

Mathematical & Computational Biology Seminar

Organizer: Valerie Hower

Wednesday, 2:00–3:00pm, 939 Evans

Aug. 26 **Paul Jenkins**, UC Berkeley

An asymptotic sampling formula for the coalescent with recombination

Sampling distributions play an important role in population genetics analyses, but closed-form sampling formulas are generally intractable to obtain. In the presence of recombination, there is no known closed-form sampling formula that holds for an arbitrary recombination rate, and sample configuration probabilities must typically be evaluated by computationally-intensive Monte Carlo techniques. In this talk, I describe how it is possible to obtain useful closed-form results in the case the population-scaled recombination rate ρ is large but not necessarily infinite. Specifically, I consider an asymptotic expansion of a two-locus sampling formula in inverse powers of ρ and obtain closed-form expressions for the first few terms in the expansion. This yields an asymptotic sampling formula for approximating two-locus likelihoods, which applies to arbitrary sample sizes and configurations. It is also universal in the sense that the functional form of the asymptotic sampling formula is common to all models of mutation. Two applications of the asymptotic sampling formula will be discussed: evaluating two-locus likelihoods in a pairwise composite likelihood, and in classifying the maximum likelihood estimate of ρ as either finite or infinite. This is joint work with Yun Song.