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Genetic variation in natural populations: a modeller's perspective

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The thesis is available at

http://physics.gu.se/~rmarina/Marina_Rafajlovic/Home_files/PhD.pdf

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Abstract

Thanks to advances in genome sequencing, empirical patterns of within- and between-species genetic variation are readily available. By studying these patterns much has been learned about the evolutionary histories of species. But the causes and consequences of different evolutionary histories are still difficult to tell apart. To this end, comparative analyses of genetic variation under different models are required. This thesis analyses genetic variation under specific models that are relevant for a number of biological species.

Firstly, this thesis discusses a method for inferring the population-size history of the population in question using simulated, as well as empirically observed frequency spectra of mutations. The method performs well when applied to simulated data, provided that a large number of mutations is sampled. However the estimation based on empirical data is biased. Secondly, the thesis studies a mainland-island colonisation model. The model allows for different levels of multiple paternity in the population. Multiple paternity promotes genetic variation. This effect is much larger during colonisation than on the long run. Therefore, multiple paternity may facilitate the establishment of species in new areas. Thirdly, this thesis analyses a colonisation model for species that reproduce both sexually and asexually, and have limited dispersal capabilities. Due to limited dispersal capabilities, sexual reproduction may be hindered locally, especially during colonisation. Unless the individuals are highly sexual, a few clones establish the front of the colonisation forming wide clonal colonies. Finally, this thesis analyses a joint effect of migration, selection and random genetic drift during adaptation in subpopulations subject to different environments. When divergent adaptation is driven by mutations, the frequency at which mutations appear, as well as how strongly they are selected for are the decisive parameters for whether or not subpopulations can adapt to their respective environments despite migration and drift. This remains to be analysed further.

Keywords: *coalescent process, site frequency spectrum, multiple paternity, dominant clone, divergent selection.*