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Stochastic Process Models in Population Genetics: Forward and Backward in Time

概要

Classical stochastic process models in population genetics describe how a population of genes evolves forward in time under random drift, mutation, selection and recombination. Examples are the Wright-Fisher diffusion process; Moran models, which are birth and death processes; and Cannings models, where parents have an exchangeable offspring distribution. Coalescent models, which are random trees or graphs, describe the ancestral lineages of samples of genes back in time. These backwards and forwards models belong together technically as dual stochastic processes. This talk will discuss examples of forwards and backwards in time models. Forwards the models are the Wright-Fisher diffusion process; Fleming-Viot diffusion process describing DNA sequence evolution; and Moran model with multiple offspring and selection. The backwards models describing ancestral lineage history are respectively the Kingman coalescent process; Gene trees which are perfect phylogenies constructed from mutation patterns on DNA sequences; and branching coalescing lineage graphs.

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