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A Semi-Analytical Study on SEIR Model with Vaccinated Effects

V. Ananthaswamy[1,†], B. Sathyapriya[2] and M. Shruthi[2]

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Abstract This research describes the dynamics of COVID-19 propagation using a mathematical model that considers vaccination and self-defence. Furthermore, the impact of vaccination on the development of disease transmission has been investigated. Our findings specifically show that putting into practice the best control measures, including time-dependent interventions, lowers the total infection load and disease transmission. Five different compartments (Susceptible, Exposed, Vaccinated, Infected, and Recovered) are used in this study to examine an epidemiological model of COVID-19 dynamics. Approximate analytical solutions to the model's system of equations were obtained using the homotopy analysis method (HAM). The numerical simulation using MATLAB was employed to validate the accuracy and effectiveness of the solutions obtained through the Homotopy Analysis Method (HAM) by comparing the results. Excellent agreement is found when comparing the approximate analytical solution and the numerical simulation. The five-compartment model includes many more aspect parameters that are explored and graphically represented. These parameters include recovery rate and vaccination rate, among others. Moreover, it underscores the potential of the HAM as a powerful tool for exploring epidemic models and formulating control strategies.

Keywords Epidemic model, COVID-19, non-linear initial value problem, Homotopy Analysis Method (HAM), numerical simulation

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1. Introduction

COVID-19 is a pandemic brought on by the corona virus, which began with a COVID-19 outbreak in Wuhan, China, in December 2019 [45]. The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was the cause of it. It started to spread early in 2020, first to Asia and then the rest of the world. After having declared the outbreak to be a public health emergency of international concern on January 30, 2020, the World Health Organization (WHO) officially declared the pandemic on March 11, 2020. A wide spectrum of symptoms, from minor symptoms to potentially fatal problems, can be caused by the COVID-19 virus. Headache, loss

†the corresponding author.
Email address: ananthu9777@gmail.com (V. Ananthaswamy), bspriyamaths08@gmail.com (B. Sathyapriya), mshruthi353@gmail.com (M. Shruthi).
[1]Research Centre and PG Department of Mathematics, the Madura College (Affiliated to Madurai Kamaraj University), Madurai, Tamil Nadu, India.
[2]Research Scholar, Research Centre and PG Department of Mathematics, the Madura College (Affiliated to Madurai Kamaraj University), Madurai, Tamil Nadu, India.

of taste and smell, runny nose, cough, sore throat, muscle pain, diarrhoea, high fever, and breathing difficulties are common indications and symptoms. The respiratory route is the main way in which the disease is transmitted. It happens when an infected individual exhales droplets and microscopic airborne particles that they cough, sneeze, sing, or inhale.

Precautionary steps to reduce the chance of illness consist of receiving a vaccination, remaining at home, avoiding crowded places, keeping a safe distance from other people, wearing a mask in public, washing your hands regularly for at least 20 seconds each time, practicing good respiratory hygiene, and keeping our hands clean while touching our mouth, nose, or eyes. Common mitigation tactics used during the public health emergency included quarantines, travel limitations, lockdowns, mask mandates, and contact tracking of the infected [44]. People ought to get vaccinated as soon as it is their turn. They ought to follow the vaccination recommendations made by their local authorities in order to safeguard themselves against COVID-19.

Zelenkov et al. [43] described a method that uses genetic algorithms to rebuild real transition rate distributions. This allows one to build a model that can describe multiple COVID pandemic peaks. In order to combine data-centric and analytical approaches, a model combining variant-aware compartmental models and machine learning was developed by Baccega et al. [5]. Furthermore, it unveiled a state-of-the-art system for ongoing forecasting and monitoring that fluidly combines compartmental models with predictive models based on machine learning. Gatto et al. [15] proposed an alternate hybrid strategy based on machine learning to address this issue, which omits the need to recalculate hyperparameters and just employs the initial set. Using sensitivity research, Rahman et al. [34] used the partial rank correlation coefficient technique to identify the most important components. The endemic equilibrium conditions and local asymptotic stability of the suggested COVID-19 model were demonstrated by Batistela et al. [6].

The compartmental model, which is expressed by a system of seven ODEs, is one of the new findings. Additional discoveries include numerical simulations by Lemos-Paiao et al. [23] employing real data from the Portuguese health authorities, evidence of positivity and boundedness of solutions, examination of equilibrium points and their stability analysis, and so forth. The utilization of the Monte Carlo method with Bayesian sequential design for particle filtering, as demonstrated by Li et al. [24], enables the model to be regenerated every day and to adjust to novel patterns in the daily incoming data.

Ramezani et al. [35] examined the accuracy level of our model by testing it against publicly available cumulative infection and mortality data for several US states. The findings of this study provide new light on the herd immunity and reproduction rate that is now prevalent in the US. Furthermore, the average COVID-19 reproduction number in the US was found to be 12.6 days; this puts the virus in the same category as measles and mumps as one of the most contagious diseases. A spectral technique was presented by Olivares et al. [33] that enables a polynomial extension of the stochastic state variables of the optimal control model to express the uncertainty propagation through the state variables. For compartmental epidemiological models, this method is used to create and resolve robust optimum control problems. More precisely, a polynomial chaotic expansion based on statistical moments was utilized.

Deng's [11] explanation of transmission parameters for current compartmental