Abstract Submitted
for the MAR17 Meeting of
The American Physical Society

Minimal-assumption inference from population-genomic data DANIEL WEISSMAN, Emory University, OSKAR HALLATSCHEK, UC Berkeley — Samples of multiple complete genome sequences contain vast amounts of information about the evolutionary history of populations, much of it in the associations among polymorphisms at different loci. Current methods that take advantage of this linkage information rely on models of recombination and coalescence, limiting the sample sizes and populations that they can analyze. We introduce a method, Minimal-Assumption Genomic Inference of Coalescence (MAGIC), that reconstructs key features of the evolutionary history, including the distribution of coalescence times, by integrating information across genomic length scales without using an explicit model of recombination, demography or selection. Using simulated data, we show that MAGIC's performance is comparable to PSMC' on single diploid samples generated with standard coalescent and recombination models. More importantly, MAGIC can also analyze arbitrarily large samples and is robust to changes in the coalescent and recombination processes. Using MAGIC, we show that the inferred coalescence time histories of samples of multiple human genomes exhibit inconsistencies with a description in terms of an effective population size based on single-genome data.

Daniel Weissman
Emory University

Date submitted: 11 Nov 2016 Electronic form version 1.4