Modeling evolution using the probability of fixation

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Abstract

Here I will describe, and attempt to explain, the surprisingly complex history of a class of widely used population-genetic models. The distinguishing feature of these models is that they express the rate of evolution as the product of 1) the rate at which a particular mutant originates within the population and 2) the probability that a newly introduced mutant of that type will go to fixation. Although from today's perspective it might seem very obvious to go from a probability of fixation such as 2s (a classical result due to Haldane, 1927) to expressing the rate of evolution as K=2Nu*2s=4Nus, in fact such models were wholly absent from the classical literature and only emerged as part of the molecular revolution during the late 1960s. Indeed, I will argue that such models are incompatible with the Modern Synthesis, and in essence formalize verbal models for evolution first proposed by the so-called Mutationists at the turn of the century. I will also describe the subsequent development of these models from the 1980s until today, highlighting in particular a highly parallel structure in which multiple independent literatures reinvented the same basic set of elaborations.

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