

GLOBAL AND LOCAL DYNAMICS OF COVID-19 UNDER VACCINATION: STABILITY AND SENSITIVITY INSIGHT

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Abstract. Coronavirus infection disease (COVID-19) is a highly contagious illness that spreads rapidly through a population, influenced by the number of susceptible and infected individuals and their social interactions. The susceptible-exposed-infectious-vaccinated-recovered (SEIVR) epidemic model can help control outbreaks by simulating direct transmission dynamics. Graphical representations illustrate the behavior of susceptible, exposed, infected, vaccinated, and recovered individuals for basic reproduction less than 1 and greater than 1. This model can predict real-world outcomes and inform strategies to mitigate the spread of infectious diseases. Furthermore, the impact of COVID-19 on the effectiveness of vaccination in reducing morbidity and mortality can provide valuable information for public health interventions. Stability analysis is carried out at equilibrium points. SEIVR model is validated by numerical simulation using MATLAB.

Keywords. Covid-19 Model; Nonlinear differential equation ; SEIVR model; Epidemic model; stability analysis

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1 Introduction

Epidemiology, as a fundamental component of medical research and public health, extensively employs mathematical modelling to understand the transmission and progression of infectious diseases. Since the early twentieth century, researchers have developed deterministic and stochastic mathematical models to gain valuable insights into disease dynamics and transmission mechanisms [1, 2, 19]. In particular, deterministic compartmental models use systems of differential equations to describe the movement of individuals among different epidemiological classes representing various stages of disease progression [3, 4, 11, 5]. Such models provide a useful mathematical framework for understanding disease transmission, predicting disease outbreaks, estimating epidemiological parameters, evaluating control strategies, and supporting evidence-based public health decisions. The pioneering work of Kermack and McKendrick in 1927 laid the foundation of modern mathematical epidemiology through the development of the classical epidemic model [7]. Since then, numerous mathematical models have been developed and extended to incorporate different epidemiological characteristics and intervention strategies [10].