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Computational Approaches to the Population Genetics of Early HIV Infection

During HIV infection, the immune system mounts a vigorous response in the form of T cell and antibody attack. In early HIV infection, this response has been shown to be a significant selective force on the infecting HIV population. Through mutation, the HIV population can escape such selection.

From a population genetics perspective, modeling early HIV infection posses significant challenges. The immune system mediated selection is complex, HIV mutation rates are high, and the dynamics of the HIV population are non-linear. The combination of these issues in a single model raises many novel theoretical and computational population genetics related questions.

In this talk I will discuss a population genetics model of early HIV infection. Using this model as a basis, I will then discuss several computational approaches that can be used to investigate the nature of HIV evolution under immune system attack during early infection.