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Local and global stability of an HCV viral dynamics model with two routes of infection and adaptive immunity

Communication Info

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Abstract

The aim of this article is to formulate and study a mathematical model describing hepatitis C virus (HCV) infection dynamics. The model includes two essential modes of infection transmission, namely, virus-to-cell and cell-to-cell. The effect of therapy and adaptive immunity are incorporated in the suggested model. The adaptive immunity is represented by its two categories, namely, the humoral and cellular immune responses. Our article begins by establishing some mathematical results through proving the model's well-posedness in terms of existence, positivity and boundedness of solutions. We present all the steady states of the problem that depend on specific reproduction numbers. It moves then to the theoretical investigation of the local and global stability analysis of the free disease equilibrium and the four disease equilibria. Finally, our article presents some numerical simulations to validate the analytical study of the global stability. Numerical simulations have shown the effect of the drug therapies on the system's dynamical behavior.

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