Jun 1st, 9:30 AM - 10:00 AM

Modeling stochastic viral evolution: A multiscale Wright Fisher model

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https://scholarscompass.vcu.edu/bamm/2018/friday/5

Abstract

Viral evolution is influenced by both demographic changes during infection at the in-host level and transmission at the between-host level. Here we implement a Wright-Fisher model at both the host and the population level. We analyze how key parameters including bottleneck size, time between transmission events, and selection impact probability of fixation and time to fixation. Both host population and bottleneck size have a role in determining probability of fixation. As the time between transmission events increases, generations to fixation is practically entirely dependent on host population size. This model provides a quantitative framework to study how population dynamics alter evolutionary dynamics in viruses across scales.

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