



A Study on Corona Virus Transmission Dynamics: Stability and Hopf Bifurcation Analysis of the SIR Model with Time Delay

¹N.Ramesh, ²B. Ravindra Reddy

¹Department of Mathematics, AVN Institute of Engineering & Technology, Hyderabad, India.

²Department of Mathematics, JNTUCEH, Kukatpally, Hyderabad, India.

(Received: 02 September 2023)

Revised: 14 October

Accepted: 07 November

KEYWORDS

SIR model, stability, Hopf bifurcation, COVID-19, basic reproduction number.

ABSTRACT:

In this research, we use the SIR (Susceptible, Infectious, and Recovered) model framework to mathematically simulate the spread of Corona virus Disease (COVID-19) in India. The effect of delay is accounted for by include a Hopf bifurcation parameter, and the research is limited to two states in India: Telangana and Andhra Pradesh. Local asymptotic stability of both the disease-free and epidemic equilibria is investigated. The ODE model indicates that the fundamental reproduction number R_0 is tightly influenced by the dynamics. In circumstances where R_0 is smaller than 1, the disease-free equilibrium is judged stable, leading to the extinction of the illness. When R_0 is greater than 1, on the other hand, a special endemic equilibrium develops. The purpose of this article is to provide an initial value estimate for the COVID-19 pandemic in India using actual data. This particular SIR model for COVID-19 is one among several pandemic models currently under examination in India. Furthermore, the COVID-19 SIR model presented in this paper is applicable with or without time delay. Theoretical findings are substantiated through numerical experiments to enhance comprehension of the model's dynamics.

1. Introduction

The field of epidemiology has become more important in modern times. The SIR model, created in the early 20th century by Ronald Ross, William Hamer, and others, is based on a set of three coupled non-linear ordinary differential equations. Kermack and McKendrick did some of the first theoretical work on infectious illness models between 1927 and 1933 [1]. On March 11, 2020, the World Health Organization (WHO) declared a pandemic on account of the new Coronavirus Disease-2019 (COVID-19), which emerged at the end of 2019 in Wuhan, China and rapidly spread across continents. On January 30, 2020 [2], The Thrissur district of Kerala was the site of the first confirmed case of the pandemic in India. Following the work of G. Ranjith Kumar, K. Lakshmi Narayan, and B. Ravindra Reddy [3], this investigation examines the stability and Hopf bifurcation analysis of the SIR epidemic model with time delay. Other relevant research includes dynamics of a SIR Epidemic Model with a saturated incidence rate under stochastic influence [4], mathematical modeling of infectious diseases [5], a

time delay epidemic model for COVID-19 [6], modeling the spread of COVID-19 [7], transmission dynamics of the COVID-19 outbreak and government intervention effectiveness [8], estimation of the final size of the COVID-19 epidemic [9], stability analysis of an epidemic model with infected immigrants and optimal vaccination [10], dynamics of a SI model with time delay and diffusion [11], compartmental models in epidemiology [12], epidemiological modeling of online social network dynamics [13], perspectives on the basic reproductive ratio [14], computation of threshold conditions for epidemiological models and global stability of the disease-free equilibrium [15], a geometric approach to global stability problems [16], global stability of SEIR models in epidemiology [17], evaluation of mathematical models for the COVID-19 outbreak [18], a brief history of R_0 and its calculation [19], study of the simple SIR epidemic model [20], and a study on COVID-19 transmission dynamics with stability analysis of the SEIR model and Hopf bifurcation for the effect of time delay [21]. The dynamics of the COVID-19 epidemic in India are the



major subject of this article. Telangana and Andhra Pradesh are modeled mathematically because of the large differences in their epidemic patterns. The situation in these states is analyzed using the SIR model, and the findings are compared. Parameters are calculated from real-time data gathered every 15 days from April to September of 2020, and these estimates are utilized in MATLAB simulations.

2. Mathematical Model

To better understand and foretell the spread of an epidemic, we detail the mechanistic transmission model below. This approach depends on segmenting the population into three well defined subsets, each representing a different infectiousness condition. As a result, people are divided into three categories: "susceptible," "infected," and "recovering."

The foundational assumption of the model is that the overall population size remains constant over time, signifying that there is no fluctuation in the total population size. "In other words,

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

So, the SIR model, including births and deaths, can be defined as

$$\begin{aligned} \frac{dS}{dt} &= A - \beta SI - \alpha S \\ \frac{dI}{dt} &= \beta SI - \gamma I - \alpha I \\ \frac{dR}{dt} &= \gamma I - \alpha R \end{aligned} \quad (1)$$

With initial conditions $S(0) \geq 0$, $I(0) \geq 0$ and $R(0) \geq 0$

Where $S(t)$ and $I(t)$ represent the number of susceptible and infected populations, respectively.

β - represents the rate of transmission,

α - represents the death Coefficient of I,

A - represents the birth rate of people,

γ - represents the recovery rate.

3. Equilibrium Analysis

There are two equilibria for system (1).

- (i) COVID-19 Disease-Free Equilibrium

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

- (ii) COVID-19 Endemic Equilibrium

$$E_1 = \left(\frac{\gamma + \alpha}{\beta}, \frac{A\beta - \alpha(\alpha + \gamma)}{\beta(\alpha + \gamma)} \right)$$

The basic reproduction number for the model is

$$R_0 = \frac{A\beta}{\alpha(\alpha + \gamma)} \quad (2)$$

4. Local Stability Analysis

In this section, we shall investigate the stability analysis of disease-free equilibrium E_0 and epidemic equilibrium E_1 . The Jacobian matrix of system (1)

$$J = \begin{bmatrix} -\beta I - \alpha & -\beta S \\ \beta I & \beta S - \gamma - \alpha \end{bmatrix} \quad (3)$$

4.1 Stability of COVID-19 disease-free equilibrium

Theorem: The disease-free equilibrium is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

Proof: For the disease-free equilibrium at the point E_0 , the system (3) reduces to

$$J = \begin{bmatrix} -\alpha - \lambda & -\beta S \\ 0 & -\beta S - \gamma - \alpha - \lambda \end{bmatrix} \quad (4)$$

With characteristic equation

$$(-\alpha - \lambda)(\beta S - \gamma - \alpha - \lambda) = 0$$

The characteristic roots are given by

$$\lambda_1 = -\alpha, \lambda_2 = \frac{\beta A}{\alpha}(\gamma + \alpha)$$

then the system is stable if $\frac{\beta A}{\alpha} < (\gamma + \alpha)$ i.e., $R_0 < 1$.

Hence the given system is stable if $R_0 < 1$ and unstable if $R_0 > 1$.

4.2 Stability of COVID-19 Endemic Equilibrium

For the Endemic Equilibrium E_1 the system (3) reduces to

$$J = \begin{bmatrix} \beta I - \alpha & -\beta S \\ \beta I & 0 \end{bmatrix} \quad (5)$$

With characteristic equation

$$\lambda^2 + P_1\lambda + P_2 = 0$$

$$\text{Where } P_1 = (-\beta I - \alpha), P_2 = \beta^2 SI$$

$$T_r(J) = -\beta I - \alpha$$



$$= -(\beta I + \alpha) < 0 \quad \text{when } I^* > 0, R_0 > 1$$

Det (J) = $\beta^2 SI > 0$ $R_0 > 1$ is unstable.

5. Delayed SIR model

This part of the paper is devoted to constructing the dynamical model for our proposed problem. The disease is assumed to have an incubation period of the virus $\tau > 0$. The incubation period represents the delay time from exposure to the development of symptoms of the virus. The bilinear transmission incidence will be a function of $(t - \tau)$. The process dynamics model can be described as

$$\begin{aligned} \frac{dS}{dt} &= A - \beta S(t - \tau) I(t - \tau) - \alpha S \\ \frac{dI}{dt} &= \beta S(t - \tau) I(t - \tau) - \gamma I - \alpha I \end{aligned} \quad (6)$$

6. LOCAL STABILITY ANALYSIS

In this section, we shall investigate the stability analysis of disease-free equilibrium E_0 and endemic equilibrium E_1

The Jacobian matrix of system (6)

$$J = \begin{bmatrix} -\beta I e^{-\lambda\tau} - \alpha & -\beta S e^{-\lambda\tau} \\ -\beta I e^{-\lambda\tau} & \beta S e^{-\lambda\tau} - \gamma - \alpha - \lambda \end{bmatrix} \quad (7)$$

6.1 Stability of COVID-19 disease-free equilibrium

Theorem: The disease-free equilibrium is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$

Proof: For the disease-free equilibrium at the point E_0 , the system (7) reduces to

$$J = \begin{bmatrix} -\alpha - \lambda & -\beta S e^{-\lambda\tau} \\ 0 & \beta S e^{-\lambda\tau} - \gamma - \alpha - \lambda \end{bmatrix} \quad (8)$$

With characteristic equation

$$(\alpha - \lambda) (\beta S e^{-\lambda\tau} - \gamma - \alpha) - \lambda = 0$$

The characteristic roots are given by

$$\lambda_1 = -\alpha, \lambda_2 = \beta S e^{-\lambda\tau} - \gamma - \alpha$$

Then the system is stable if $\frac{\beta A}{\alpha} e^{-\lambda\tau} < (\gamma + \alpha)$

$$\frac{\beta A}{\alpha} < (\gamma + \alpha)$$

$$\frac{\beta A}{\alpha(\alpha + \gamma)} < 1$$

$$R_0 < 1$$

Hence the given system is stable if $R_0 < 1$ and unstable if $R_0 > 1$.

6.2 Stability of COVID-19 Endemic Equilibrium

In COVID-19 infection, the effects of time delay τ is a bifurcation parameter and it goes through a stationary values. The COVID-19 equilibrium occurs through direct stability and Hopf bifurcation. For the endemic equilibrium E_1 the system (7) reduce to

$$J = \begin{bmatrix} -\beta I e^{-\lambda\tau} - \alpha - \lambda & -\beta S e^{-\lambda\tau} \\ \beta I e^{-\lambda\tau} & \beta S e^{-\lambda\tau} - \gamma - \alpha - \lambda \end{bmatrix} \quad (9)$$

The characteristic equation of (9) for the endemic equilibrium is

$$\lambda^2 + x_1 \lambda + x_2 + e^{-\lambda\tau} (x_3 \lambda + x_4) = 0 \quad (10)$$

Where $x_1 = 2\alpha + \gamma$, $x_2 = \gamma\alpha + \alpha^2$

$$x_3 = \beta I - \beta S, x_4 = \gamma\beta I - \alpha\beta I - \beta S\alpha$$

we need to find the necessary and sufficient condition for every root of the characteristic equation (10)

Case 1: If $\tau = 0$ equation (10) becomes

$$\lambda^2 + (x_1 + x_3) \lambda + (x_3 + x_4) = 0 \quad (11)$$

By Routh-Hurwitz criteria, all roots of (11) are real and negative, or complex conjugate with the negative real part of

$$x_1 + x_3 > 0 \text{ \& } x_2 + x_4 > 0$$

Hence, the system (6) without delay is locally asymptotically stable when $R_0 > 1$.

Case 2: If $\tau > 0$

put $\lambda = \omega i$ in (10), we get

$$(\omega^2 + x_2 + x_4 \cos \omega\tau + \omega x_3 \sin \omega\tau) + i(x_1 \omega + x_1 \omega \cos \omega\tau - x_4 \sin \omega\tau) = 0 \quad (12)$$

Separating the real and imagine

$$\begin{aligned} \omega^2 - x_2 &= x_3 \omega \sin \omega\tau + x_4 \cos \omega\tau \\ -x_1 \omega &= -x_4 \sin \omega\tau + x_3 \omega \cos \omega\tau \end{aligned} \quad (13)$$

Which is equivalent to

$$\omega^4 + \omega^2(x_1^2 - 2x_2 - x_3^2) + (x_2^2 - x_4^2) = 0 \quad (14)$$

Thus if $x_1^2 - 2x_2 - x_3^2 > 0$, $x_2^2 - x_4^2 > 0$

Then, there is no ω such that $i\omega$ is an Eigen value of the characteristic equation (10)



i.e., λ will never be a purely imaginary root of equation (10). Thus, the real part of all the Eigen value of equation (10) is negative for all $\tau \geq 0$.

Hence, the endemic equilibrium is asymptotically stable for all τ .

If the following conditions hold:

- (i) $R_0 > 1$
- (ii) $(x_1 + x_2) > 0, (x_3 + x_4) > 0$
- (iii) $x_1^2 - 2x_2 - x_3^2 > 0, x_2^2 - x_4^2 > 0$ (15)

If any one of $x_1^2 - 2x_2 - x_3^2, x_2^2 - x_4^2$ is negative. There is a unique positive ω_0 satisfying (14). That is, there is a single pair of purely imaginary roots $\pm \omega i$ to (10)

From (13) τ_k corresponding to ω_0 can be obtained

$$\Delta = \begin{vmatrix} x_3 \omega & x_4 \\ -x_4 & x_3 \omega \end{vmatrix} = x_3^2 \omega^2 + x_4^2$$

$$\cos \omega_0 \tau_k = \frac{1}{\Delta} \begin{vmatrix} \omega^2 - x_2 & x_3 \\ -x_1 \omega & -x_4 \end{vmatrix}$$

$$= \frac{1}{\Delta} (x_2 x_4 - \omega^2 x_4 + x_1 x_3 \omega^2)$$

$$\tau_k = \frac{1}{\omega_0} \cos^{-1} \left[\frac{(x_4 - x_1 x_3) \omega^2 - x_2 x_4}{x_3^2 \omega^2 + x_4^2} \right] + \frac{2n\pi}{\omega_0} \quad (16)$$

For $\tau = 0$, E_1 is stable, it remains stable for

$$\tau < \tau_0 \text{ if } \left| \frac{d R_e(\lambda)}{dt} \right|_{\lambda=i\omega_0} > 0$$

Differentiating (10) with respect τ , we get

$$\frac{d\lambda}{d\tau} [2\lambda + x_1 + x_3 e^{-\lambda\tau} - \tau e^{-\lambda\tau} (x_3 \lambda + x_4)] = \lambda e^{-\lambda\tau} (x_3 \lambda + x_4) \quad (17)$$

$$\left[\frac{d\lambda}{d\tau} \right]^{-1} = \left[\frac{2\lambda + x_1 + x_3 e^{-\lambda\tau} - \tau e^{-\lambda\tau} (x_3 \lambda + x_4)}{\lambda (x_3 \lambda + x_4) e^{-\lambda\tau}} \right]$$

$$\left[\frac{d\lambda}{d\tau} \right]^{-1} = \frac{2\lambda + x_1}{\lambda (x_3 \lambda + x_4) e^{-\lambda\tau}} + \frac{x_3}{\lambda (x_3 \lambda + x_4)} - \frac{\tau}{\lambda}$$

$$= \frac{(2\lambda + x_1) e^{-\lambda\tau}}{\lambda (x_3 \lambda + x_4)} + \frac{x_3}{\lambda (x_3 \lambda + x_4)} - \frac{\tau}{\lambda}$$

$$\left[\frac{d\lambda}{d\tau} \right]^{-1} = \frac{2\lambda + x_1}{-\lambda (\lambda^2 + x_1 \lambda + x_2)} + \frac{x_3}{\lambda (x_3 \lambda + x_4)} - \frac{\tau}{\lambda}$$

$$\left| \frac{d R_e(\lambda)}{dt} \right|_{\lambda=i\omega_0} = \left| R_e \left(\frac{d\lambda}{d\tau} \right) \right|_{\lambda=i\omega_0}$$

$$= R_e \left[\frac{2i\omega_0 + x_1}{-i\omega_0(-\omega_0^2 + x_1 i \omega_0 + x_2)} + \frac{x_3}{i\omega_0(x_3 i\omega_0 + x_4)} - \frac{\tau}{i\omega_0} \right]$$

$$= R_e \left[\frac{1}{\omega_0} \left(\frac{2i\omega_0 + x_1}{x_1 \omega_0 + (\omega_0^2 - x_2)i} + \frac{x_3}{(-x_3 \omega_0 + x_4 i)} - i\tau \right) \right]$$

$$= \frac{1}{\omega_0} \left[\frac{2\omega_0(\omega_0^2 - x_2) + x_1^2 \omega_0}{x_1^2 \omega_0 + (\omega_0^2 - x_2)^2} - \frac{x_3^2}{(x_3^2 \omega_0^2 + x_4^2)} \right]$$

$$= \frac{2\omega_0^2 + (x_1^2 - 2x_2 - x_3^2)}{(x_3^2 \omega_0^2 + x_4^2)}$$

Under the condition $x_1^2 - 2x_2 - x_3^2 > 0$

$$\text{We have } \left| \frac{d R_e(\lambda)}{dt} \right|_{\lambda=i\omega_0} > 0$$

Therefore, the transversality condition holds, and Hopf bifurcation occurs at $\omega = \omega_0, \tau = \tau_0$

7. Numerical Simulation

Simulation for the dynamical system of the classical SIR model (1) and the time delayed SIR model (6) is compared to real data collected by the official website of PRS (Parliament and State) Legislative Research [18]. COVID-19 data was collected every 15 days from April to September for the year 2020. The COVID-19 has unspecified parameter values for the real-time data of the SIR model. The pandemic in India should be determined by these model values. COVID-19 data are therefore important in developing and validating the non-linear ODE. Let us consider the parameters $A = 90, \alpha = 0.000001, \beta = 0.000002, \gamma = 0.00001$.

In that event (14) has no positive roots, at that point, COVID-19 infectious equilibrium is locally asymptotic stable. On the off chance that $R_0 = 16363636.3671$, at that point the COVID-19 disease equilibrium $E_1 = (5.5, 8181817.682)$ has positive real roots and others have negative real roots. It is not hard to evaluate the bifurcation stationary value to be $\tau = 0$.

In figure1, we compared COVID-19 real-infected cases and estimation values without time delay, when $\tau = 0$ in Telangana state.

In figure 2, we compared COVID-19 real-infected cases and estimation values without time delay, when $\tau = 0$ in Andhra Pradesh state.

In figure 3, we compared COVID-19 real-infected cases and estimation values without time delay, when $\tau = 0$ of Telangana and Andhra Pradesh states.

In figure 4, we compared COVID-19 real-infected cases and estimation cases with time delay, when $\tau = 0.2$ of Telangana and Andhra Pradesh states.



In figure 5, we compared COVID-19 real-infected cases and estimation cases with time delay, when $\tau = 0.9$ of Telangana and Andhra Pradesh states.

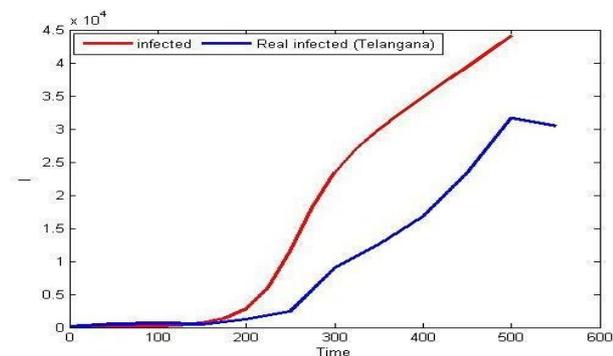


Figure 1. the time series of the system (6) is asymptotic stable when $\tau = 0$ and the real-time data of Telangana with the parameter values $A = 90$, $\alpha = 0.000001$, $\beta = 0.000002$, $\gamma = 0.00001$.

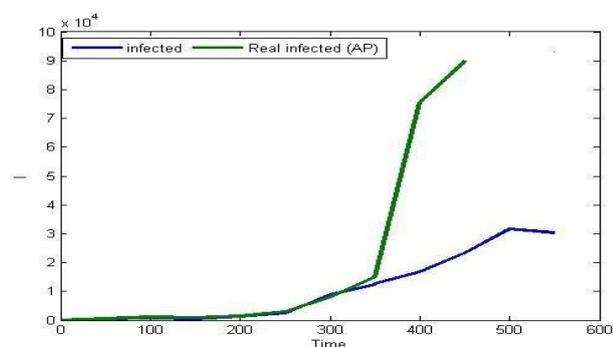


Figure 2. the time series of the system (6) is asymptotic stable when $\tau = 0$ and the real-time data of Andhra Pradesh with the parameter values $A = 90$, $\alpha = 0.000001$, $\beta = 0.000002$, $\gamma = 0.00001$.

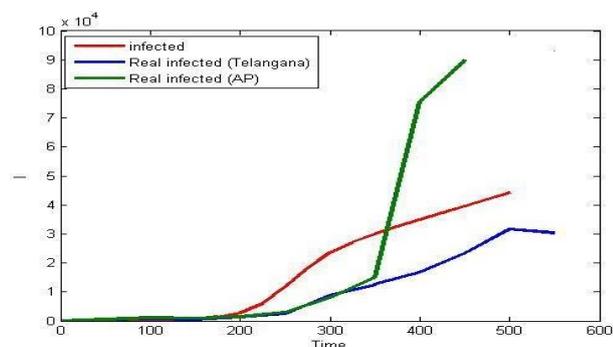


Figure 3, the time series of the system (6) is asymptotic stable when $\tau = 0$ and the real-time data of both Telangana and Andhra Pradesh with the parameter values $A = 90$, $\alpha = 0.000001$, $\beta = 0.000002$, $\gamma = 0.00001$.

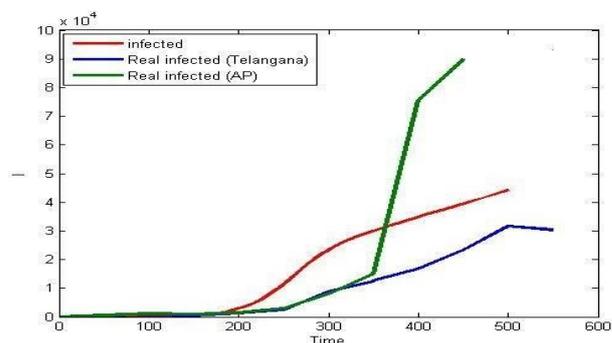


Figure 4, the time series of the system (6) is asymptotic stable when $\tau = 0.2$ and the real-time data of both Telangana and Andhra Pradesh with the parameter values $A = 90$, $\alpha = 0.000001$, $\beta = 0.000002$, $\gamma = 0.00001$.

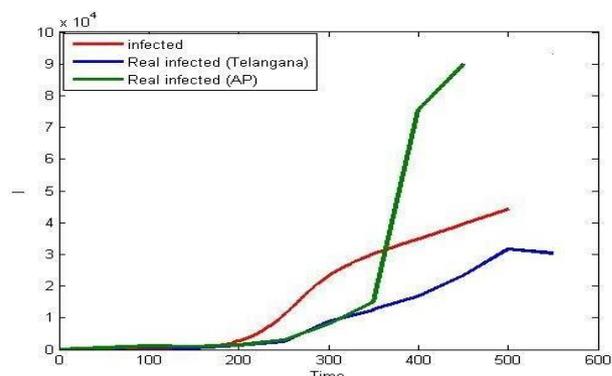


Figure: 5, the time series of the system (6) asymptotic stable when $\tau = 0.9$ and real time data of both Telangana and Andhra Pradesh with the parameter values $A = 90$, $\alpha = 0.000001$, $\beta = 0.000002$, $\gamma = 0.00001$.

8. Conclusion

In this manuscript, we have examined an SIR model for COVID-19 infection that incorporates a time delay. We analyze the model's global dynamic behavior and determine the system's threshold value, R_0 . Asymptotically stable is the equilibrium E_0 , where no diseases exist, where R_0 is smaller than 1. The stability of the resulting linearized system is guaranteed by the absence of real positive roots in equation (6). When $\tau = 0$, the polynomial equation (15) has a single real positive root, suggesting that the equilibrium of infection with COVID-19 is stable. Conversely, when $\tau = 0$, the equilibrium solution becomes unstable, leading to Hopf bifurcation. Our theoretical findings are further supported by numerical simulations. From Figure -3, we observed that the Andhra Pradesh state estimation



values are nearly equal to the real infected cases. In figures 4 and 5 we observed different functional responses and added new compartments of $\tau = 0.2$ and $\tau = 0.9$ in both states.

References

1. H. S Rodrigues, Application of SIR epidemiological model: new trends. *arXiv preprint* (2016) *arXiv:1611.02565*.
2. J.Mackolil, B. Mahanthesh, Mathematical Modelling of Coronavirus disease (COVID-19) Outbreak in India using Logistic Growth and SIR Models. Research Square; 2020. DOI: 10.21203/rs.3.rs-32142/v1.
3. G.Ranjith Kumar, K.Lakshmi Narayan and B.Ravindra Reddy, Stability and Hopf bifurcation analysis of SIR epidemic model with time delay.
4. G.Ranjith Kumar, K.Lakshmi Narayan and B.Ravindra Reddy, Dynamics of an SIR Epidemic Model With a Saturated Incidence Rate Under Stochastic Influence.
5. H.W.Hethcote, The mathematics of infectious diseases *SIAM Review*, 42, (2000) 599–653. <https://doi.org/10.1137/S0036144500371907>
6. M.Maleewong, Time Delay Epidemic Model for COVID-19 (2020). <https://doi.org/10.1101/2020.05.23.20111500>
7. B.Ivorra, et al.: Mathematical modelling of the spread of the Coronavirus Disease 2019 (COVID-19) taking into account the undetected infections. The case of China, *Communications in Nonlinear Science and Numerical Simulation*, Volume 88, (2020),105303, ISSN 1007-5704, <https://doi.org/10.1016/j.cnsns.2020.105303>.
8. Y.Fang, Y.Nie & M.Penny, Transmission dynamics of the COVID-19 outbreak and effectiveness of government interventions: A data-driven analysis. *Journal of medical virology*. (2020). <https://doi.org/10.1002/jmv.25750>
9. M.Batista, Estimation of the Final Size of the Corona Virus Epidemic by the SIR Model <https://doi.org/10.1101/2020.02.16.20023606>
10. M.Sridevi and B.Ravindra Reddy, Stability Analysis of an Epidemic Model with infected Immigrants and Optimal Vaccination.
11. M.Sridevi and B.Ravindra Reddy, Dynamics of an SI Model with time delay and Diffusion.
12. F.Brasseur, Compartmental models in epidemiology, in *Mathematical Epidemiology*, vol. 1945, Berlin: Springer, 19-79,2008.
13. J.Cannarella & J.A.Spechler, Epidemiological modeling of online social network dynamics. (2014). *arXiv preprint arXiv:1401.4208*.
14. J.R.Heffernan, R.J.Smith and L.M.Wahl, Perspective on the Basic Reproductive Ratio, *J.R.Soc.Interface*, 2: 281-293,2005 <https://doi.org/10.1098/rsif.2005.0042>
15. J.C Kamgang and G.Sallet, Computation of threshold conditions for epidemiological models and global stability of the disease-free equilibrium (DFE). *Mathematical Biosciences*, Volume 213, Issue 1,2008, Pages 1-12,ISSN 0025-5564, <https://doi.org/10.1016/j.mbs.2008.02.005>.
16. Y. Li Michael and J.S Muldowney, A geometric approach to global stability problems. <https://doi.org/10.1137/S0036141094266449>
17. J.S.Muldowney, Y. Li Michael , M.Y., and P. van den Driessche, Global stability of SEIR models in epidemiology. *Mathematical Biosciences*, Volume 125, Issue 2, 1995, Pages 155-164, ISSN 0025-5564, [https://doi.org/10.1016/0025-5564\(95\)92756-5](https://doi.org/10.1016/0025-5564(95)92756-5).
18. N.Wang, et al.An Evaluation of Mathematical Models for the Outbreak of COVID-19. (2020). <https://doi.org/10.1093/pcomedi/pbaa016>.
19. J.A.P. Heester Beek, A Brief History of R0 and a Recipe for its Calculation. (2020)
20. P.Porwal, P.Shrivastava and S.K.Tiwari, Study of a Simple SIR Epidemic Model. (2015)
21. M.Radha and S.Balamuralitharan, A study on COVID-19 transmission dynamics: stability analysis of SEIR model with Hopf bifurcation for effect of time delay. *Adv Differ Equ* **2020**, 523 (2020). <https://doi.org/10.1186/s13662-020-02958-6>
22. COVID-19 data <https://prsindia.org/covid-19>.