

Numerical Methods for Branching Process Models - Applications to Processes Involving Rare Recombination And Mutation

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Abstract: Branching process models have a long history of biological applications. While the theory can be quite cumbersome, numerical methods have yielded detailed insight into some important biological processes. Here we formulate branching process models of genetic recombination and mutation, where there are both new events, modeled by immigration, and proliferation of old events by replication. We derive numerical means, variances, and distributions of biologically relevant quantities. As an example, these methods can be used to determine the relative contribution of new vs. old genetic events. The balance between new vs. old events determines the applicability of haplotype mapping and can guide treatment strategies for pathogens that acquire genetic resistance to treatment.