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SQIRV MODEL FOR OMICRON VARIANT WITH TIME DELAY

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ABSTRACT. In order to examine the dynamics of the Omicron variant, this paper uses mathematical modelling and analysis of a SQIRV model, taking into account the delay in the conversion of susceptible individuals into infected individuals and infected individuals into recovered individuals. The pandemic was eventually controlled as a result of the massive delays. To assure the safety of the host population, this concept incorporates quarantine and the COVID-19 vaccine. Both local and global stability of the model are examined. It is found that the fundamental reproduction number affects both local and global stability conditions. Our findings show that asymptomatic cases caused by an affected population play an important role in increasing Omicron infection in the general population. The most recent data on the pandemic Omicron variant from Tamil Nadu, India, is verified.

Key words and phrases: Delay; Omicron; Reproduction number; Steady states; Stability.

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1. INTRODUCTION

The Omicron variant can infect people and cause symptoms similar to previous versions. The Omicron variant, also known as B.1.1.5 29 SARS-Cov-2 Variant, was less contagious than the original COVID-19 virus and the Delta variant. Omicron was widespread across several countries and remained the dominant species as of November 24, 2021. COVID-19 vaccination remains the most effective public health measure for avoiding COVID-19 and lowering the likelihood of new variants developing. This includes the initial course, booster injections, and any additional dosages that may be required. To describe how diseases spread within groups of subpopulations, mathematical models have been developed. It is clear that interpreting COVID-19 transmission dynamics depends on a large part on the time periods. In order to improve the SIqIRV model's output in this paper, the Quarantined and Vaccinated compartments are connected nonlinearly [9]. New SQIRV mathematical model is constructed after certain improvements. Many mathematical models for COVID-19 with the vaccine and quarantine compartments have been developed ([5], [7], [10], [23], [30]).

The goal of the current research is to explore the effects of the latency period by developing two mathematical models. One is an integer model that includes a class of susceptible people who have not been spreading ([1], [6], [19], [24], [25]). The second uses a delay differential equations model, which gives newly afflicted people some time before they become infectious ([27], [28], [29]). With a nonlinear relationship between the quarantine and vaccination compartments, we created the SQIRV model. When delay factors are included in the system of differential equations, the Omicron model can be mathematically modelled in a way that is reasonably accurate to the observed occurrences. By referring to the articles ([2], [8], [13], [14], [16], [21], [22], [26]), we have added the element of delay to this model. The causes of the delays include vaccinations and quarantine. According to conventional epidemiological models, the disease tends to converge on stable points if the infection rate is kept under control. With quarantine, vaccination, and the use of delaying compounds, the pandemic of the Omicron variant may almost certainly be resisted in the current Omicron condition. The modeling's delay factors and delaying strategies, however, stand alone and are unrelated to any other kinds of transmission rates. This work also examines the stability analysis of the model and the existence and uniqueness of solutions ([3], [12], [15], [18]). It is challenging to investigate the global elements of a pestilence model framework since there are no recognised numerical methods for establishing Lyapunov capabilities for epidemic models ([4], [32]). In order to validate and confirm our theoretical findings for Omicron B.1.1.529 SARS-Cov-2, computational simulations were run at the end of the inquiry.

2. MATHEMATICAL MODEL

An Omicron mathematical model based on a consistent, non linear first request construction of common differential conditions is examined (see Fig. 1). The whole population $N(t)$ is subdivided into state factor sub-populations of people who are Susceptible individuals $S(t)$, Infected individuals $I(t)$, Quarantined individuals $Q(t)$, Recovered individuals $R(t)$ and Vaccinated individuals $V(t)$. The notions that are used to denote the parameters in this research, described in table 2.1. The corresponding values are collected from the source [35].

In the model development, there are associated concerns that: (i) Vaccines lose their effectiveness over time, causing people to lose their immunity. (ii) For Omicron, the Covid-19 vaccinations are indicated. (iii) Vaccine can be given to isolated people.

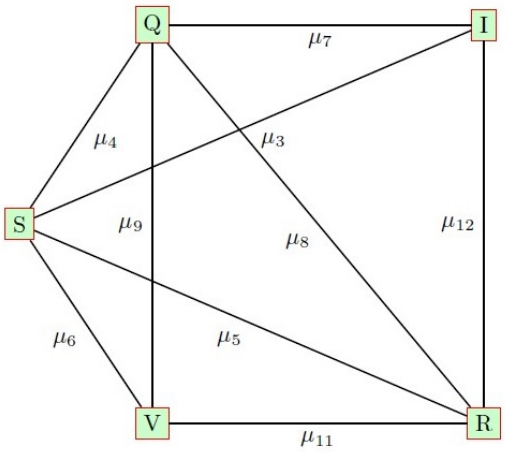

Figure 1: Network of the Model

Table 2.1: Parameters and their descriptions

Parameters	Descriptions	Values
Γ	Rate at which humans are recruited into the population	5
μ_1	The natural death rate applicable to all compartments	0.065
μ_2	Rate at which a certain fraction of susceptible individuals receives vaccination	0.0109
μ_3	Effective infectious contact rate between the susceptible and infected individual	0.0012
μ_4	The quarantine rate of the susceptible individuals	0.0107
μ_5	The rate at which the recovered compartment loses its immunities to treatment	0.0017
μ_6	The rate at which the vaccinated compartment loses its immunities to vaccination	0.0092
μ_7	The treatment rate of the infected class	0.1087
μ_8	The natural recovery rates due to quarantine	0.0146
μ_9	The contact rate between Quarantined and Vaccinated people	0.0098
μ_{10}	The death rate induced by infections of infected individuals	0.0006
μ_{11}	The rate at which recovered individual moves to vaccinated compartment	0.92
μ_{12}	The natural recovery rates transfere from infected to recovered individuals	0.045

By the assumptions made, the system of equations of the model and network is formulated as

$$\begin{aligned}
\frac{dS}{dt} &= \Gamma - (\mu_1 + \mu_2)S - \mu_3 SI + \mu_4 Q + \mu_5 R + \mu_6 V \\
\frac{dQ}{dt} &= \mu_7 I - (\mu_1 + \mu_4 + \mu_8)Q - \mu_9 QV, \\
\frac{dI}{dt} &= \mu_3 SI - (\mu_1 + \mu_7 + \mu_{10})I + \mu_{12} I, \\
\frac{dR}{dt} &= \mu_{12} I + \mu_8 Q - (\mu_1 + \mu_5 + \mu_{11})R, \\
\frac{dV}{dt} &= \mu_{11} R + \mu_2 S - (\mu_1 + \mu_6)V + \mu_9 QV
\end{aligned} \tag{2.1}$$

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

It is considered that the disease has an incubation time of the virus $\tau_1 > 0$ transferred from Susceptible period, an incubation period τ_2, and a recovered period $\tau_3 > 0$. This section of the paper is focused in constructing the dynamical model for our problem formulation. The incubation period is the delay time that passes between being susceptible and showing symptoms of the virus. The bilinear transmission incidence will be a function of $(t - \tau_1)$ and $(t - \tau_2)$. The recovery period, which will depend on $(t - \tau_3)$, is the time it takes from contracting the infection to becoming fully immune and switching to the recovered compartment. The written form of the delay differential system is

$$\begin{aligned}
\frac{dS}{dt} &= \Gamma - \mu_{21}S - \mu_3 S(t-\tau_1)I(t-\tau_2) + \mu_4 Q + \mu_5 R + \mu_6 V \\
\frac{dQ}{dt} &= \mu_7 I - \mu_{22}Q - \mu_9 QV, \\
\frac{dI}{dt} &= \mu_3 S(t-\tau_1)I(t-\tau_2) - (\mu_{23})I - \mu_{12}I(t-\tau_3), \\
\frac{dR}{dt} &= \mu_{12}I(t-\tau_3) + \mu_8 Q - \mu_{24}R, \\
\frac{dV}{dt} &= \mu_{11}R + \mu_2 S - \mu_{25}V + \mu_9 QV
\end{aligned} \tag{2.2}$$

where $\mu_{21} = \mu_1 + \mu_2$, $\mu_{22} = \mu_1 + \mu_4 + \mu_8$, $\mu_{23} = \mu_1 + \mu_7 + \mu_{10}$, $\mu_{24} = \mu_1 + \mu_5 + \mu_{11}$, and $\mu_{25} = \mu_1 + \mu_6$

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

In the system of equations, a susceptible individual is assumed to interact with an infective individual and does not move to the infected compartment until after certain time "incubation period" as of the case of Omicron. The incubation period τ_1 is only when moving from the susceptible compartment to the infected compartment. τ_2 is the infective period of the infected individual when moving from Susceptible individual to infected individual. τ_3 is the recovery period for an infected individual moving from infected compartment to the recovery compartment. Our modification of the SI_qIRV model considers the delay constants, while a detailed description can be obtained by using a system of cities connected by traffic streams.

3. EXISTENCE AND UNIQUENESS OF SOLUTIONS OF THE MODEL

Theorem 3.1. *Let Ω denote a region $|t - t_0| \leq y, |x - x_0| \leq z, x = (x_1, x_2, \ldots, x_n), x_0 = (x_{10}, x_{12}, \ldots, x_{n0})$. Also, suppose the Lipschitzian condition $|f(t, x_1) - f(t, x_2)| \leq c|x_1 - x_2|$ is satisfied by $f(t, x)$, whenever (t, x_1) and (t, x_2) is in Ω, where c is positive. A unique continuous vector solution $x(t)$ of the system in the interval $t - t_0 \leq \delta$ exists, such that $\delta > 0$.*

Proof. Let Ω denote the region $0 \leq \alpha \leq R$, we want to show that the partial derivatives of are continuous and bounded in Ω.

Let $P_1 = \frac{dS}{dt}, P_2 = \frac{dQ}{dt}, P_3 = \frac{dI}{dt}, P_4 = \frac{dR}{dt}, P_5 = \frac{dV}{dt}$

Now $|\frac{\partial P_1}{\partial S}| = |-\mu_1 + \mu_3 I + \mu_2| < \infty, |\frac{\partial P_1}{\partial Q}| = |-\mu_4| < \infty, |\frac{\partial P_1}{\partial I}| = |-\mu_3 S| < \infty,$
$|\frac{\partial P_1}{\partial R}| = |\mu_5| < \infty, |\frac{\partial P_1}{\partial V}| = |\mu_6| < \infty,$

Similarly the partial derivatives of (2.1) exist for all variables, which are finite and bounded. Hence, (2.1) has a unique solution. ∎

Theorem 3.2. *Positivity of the model. If S(0), Q(0), I(0), R(0), V(0) are nonnegative, then S(t), Q(t), I(t), R(t), V(t) are also nonnegative for all $t > 0$.*

Proof. The sum of all the equations of the system (2.1) yield

$$\frac{dN}{dt} = \Gamma - (S + Q + I + R + V)\mu_1 - \mu_{10}I, \tag{3.1}$$

such that in the absence of infections we have $\dot{N} = \Gamma - N\mu_1$. Integrating we get, $\frac{\Gamma}{\mu_1} + Ce^{-\mu_1 t}$ where C is constant.

$$N(t) = \lim_{t\to\infty}\left(\frac{\Gamma}{\mu_1} + Ce^{-\mu_1 t}\right) = \frac{\Gamma}{\mu_1}$$
$$\implies \lim_{t\to\infty} supN(t) \leq \frac{\Gamma}{\mu_1}$$

then it follows the nonnegativity for all time t>0. ∎

The model under consideration in this paper has two steady-state solutions. The model system (1) is made static, i.e. the time-independent solutions are obtained. The steady-state solution in the absence of infections i.e., $I = 0$ is given by

$$\begin{aligned} E^0 &= (S, Q, I, R, V) \\ &= \Big(\frac{\Gamma(\mu_1 + \mu_6)}{\mu_1(\mu_1 + \mu_2 + \mu_6)}, 0, 0, 0, \frac{\Gamma\mu_2}{\mu_1(\mu_1 + \mu_2 + \mu_6)}\Big) \end{aligned} \tag{3.2}$$

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

$$\begin{aligned} E^* &= (S^*, Q^*, I^*, R^*, V^*) \\ &= \Big(\frac{\mu_{33}}{\mu_3}, \frac{\mu_7 I^*}{\mu_{22} + \mu_9 V^*}, \frac{\mu_3\Gamma - \mu_{21}\mu_{33} + \mu_6 D}{\mu_{33} - \mu_4 A - \mu_5 B - \mu_6 C^*}, \\ &\quad \frac{\mu_8 Q^* + \mu_{12} I^*}{\mu_1 + \mu_5 + \mu_{11}}, \frac{\mu_2\mu_{11}R^* + \mu_2\mu_{23}}{\mu_2(\mu_1 + \mu_6 - \mu_9 Q^*)}\Big) \end{aligned} \tag{3.3}$$

where $\mu_{33} = \mu_1 + \mu_7 + \mu_{10} + \mu_{12}$, $A = \frac{\mu_7}{\mu_{22}+\mu_9 V^*}$, $B = \frac{\mu_{12}}{\mu_1+\mu_5+\mu_{11}} + \frac{\mu_7\mu_8}{(\mu_{22}+\mu_9 V^*)(\mu_1+\mu_5+\mu_{11})}$, $C = \frac{\mu_{11}B}{\mu_1+\mu_6-\mu_9 Q^*}$.

The fundamental reproduction number R_0 is calculated by using the next generation operator matrix as follows ([11], [31]):

Theorem 3.3. *Define $Xs = \{x = 0 | x_i, i = 1, 2, 3, \dots\}$. In order to compute for R_0, we distinguished new infections from all other changes in the population.Let $F_i(x)$ be the rate of new clinical manifestations of disease symptoms in compartment i, also, let V_i^+ be the rate at which individuals move into compartment i through other means and V_i^- be the rate at which individuals move out of the compartment i. Then $\dot{x}_i = f_i(x) = F_i(x) - V_i(x), i = 1, 2, 3, \dots$ and $V_i(x) = V_i^- - V_i^+$, such that F is a non negative matrix and V is a non singular matrix.*

Proof.

$$F = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \mu_7 & 0 & 0 \\ 0 & 0 & \mu_3 S & 0 & 0 \\ 0 & 0 & \mu_{12} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$V = \begin{pmatrix} \mu_1+\mu_2 & \mu_4 & 0 & \mu_5 & \mu_6 \\ 0 & \mu_1+\mu_4+\mu_7+\mu_8 & 0 & 0 & 0 \\ 0 & 0 & \mu_1+\mu_{10}+\mu_{12}+\mu_7 & 0 & 0 \\ 0 & \mu_8 & 0 & \mu_1+\mu_5+\mu_{11} & 0 \\ \mu_2 & 0 & 0 & 0 & \mu_1+\mu_6 \end{pmatrix}$$

$$V^{-1} = \begin{pmatrix} V_{11} & V_{12} & 0 & V_{14} & V_{15} \\ 0 & V_{22} & 0 & 0 & 0 \\ 0 & 0 & V_{33} & 0 & 0 \\ 0 & V_{42} & 0 & V_{44} & 0 \\ V_{51} & V_{52} & 0 & V_{54} & V_{55} \end{pmatrix}$$

where
$V_{11} = \frac{\mu_1+\mu_6}{\mu_1(\mu_1+\mu_2+\mu_6)}, V_{12} = -\frac{(\mu_1+\mu_6)(\mu_4\mu_1+\mu_4\mu_5+\mu_5\mu_8)}{(\mu_1+\mu_4+\mu_7+\mu_8)(\mu_1+\mu_5+\mu_{11})\mu_1(\mu_1+\mu_2+\mu_6)},$
$V_{14} = -\frac{\mu_5(\mu_1+\mu_6)}{\mu_1(\mu_1+\mu_2+\mu_6)(\mu_1+\mu_5+\mu_{11})}, V_{15} = -\frac{\mu_6}{\mu_1(\mu_1+\mu_2+\mu_6)},$
$V_{22} = \frac{1}{(\mu_1+\mu_4+\mu_7+\mu_8)}, V_{33} = \frac{1}{(\mu_1+\mu_{10}+\mu_{12}+\mu_7)},$
$V_{42} = \frac{\mu_2\mu_6\mu_8}{(\mu_1+\mu_4+\mu_7+\mu_8)(\mu_1+\mu_5+\mu_{11})\mu_1(\mu_1+\mu_2+\mu_6)}, V_{44} = \frac{1}{\mu_1+\mu_5+\mu_{11}},$
$V_{51} = \frac{\mu_2}{\mu_1(\mu_1+\mu_2+\mu_6)}, V_{52} = \frac{\mu_2(\mu_1\mu_4+\mu_4\mu_5+\mu_5\mu_8)}{(\mu_7+\mu_4+\mu_8+\mu_1)(\mu_1+\mu_5+\mu_{11})\mu_1(\mu_1+\mu_2+\mu_6)},$
$V_{54} = \frac{\mu_5\mu_2}{(\mu_1+\mu_5+\mu_{11})\mu_1(\mu_1+\mu_2+\mu_6)}, V_{55} = \frac{\mu_1+\mu_2}{\mu_1(\mu_1+\mu_2+\mu_6)}.$

Therefore, R_0 is the largest eigenvalue of the spectral radius given by

$$R_0(FV^{-1}) = \mu_3\Big(\frac{\Gamma(\mu_1+\mu_6)}{\mu_1(\mu_1+\mu_2+\mu_6)}\Big)\Big(\frac{1}{(\mu_1+\mu_{10}+\mu_{12}+\mu_7)}\Big) \tag{3.4}$$

∎

4. LOCAL AND GLOBAL STABILITY ANALYSIS OF THE MODEL

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

Proof. . The Jacobian matrix of (2.1) at infection free steady state solution is given by

$$J(E^0) = \begin{pmatrix} J_{11} & \mu_4 & -\mu_3 S & \mu_5 & \mu_6 \\ 0 & J_{22} & \mu_7 & 0 & 0 \\ 0 & 0 & J_{33} & 0 & 0 \\ 0 & \mu_8 & \mu_{12} & J_{44} & 0 \\ \mu_2 & \mu_9 V & 0 & \mu_{11} & J_{55} \end{pmatrix}$$

where $J_{11} = -\mu_1-\mu_2, J_{22} = -\mu_1-\mu_4-\mu_8-\mu_9 V, J_{33} = \mu_3 S-(\mu_1+\mu_7+\mu_{10}+\mu_{12}),$
$J_{44} = -\mu_1-\mu_5-\mu_{11}, J_{55} = -\mu_1-\mu_6.$

Then from the Jacobian matrix, the eigen values are $-(\mu_1+\mu_4+\mu_7+\mu_8),$
$-(\mu_1+\mu_4+\mu_{11}), \mu_3 S-(\mu_1+\mu_7+\mu_{10}+\mu_{12}),\ and\ \frac{1}{2}\Big(-(\mu_1+\mu_2)-(\mu_1+\mu_6)$
$\pm\sqrt{(\mu_1+\mu_2)^2+4\mu_2\mu_6-\mu_1\mu_2(\mu_1+\mu_6)+(\mu_1+\mu_6)^2}\Big)$

Now, the System (2.1) is stable iff $\mu_3 S-(\mu_1+\mu_7+\mu_{10}+\mu_{12})<0$, and
$\mu_1(\mu_1+\mu_2+\mu_6)>1.$
$\iff \frac{\mu_3 S}{\mu_1+\mu_7+\mu_{10}+\mu_{12}}<1,\ and\ \mu_1(\mu_1+\mu_2+\mu_6)>1$
$\iff \mu_3\Big(\frac{\Gamma(\mu_1+\mu_6)}{\mu_1(\mu_1+\mu_2+\mu_6)}\Big)\Big(\frac{1}{(\mu_1+\mu_{10}+\mu_{12}+\mu_7)}\Big)<1$
Then clearly the infection free steady state E^0 (3.2) is locally asymptotically stable if $R_0<1$. ∎

Theorem 4.2. *The infection free steady state solutions E^0 is globally asymptotically stable if $R_0 < 1$.*

Proof. We consider the Lyapunov function candidate $G(S, Q, I, R, V) : \mathbb{R}^5 \to \mathbb{R}^+$ defined as $G(S, Q, I, R, V) = \tau I$.

Differentiating the above function with respect to time, we get

$$\begin{aligned} \dot{G} &= \tau \dot{I} \\ &= \tau\Big(\mu_3 S - (\mu_1 + \mu_7 + \mu_{10} + \mu_{12})\Big) I \\ &\leq \tau\Big(\mu_3 \big(\frac{\Gamma(\mu_1 + \mu_6)}{(\mu_1(\mu_1 + \mu_2 + \mu_6)}\big)\big(\frac{1}{(\mu_1 + \mu_{10} + \mu_{12} + \mu_7)}\big) - 1\Big) I \end{aligned} \tag{4.1}$$

Taking $\tau = \frac{1}{\mu_1+\mu_{10}+\mu_{12}+\mu_7}$, then $\dot{G} = (R_0 - 1)I \implies (R_0 - 1)I \leq 0$

$\dot{G} = 0$, when I=0, then $S \to \frac{\Gamma(\mu_1+\mu_6)}{\mu_1(\mu_1+\mu_2+\mu_6)}, N \to \frac{\Gamma}{\mu_1}$ as $t \to \infty$.

Therefore $\{(S, Q, I, R, V) \in \Omega | \dot{G} \leq 0\}$ is the singleton set E^0. Hence from the La-Salle invariance principle [20], when $R_0 < 1$, the global stability of infection free steady state is globally asymptotically stable. ∎

Theorem 4.3. *The infection persistent steady state solution E^* of (2.1) is locally asymptotically stable if $R_0 > 1$.*

Proof. The Jacobian matrix of (2.1) at infection persistent steady state solutions is given by

$$J(E^0) = \begin{pmatrix} H_{11} & \mu_4 & -\mu_3 S^* & \mu_5 & \mu_6 \\ 0 & H_{22} & \mu_7 & 0 & -\mu_9 Q^* \\ \mu_3 I^* & 0 & H_{33} & 0 & 0 \\ 0 & \mu_8 & \mu_{12} & H_{44} & 0 \\ \mu_2 & \mu_9 V^* & 0 & \mu_{11} & H_{55} \end{pmatrix}$$

where $H_{11} = -\mu_1 - \mu_2 - \mu_3 I^*, H_{22} = -\mu_1 - \mu_4 - \mu_7 - \mu_8 - \mu_9 V^*$,
$H_{33} = \mu_3 S^* - (\mu_1 + \mu_7 + \mu_{10} + \mu_{12}), H_{44} = -\mu_1 - \mu_5 - \mu_{11}, H_{55} = -\mu_1 - \mu_6 + \mu_9 Q^*$.

The characteristic polynomial is $\lambda^5 + a_1\lambda^4 + a_2\lambda^3 + a_3\lambda^2 + a_4\lambda + a_5$
where

$$\begin{aligned} a_1 &= \mu_{21} + \mu_3 I^* - \mu_9 Q^* + \mu_{22} + \mu_9 V^* + \mu_{24} + \mu_{25} \\ a_2 &= (\mu_{21} + \mu_3 I^* - \mu_9 Q^*)(\mu_{22} + \mu_9 V^* + \mu_{24}) + (\mu_{21} + \mu_3 I^*)(\mu_{25} - \mu_9 Q^*) \\ &\quad -\mu_2\mu_6 + \mu_9 Q^* \mu_9 V^* \\ a_3 &= (\mu_{21} + \mu_3 I^* - \mu_9 Q^*)(\mu_{22} + \mu_9 V^*)\mu_{24} - \mu_3 I^*(\mu_4\mu_7 + \mu_3 S^* \mu_9 Q^* + \mu_5\mu_{12} \\ &\quad +\mu_9 Q^* \mu_{24}) - [\mu_9 Q^*((\mu_{21} + \mu_3 I^*)(\mu_{22} + \mu_9 V^*) + \mu_{21}\mu_{24}) + \mu_2\mu_6((\mu_{22} + \mu_9 V^*) \\ &\quad +\mu_{24})] + (\mu_{21} + \mu_3 I^*)((\mu_{22} + \mu_9 V^*)\mu_{25} + \mu_{24}\mu_{25} + \mu_9 Q^* \mu_9 V^*) + \mu_3 I^* \mu_3 S^* \\ &\quad (\mu_{22} + \mu_9 V^* + \mu_{24} + \mu_{25}) + \mu_9 Q^*(\mu_2\mu_4 + \mu_8\mu_{11}) + \mu_{24}((\mu_{22} + \mu_9 V^*)\mu_{25} \\ &\quad +\mu_9 Q^* \mu_9 V^*) \\ a_4 &= (\mu_{21} + \mu_3 I^*)(\mu_9 Q^*(\mu_8\mu_{11} + \mu_{24}\mu_9 V^*) + (\mu_{22} + \mu_9 V^*)\mu_{24}(\mu_{25} - \mu_9 Q^*)) \\ &\quad -\mu_3 I^*\big(\mu_3 S^* \mu_9 Q^*(\mu_{22} + \mu_9 V^* + \mu_{24}) + \mu_4\mu_7(\mu_{24} + \mu_{25}) + \mu_5\mu_{12}(\mu_{22} \\ &\quad +\mu_9 V^* + \mu_{25}) + \mu_5(\mu_7\mu_8 + \mu_6\mu_9 V^*) + \mu_6\mu_{12}\mu_{11}\big) + \mu_4\mu_9 Q^*(\mu_5\mu_7 + \mu_2\mu_{24}) \\ &\quad +\mu_5\mu_9 Q^*(\mu_3 I^*\mu_{12} + \mu_2\mu_8) \end{aligned}$$

$$\begin{aligned} a_5 &= \mu_3 I^*([\mu_5\mu_9 Q^*(\mu_7\mu_8 + \mu_{12}(\mu_{22} + \mu_9 V^*)) + \mu_4\mu_9 Q^*\mu_{12}\mu_{11}] + (\mu_8\mu_9 V^* \\ &\quad +\mu_{24}\mu_9 V^*)(\mu_3 S^*\mu_9 Q^* - \mu_6\mu_7) + \mu_{24}(\mu_9 Q^* + \mu_{25})(\mu_4\mu_7 - \mu_3 S^*(\mu_{22} \\ &\quad +\mu_9 V^*)) - [\mu_{12}(\mu_{22} + \mu_9 V^*)(\mu_6 u + \mu_5\mu_{25}) + \mu_5(\mu_7\mu_8\mu_{25} + \mu_9 Q^*\mu_{12}\mu_{11})] \end{aligned}$$

Using the Descartes rule of sign [17] and Routh-Hurwitz method, the quartic polynomial has unique positive real roots, if and only if $a_1 > 0, a_2 > 0, a_3 > 0, a_4 > 0$ and $a_5 < 0$. That is $\mu_{21} + \mu_3 I^* - \mu_9 Q^* > 0$. Then the infection persistent steady state $(S^*, Q^*, I^*, R^*, V^*)$ (3.3) is locally asymptotically stable when $R_0 > 1$. ∎

Theorem 4.4. *The infection persistent steady state solution of* (2.1) *is globally asymptotically stable if* $R_0 > 1$.

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

$$\begin{aligned} \Upsilon &= \Big(S - S^* - S^* ln\frac{S^*}{S}\Big) + \Big(Q - Q^* - Q^* ln\frac{Q^*}{Q}\Big) + \Big(I - I^* - I^* ln\frac{I^*}{I}\Big) \\ &\quad +\Big(R - R^* - R^* ln\frac{R^*}{R}\Big) + \Big(V - V^* - V^* ln\frac{V^*}{V}\Big) \end{aligned} \tag{4.2}$$

The derivative of Υ(S,Q,I,R,V) along the solutions of (4.2) is given by

$$\dot{\Upsilon} = \frac{(S - S^*)}{S^*}\frac{dS}{dt} + \frac{(Q - Q^*)}{Q}\frac{dQ}{dt} + \frac{(I - I^*)}{I}\frac{dI}{dt} + \frac{(R - R^*)}{R}\frac{dR}{dt} + \frac{(V - V^*)}{V}\frac{dV}{dt} \tag{4.3}$$

From the first equation (2.1),

$$\begin{aligned} \Gamma &= \mu_{21}S^* + \mu_3 S^* I^* - \mu_4 Q^* - \mu_5 R^* - \mu_6 V^* \\ \mu_{22} &= \mu_7\frac{I^*}{Q^*} - \mu_9 V^*, \mu_{23} = \mu_3 S^* - \mu_{12}\frac{R^*}{I^*}, \\ \mu_{24} &= \mu_{12}\frac{I^*}{R^*} + \mu_8\frac{Q^*}{R^*}, \mu_{25} = \mu_{11}\frac{R^*}{V^*} + \mu_2\frac{S^*}{R^*} + \mu_9\frac{Q^*}{V^*} \end{aligned} \tag{4.4}$$

By using (2.1), (4.4) in (4.2) and simplifying we get

$$\begin{aligned} \dot{\Upsilon} &= \frac{(S - S^*)}{S}\Big[\mu_{21}(S^* - S) + \mu_3 S(I^* - I) + \mu_3 I(S^* - S) + \mu_4(Q - Q^*) \\ &\quad +\mu_5(R - R^*) + \mu_6(V - V^*)\Big] + \mu_7(Q - Q^*)\Big[\frac{I}{I^*} - \frac{Q}{Q^*} - \frac{Q^* I}{QI^*} + 1\Big] \\ &\quad +\mu_3(I - I^*)(S - S^*) + \mu_{12}(I - I^*)\Big[\frac{R}{R^*} - \frac{I}{I^*} - \frac{I^* R}{IR^*} + 1\Big] \\ &\quad +\mu_{12}(R - R^*)\Big[\frac{I}{I^*} - \frac{R}{R^*} - \frac{R^* I}{RI^*} + 1\Big] \\ &\quad +\mu_8(R - R^*)\Big[\frac{Q}{Q^*} - \frac{R}{R^*} - \frac{R^* Q}{RQ^*} + 1\Big] \\ &\quad +\mu_{11}(V - V^*)\Big[\frac{R}{R^*} - \frac{V}{V^*} - \frac{V^* R}{VR^*} + 1\Big] \\ &\quad +\mu_2(V - V^*)\Big[\frac{S}{S^*} - \frac{V}{V^*} - \frac{V^* S}{SR^*} + 1\Big] \end{aligned} \tag{4.5}$$

Hence, for all $S, Q, I, R, V > 0$, $\dot{\Upsilon}(S, Q, I, R, V) \leq 0$ holds when $S = S^*, Q = Q^*, I = I^*, R = R^* \; and \; V = V^*$. Therefore $\{(S^*, Q^*, I^*, R^*, V^*) \in \Omega | \dot{\Upsilon} \leq 0\}$ is the singleton set E^*. Hence from the La-Salle invariance principle [20], the infection persistent steady state solutions of (2.1) is globally asymptotically stable when $R_0 > 1$. ∎

5. NUMERICAL ANALYSIS

On December 15th, Tamil Nadu reported the first case of the Omicron strain of SARS-CoV-2 by a visitor from another country. For this paper, we used data from Tamilnadu, India ([33]). Just three weeks after the first confirmed Omicron case was recorded, Tamil Nadu was infected with the extremely infectious and quickly spreading variant of SARS-CoV-2. The number of daily cases started to increase on December 29, when 739 people tested positive. They rapidly grew to over 10,000 on January 8. After another 38 days, there were 36,000 cases. The daily cases, on the other hand, went from 1,000 to 7,000 in just 7 days. According to a statement made public by the Tamil Nadu public health department, 18.4% of the samples sequenced in the state from January to March 2022 included the Omicron BA.2 subvariation. Tamilnadu achieves a death rate of zero on March 11. The state of Tamilnadu obtains a safe situation against the spread of Omicron viruses on March 31st without any fatalities.Total number of positive cases, recovered cases and deaths as on 31st march 2022 are 3452825, 3414494 and 38025 respectively in Tamilnadu ([34],[35],[36]). The initial conditions are S(0) = 30095, Q(0) = 322, I(0) = 35, R(0) = 51, V(0) = 42846. Mathematica and Matlab are used to calculate the numerical solution. The values of the parameters are listed in the Table 2.1.

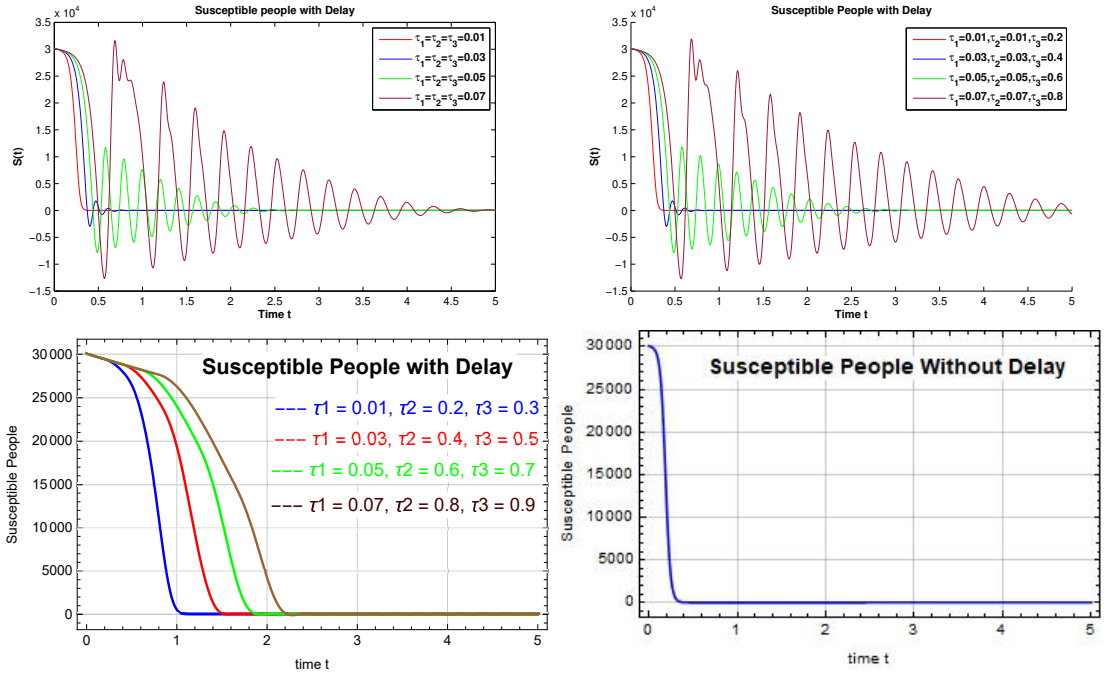

Figure 2: Susceptible people S(t) against time t

Remark 5.1. Figure 2 depicts the Susceptible individual against time t with different delays (τ_1, τ_2, τ_3) among them and without delay in the overall condition of Tamilnadu. The number of susceptible people varies over time with varied time lags and approaches stability at a specific moment.

Remark 5.2. The Quarantined People of the Host of Human Population against the Time t in the State of Tamilnadu are shown in Figure 3. The Omicron virus spreads less when infected people are quarantined. The number of isolates in this instance varies with the time lag and reaches equilibrium at a specific point.

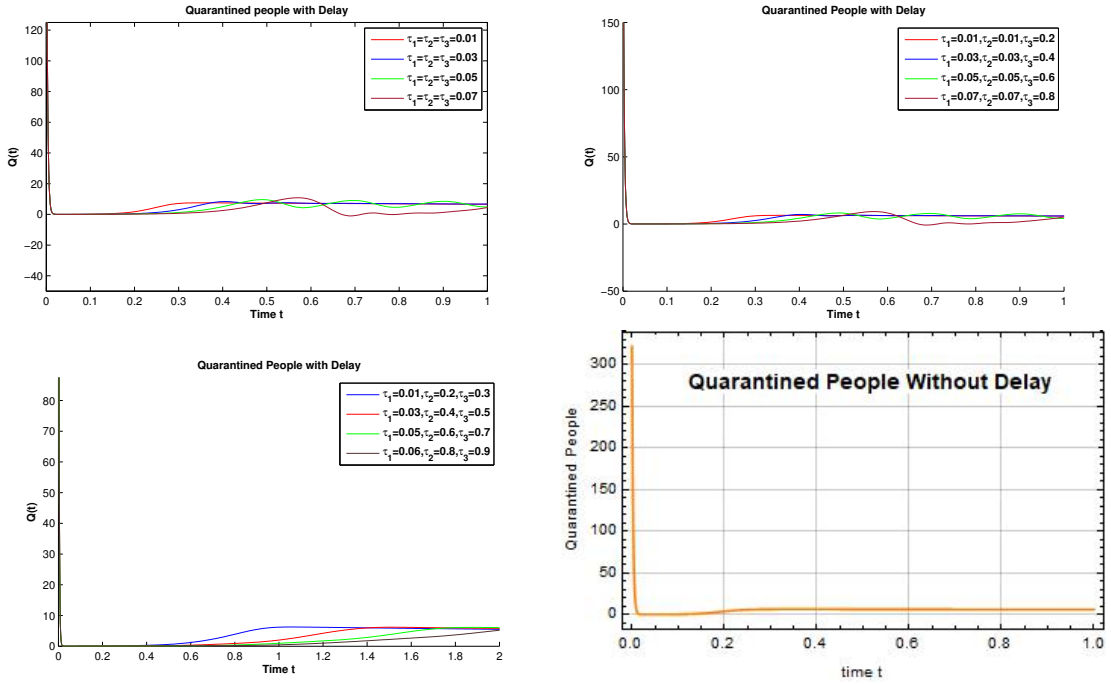

Figure 3: Quarantined people Q(t) against time t

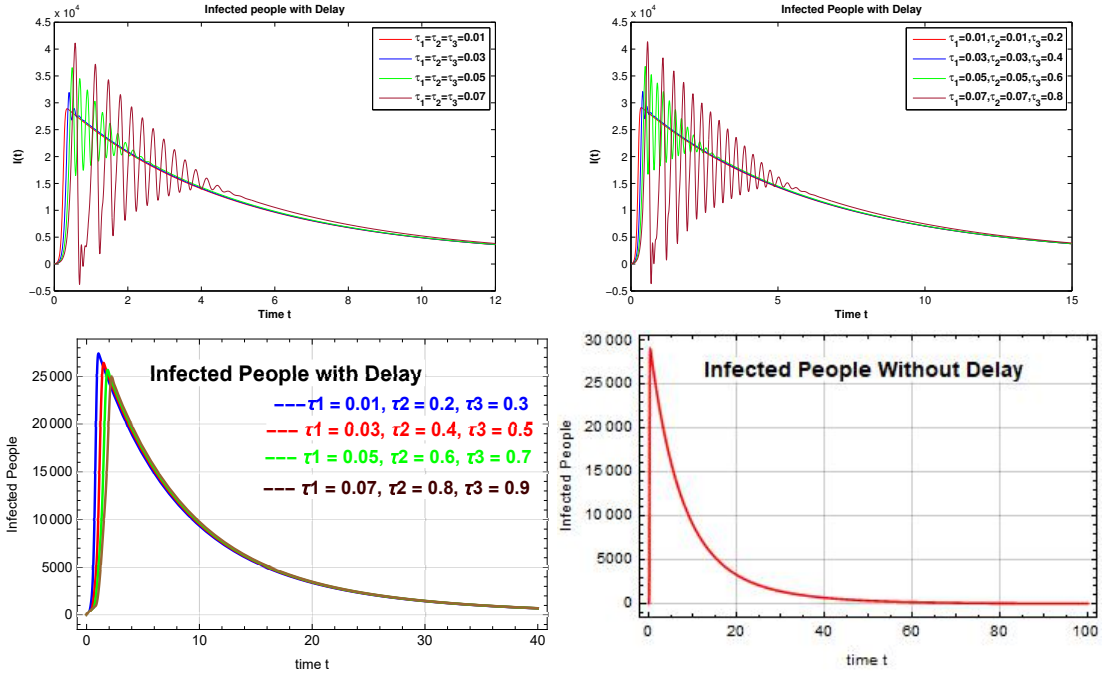

Figure 4: Infected People I(t) against time t

Remark 5.3. The various victim stages are illustrated in relation to the various time delays in Figure 4. Some districts experience a significant incidence of disease among the population from December 25 to March 11 of 2022, which is known as the Omicron period.

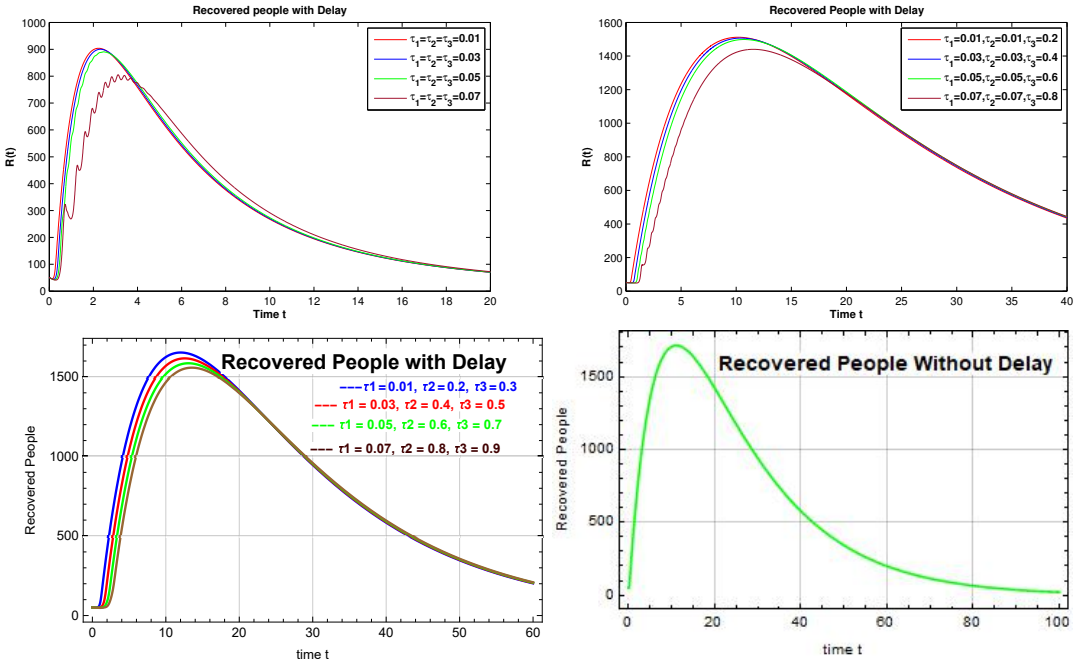

Figure 5: Recovered people R(t) against time t

Remark 5.4. According to Figure 5, the number of recoveries increases exponentially as the government increases the number of people receiving quarantine and vaccine, until stabilising at some point. It discusses the frequency of infected, quarantined, and vaccinated individuals during Omicron's recovery period in the Tamil Nadu state.

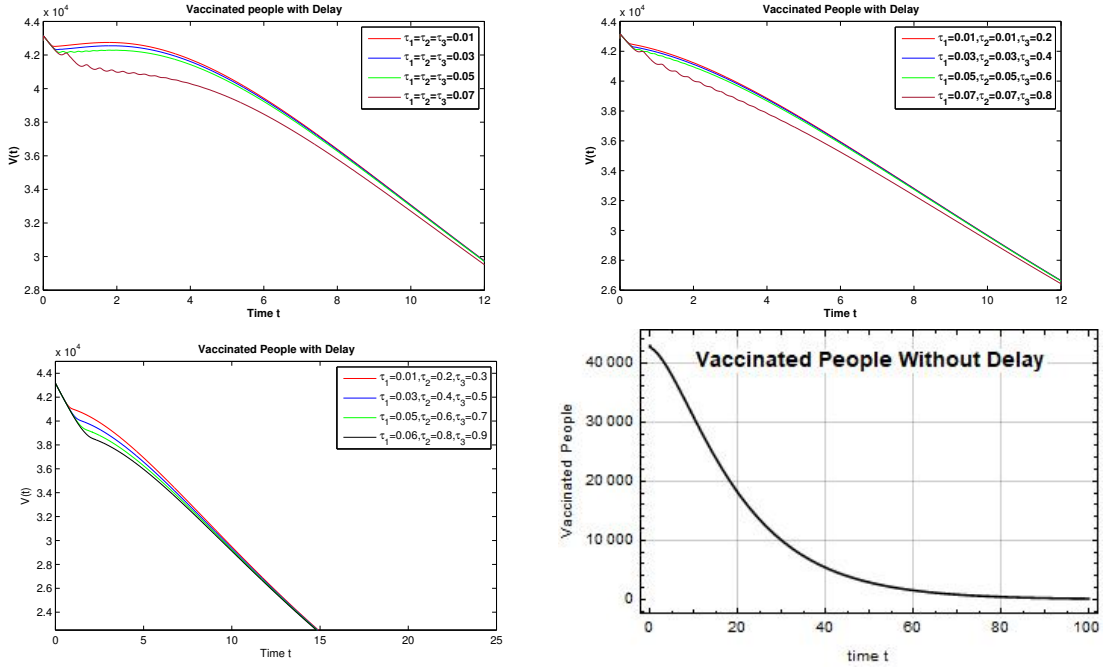

Figure 6: Vaccinated People V(t) against time t

Remark 5.5. Vaccination is the single most significant factor in preventing the spread of viruses. Figure 6 shows that as the population of vaccination recipients increases, the spread of the virus is stopped, and over time, the connection between the two becomes stable.

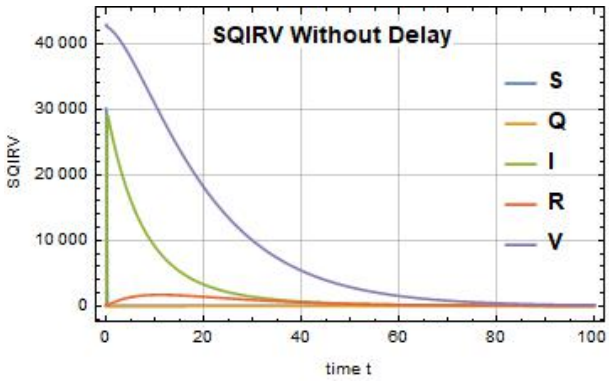

Figure 7: S(t),Q(t),I(t),R(t),V(t) against time t without delay

Remark 5.6. Figure 7 represents the stability of the model SQIRV without delay. When people received their vaccinations in accordance with government instructions, the infection rate gradually dropped to a low level.

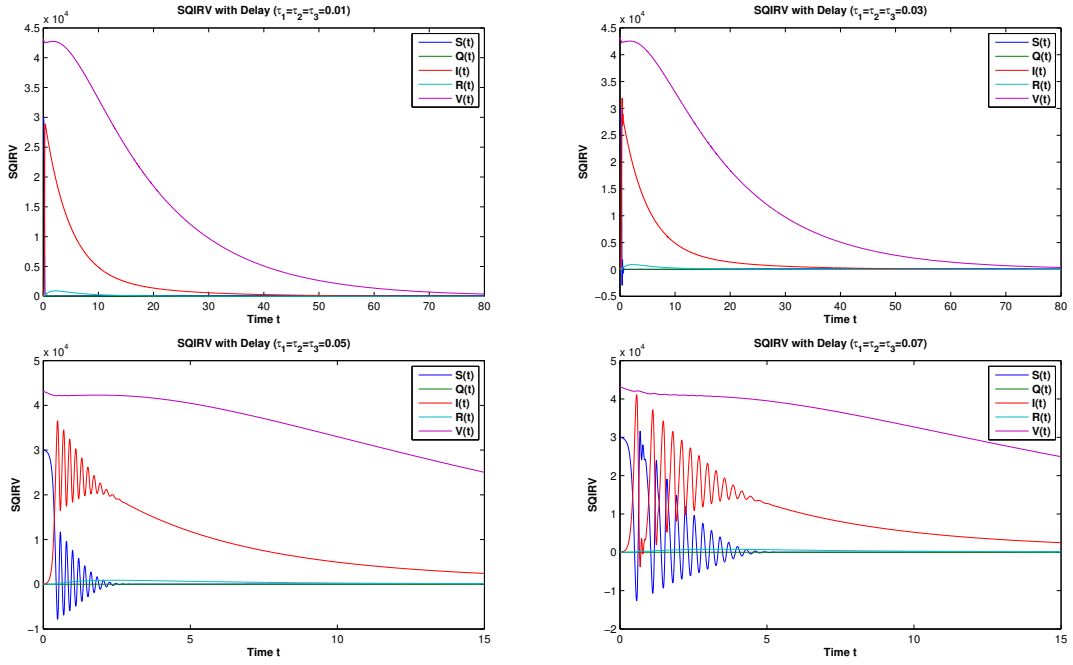

Figure 8: Stability condition of the Tamilnadu against time t with the delay relation $\tau_1 = \tau_2 = \tau_3$

Remark 5.7. The stability of the model with different delays can be seen in Figure 8, where $\tau_1 = \tau_2 = \tau_3$. The system demonstrates the correspondence of stability of this model without delay for the small values of equal time delays (0.01, 0.03).

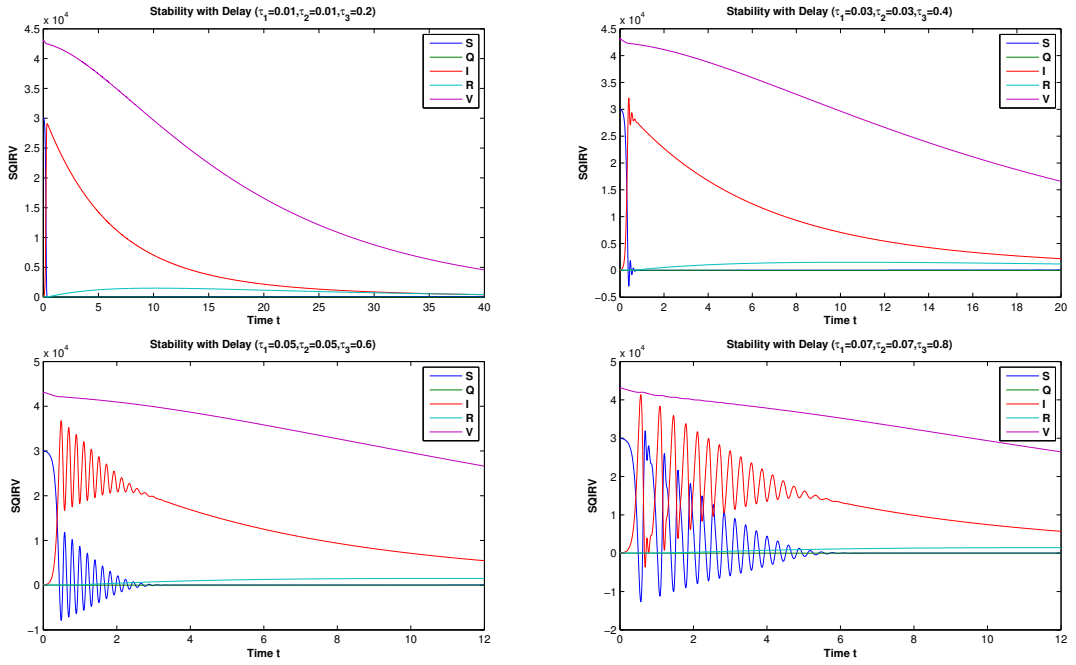

Figure 9: Stability condition of the Tamilnadu against time t with the delay relation $\tau_1 = \tau_2 \neq \tau_3$

Remark 5.8. According to Figure 9, the system reaches stability much like the integer model does for small delays of $\tau_1 = \tau_2 \neq \tau_3$. The system deviates from the integer model and achieves model stability for larger values, such as $\tau_1 = \tau_2 = 0.05, 0.07$ and $\tau_3 = 0.6, 0.8$.

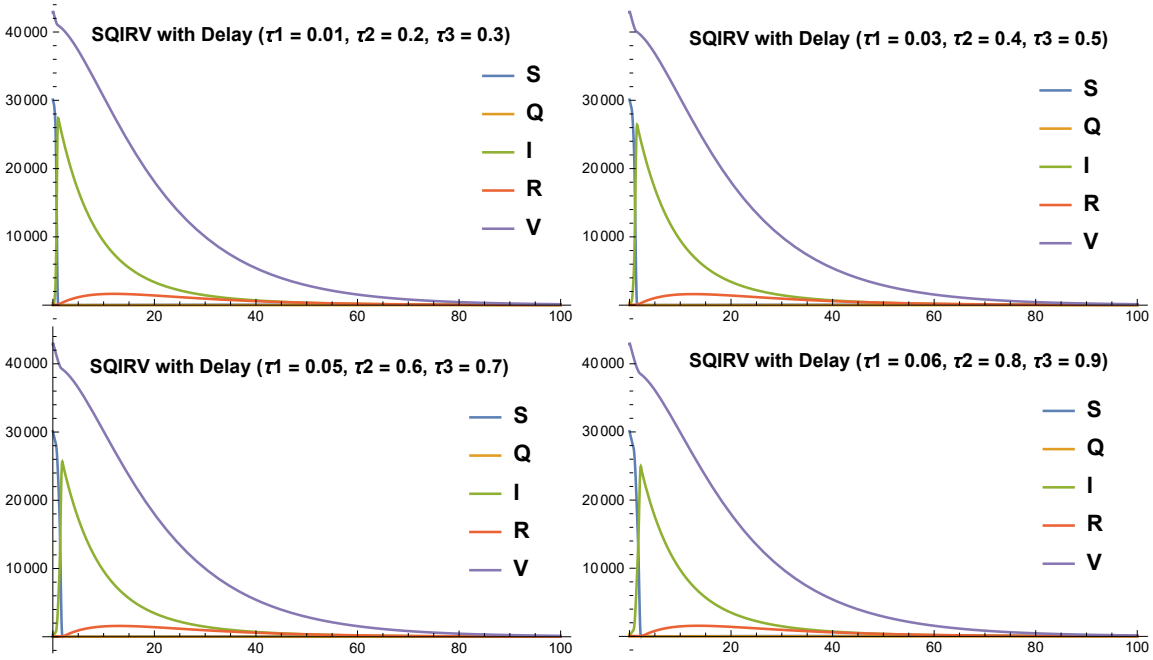

Figure 10: Stability condition of the Tamilnadu against time t with the delay relation $\tau_1 \neq \tau_2 \neq \tau_3$

Remark 5.9. The stability for varied delays $\tau_1 \neq \tau_2 \neq \tau_3$ is shown in Figure 10. As with the integer model, the system stabilises. The delay system described in (3.1) provides the best prediction for all lag values for the various delay values.

All Figures show how persons in Tamilnadu were infected and confirmed with the Omicron variant in the beginning and recovered by the end of March 31st, 2022. It is obvious from Figure 3 that once the infected population increases, all other compartments increase as well. The figures show that when the Omicron variant was first discovered, its spread was rapid, and when the government implemented quarantine and vaccination at a high rate, the variant's spread was reduced to a safe level.

6. CONCLUSIONS

We arrive at the conclusion from the data that the host community will be protected from the Omicron variation if the number of separated, recovered, and vaccinated individuals rises. We also discovered that the second wave of SARS Cov-2 Omicron variant is less likely to spread if the intercessions are properly adhered to. According to Table 2.1, as of March 31, the number of infected people in Tamilnadu districts has decreased to low level with no death based on RT PCR sample tests. Covid-19 vaccinations helped people avoid infection with the SARS CoV-2 Omicron variant. The data acquired from Tamil Nadu together with our SQIRV mathematical model, suggest that the Omicron variant infection has stabilised after few months. This model outperforms other mathematical models by taking into account the nonlinear force of quarantine, vaccine, infection, and care, as well as the right inclusion of valuable parameters. The principles of reproduction number calculated with this model are an outbreak threshold that determined whether or not the disease would go further in Tamilnadu where $R_0 < 1$. These model's fundamentals of positivity and boundedness have been examined and validated. There are infection-free steady-state solutions that are asymptotically stable locally and globally when $R_0 < 1$. Also When $R_0 > 1$ is present, infection-present steady-state solutions that are stable locally and globally are discovered. The delay model, which is discussed in this research provided better recommendations for how to prevent the host population in the event of a pandemic. Finally, the SQIRV Model is used to validate the most recent Omicron variant pandemic data from the Indian state of Tamilnadu.

DECLARATIONS

Conflict of interest/Competing interests. The authors declare that they have no competing interests.

Availability of data and materials. Data sharing not applicable to this article as no datasets were generated or analyzed during the current study.

Authors' contributions. All authors contributed equally to this work. The authors declare that they have read and approved the final manuscript.

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