

Virginia Commonwealth University VCU Scholars Compass

Biology and Medicine Through Mathematics Conference

2022

May 19th, 9:30 AM - 10:00 AM

Multi-strain epidemic model with infected vaccinated and reinfected recovered population: application to COVID-19 pandemic

Olusegun Michael Otunuga Augusta University, ootunuga@augusta.edu

Follow this and additional works at: https://scholarscompass.vcu.edu/bamm

Part of the Disease Modeling Commons, Life Sciences Commons, and the Physical Sciences and Mathematics Commons

https://scholarscompass.vcu.edu/bamm/2022/thur/3

This Event is brought to you for free and open access by the Dept. of Mathematics and Applied Mathematics at VCU Scholars Compass. It has been accepted for inclusion in Biology and Medicine Through Mathematics Conference by an authorized administrator of VCU Scholars Compass. For more information, please contact libcompass@vcu.edu.

Title: Multi-strain epidemic model with infected vaccinated and re-infected recovered population: application to COVID-19 pandemic.

In this work, an innovative multi-strain *SVEIR* epidemic model is developed for the study of the spread of a multi-strain infectious disease in a population infected by mutations of the disease. The population is assumed to be completely susceptible to *n* different variants of the disease, and those who are vaccinated and recovered from a specific strain $k (k \le n)$ are immune to previous and present strains $j = 1, 2, \dots, k$, but can still be infected by newer emerging strains $j = k + 1, k + 2, \dots, n$. The model is designed to simulate the emergence and dissemination of viral strains. A bound for the herd immunity threshold is calculated. Also, 2^n different equilibrium points are calculated and the conditions for existence, local, and global stability of these equilibrium points investigated. The question as to whether it is possible for the population to have an endemic with more than one strain of the virus is answered by studying the stability analysis of all equilibrium points that are not disease-free equilibrium point. The effect of vaccines on the population is also analyzed. The validity of the work done is verified through numerical simulations by applying the proposed model and strategy to analyze the multi-strains of the COVID-19 virus in the United State.