A SINGULARLY PERTURBED HIV MODEL WITH TREATMENT AND ANTIGENIC VARIATION

Jorge P. Zubelli\textsuperscript{1} and Nara Bobko\textsuperscript{2}

\textsuperscript{1}Instituto Nacional de Matemática Pura e Aplicada
Rio do Janeiro, RJ 22460-320, Brazil
zubelli@impa.br

\textsuperscript{2}Instituto Nacional de Matemática Pura e Aplicada
Rio do Janeiro, RJ 22460-320, Brazil
narab@impa.br

Abstract

The dynamics of the virions of HIV is much faster than the dynamics of the cells that host the viruses. While CD4\textsuperscript{+} T cells have a half-life of the order of days, virions have a half-life of about a few hours. These two intrinsic time scales of the HIV-1 dynamics leads to a singularly perturbed system. In order to deal with perturbed problems, multiscale analysis techniques have been used in many areas, including biological modeling of infectious diseases in [2, 3].

Using Tikhonov’s theorem, we perform a multiscale analysis of a within-host HIV model. This theorem leads to a way of approximating the solutions of the perturbed system by solutions of a reduced system. The interest in such a reduction lies on the fact that, in many cases, the complexity of the problem is considerably reduced. Indeed, for certain parameters, the system becomes very stiff and the respective reduced system offers a robust approximation, as we shall see here. Furthermore, we show that this reduced system is globally asymptotically stable by using Lyapunov’s stability theory.

REFERENCES