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Quantifying convergence of the Kingman coalescent via the ancestral process per generation

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Error threshold being the forefront of the issue for computationally-intensive methodologies and statistical models based on Kingman's coalescent, six main points arise: (i) discrepancy between the exact and linearized non-coalescence probability; (ii) validity of the linearized coalescence probability; (iii) conditional probabilities of single-pair and multi-coalescences given at least one coalescence; (iv) parity of reduced ancestral processes that suppress multi-coalescences, when compared to the exact ancestral process; (v) genealogical topology; and (vi) subsequent inter-arrival times. Regions of adherence and detraction from the Wright-Fisher ancestral process were identified, in terms of transition probabilities and expected inter-arrival times, due to the linearization of Kingman's coalescent that neglects multi-coalescence events. Empirically, expected genealogical parity of the single-pair restricted Wright-Fisher haploid model exceeds 99% where $n \leq \frac{1}{2} \sqrt[3]{N}$; similarly, per expected interval where $n \leq \frac{1}{2} \sqrt{\frac{N}{6}}$. Quantitative parametric analysis on the varieties of multi-coalescence events in restricted Wright-Fisher models, rather than stochastic realization, avoids elaboration of the genealogical sample space under multi-coalescence. Mutational activity, such as site frequency spectra, will not be accurately measured with the Kingman coalescent when sample sizes exceed these criteria.

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