

Abstract Submitted
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Modelling Spread of Oncolytic Viruses in Heterogeneous Cell Populations MICHAEL ELLIS, HANA DOBROVOLNY, Texas Christian University — One of the most promising areas in current cancer research and treatment is the use of viruses to attack cancer cells. A number of oncolytic viruses have been identified to date that possess the ability to destroy or neutralize cancer cells while inflicting minimal damage upon healthy cells. Formulation of predictive models that correctly describe the evolution of infected tumor systems is critical to the successful application of oncolytic virus therapy. A number of different models have been proposed for analysis of the oncolytic virus-infected tumor system, with approaches ranging from traditional coupled differential equations such as the Lotka-Volterra predator-prey models, to contemporary modeling frameworks based on neural networks and cellular automata. Existing models are focused on tumor cells and the effects of virus infection, and offer the potential for improvement by including effects upon normal cells. We have recently extended the traditional framework to a 2-cell model addressing the full cellular system including tumor cells, normal cells, and the impacts of viral infection upon both populations. Analysis of the new framework reveals complex interaction between the populations and potential inability to simultaneously eliminate the virus and tumor populations.

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