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Stochastic Models in Population Genetics : Coalescent, Ancestral Process

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Abstract

The aim of these talks is to present a brief review of genealogical or coalescent methods, which are very useful in interpreting and understanding a wide range of population genetic data. A lot of different models will be showed, from discrete to continous ones, from simple to more complicated ones, taking into account different evolutionary aspects like mutation, selection, variable population size, geographical structure, etc.

Main subjects of the talks :

Wright-Fisher Model, then with mutation, selection

Most Recent Common Ancestor, Tree Length, Estimating Mutation Rate

Continuous Model : Kingman's Coalescent, Ancestral Process

Generalizing to : variable population size, geographical structure, segregation, selection, recombination...