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Sampling HIV intrahost genealogies based on a model of acute stage CTL response

Genealogy based methods have become a common tool in analyzing intrahost HIV evolution. These methods require a coalescent model which implicitly describes the role of evolutionary forces in shaping HIV genealogies. Currently, HIV genealogies are constructed assuming variants of the Kingman coalescent. The Kingman coalescent is a generic coalescent model that does not explicitly account for the special features of HIV evolution. For example, the Kingman coalescent does not account for the role of CTL attack.

In this talk we introduce a coalescent model of the acute stage that explicitly incorporates the role of early CTL attack. Using this coalescent model, we develop a computational method that allows us to sample HIV genealogies shaped by CTL attack. We show that such genealogies are different in form than Kingman coalescent genealogies. We use our genealogy sampler to explore the type of CTL attack that is best at controlling HIV diversity. Our work is a first step in developing computational tools that can use HIV genetic data to infer parameters describing CTL attack.