

Abstract

The co-infection of covid-19 and dengue fever has led to unfavorable outcomes because of high rates and extended hospital stays or isolation. This situation poses a significant threat to economic stability and has already burdened nations' healthcare systems. Covid-19, known as a novel coronavirus caused by handshaking or transmitted through drops from the nose when a covid-19 contaminated person wheezes and abducts, and dengue fever is caused when infected mosquitos bite a healthy individual. Both diseases exhibit predominantly similar symptoms, making it exceptionally challenging to conduct epidemic research aimed at controlling co-infection of both diseases.

Covid-19, dengue fever, and their co-infection have become a societal challenge. So, in this research, our primary objective is to examine and explore the stability of these dangerous diseases in the human population. We consider compartmental fractional order models to understand the complex dynamics of these diseases. Subsequently, we discuss their control measures, which significantly contribute to explaining how to eradicate these diseases from society. The reason for selecting these fractional models is to fill some flaws and gaps in the mathematical analysis performed. So, firstly, we discuss the covid-19 fractional order model and its theoretical analysis along with its stability locally and globally, and then an optimal control problem is developed for control measures. After that, we discuss its fuzzy fractional analysis to handle uncertainty in the data. Then, we present a dengue fractional order model with its complete theoretical and optimal control analysis. Lastly, we develop a covid-19 and dengue fever co-infection model and its optimal control analysis. A comprehensive mathematical analysis of this model is undertaken to forecast the dynamics of this co-infection model in humans. The study assists public health services in controlling or reducing the burden of this deadly disease.

We solve the fractional optimal control problems using well-established numerical techniques to verify our theoretical results. The study offers a quantitative analysis of deterministic epidemic models, focusing on varying vaccination and treatment coverage levels. We also examine the influence of threshold parameters across diverse vaccination and treatment coverage levels to extract valuable findings. The numerical results obtained using MATLAB confirm our assertion that co-infection could be eradicated more swiftly when a human population adopts appropriate vaccination and treatment alongside heightened awareness across different coverage levels.