A Scalable Engineering Combination Therapies for Evolutionary Dynamic of Macrophages

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Résumé

Abstract

The study of human immunodeficiency virus (HIV) has been the subject of mas- sive scientific research in recent years. Some works have focused on the evolution of the virus mutations developed against the immune system or the combination design therapy. But most of these models are too complex to analyze them in details and to design an optimal combination therapy. The main objective of this paper is about the analysis of the stability and optimal control techniques applied to HIV combination therapy in a nonlinear model, which take in account the mutations and latent cells. We use a L1 controller that stabilize the evolutionary dynamics of HIV disease. Be- cause of the positive nature of the system, this problem can be solved with a scalable iterative algorithm that finds the best medication.Therefore, following recent work of V. Jonsson and R. Murray we introduce a similar algorithm to solve the combination therapy design problem. We obtain efficient results for this nonlinear model and our results show that control theory can still be applied and is powerful on more complex and realistic models.

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