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

We will discuss continuous-time, multi-type branching problems to model aspects of HIV-virus and T-cell dynamics in the blood stream. We are motivated by observations of viral load in HIV+ patients on anti-retroviral treatment (ART). While on ART for HIV, an infected individual's viral load remains non-zero, though it is very low and undetectable by routine testing. Further, blood tests show occasional viral blips: very short periods of detectable viral load. We hypothesize that this very low viral load can be explained principally by the activation of cells latently infected by HIV before the initiation of treatment, which constitute a reservoir that has been observed to decay in time. Viral blips then represent large deviations from the mean. Modeling this system as a sub-critical 3-type branching process (latently infected cells, activated cells, virus), 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. This technique also allows us to calculate extinction probability distributions in time, which we relate to extinction of the latent reservoir. We also consider related problems including a 2-type super-critical branching process (virus and target cells only) with small initial numbers representing early HIV infection dynamics, to assess probabilities of infection initiation and early-time viral loads.