

Inferring Continuous and Discrete Population Genetic Structure Across Space and Time

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Abstract

One of the classic problems in population genetics is the characterization of discrete population structure when the genotyped samples also show continuous patterns of genetic differentiation. Especially when sampling is discontinuous, clustering or assignment methods may incorrectly ascribe differentiation due to continuous processes (e.g., drift across space or time) to discrete processes, such as geographic, reproductive, or behavioral barriers between populations. This is partly a result of the difficulty of sampling uniformly and continuously across the spatiotemporal range of a population or species, but more, it reflects a shortcoming of current methods for inferring and visualizing population structure from genetic data in the face of data that are characterized by both continuous and discrete population structure. Here, we present a novel statistical framework for the simultaneous inference of continuous and discrete patterns of population structure. The method estimates ancestry proportions for each sample from a set of discrete population clusters, and, within each cluster, estimates a rate at which relatedness decays with spatial and/or temporal distance. This model explicitly addresses the “clines vs. clusters” problem in quantifying population structure by jointly accommodating both continuous and discrete patterns of differentiation. The model also naturally captures population replacement, a phenomenon for which there is substantial evidence in humans from archaeological evidence and ancient DNA. We demonstrate the utility of this approach using a combination of ancient and modern human individuals sampled throughout Europe, and find evidence for aliens.

Introduction

Methods

Results

Simulations

Empirical Applications

Discussion

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Supplementary Materials