



Spatial population models

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Abstract. These notes are intended to provide a very rapid introduction to some of the mathematical models of theoretical population genetics. We shall be particularly concerned with models that are designed to capture the interplay between spatial structure and various forces of evolution. However, we begin with a brief review of some classical non-spatial models (the Wright-Fisher and Moran models and their diffusion approximations) and the corresponding (backwards in time) Kingman coalescent which describes the genealogical relationships between individuals sampled at random from the population.

Our first spatial model is Kimura's stepping stone model of subdivided populations, which we use to capture information about the way in which the correlation between genetic types of individuals sampled from the population decays with spatial separation.

The stepping stone model is not a particularly natural model for populations evolving in a spatial continuum and we next turn our attention to the challenges of modelling evolution in a spatial continuum, describing, in particular, Felsenstein's 'pain in the torus'. The spatial Lambda-Fleming-Viot model is then presented as one resolution of the pain in the torus, and the rest of the notes are devoted to developing that model and illustrating how it captures some of the features seen in data, before using it to investigate the interplay between spatial structure and natural selection.

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