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*Dirichlet approximation of equilibrium distributions in Cannings models with mutation*

**Abstract**

Consider a haploid population of fixed finite size with a finite number of allele types and having Cannings exchangeable genealogy with neutral mutation. The stationary distribution of the Markov chain of allele counts in each generation is an important quantity in population genetics but has no tractable description in general. We provide upper bounds on the distributional distance between the Dirichlet distribution and this finite population stationary distribution for the Wright-Fisher genealogy with general mutation structure and the Cannings exchangeable genealogy with parent independent mutation structure. In the first case, the bound is small if the population is large and the mutations do not depend too much on parent type; "too much" is naturally quantified by our bound. In the second case, the bound is small if the population is large and the chance of three-mergers in the Cannings genealogy is small relative to the chance of two-mergers; this is the same condition to ensure convergence of the genealogy to Kingman's coalescent. These results follow from a new development of Stein's method for the Dirichlet distribution based on Barbour's generator approach and a probabilistic description of the semigroup of the Wright-Fisher diffusion due to Griffiths, and Li and Tavaré. Joint work with Han L. Gan (Northwestern) and Adrian Röllin (NU Singapore).