_3\zeta_6\zeta_8 - \zeta_3\zeta_{33}\zeta_5\zeta_{10} - \zeta_3\zeta_9\zeta_6\zeta_{10} - \zeta_4\zeta_{33}\zeta_5\zeta_{11} \\
&\quad - \zeta_4\zeta_9\zeta_6\zeta_{11} - \zeta_4\zeta_5\zeta_{55}\zeta_{11} - \zeta_4\zeta_6\zeta_8\zeta_{12} - \zeta_4\zeta_5\zeta_{10}\zeta_{12} \\
&\quad - \zeta_3\zeta_6\zeta_8\zeta_{66} - \zeta_3\zeta_5\zeta_{10}\zeta_{66}]
\end{aligned}$$

$$\begin{aligned} b_7 &= \zeta_2 I^*[\zeta_{44}\zeta_{22}\zeta_{33}\zeta_{55}\zeta_{66} - \zeta_4\zeta_{33}\zeta_5\zeta_{55}\zeta_{11} - \zeta_4\zeta_9\zeta_6\zeta_{55}\zeta_{11} - \zeta_{44}\zeta_4\zeta_6\zeta_8\zeta_{12} \\ &\quad -\zeta_4\zeta_{33}\zeta_5\zeta_{10}\zeta_{12} - \zeta_4\zeta_9\zeta_6\zeta_{10}\zeta_{12} - \zeta_{44}\zeta_3\zeta_6\zeta_8\zeta_{66} - \zeta_3\zeta_{33}\zeta_5\zeta_{10}\zeta_{66} \\ &\quad -\zeta_3\zeta_9\zeta_6\zeta_{10}\zeta_{66}] \end{aligned}$$

By using Descartes rule of sign [17], we can get there are no positive real roots.

Also by Routh-Hurwitz stability criterion [5], the real parts of the complex roots are also negative if $\zeta_2 I* > 0, 1 - R_0 > 0, R_0 < 1$. Then the infection persistent steady state $(S^*, E^*, I^*, Q^*, R^*, V^*)$ is locally stable when $R_0 < 1$. □

Theorem 4.4. *The infection persistent steady state solution of (1) is globally asymptotically stable if* $R_0 > 1$.

Proof. We Consider a Volterra type Lyapunov function of the form P(S, E, I, Q, R, V) : $\{(S, E, I, Q, R, V) \in \Omega | S, E, I, Q, R, V > 0\} \to R^+$ defined as

$$\begin{aligned} P &= \Big(S - S^* - S^* ln\frac{S^*}{S}\Big) + \Big(Q - Q^* - Q^* ln\frac{Q^*}{Q}\Big) + \Big(I - I^* - I^* ln\frac{I^*}{I}\Big) \\ &\quad +\Big(R - R^* - R^* ln\frac{R^*}{R}\Big) + \Big(V - V^* - V^* ln\frac{V^*}{V}\Big) \end{aligned} \tag{11}$$

The derivative of P(S,E,I,Q,R,V) along the solutions of (11) is given by

$$\begin{aligned} \dot{P} &= \frac{(S - S^*)}{S}\frac{dS}{dt} + \frac{(E - E^*)}{E}\frac{dE}{dt} + \frac{(I - I^*)}{I}\frac{dI}{dt} + \frac{(Q - Q^*)}{Q}\frac{dQ}{dt} \\ &\quad +\frac{(R - R^*)}{R}\frac{dR}{dt} + \frac{(V - V^*)}{V}\frac{dV}{dt} \end{aligned} \tag{12}$$

From the first equation (1),

$$\begin{aligned} P &= \zeta_1 S^* + \zeta_2 S^* I^* - \zeta_3 R^* - \zeta_4 V^* \\ \zeta_{22} &= \zeta_2\frac{S^* I^*}{E^*}, \zeta_{33} = \zeta_6\frac{E^*}{I^*}, \\ \zeta_{44} &= \zeta_5\frac{E^*}{Q^*} - \zeta_9\frac{I^*}{Q^*}, \zeta_{55} = \zeta_8\frac{I^*}{R^*} + \zeta_{10}\frac{Q^*}{R^*}, \\ \zeta_{66} &= \zeta_{11}\frac{Q^*}{V^*} + \zeta_{12}\frac{R^*}{V^*} \end{aligned} \tag{13}$$

By using (1), (12) in (11) and simplifying we get

$$\begin{aligned} \dot{P} &= \frac{(S - S^*)}{S}\Big[\zeta_1(S^* - S) + \zeta_2 S(I^* - I) + \zeta_2 I(S^* - S) + \zeta_3(R - R^*) \\ &\quad +\zeta_4(V - V^*)\Big] + \zeta_1 S^* I^*\Big[\frac{SI}{S^* I^*} - \frac{E}{E^*} - \frac{E^* SI}{ES^* I^*} + 1\Big] \\ &\quad +\zeta_6 E^*\Big[\frac{E}{E^*} - \frac{I}{I^*} - \frac{I^* E}{IE^*} + 1\Big] \\ &\quad +\zeta_5 E^*\Big[\frac{E}{E^*} - \frac{Q}{Q^*} - \frac{Q^* E}{QE^*} + 1\Big] \end{aligned}$$

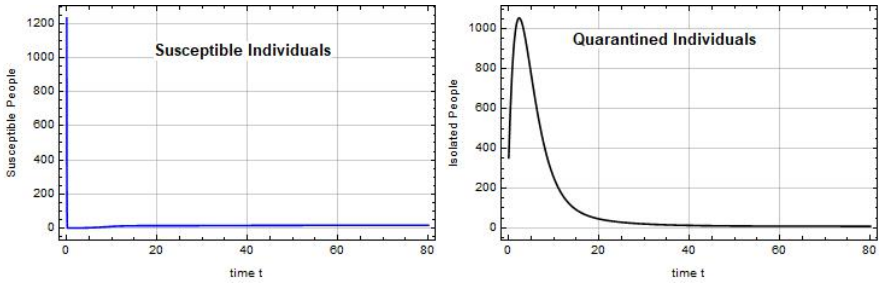
$$
\begin{aligned}
&+\zeta_9 I^*\Big[\frac{I}{I^*}-\frac{Q}{Q^*}-\frac{Q^*I}{QI^*}+1\Big]\\
&+\zeta_8 I^*\Big[\frac{I}{I^*}-\frac{R}{R^*}-\frac{R^*I}{RI^*}+1\Big]\\
&+\zeta_{10} Q^*\Big[\frac{Q}{Q^*}-\frac{R}{R^*}-\frac{R^*Q}{RQ^*}+1\Big]\\
&+\zeta_{11} Q^*\Big[\frac{Q}{Q^*}-\frac{V}{V^*}-\frac{V^*Q}{VQ^*}+1\Big]\\
&+\zeta_{12} R^*\Big[\frac{R}{R^*}-\frac{V}{V^*}-\frac{V^*R}{VR^*}+1\Big] \qquad (14)
\end{aligned}
$$

Hence, for all $S, E, I, Q, R, V > 0$, $\dot{P}(S, E, I, Q, R, V) \leq 0$ holds when $S = S^*, E = E^*, I = I^*, Q = Q^*, R = R^*, V = V^*$ and $S^*I = S^*I$.

Therefore $\{(S^*, E^*, I^*, Q^*, R^*, V^*) \in \Omega | \dot{P} \leq 0\}$ is a singleton set. Hence from the La-Salle invariance principle [21], the infection persistent steady state solutions of (1) is globally asymptotically stable when $R_0 > 1$. □

5. Numerical Simulations

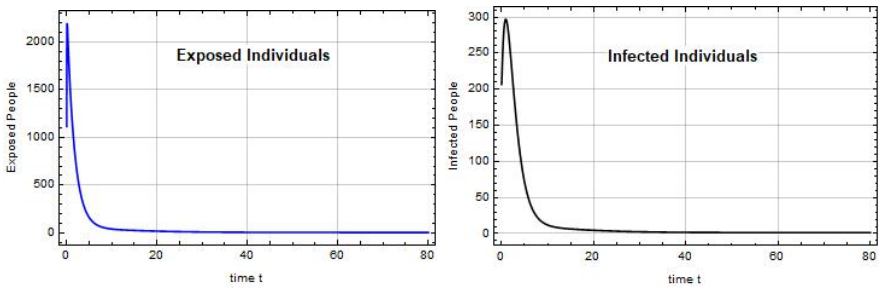
We utilised the data from the papers [9], [10] to validate our theoretical analysis. The following are the data's numerical values that correspond to the study's defined parameters: Up till March 11, 2022, 329778 positive cases and 329737 recovered individuals were discovered in Coimbatore of Tamil Nadu. On March 11, 2022, it was discovered that there were 41 recovered individuals, 207 active cases, 13 positive cases, 2083 individuals who had received vaccinations, and 51 fatalities. As a result, we used the following values to fit the data to our suggested model: S(0) = 1233, E(0) = 1114, I(0) = 207, Q(0) = 353, R(0) = 41, and V(0) = 2083. The numerical values are simulated using Mathematica. The table 1 contains a list of the variables' and parameters' values.



(a) Susceptible S(t) (b) Isolated Q(t)

FIGURE 1. Susceptible S(t) and Isolated Q(t) people against time t

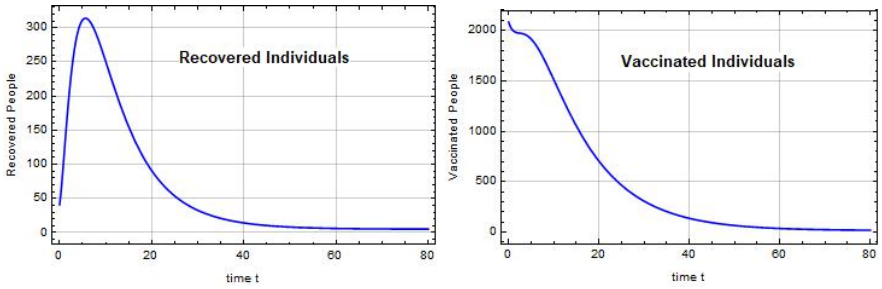
The impact of the Omicron variant can be observed in Figure 1(a,b) in the Coimbatore district of Tamil Nadu for the Susceptible Individual and the Quarantined Individual against time t.



(a) Exposed E(t) (b) Infected I(t)

FIGURE 2. Exposed E(t), Infected I(t) people against time t

Figure 2(a,b) plots the rates of host population exposure and infection against time (t) in Coimbatore. Figures 1 and 2 depict the first Omicron variant infection and recovery of individuals in Coimbatore of Tamilnadu. The figures make it clear that as the exposed population grows, so do the other compartments. After almost 15 days in our model, we observe an increased availability of susceptible individuals due to the loss of immunity. A infection free field will also exist after 30 days if there is an increase in isolated and vaccinated classes.

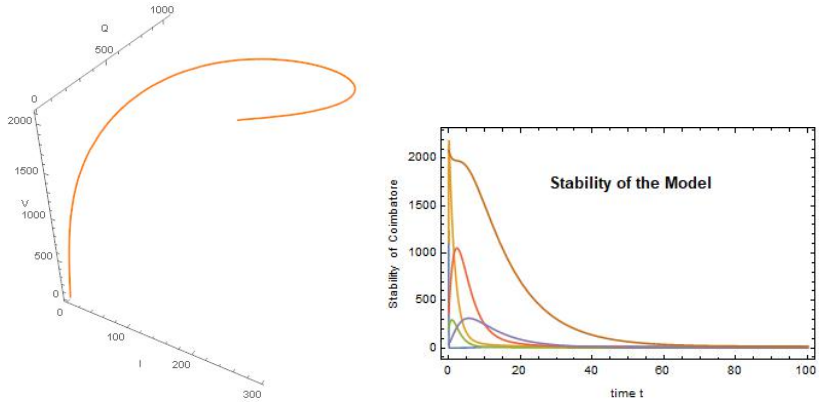


(a) Recovered R(t) (b) Vaccinated V(t)

FIGURE 3. Recovered R(t), Vaccinated V(t) people against time t

The rate of people who came back and received vaccinations has risen over time, as shown in Figure 3(a,b). Figure 3 demonstrates the Omicron variant's initial rapid spread and how, after the government heavily promoted vaccination and quarantine, the variant's spread was slowed to a safe level and people began

to recover. People were able to avoid infection at a high rate thanks to COVID-19 vaccinations.



(a) 3D of IQV (b) Stability of SEIQRV

FIGURE 4. Stability of the system against time t

The relationship between the rates of isolated, recovered, and vaccinated individuals during the COVID-19 infection period in Coimbatore, Tamil Nadu, is shown in Figure 4(a,b). Figure shows the stability of the Coimbatore district's COVID-19 mathematical model. When people received their vaccinations in accordance with government recommendations, the infection rate gradually dropped to a low level. The data shows that as of March 11 there were 13 infected patients in the Coimbatore district, based on RT PCR sample tests of 1233, with no fatalities. Figure 4 shows that the infected rate drops during a brief period of rapid spread with the reproduction number $R_0 < 1$. The system in the Coimbatore district is stable as a result.

6. Conclusions

The parameters defined from the data of Coimbatore of Tamilnadu are used in this paper to create a dynamic SEIQRV Model. The outbreak threshold for the illness in Coimbatore of Tamilnadu, where $R_0 1$, was defined by the principles of reproduction number estimated using this model.The basics of positivity and boundlessness in these models have been investigated and confirmed. There are steady-state solutions that are immune to infection and are asymptotically stable both locally and globally when $R_0 < 1$. Additionally, when $R_0 < 1$ is present, infection-present steady-state solutions are found to be locally stable, and when $R_0 > 1$ is present, infection-present steady-state solutions are discovered to be globally stable. At the extremely foremost, Coimbatore of Tamilnadu data from the current Omicron variant pandemic in India are verified. This research can be expanded in the future to cover additional non-integer-order derivative types.

Conflicts of interest : The authors declare that they have no competing interests.

Data availability : Data sharing not applicable to this article as no datasets were generated or analyzed during the current study.

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