

On a Class of Genetic Genealogical Tree Models

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The field of Feynman-Kac path measures, and their genealogical tree interpretation models is one of the most active contact points between probability, statistics, biology, physics, and engineering sciences, including rare event analysis, and advanced signal processing.

The common aspect of all these applications is that they represent path integration of free Markov particle evolutions, weighted by some potential functions. The models we consider belong to the general class of branching and interacting particle systems. Particles explore the state space as a free Markov evolution; during their exploration particles with low potential are killed, while the ones with high potential value duplicate. From a more probabilistic point of view, these genetic type particle models can also be interpreted as stochastic linearization, or as sophisticated interacting acceptance-rejection type simulation techniques.

In the first part of this talk we give an overview of these application model areas. In the second part, we briefly present some of the recent mathematical ideas that have improved our understanding of these stochastic algorithms, including propagation of chaos analysis with precise algebraic tree-based functional representations of particle block distributions.