



THE UNIVERSITY OF
CHICAGO

Department of Statistics

MASTER'S THESIS PRESENTATION

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Inferring Population Structure with Pooled Genetic Data

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ABSTRACT

Population structure is of great interest since it is potentially a confounder in association studies. It is also valuable in inferring evolution of human history. Various methods were proposed and showed accurate in both simulations and real datasets. However, with denser markers and accumulated individuals, computation for model-based methods is notoriously expensive, and working with summary-level data is computationally cheaper. In addition, due to privacy individual genotypes are usually not reported in publication. It is thus desirable to learn population structure from summary-level data. In this paper, we show that proportions of populations in a pooled dataset can be restored, given the reference panel for underlying populations. We demonstrate our method with simulations and data in 1000 Genome Project. The method helps match cases with publicly available controls and potentially provides better statistical power.

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