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Evolution in a spatial continuum.

Abstract:

Classical models for gene flow fail in (at least) three ways. First they cannot explain patterns in data observed over large scales, second they predict much more genetic diversity than is observed and third they assume that genetic loci evolve independently. In collaboration with Nick Barton we recently proposed a new framework for modelling populations evolving in a spatial continuum that addresses these issues. In this talk we describe the new framework and some asymptotic results for the genealogy of a sample from a population living on a two-dimensional torus. These results are joint work with Amandine Veber.