Linear and Nonlinear Analysis
Yokohama Publishers
ISSN 2188-8167

Volume 9, Number 3, 2023, 221–229

A MATHEMATICAL MODELLING OF TWO DISEASES: INFLUENZA AND SARS-COV-2

DIPAK MAJI AND ADITYA GHOSH

Abstract. A mathematical model is considered here which depicts the interactive behaviour of a patient who is suffering either in Influenza or COVID-19 and have a chance to get infected by other disease after recovering from one. The model considers different variables to portray the clear picture of the behaviour of two diseases. The situation where a person suffers in either one of the disease or protected from one disease but suffering in other disease is consider by four different variables. In this work the disease-free equilibrium is considered to find out the stability for the same and the stability analysis has been done. The analysis provides some important outcome for different parameter. Numerical simulation is also performed to justify the derived results.

1. Introduction

As the COVID-19 is still not over completely, rather than it is changing its nature and appears in different forms. It was started in Dec 2019 at Wuhan, China and gradually spread all over the world and so for India. Many patients were died not only in COVID-19 caused by the virus SARS-CoV-2 but specially by other disease which was present along with COVID-19. This incident is known as comorbidity. Starting from May 2020 the highest number of deaths in India and second highest in world was reached by 5th September 2020 with case fatality rate of 1.75 percent. Due to the sudden outbreak of COVID-19, the main attack was on respiratory system of human being and if the person already had any other respiratory problem, those cases were becoming critical. Pneumonia was one of the major diseases for comorbidity along with COVID 19 with immediate cause of death (around 54 percent). Dyspnea, fever and cough also were responsible for the same. Vaccination was started on 16/01/2021 and at present the few vaccines are used for the same [1]. Sometimes, some virus can also block the growth of other virus if they both are residing in the same host ([10]). Here we try to see the interaction of SARS-COV-2 with Influenza virus and try to understand the mutual behavior of them and do stability analysis for the interactive model. One competitive model is considered here by taking SARS-COV-2 and Influenza virus and their interactive nature is considered. There are many articles regarding interactive behavior of SARS -COV-2([4, 7, 9, 11]). There are many antiviral medicines available in the market for the influenza. By the use of antiviral medicines, influenza can be prevented. During

2020 *Mathematics Subject Classification.* 35A01, 65L10, 65L12, 65L20, 65L70.

Key words and phrases. Modelling, influenza, Covid, Stability, disease free equilibrium, interactive model.

the infected period of influenza, people should drink plenty of water of fluid and sufficiently rest. Antiviral medicine cannot remove the symptoms of the influenza but it can reduce the appearance and the duration of the disease. Every person need not go for active antiviral treatment for influenza but should take action based on several factors. If the persons are very ill and suffering for disease also, then there is a risk factor and the person's needs antiviral medicines. If a person is suffering influenza for more than 48 hours with all symptoms of the influenza, then it is advisable to the consult a doctor for treatment. The dynamics of the influenza [5,8] have been studied by various researcher such as Andresen et al [6], Hethcote [3], who have also suggested mathematical models for the transmission dynamics of the influenza.

2. Mathematical assumption

Here the mathematical model is considered which is based on a system of ordinary differential equations and it is of compartmental model. A SEIR model was discussed by Pinky,L. [10]. In that work Infected disease was considered in exposed class also and both co-infection classes, which is a very complicated dynamics to study. The exposed class and co-infected class are not considered in our work.

The total population N(t) of the mathematical model is divided into six different classes namely S(t) proportion of the human population which is susceptible at time t. $I_1(t)$ proportion of the human population which is infected at time t by the virus -1 (influenza) and $I_2(t)$ proportion of the human population which is infected at time t by the virus -2 (SARS-COV-2) and $S_1^{(2)}(t)$ proportion of the human population which are recovered from virus-2 are immune to virus-2 but now are susceptible to virus-1 at time t and $S_2^{(1)}(t)$ proportion of the human population which are recovered from virus -1, they are immune to virus-1 but now are susceptible to virus-2 at time t, R(t) be the proportion of the human which are recovered at time t. Initially the population are susceptible to both viruses (Influenza and SARS-COV2). Population can be infected by either virus with the force of infection $k_i (i = 1, 2)$ and move into the infected components. Our assumption is that virus -1(Non-SARS-COV-2 such as influenza) and virus -2 is (SARS-COV-2). Some susceptible are infected at a time by virus -1 with the rate k_1 and some are infected by virus-2 with the rate k_2,after some time infected are recovered from virus -1 but now they are susceptible to virus-2 ($S_2^{(1)}(t)$) at the rate δ_1 again those susceptible belong to the $I_2(t)$ components at the rate μ_1. Population on $I_2(t)$ classes are recovered from virus-2 but now they are susceptible to virus-1 ($S_1^{(2)}(t)$) at the rate δ_2 again those susceptible belong to the $I_1(t)$ components at the rate μ_2. Both of the infected are recovered at the rate $\delta_i (i = 1, 2)$. The natural death rate μ is applicable in each of the classes of the model.

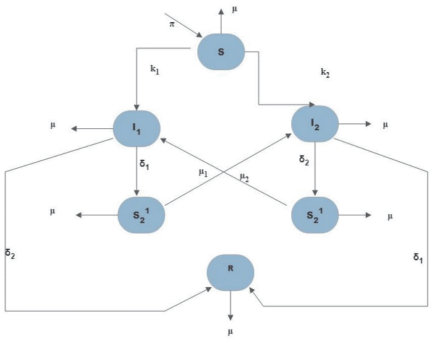

FIGURE 1. Model Diagram

3. Model diagram

The model diagram is a block diagram which is the interaction between different variables. The Fig-1 represent the diagram corresponding to the model.

4. Model equations

The mathematical model can be represented by the following first order system of ODE

$$\frac{dS}{dt} = \pi - k_1 S - k_2 S - \mu S \tag{4.1}$$

$$\frac{dI_1}{dt} = k_1 S - \delta_1 I_1 + \mu_2 S_2^{(1)} - \mu I_1 - \delta_2 I_1 \tag{4.2}$$

$$\frac{dI_2}{dt} = k_2 S - \delta_2 I_2 + \mu_1 S_1^{(2)} - \mu I_2 - \delta_1 I_2 \tag{4.3}$$

$$\frac{dS_1^{(2)}}{dt} = \delta_2 I_2 - \mu_2 S_1^{(2)} - \mu S_1^{(2)} \tag{4.4}$$

$$\frac{dS_2^{(1)}}{dt} = \delta_1 I_1 - \mu_1 S_2^{(1)} - \mu S_2^{(1)} \tag{4.5}$$

$$\frac{dR}{dt} = \delta_1 I_2 + \delta_2 I_1 - \mu R \tag{4.6}$$

The details of the parameters are described in Table-1:

TABLE 1. Parameter Details

Parameter	Description	Value	Reference
k_1	Infected rate of disease-1(Influenza)	0.35 per day	[7]
k_2	Infected rate of disease-2(Covid)	0.41 per day	[?]]
δ_1	Recovery rate from disease-1(Influenza)	0.21 per day	[1]
δ_2	Recovery rate from disease-2(Covid)	0.10 per day	[10]
π	Recruitment Rate	0.0381 per day	[10]
μ	Average Life Span	0.00003914 per day	[3]
μ_1	Infection rate of virus -2 which is recovered from virus -1	0.12 per day	[9]
μ_2	Infection rate of virus -1 which is recovered from virus-2	0.21 per day	[11]

5. Positivity of the solution

The model of the system $(1)-(6)$ monitors the changes in the human populations. It is therefore important to prove that the solution of the system with on negative initial conditions will remain non-negative for all $t > 0$, thus we have the following theorem.

Theorem 5.1. *If Given that the initial condition of the system is* $S(0) \geq 0, I_1(0) \geq 0, I_2(0) \geq 0, S_1^{(2)} \geq 0, S_2^{(1)} \geq 0, R \geq 0$*, then all the solutions will be non negative.*

Proof. Using standard inequality system, we can show the positivity of the system as follows,

$$\frac{ds}{dt} \geq \pi - (k_1 + k_2 + \mu)S \tag{5.1}$$

Here this represent a linear differential equation with intregrating factor, $e^{(k_1+k_2+\mu)t}$
By multiplying both side with the integrating factor and integrating, we get the following,
$S \geq \pi(k_1 + k_2 + \mu) + \frac{C}{(k_1+k_2+\mu)} e^{(k_1+k_2+\mu)t}$, where C is the integrating constant.
As $t \to \infty$, $S \geq \pi(k_1 + k_2 + \mu)$
Which shows that $S(t)$ is positive.
Similarly for all remaining variable positivity can be shown. □

6. Boundedness

We show that the all solutions of the system are bounded. The analysis of the system $(1) - (6)$ be analysed in the region ω of the biological interest. Thus, we have the following theorem on the system $(1) - (6)$ for boundedness property.

Theorem 6.1. *The feasible region* ω *defined by* $\omega = \{S, I_1, I_2, S_2^{(1)}, S_1^{(2)}, R | 0 \leq N \leq max\{N(0), \frac{\pi}{\mu}\}\}$ *with all positive initial conditions, is positively invariant and attracting with respect to system* $(1) - (6)$*, where* $N = S + I_1 + I_2 + S_2^{(1)} + S_1^{(2)} + R$

Proof. Here at time t, the total population is defines as
$N = S + I_1 + I_2 + S_2^{(1)} + S_1^{(2)} + R$. By taking derivative and putting all value from equations $(1) - (6)$, the following can be obtained,

$$\frac{dN}{dt} = \pi - \mu N \tag{6.1}$$

As the equation is a linear differential equation, the integrating factor is $e^{\mu t}$
By multiplying both side with the integrating factor and taking the initial condition as $N(0) = N_0$, the following solution can be obtained

$$N \leq \frac{\pi}{\mu} + ke^{-\mu t} \tag{6.2}$$

Where $k = N_0 - \frac{\pi}{\mu}$
As $t \to \infty$, $0 \leq N \leq \frac{\pi}{\mu}$ □

7. Existence of equilibrium points

In the absence of influenza ($I = 0$), system $(1) - (6)$ has disease free equilibrium, which is given by,
$E_0 = (\ \frac{\pi}{(k_1+k_2+\mu)}, 0, 0, 0, 0)$

If no one can be infected by virus - 1(influenza) but infected by virus-2 (SARS-COV-2) then equilibrium point will be

$$E_1 = \Big(\frac{\pi}{(k_1+k_2+\mu)}, 0, \frac{\pi k_2}{(k_1+k_2+\mu)(\delta_1+\delta_2+\mu)}, 0, \frac{\pi k_2 \delta_2}{(k_1+k_2+\mu)(\delta_1+\delta_2+\mu)(\mu_1\mu_2)}, \frac{\pi k_2 \delta_1}{(k_1+k_2+\mu)(\delta_1+\delta_2+\mu)\mu}\Big)$$

Again, if we consider $I_2 = 0$ i.e. no one can be infected by virus-2 (SARS-COV-2) but the population is infected by virus -1. The equilibrium point will be

$$E_2 = \Big(\frac{\pi}{(k_1+k_2+\mu)}, \frac{\pi k_1}{(k_1+k_2+\mu)(\delta_1+\delta_2+\mu)}, 0, 0, \frac{\pi k_2}{(k_1+k_2+\mu)\mu}, \frac{\pi k_1 \delta_2}{(k_1+k_2+\mu)(\delta_1+\delta_2+\mu)\mu}\Big)$$

8. Stability analsysis

Theorem 8.1. *The disease-free equilibrium point E_0 is locally asymptotically stable if the transmission rate of those, who are recovered by one disease will not be affected by another disease.*

Proof. Linearizing the system $(1)-(6)$ around the equilibrium point E_0, the following matrix can be obtained,

$$\begin{bmatrix} -(k_1+k_2+\mu) & 0 & 0 & 0 & 0 & 0 \\ k_1 & -(\delta_1+\delta_2+\mu) & 0 & \mu_2 & 0 & 0 \\ k_2 & 0-(\delta_1+\delta_2+\mu) & 0 & \mu_1 & 0 & \\ 0 & 0 & \delta_2 & -(\mu_1+\mu_2) & 0 & 0 \\ 0 & \delta_1 & 0 & 0 & -(\mu_1+\mu_2) & 0 \\ 0 & \delta_2 & \delta_1 & 0 & 0 & -\mu \end{bmatrix}$$

From the jacobian matrix the eigen values can be obtained as
$\lambda_1 = -(k_1+k_2+\mu)$
$\lambda_2 = -\mu$
Others eigen value will be root of the following equation,
$\{-(\delta_1+\delta_2+\mu)-\lambda\}\{-\mu-\lambda\}\{-(\delta_1+\delta_2+\mu)-\lambda\}\{-(\mu+\mu_1)-\lambda\}\{-(\mu+\mu_2)-\lambda\}-\mu_1\mu_2\delta_2 = 0$

Case − I : If $\mu_1 = 0$ i.e. $S_2^{(1)}$ does not belong to the I_2 class, then different eigen values of the system are
$-(\delta_1+\delta_2+\mu), -(k_1+k_2+\mu), -\mu$
Which shows the system will be asymptotically stable.

Case − II : If $\mu_2 = 0$ i.e. $S_1^{(2)}$ does not belong to the I_1 class, then different eigen values of the system are
$-(\delta_1+\delta_2+\mu), -(k_1+k_2+\mu), -\mu$
Which shows the system will be asymptotically stable.

Case − III : If $\mu_1 = 0$ and $\mu_2 = 0$, then different eigen values of the system are
$-(\delta_1+\delta_2+\mu), -(k_1+k_2+\mu), -\mu$
Which shows the system will be asymptotically stable. □

9. Numerical simulation

Based on the Numerical simulation on Matlab we got the following figures i.e figure2-figure 7.

10. Results and discussion

Here the model is highly non-linear in nature. The results shows that the disease-free equilibrium point will be always asymptotically stable if the rate of propagation to one disease will be zero provided it has been safe already protected from another disease. It means that the person is already recovered from the influenza but he/ she has no chance to affected by covid. In this case the disease-free case is stable. The model is stable also it means the person is already recovered from the covid but he/ she has no chance to affected by Influenza. The following diagram shows the

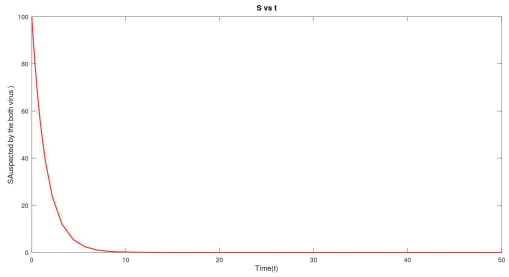

FIGURE 2. suspected vs time

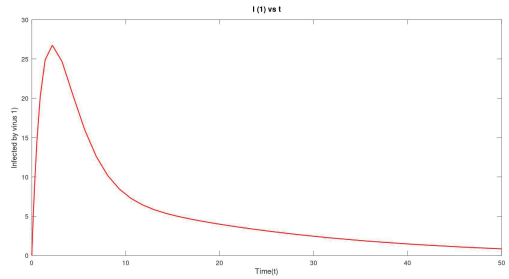

FIGURE 3. Infected by virus 1 vs time

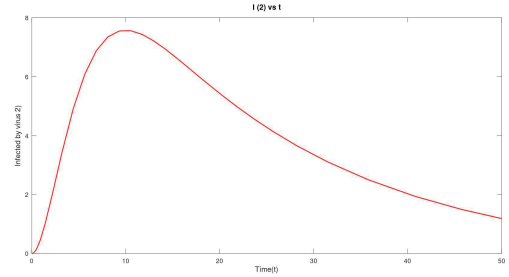

FIGURE 4. Infected by virus2 vs time

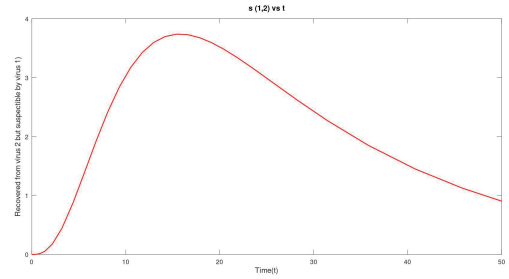

FIGURE 5. suspectable to virus 1 but recovered from2 vs time

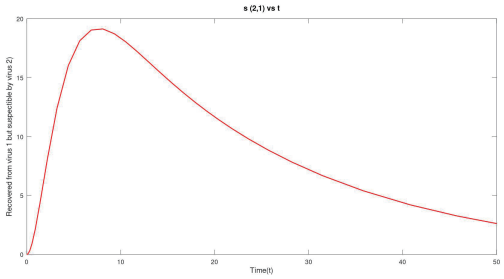

FIGURE 6. suspectable to virus 2 but recovered from virus 1 vs time

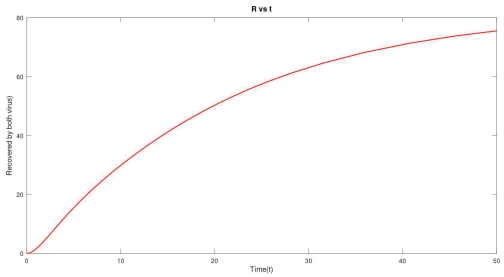

FIGURE 7. Recovered vs time

justification for the claim. Here Fig1 shows the growth rate of susceptible disease-1 for Disease-free equilibrium. The curve started from a high note and gradually minimizing and tending to zero, which indicates that susceptible population is showing decay, which means the disease is minimizing. In the same sense the Fig6 shows the growth rate of recovered population, which is growing. This means the number of recovered persons increasing day by day which might lead to a stable position. Fig2 – Fig5 show the growth rate of other variables namely (Influenza, Covid etc.) which also showing stability.

The epidemic model involving two viruses is considered here. Such kind of virus infection is seen very frequently. By our model, it can be observed that, the absence of one virus shows significance results. Though our model has many limitations, despite of that, we try to provide the impact of absence of one virus or the impact of parameter in the model.

11. CONCLSTION

This model is very realistic and interesting. Normally the idea is that one disease accelerates other disease. But there are some situations, where one virus block or supress another virus if they live in the same host. Here we try to explore two different viruses in the same host. In our model we try to observe the viruses individually as well as coherently. Till now, we are able to consider the disease-free case, where some interesting results are observed. The rate of infection of one disease for those population, which have been recovered from other disease,

plays an important role for that. If the rate is zero, then the model is becoming asymptotically stable.

References

[1] *https://covid19.who.int/data*

[2] H. Achdout, E. B. Vitner, B. Politi, S. Melamed, Y. Yahalom-Ronen, H. Tamir, N. Erez, R. Avraham, S. Weiss, L. Cherry, E. Bar-Haim, E. Makdasi, D. Gur, M. Aftalion, T. Chitlaru, Y. Vagima, N. Paran and T. Israely, *Increased lethality in influenza and SARA-CoV-2 coinfection is prevented by influenza immunity but not SARS-CoV-2 immunity*, Nat Commun **12** (2021): Article number: 5819.

[3] V. Andersen, J. Lin and S. A. Levin, *The dyanamics of co circulating influenza strains conferring partial cross–immunity*, J.Math. Biol. **35** (1997), 825–842.

[4] M. L. Blascom J. Buesa, J. Colomina, M. J. Forner, M. J. Galindo, J. Navarro, J. Noceda, J, Redón, J. Signes-Costa and D. Navarro, *Co-detection of respiratory pathogens in patients hospitalized with coronavirus viral disease–2019 pneumonia*, J. Med. Virol. **92** (2020), 1799–1801.

[5] D. J. D. Earn, J. Dushoff and S. A. Levin, *Ecology and evoluation of the flu*, 2002.

[6] H. W. Hethcote, *The mathematics of influenza diseases*, Siam Rev. **42** (2000), 599–653.

[7] D. Kim, J. Quinn, B.Pinsky, N. H. Shah and I. Brown, *Rates of coinfection between SARS-CoV-2 and other respiratory pathogens*, JAMA. **26** (2020), 2085–2086.

[8] E. W. Larson, J. W. Dominik, A. H. Rowberg and G. A. Higbee, *Influenza virus population dynamics in the respiratory tract of experimentally infected mice*, Infect Immun. **13** (1976), 438-447.

[9] M. D. Nowak, E. M. Sordillo, M. R. Gitman and A. E. Paniz, *Co-infection in SARS-CoV-2 infected patients: where are influenza virus and rhinovirus/enterovirus ?*, J. Med. Virol. **92** (2020), 1699–1700.

[10] L. Pinky and H. M. Dobrovolny, *SARS-CoV-2 coinfections: could inflfluenza and the common cold be benefificial?*, J. Med. Virol. **92** (2020), 2623–2630.

[11] Q. Xing, G.-J. Li, Y. H. Xing, T. Chen, W.-J. Li, W. Ni, K. Deng, R.-Q. Gao, C.-Z. Chen, Y. Gao, Q. Li, G.-L. Yu, J.-N. Tong, W. Li, G.-L. Hao, Y. Sun, A. Zhang, Q. Wu, Z.-P. Li and S-L. Pan *Precautions are needed for COVID-19 patients with coinfection of common respiratory pathogens*, Lancet. doi: 10.2139/ssrn.3550013, 2020

Manuscript received 10 April 2022
revised 15 November 2022

Dipak Maji
Department of mathematics , Adamas University ,Kolkata,700126, West Bengal, India
E-mail address: dipak.maji@stu.adamasuniversity.ac.in

Aditya Ghosh
Department, Adamas University, Barasat, Kolkata, 700126,West Bengal, India
E-mail address: aditya.ghosh@adamasuniversity.ac.in