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Mathematical analysis of an influenza A epidemic model with discrete delay

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Abstract

Recently, a large number of mathematical models that are described by delay differential equations (DDEs) have appeared in the life sciences. In this paper, we present a delay differential model to describe influenza A (H1N1) dynamics. We begin by presenting the model with a brief discussion, followed by proving the positivity and boundedness of the model solution. We establish sufficient conditions for the global stability of the equilibria (the infection free equilibrium and the infected equilibrium), these conditions are obtained by means of the Lyapunov LaSalle invariance principle of the system. Also we have carried out bifurcation analysis along with an estimated length of delay to preserve the stability behaviour. In particular, we show the threshold dynamics in the sense that if (reproduction number) $R_0 < 1$ the infectious population disappear so the disease dies out, while if $R_0 > 1$ the infectious population persist. Sensitivity analysis of the influenza A (H1N1) model reveals which parameter values have a major impact on the model dynamics. Numerical simulations with application to H1N1 infection are given to verify the analytical results.

Keywords: H1N1 Model, Delays, Stability analysis, Sensitivity analysis.

Mathematical Subject Classification (2010): 92B05, 93D05, 34D23, 90C31.

1 Introduction

Over the past one hundred years, mathematics has been used to understand and predict the spread of diseases, relating important public-health questions to basic transmission parameters. From prehistory to the present day, diseases have been a source of fear and superstition. A comprehensive picture of disease dynamics requires a variety of mathematical tools, from model creation to solving differential equations to statistical analysis. Although mathematics has been so far done quite well in dealing with epidemiology but there is no denying that there are certain factors which still lack proper mathematization.

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