Modeling, Analysis, and Simulation of Measles Disease Transmission Dynamics

Motivation:

Measles is an acute, highly infectious viral disease caused by morbillivirus (measles virus), for which humans are the only reservoirs. Recently, there has been an in- crease in measles infections in sub-Saharan Africa, with 17,500 cases altogether as of January 2022, a 400% spike from cases reported in 2021. Regardless of the availability of measles immunization, there were 207,500 predicted measles mortalities globally in 2019, of which 147,900 (more than 70%) were in African nations. Globally, it was forecast that 134,200 children would die from measles in 2015, making it the highest public health issue. Currently, crises in countries such as Afghanistan, Ethiopia, Somalia, and Ukraine are forcing millions of children to leave their homes. Immu- nization programs and other crucial children's health ser- vices have been interrupted in these countries. Hence the severity of the desease motivated the authors to do this research.

Contribution:

In accordance with each of the most recent articles on the dynamics of measles transmission, all of the studies do not develop an epidemiological or mathematical model of measles infection outbreak that emphasizes the persistence of the measles virus on objects, surfaces, or in the atmosphere. Therefore, the goal of this work is to construct an SVIRP deterministic mathematical model while also improving the SVIR deterministic mathematical model by introducing a compartment for the host of the measles virus's capability to survive in the atmosphere and other infected materials.

Methodology:

The authors have modified the SEVIR model by SVIR considering a new compartment called pathogen population P that has the highest impact on the transmission of the disease. From the model, they first estimated the disease-free equilibrium, calculated the effective reproduction number (REff), and established the stability analysis. The local stability analysis of the DFEP is justified using linearization. The Cas tillo–Chavez stability criterion is used to demonstrate the global stability of the disease-free equilibrium point, while the linearization method is used to justify its local stability analysis and gives a result of REff <1. The stability analysis of endemic equilibrium point is explained by defining a Lyapunov function, and its global stability exists when REf f > 1. To identify the effect of parameters on the transmission dynamics, they performed

sensitivity index and numerical simulation. To study the sensitivity, Maple 18 software is used.

Conclusion:

In this study, they have formulated and analyzed a mathematical model of transmission dynamics of measles considering the indirect contact that causes infection on the susceptible individuals due to touching infected objects, inhaling polluted air, and other modes of transmission of measles virus. To formulate the model, they first reviewed some of recent published papers and articles that worked on measles disease and modifed the SEVIR model by SVIR considering a new compartment called pathogen population P that has a highest impact on the transmission of the disease. From numerical simulation, it is obtained that the indirect contact rate has an extreme impact on the transmission dynamics of measles. Therefore, they conclude by saying that the rate of indirect contact must be minimized to reduce the number of infected in- dividuals. Also, they found that working on reducing the infection rates and infective contribution to the pathogen concentration in the environment. In addition, enhancing the treatment rate of infective and vaccination brings a significant contribution to reducing the disease effect in the community.