

# Modeling the Dynamics of HIV-1 Decline in Patients on Protease Inhibitor Monotherapy

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Abstract text. Mathematical models shed light on the dynamics of HIV-1 infection in vivo. In this talk, we generalize one of the early models of the dynamics of HIV-1 introduced by Perelson et al. on a nonempty closed subset of real numbers, a so called time scale, see [1] and [2]. We first calculate the total concentration of plasma virions on different time scales and then compare all these models to data obtained from patients. Data we use here is permitted by Perelson, see [3]. In order to achieve our goal, we use MathLab with nonlinear least squares method, estimate parameters such as the virion clearance rate and the rate of loss of infected cells, and calculate adjusted R-squared values of the total concentration of plasma virions on different time scales. We also discuss the results from the fit of the total viral concentrations when the unit of time is in days and in hours.

**Keywords.** Time scales, HIV, dynamic equations, difference equations, systems.

This is a joint work with Gulsah Yeni.

## References

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- [3] A. S. Perelson and P.W. Nelson, Mathematical Analysis of HIV-1 Dynamics in Vivo, *SIAM Rev.* **41** (1999), 3–44.