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Continuous-time branching processes to model viral load in treated HIV+ individuals

We will discuss a continuous-time, multi-type branching model of HIV viral dynamics in the blood stream. We are motivated by observations of viral load in HIV+ patients on anti-retroviral treatment (ART). ARTs very effectively limit viral replication. However, while on ARTs, an HIV+ individual's viral load remains non-zero, and blood tests show occasional viral blips: short periods of increased viral load. We hypothesize that this low viral load can be attributed to activation of cells latently infected by HIV before treatment initiation. Blips then represent small-probability deviations from the mean. Modeling this system as a branching process, we derive equations for the probability generating function. Using a novel numerical approach we extract probability distributions for viral load yielding blip amplitudes consistent with patient data. We then compute distributions on duration of these blips through direct numerical simulation. Our stochastic model of latent cell activation reproduces features of treated HIV infection. It can be used to provide insight into variability of treatment outcomes for HIV+ individuals not available in deterministic models.