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Computational Model of Genetic Demographic Networks

Demographic network is defined as a set of populations evolving from a single ancestral population with a beginning at the time 0. The structure of the network is described by two types of events: split of a single population into two populations and merger of two populations. Additionally, we incorporate migration between populations coexisting in the model.

There are several models available in the literature that can be used to analyze data from such demographic networks. Most of them are based on backward-time coalescent simulations and require considerable computational power. In this paper we introduce a forward-time and time-continuous model that allows to calculate the exact values of the entries of the infinite matrixes $R_{ij}(t)$ being the joint distributions of pairs of alleles sampled at the time t from populations i (first allele from a pair) and j (second allele). We assume that individuals in each population in the network are described by the same allelic space model and we introduce mutation to the model using intensity matrices Q_i of the Markov chain of the mutation process in population i. Mutation model is assumed unchanged between two adjacent demographic events. Population size growth can be specified for each population. Evolution of the joint distributions between network events is described by Lyapunov differential equations.

In our work we present mathematical details of the model and a computer program implementing this model along with several applications. We also discuss some improvements to our model, such as optimization of the computational complexity for some common mutation models and calculating the joint distributions of a sample of size greater that 2.

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