

The use of haplotype statistics to infer demographic parameters

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A population's demographics in the past leaves its fingerprint on the current genetic polymorphism. Recently, there has been an enormous growth in the amount of genetic data available. The current methods for handling genetic data are geared for a small number of sequences and are not appropriate for large samples. In our work, we developed new methods that are based on the tools and concepts of statistical mechanics, and can treat large samples smoothly.

One of the tools that we developed is a model for allele frequency distribution. By comparing the solution of the model to simulated and real data, one can retrieve the demographic parameters of the past (e.g. population size and growth rate). Our method is superior to the common methods in that it gives an unbiased estimator of the growth rates, and can also be applied to cases where the mutation rate is too small for the phylogenetic tree to be reconstructed.