THE UNIVERSITY OF CHICAGO

Department of Statistics

MASTER'S THESIS PRESENTATION

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Statistical Approaches to Investigate Population Structure in Ancient DNA

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ABSTRACT

The field of ancient DNA (aDNA) has seen rapid growth in the last few years. For example, the amount of available aDNA data has increased dramatically (from 1-3 individuals to >1000 today). A central goal in aDNA is to better understand the relationship between different ancient populations. Many of the pre-existing approaches to study population structure in aDNA are difficult to interpret and only utilize a fraction of the reads. Here, we present scalable approaches to investigate population structure that are easier to interpret, and that do not discard any of the data. First, we develop an approach to estimate genetic distances between individuals using all the read level-data. The main idea here is that we can provide a standard summary statistic (the genetic distance matrix) that can be used as input for various downstream statistical procedures, such as PCA. Next, we develop a statistical method to infer and visualize genetic variation across time and space using read-level data. More formally, we model hetereozygosity as a Gaussian Process across time and space. We apply our methods to a dataset of 153 ancient individuals from Great Britain sampled between 3000-6000 years ago.

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