

The geometry of admixture in population genetics: the blessing of dimensionality

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Abstract

We present a geometry-based interpretation of the f -statistics framework, commonly used to determine phylogenetic relationships from genetic data. The focus is on the determination of the mixing coefficients in population admixture events subject to post-admixture drift. The interpretation takes advantage of the high dimension of the dataset and analyzes the problem as a dimensional reduction issue. We show that it is possible to think of the f -statistics technique as an implicit transformation of the genetic data from a phase space into a subspace where the mapped data structure is more similar to the ancestral admixture configuration. The positive effect of the map can be explicitly assessed. The overarching geometric framework provides slightly more general formulas than the f -formalism by using a different rationale as a starting point. Explicitly addressed are two- and three-way admixtures. The mixture proportions are provided by suitable linear fits in two or three dimensions that can be easily visualized. The developments and findings are illustrated with numerical simulations from real world datasets.

Keywords: population admixture; f -statistics; genetic drift; dimensional reduction

Introduction

The determination of admixture proportions in hybrid populations is a central topic in population genetics. At large evolutionary time scales, a population admixture event can be thought of as a sudden process in which a new lineage emerges as the genetic weighted combination of two or more donors, in its simplest formulation.

The formalism known as f -statistics Patterson *et al.* (2012); Haak *et al.* (2015); Lazaridis *et al.* (2016); Peter (2016); Lipson (2020); Eadaoin Harney *et al.* (2021); Peter (2022), which deals with allele-sharing correlations between two, three and four populations, is a commonly used technique to determine the admixture coefficients. Despite their simple computation and definition, the f -statistics outcome assessment may not be straightforward Lipson (2020). We develop a geometry-based interpretation of f -statistics intended to deepen understanding of the population admixture problem. Geometric-like methods have already been raised in the past Cavalli-Sforza (1966); Cavalli-Sforza and Piazza (1975); Cavalli-Sforza *et al.* (1994); Long (1991); Oteo-García (PhD thesis, 2020); Agrawal-Tamir *et al.* (2021). The strength of our approach is to take advantage of the high dimensionality of the problem, broadening the f -formalism toolkit.

Whenever the genetic information from the original populations is available, determining the admixture proportions is straightforward. However, the evolutionary history of the original populations manifests itself, for example, in random changes in allele frequencies, a phenomenon known as genetic drift. Although ancient DNA can sometimes aid in estimating admixture proportions by providing better proxies, the time elapsed since

admixture and the possibility that the putative parents themselves are extinct make accurate estimates difficult. Moreover, a population may experience over time continuous, discrete, occasional, or repeated genetic influx from other or multiple others, which makes the issue more challenging. The present study is concerned with the approximation of admixture proportions in populations that are assumed to have evolved in time via genetic drift. A dataset with population allele frequencies corresponding to a large number of Single Nucleotide Polymorphisms (SNPs) is the common starting point for dealing with this question.

The population admixture problem may be posed as a geometric issue in a phase space, the allele frequency space, where each population is represented by a point and each axis corresponds to a SNP in the dataset Oteo-García and Oteo (2021). With only three SNP, Figure 1 outlines the nature of the problem. Populations i, a', b', x, b, j , are assumed to be related by phylogenetic trees and are located in phase space by their position vectors whose coordinates are given by the allele frequencies in the dataset. At the time of admixture, we have three co-linear points, a', x', b' , with a' and b' the donors and x' the hybrid. Then, they describe Brownian-like trajectories because allele frequencies undergo small random changes as a result of genetic drift, resulting in population proxies a, x, b .

Populations i and j , which appear as spectators in the Figure 1, will be referred to as auxiliary populations and will play an important role. Any population related to the admixture contributors via phylogenetic trees may be considered as auxiliary. The Brownian-like trajectory depicted from b to j is

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the most complex ecosystems of all even in some cases where they are subject to intense management This complexity which equally comprises biotic and abiotic factors varying both in time and space makes extremely high demands on the adaptational capacity and thus flexibility of the carriers of such an ecosystem Longevity combined with immobility during the vegetative phase however appears to contradict the obvious necessity of adaptational flexibility in forest tree populations when compared with short lived and or mobile organisms

Population Genetics of Multiple Loci Freddy B.

Christiansen,2000-01-10 Population Genetics of Multiple Loci F B Christiansen University of Aarhus Denmark This is a very beautiful and powerful study of an area that Christiansen has dominated for many years Marcus Feldman Stanford University USA Population genetics thrives on the constant interaction between theoretical and empirical knowledge In the first instance population genetics was developed using one locus two allele models for genetic variation The simplicity of these models opened up theoretical developments in population and evolutionary genetics to biologists without specialist training in mathematics Population genetics of multi allelic loci is more complex and requires more mathematical insight and its study is predominantly undertaken by mathematical biologists Traditional formulations of multi locus theory do not simplify by assuming two alleles per locus In this elegant presentation the author provides a formulation of multi locus population genetics that retains the simplicity of two allele models Provides an accessible and natural extension of classical population genetics to multiple loci Exposes the population genetic aspects of sexual reproduction Describes the complexity of evolutionary interactions among genes Provides the background for insight into the functioning of genetic algorithms applied in computer science Written by a world leader in the field The book is divided into two main sections Part I Recombination and Segregation includes coverage of random mating inbreeding migration and mixing Part II Selection covers numerous phenomena involving natural selection including viability fertility mutation and migration The author has successfully presented the theory in a way that is intelligible to anyone with a reasonably good background in basic mathematics and is devoted to learning multiple loci population genetics The text is primarily aimed at advanced undergraduate and postgraduate students and researchers interested in genetics and population biology It is also essential reading for those working or researching in biomathematics and adaptive computing

NBS Special Publication ,1970 **Theory of Population Genetics and Evolutionary Ecology** Joan Roughgarden,1979 This is a reprint of a classic which synthesizes population genetics and population genetics to form one of the first books on evolutionary ecology Written by one of the foremost authorities in the field it is designed as an introduction useful to readers at various levels from diverse backgrounds It features balanced readable coverage of both elementary and advanced topics that are essential to those interested in evolutionary biology ecology animal behavior sociobiology and paleobiology

Mathematical Population Genetics 1

Warren J. Ewens,2012-10-01 Population genetics occupies a central role in a number of important biological and social undertakings It is fundamental to our understanding of evolutionary processes of plant and animal breeding programs and of

various diseases of particular importance to mankind This is the first of a planned two volume work discussing the mathematical aspects of population genetics with an emphasis on the evolutionary theory This first volume draws heavily from the author's classic 1979 edition which appeared originally in Springer's Biomathematics series It has been revised and expanded to include recent topics which follow naturally from the treatment in the earlier edition e g the theory of molecular population genetics This book will appeal to graduate students and researchers in mathematical biology and other mathematically trained scientists looking to enter the field of population genetics Mathematical Reviews ,1994

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Acta Botanica Academiae Scientiarum Hungaricae ,1983 **Journal of Mathematical Biology** ,1985 Publishes papers in which mathematics is used to understand biological phenomena and mathematical papers which answer questions arising from models of biological phenomena Principles of Population Genetics Daniel L. Hartl,Andrew G. Clark,1989 Darwinian evolution in mendelian populations Random genetic drift Mutation and the neutral theory Natural selection Inbreeding and other forms of nonrandom mating Population subdivision and migration Molecular population genetics Evolutionary genetics of quantitative characters Ecological genetics and speciation **Genetic Diversity in Establishing Plant Populations** Steven H. Rogstad,Stephan Pelikan,2011-09-02 The new research described in this book demonstrates that the interplay of a host of founding conditions can frequently produce profound differences in population expansion rates and maintenance of genetic diversity in contrasting populations that differ often only to slight degrees in initial founding conditions The goals of this book are twofo Proceedings of the National Academy of Sciences of the United States of America National Academy of Sciences (U.S.),1926 Foundations of Biology Paul Weingartner,Georg Dorn,1986 *The American Naturalist* ,2009

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