

A mathematical model for the therapy of the HIV infection

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Abstract

In [17] it was introduced a model to describe the dynamics of the HIV infection when the patient is under chemotherapy (either RTI or PI). The main idea in [17] was to introduce the effectiveness of the drug as a dynamical variable. In this paper we pursue the idea starting from an analysis of the fitness of the virus during the therapy. We introduce an adaptive model in which the ability of the viruses to infect the target cells is related to the number of contacts between viruses and T -cells that have been inhibited by the drug. This approach is similar to the model proposed in [10] for a predator-prey system. However the biological interpretation is different here because in this context the adaptation of the virus is due to the development of resistant virus strains. We analyze different combination therapies with three antiviral drugs, which consist of reverse transcriptase inhibitors (RTI) and protease inhibitors (PI) and we show the possibility of very long latency periods, during which the viral load goes below the detectable level. These periods are followed by a rebound followed by the re-establishing of the conditions previous to the therapy. This dynamics is in good qualitative agreement with the available clinical data.

[10] V.W. Noonburg: “Competing species model with behavioral adaptation”, *J. Math: Biol.* 15 (1982), 239–247.

[17] M. Sammartino - L. Seta: “A model for the chemotherapy of the HIV infection with antigenic variation”, *Proceedings of WASCOM 2001*, World Sci. Publishing, River Edge, NJ (2002), 521–526.