

Marek Kimmel,
Department of Statistics, Rice University,
and Silesian University of Technology, Gliwice, Poland

Simple but interesting genetic models

Abstract

The talk describes two simple models concerning aspects of genetic drift, mutation and recombination, combined with demography.

In the first model, we investigate how the estimates of the distributions of the time to coalescence depend on the model within which they have been formulated. Most widely used models assume simplifications such as deterministic population size. The question arises how robust they are for populations evolving stochastically. One interesting example which comprises stochasticity is O'Connell limit theory of genealogy in branching processes. Our paper explores how fast, in terms of number of generations, the limiting distributions of O'Connell are adequate descriptions of transient distributions. We perform extensive simulations of slightly supercritical branching processes and compare the results with O'Connell limits. Coalescent computations under the Wright-Fisher model are compared with limiting O'Connell results and with full genealogy-based expectations. These expectations are used to estimate the corrected age of the root of the mitochondrial polymorphism of modern humans based on DNA from humans and Neanderthal fossils.

In the second model, we extend the theoretical treatment of the Moran model of genetic drift with recombination and mutation, previously introduced by us for two loci, to the case of n loci. In the works of Griffiths, Hudson and Kaplan and others important properties were established using the coalescent approach. The specific framework we use allows finding close-form relationships, which however are limited to a set of distributions, which jointly characterize allelic states at a number of loci at the same or different chromosome(s) but which do not jointly characterize allelic states at a single locus on two or more chromosomes. However, the system is sufficiently rich to allow computing all possible multipoint linkage disequilibria under recombination, mutation and drift. We explore the algorithms enabling construction of the transition probability matrices of the Markov chain describing the process. We find that asymptotically the effects of recombination become indistinguishable, at least as characterized by the set of distributions we consider, from the effects of mutation and drift. Mathematically, the results are based on the theory of semigroups of operators.

Research carried out jointly with Adam Bobrowski, Krzysztof Cyran and Tomasz Wojdyla.