Population models as partial observations of genealogical models

Abstract:
Classical models of biological populations, for example, Markov branching processes, typically model population size and possibly the distribution of types and/or locations of individuals in the population. The intuition behind these models usually includes ideas about the relationships among the individuals in the population that cannot be directly recovered from the model. This loss of information is even greater if one employs large population approximations such as the diffusion approximations popular in population genetics. “Lookdown” constructions provide representations of population models in terms of countable systems of particles in which each particle has a “type” which may record both spatial location and genetic type and a “level” which incorporates the lookdown structure which in turn captures the genealogy of the population. The original population model can then be viewed as the result of the partial observation of the more complex model. We will exploit ideas from filtering of Markov processes to make the idea of partial observation clear and to justify the lookdown construction.

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