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Research Article

The Fractional SIRC Model and Influenza A

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This paper deals with the fractional-order SIRC model associated with the evolution of influenza A disease in human population. Qualitative dynamics of the model is determined by the basic reproduction number, R_0. We give a detailed analysis for the asymptotic stability of disease-free and positive fixed points. Nonstandard finite difference methods have been used to solve and simulate the system of differential equations.

1. Introduction

Influenza is transmitted by a virus that can be of three different types, namely A, B, and C [1]. Among these, the virus A is epidemiologically the most important one for human beings, because it can recombine its genes with those of strains circulating in animal populations such as birds, swine, horses, and so forth [2, 3]. Over the last two decades, a number of epidemic models for predicting the spread of influenza through human population have been proposed based on either the classical susceptible-infected-removed (SIR) model developed by Kermack and McKendrick [4].

Casagrandi et al. [5] have introduced SIRC model by adding a new compartment C, which can be called cross-immune compartment, to the SIR model. This cross-immune compartment (C) describes an intermediate state between the fully susceptible (S) and the fully protected (R) one. They have studied the dynamical behaviors of this model numerically [6]. Jódar et al. [7] developed two nonstandard finite difference schemes to obtain numerical solutions of a influenza A disease model presented by Casagrandi et al. [5]. Very recently Samanta [6] considered a nonautonomous SIRC epidemic model for Influenza A with varying total population size and distributed time delay.