Reconstruction of an HIV Transmission History in a Bayesian Coalescent Framework

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Abstract. We examine the relationship between viral evolutionary history and transmission history using a Bayesian coalescent approach. For 11 patients in a known heterosexual HIVtransmission chain, at least one sample was obtained and two regions were amplified and cloned. Timed evolutionary histories were inferred and a population genetic perspective was adopted to evaluate the compatibility with the timed history of infection events. We show that particular clusterings in the *pol* and *env* genealogies result in divergence times incompatible with the transmission history. In addition, we could infer the direction of transmission for several infections. For the earliest transmission, with an unknown direction, no clear population genetic preference for a transmission direction could be obtained. Furthermore, we introduce a new demographic prior whereby we condition the viral population history for each patient separately on the intra-host taxa. Crucially, the demographic history is shared between patients, such that strength is given from patients with sumptuous within-host information to patients with more concise within-host sampling schemes. We use this model to characterize the bottleneck associated with HIV transmission. Finally, we demonstrate its utility in estimating the evolutionary rates at the within and between host level

for both the *pol* and *env* region of the HIV-1 genome. We hereby find that multiple transmissions are required before the action of drift at transmission leads to a measurably slower rate of HIV-1 evolution at the epidemic scale.