

Stochastic Modeling Reveals New Mechanisms of Pathogen Evolution

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Abstract

Epidemiological and evolutionary processes are inherently stochastic since we can never know with certainty exactly how many descendants an individual will leave, what the phenotypes of those descendants will be, or what environments they will encounter. Despite this, models of pathogen evolution have nearly all been deterministic, treating values such as transmission and virulence as parameters that can be known ahead of time. We present a broadly applicable analytic approach for modeling pathogen evolution in which vital parameters such as transmission and virulence are treated as random variables, rather than as fixed values. We start from a general stochastic model of evolution and show how to derive from this specific equations for the evolution of transmission and virulence. We illustrate this using an SIR model for the pathogen but show how our approach can be applied to other models of pathogen dynamics. We show that allowing transmission and virulence to have distributions of possible values does more than just introduce noise into our results, it reveals new evolutionary forces that are invisible to deterministic models. In particular, since the virulence and transmission potential of a pathogen are now random variables, they can covary within an individual. We show that this within individual covariation has a clear biological interpretation and will be predictably different for different kinds of pathogens. Finally, we discuss general principles concerning how stochastic variation in vital parameters can influence evolutionary epidemiological dynamics. This research is confined to between-host evolution.
