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Exact inference from non-neutral Wright-Fisher bridges

Recent advances in genome sequencing technology have allowed for the collection of vast datasets and enabled inference from allele frequency time series data, for which the Wright-Fisher diffusion is a standard model. Owing to the intractability of the Wright-Fisher diffusion transition density, most approaches have relied on time-discretisation which introduces a bias that is difficult to quantify. I will describe an MCMC algorithm for a discretely observed Wright-Fisher diffusion which acts directly on the space of diffusion paths, with no discretisation. The method is thus exact in the sense that the MCMC output targets the true posterior distribution of the underlying path, and of static parameters quantifying evolutionary forces such as mutation and selection.
This is joint work with Jaromir Sant, Paul A. Jenkins, and Dario Spanò.