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Modeling the evolution of HIV-1 across the within- and between-host scales

HIV-1 is a rapidly replicating retrovirus with dramatically different numbers of replications between scales: within host there are an estimated 4 million cells newly infected each hour whereas between hosts, in the majority of cases, new infections are started by a single virus strain. The rate of evolution of the virus between these fitness landscapes differs, with a greater rate within than between hosts.

We simulate the within-host evolution using a compartmental model with a latent reservoir and stochastically simulate the transmission bottleneck. As the virus evolves within-host, this increased evolution is coupled to between-host fitness by allowing transmission fitness to drift. i.e. there is greater variance of transmission fitness when the virus is a member of a more evolved within-host compartment.

Linking the within- and between-host scales through a stochastic, competitive transmission bottleneck, our results suggest that both the HIV latent reservoir and bottleneck effects contribute to the observed rate of between-host evolution, over the epidemic.