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Inference with selection, varying population size and evolving population structure: Application of ABC to a forward-backward coalescent process with interactions

Abstract: This is joint work with Clotilde Lepers, Matthieu Porte, Sylvie Méléard and Viet Chi Tran.

Genetic data are often used to infer history, demographic changes or detect genes under selection. Inferential methods are commonly based on models making various strong assumptions: demography and population structures are supposed *a priori* known, the evolution of the genetic composition of a population does not affect demography nor population structure, and there is no selection nor interaction between and within genetic strains. We present a stochastic birth-death model with competitive interaction to describe an asexual population, and we develop an inferential procedure for ecological, demographic and genetic parameters. We first show how genetic diversity and genealogies are related to birth and death rates, and to how individuals compete within and between strains. Second, we develop an Approximate Bayesian Computation framework for analyzing genetic data. By analyzing simulated data, we show that the procedure give accurate estimate of the parameters of the model. We finally carry an illustration on real data and analyze the genetic diversity of microsatellites on Y-chromosomes sampled from Central Asia populations in order to test whether different social organizations show significantly different fertilities.