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Benjamin Allen* (allenb@emmanuel.edu), 400 The Fenway, Boston, MA 02115. *How to compute the fixation probability of just about anything (under weak selection).*

Evolution is driven by the arrival and fixation of mutations. “Fixation” refers to a single new mutation ultimately spreading throughout a population. The probability that this occurs depends on the mutation’s effect on the bearer, as well as interactions with other organisms, spatial structure, mating, replacement patterns, and other factors. Calculating fixation probabilities can therefore be difficult, even in idealized mathematical models. I will present recent work on a unifying mathematical framework for modeling natural selection in populations with arbitrary spatial structure and behavioral interactions. This framework leads to a general polynomial-time algorithm for calculating fixation probabilities, under the assumption that selection is weak. I will apply this method to compute fixation probabilities of weakly selected mutations in graph-structured populations. (Received January 24, 2022)