

A STUDY ON MATHEMATICAL MODEL IN EPIDEMIOLOGY-THE SPREAD OF THE SEVERE ACUTE RESPIRATORY SYNDROME EPIDEMIC

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ABSTRACT

Specifically, we simulate the Severe Acute Respiratory Syndrome pandemic using the twin epidemic theory, which states that there are two epidemics in a community and that immunity to one severe disease is conferred by a minor infection to the other. A consistent background infection level was found during the SARS outbreak, which persisted for a lengthy period of time and then began to drop gradually, on top of which sprang unexpected local outbreaks. This was confirmed by laboratory testing. SARS is a serious threat to human health across the world, and it has the potential to have a disastrous impact on the world's economy and growth. As a result, it is extremely essential and vital to investigate the dynamics of transmission using qualitative and quantitative mathematical models, and to anticipate and prevent infectious disease as early as possible.

KEYWORDS: Severe, Epidemic, Infection, Mathematical, Syndrome.

I. INTRODUCTION

In recent years, medical researchers and scientists have paid close attention to the emergence of novel infectious illnesses and the agents that cause them, as well as the causative agents that are responsible for these diseases. Severe acute respiratory syndrome (SARS) is one such illness that has caused widespread dread around the world. Known as SARS, the severe acute respiratory syndrome (SARS) is a respiratory illness that was initially discovered in China's southern province of Guangdong in 2003. It has been suggested that SARS may be caused by infection with a new corona virus. Since November 2002, the pandemic of Severe Acute Respiratory Syndrome has been wreaking havoc on human society all over the world. It has resulted in a significant catastrophic danger in terms of sudden fatalities, interruption of the tourism sector, economic downturn, and so on. It is a significant concern to the medical establishment and a threat to foreign travellers because SARS is spreading. It is having a significant negative economic impact in areas of East Asia and is spreading around the world. The large number of instances of SARS transmission to health-care professionals demonstrates the severe threat that SARS poses to the medical community as a whole. The capacity of SARS to spread swiftly on a worldwide scale, on the other hand, has proven to be its most remarkable characteristic. An individual who has been exposed to SARS may get infected after an incubation period of 2-7 days, with 3-5 days being the most frequent duration. The vast majority of infected persons either recover completely within 7-10 days or die in a seven to ten percent mortality rate. Individuals over the age of 40, particularly those with pre-existing medical conditions such as heart or liver illness, appear to be at greatest risk of developing SARS. Its symptoms are comparable to those of pneumonia or other respiratory diseases, and include a high temperature, shortness of breath, a dry cough, a headache, stiff or achy muscles, tiredness, and diarrhoea. It is contagious among children. These signs and symptoms, on the other hand, are not all the same. For example, the illness appears to be milder in the United States than it is in Asia. The virus's mechanism of transmission is not

completely understood at this time. SARS appears to be transmitted mostly through direct contact between people. However, it might also be spread by infected items, air, or other means. The illness is now incurable because to the lack of a viable pharmacological treatment, and a vaccination against the disease has not yet been produced. The conventional SIR epidemic model has a tough time explaining this phenomenon. It is striking how similar the pattern found in the SARS pandemic is to the pattern observed in the coronavirus-mediated outbreaks that afflicted pigs between 1983 and 1985. We postulate that coronaviruses have a high mutation and recombination rate throughout the SARS epidemic, and that minor changes can modify the tissue tropism of coronaviruses in a given pandemic. There are two epidemics: the first is SARS, which is caused by a coronavirus, which we refer to as virus A. The second epidemic is Ebola, which is caused by a coronavirus. The spread of another pandemic, which is hypothesised to have happened before to SARS and which is considered to be very infectious due to both the nature of the virus and its relative innocuousness, is facilitated by the consumption of infected food and the contact with contaminated surfaces. It has been determined that the outbreak was caused by a coronavirus, which we refer to as virus B, which causes gastroenteritis. This is inferred from the observation that diarrhoea was observed in the population for around one day before to the SARS outbreak, which is a reasonable assumption. The most likely source of virus A's emergence is a mutation or recombination event in virus B's genome.

II. LITERATURE REVIEW

Anderson Luiz Pena da Costa et al (2021) The transmission elements of irresistible diseases is powerless to changes represented by a few factors, whose acknowledgment is basic for the reasonable improvement of techniques for anticipation and control, just as for creating wellbeing approaches. In this unique circumstance, mathematical modelling can give helpful bits of knowledge concerning transmission examples and recognition of boundaries to alleviate disease in the populace. To instructionally introduce the mathematical modelling of irresistible diseases for wellbeing understudies and experts as a device in the study of disease transmission. A complete writing survey was led with articles acquired from PubMed, Web of Science, and Google Scholar data sets with the term irresistible diseases mathematical modeling. There are two principle kinds of models worked with a premise on fixed or probabilistic rates that portray people's development in compartments that assign stages in the regular history of the disease. In this sense, deterministic models are non-probabilistic and stochastic models are probabilistic, the first aides in fostering a prospection of potential situations in the study of disease transmission, while the second is more material in the investigation of the impact of factors in the transmission elements. The irresistible specialists are in a steady course of natural advancement, just as the climate and human originations, culture, and conduct, inferring a consistent change in the epidemiological profile of irresistible diseases, where the mathematical modeling can offer help to the dynamic cycles concerning the study of disease transmission and general wellbeing.

Chayu Yang (2020) we suggest a mathematical model to explore the momentum flare-up of the Covid disease 2019 (COVID-19) in Wuhan, China. Our model portrays the different transmission pathways in the contamination elements, and stresses the job of the ecological supply in the transmission and spread of this disease. Our model additionally utilizes non-steady transmission rates which change with the epidemiological status and natural conditions and which mirror the effect of the on-going disease control measures. We lead a definite examination of this model, and show its application utilizing freely announced information. Among different discoveries, our insightful and mathematical outcomes show that the Covid contamination would stay endemic, which requires long haul disease counteraction and intercession programs.

A. Huppert (2013) we talk about how much disease transmission models give dependable expectations. The idea of expectation is outlined as it is perceived by modelers, and delineated by some work of art and ongoing models. A precondition for a model to give legitimate expectations is that the suppositions fundamental it relate to the truth, however such correspondence is constantly restricted—all models are rearrangements of the real world. A focal precept of the modeling venture is the thing that we might call the 'strength theory': a model whose suspicions around compare to reality will make expectations that are roughly substantial. To look at which of the expectations made by a model are dependable, it is fundamental to inspect the results of various models. Along these lines, if an exceptionally worked on model makes a forecast, and if the equivalent or a very much like expectation is made by a more intricate model that incorporates a few systems or subtleties that the primary model didn't, then, at that point, we acquire some certainty that the expectation is hearty. A significant advantage got from mathematical modeling action is that it requests straightforwardness and exactness in regards to our presumptions, accordingly empowering us to test our comprehension of the disease the study of disease transmission by contrasting model outcomes and noticed examples. Models can likewise aid dynamic by making projections seeing significant issues, for example, intercession initiated changes in the spread of disease.

Dr. V.H. Badshah et al (2013) this review targets giving the Considerable job of relationship of mathematical modeling and dynamical parts of some pandemic diseases. This review stresses a comprehension of deterministic modeling applied to the populace elements of contamination diseases. Here we are essentially underscoring the authentic foundation of mathematical modeling and job of elements in various contamination diseases like measles, AIDS, Cholera, Plague, Malaria, T.B., and Dengue and so on Our examination is zeroing in on authentic parts of bioepidemiological mathematical review.

Mikayla C. Chubb (2009) the creators of this paper advocate for the extended utilization of mathematical models in the study of disease transmission and give an outline of the standards of mathematical modeling. Mathematical models can be utilized all through the epidemiological exploration measure. At first they might assist with refining concentrate on inquiries by outwardly communicating complex frameworks, coordinating writing look, and recognizing touchy factors. In the review configuration stage, models can be utilized to test examining methodologies, to assess test size and power, and to anticipate results for contemplates unrealistic because of time or moral contemplations. Whenever information are gathered, models can aid the translation of results, the investigation of causal pathways, and the joined examination of information from numerous sources. At long last, models are regularly utilized during the time spent applying research discoveries to general wellbeing practice by assessing populace hazard, foreseeing the impacts of mediations, and adding to the assessment of progressing programs. Mathematical modeling can possibly make critical commitments to the area of the study of disease transmission by upgrading the exploration cycle, filling in as an apparatus for imparting discoveries to policymakers, and encouraging interdisciplinary coordinated effort.

III. THE STEADY STATES OF THE SYSTEM

In this part, we will compute the steady states of the model that we have constructed. There are numerous stable states in the environment, including when both illnesses are absent (uninfected equilibrium), and if a disease (either one or both at the same time) is prevalent.

Table 1: Parameters of the SARS epidemic model

Parameters	Description
λ	Constant rate of inflow of individuals into the susceptible class due to immigration or births
γ	Constant rate of removal of the susceptibles due to deaths by natural causes and not due to infection Transmission rate of virus A Transmission rate of virus B
α	Constant removal rate of infectives with virus A
β	Constant removal rate of infectives with virus B
μ	
τ	

Set

$$\frac{dS(t)}{dt} = 0 = \frac{dI_A(t)}{dt} = \frac{dI_B(t)}{dt},$$

We will obtain

$$\begin{aligned} \lambda - \gamma S - \alpha SI_A - \beta SI_B &= 0 \\ -\mu I_A + \alpha SI_A &= 0 \\ -\tau I_B + \beta SI_B &= 0 \end{aligned}$$

Presently tackling the above mentioned, we get the disease free harmony point as $E_1 = (\lambda/\gamma, 0, 0) = (\tilde{S}, \tilde{I}_A, \tilde{I}_B)$

At the point when $I_B = 0$, the one disease state balance point is provided by $E_2 = (\hat{S}, \hat{I}_A, \hat{I}_B)$ where

$$\begin{aligned} \hat{S} &= \frac{\mu}{\alpha} \\ \hat{I}_A &= \frac{\lambda - \alpha - \gamma\mu}{\mu\alpha} \\ \hat{I}_B &= 0 \end{aligned}$$

Where $\frac{\lambda\alpha}{\gamma} > \mu$

At the point when $I_A = 0$, the one disease state harmony point is provided by $E_3 = (S^*, I_A^*, I_B^*)$

$$S^* = \frac{\tau}{\beta}$$

$$I_A^* = 0$$

$$I_B^* = \frac{\lambda\beta - \gamma\tau}{\tau\beta}$$

Where $\lambda\beta > \gamma\tau$

IV. STABILITY OF THE EQUILIBRIUM POINTS

In this part, we give a few outcomes on the strength of the harmony focuses.

Theorem 1: the disease free harmony $E_1 = (\lambda/\gamma, 0, 0) = (\tilde{S}, \tilde{I}_A, \tilde{I}_B)$ is locally asymptotically steady if and provided that $\frac{\lambda\alpha}{\gamma} < \mu$ and $\frac{\lambda\beta}{\gamma} < \tau$.

Confirmation: We figure the jacobian framework of the framework about the harmony point E_1 . The jacobian lattice is provided by

$$\begin{pmatrix} -\gamma & \frac{-\lambda\alpha}{\gamma} & \frac{-\lambda\beta}{\gamma} \\ 0 & -\mu + \frac{\lambda\alpha}{\gamma} & 0 \\ 0 & 0 & -\tau + \frac{\lambda\beta}{\gamma} \end{pmatrix}$$

The Eigen upsides of the above framework are

$$-\gamma, -\mu + \frac{\lambda\alpha}{\gamma}, -\tau + \frac{\lambda\beta}{\gamma}$$

Presently, the harmony E_1 is locally asymptotically steady if and provided that all the Eigen upsides of the jacobian grid have negative genuine parts. However, all the Eigen esteems will have negative genuine parts if and provided that the condition $\frac{\lambda\alpha}{\gamma} < \mu$ and $\frac{\lambda\beta}{\gamma} < \tau$ is fulfilled. This demonstrates the hypothesis.

Theorem 2: The disease state balance $E_2 = (S, I_A, I_B)$ is locally asymptotically steady if and provided that $\frac{\lambda\alpha}{\gamma} > \mu$ and $\frac{\mu}{\alpha} < \frac{\tau}{\beta}$

Verification: We register the jacobian network of the framework about the balance point E_2 . The jacobian grid is provided by

$$\begin{pmatrix} \frac{-\lambda\alpha}{\mu} & -\mu & \frac{-\mu\beta}{\alpha} \\ \frac{\lambda\alpha - \gamma\mu}{\mu} & 0 & 0 \\ 0 & 0 & -\tau + \frac{\mu\beta}{\alpha} \end{pmatrix}$$

The trademark condition of the jacobian framework is given by

$$\left(-\tau + \frac{\mu\beta}{\alpha} - x\right)\left(x^2 + \frac{\lambda\alpha}{\mu}x + \lambda\alpha - \gamma\mu\right) = 0$$

One Eigen esteem is $x = -\tau + \frac{\mu\beta}{\alpha}$ and this Eigen worth will have negative genuine part when

$$\frac{\mu}{\alpha} < \frac{\tau}{\beta}$$

To finish up with regards to the next Eigen esteems, we apply the Routh-Hurwitz basis to the polynomial

$$\left(x^2 + \frac{\lambda\alpha}{\mu}x + \lambda\alpha - \gamma\mu\right)$$

In this way, the other Eigen upsides of the framework will have negative genuine parts if and provided that

$$\frac{\lambda\alpha}{\gamma} > \mu$$

Consequently, from the last two conditions, the theorem is demonstrated.

V. CONCLUSION

In this paper, we investigated a basic model of SARS transmission based on the double epidemic hypothesis and found it to be accurate. In the model, we have discovered three stable states: a disease-free state, a disease state where the infectives with virus B are absent, and a third disease state with a zero number of infectives with virus A. We employ the linear stability analysis to derive the criteria for the local asymptotic stability of the three steady states under consideration. In this study, we discovered that infection induced by virus A, which is the SARS virus, may be suppressed when the following factors are present $\frac{\lambda\beta}{\gamma} > \tau$ and $\frac{\tau}{\beta} < \frac{\mu}{\alpha}$. The milder infection produced by virus B, on the other hand, serves as a vaccination against the SARS virus. Because of this, there is a potential in the future that a vaccine approach to combat the SARS pandemic will be developed with the aid of this research.

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