

REPORT FOR ABEL VISITING SCHOLAR PROGRAM

Research Subject: Dynamics of a Mathematical Model of COVID-19 Incorporating the Effect of Vaccine

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Host researchers: Prof. Alan Rendall and Dr. Burcu Gürbüz

This report concentrates on the progress of the project entitled “Dynamics of a Mathematical Model of COVID-19 Incorporating the Effect of Vaccine” during a research stay at the Johannes Gutenberg-University Mainz with an IMU-Abel Grant.

With the help of Host researchers, Prof. Alan Rendall and Dr. Burcu Gürbüz, I have initiated the project to develop a compartmental mathematical model with a particular focus on the vaccine efficacy and virus concentration in the environment during the COVID-19 pandemic. In the research propose we previously presented to IMU, we were planing to develop a SIARCV mathematical model. Here, Susceptible class (S), Asymptotically Infected class (A), Infected class (I), Recovery class (R), Vaccinated class (V), and density of the virus (C) in the environment are taken into consideration. However, during the research stay, our mathematical and numerical investigations have shown that it is not straightforward to analyse previously proposed SIARCV model. In order to make the model mathematically more attainable, we have replaced the Asymptomatic class (A) with Exposed class (E).

1. Equilibrium points or steady states of a system are constant solutions of a differential equation have been computed using

$$\frac{dF}{dt} = 0, \text{ where } F = \{S, E, I, V, R, C\}.$$

It has been found that the mathematical model has two equilibria: a unique disease free equilibrium and endemic equilibrium. For a disease free equilibrium, since there are no infected individuals in the population, we assumed that density of the virus is zero. Thus only Susceptible, Vaccinated and Recovered classes may present in the population and we may state this as $(S^*, 0, 0, V^*, R^*, 0)$.

2. The local stability analysis around the unique disease free equilibrium has been investigated by finding the Jacobian matrix of the system. Here, we have used linearisation argument. Thus the corresponding linearised system is used to determine stability of the system around disease free equilibrium. We have also found that determinant of the Jacobian matrix is associated with the basic reproduction number.
3. Next Generation Method has been used to derive the basic reproduction number of the compartmental model. We have found an excellent agreement between the analytical results obtained using Next Generation Method and the determinant of the Jacobian Matrix around disease free equilibrium mentioned above.
4. We have also written the Matlab code for the system using ode45 and also developed the code for parameter estimation using nonlinear least square method.

Due to the limited time, parameter estimation could not be performed to find optimum parameters. We will continue to communicate via online meetings to complete the project.

To the best of our knowledge, there are only a few mathematical models considering the effect of vaccination and the density of the virus in the environment. Thus, this work will contribute to expand our knowledge of the current pandemic and may open new directions to the modeling of infectious diseases. Therefore, this work may be regarded as an important step for further studies on infectious diseases.

Finally, I am grateful to the Selection Committee of the Abel Visiting Scholar Program for supporting my research stay.

Dr. Aytül Gökçe