

ROLAND REGÖS

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Estimating the Mutational Fitness Effects Distribution during early HIV infection

Co-Authors: Eva Bons, Frederic Bertels

The evolution of HIV during acute infection is often considered a neutral process. Recent analysis of sequencing data from this stage of infection, however, showed high levels of shared mutations between independent viral populations. This suggests that selection might play a role in the early stages of HIV infection. We adapted an existing model for random evolution during acute HIV-infection to include selection. Simulations of this model were used to fit a global mutational fitness effects distribution (MFED) to previously published sequencing data of the env gene of individuals with acute HIV infection. Measures of sharing between viral populations were used as summary statistics to compare the data to the simulations.

We confirm that evolution during acute infection is significantly different from neutral. The distribution of mutational fitness effects is best fit by distribution with a low, but significant fraction of beneficial mutations and a high fraction of deleterious mutations. While most mutations are neutral or deleterious in this model, about 5% of mutations is beneficial. These beneficial mutations will, on average, result in a small but significant increase in fitness. When assuming no epistasis, this indicates that at the moment of transmission HIV is near, but not on the fitness peak for early infection.