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# 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 linage 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); Éadaoin 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); Agranat-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 $i, a', b', a, b, j$, are assumed to be related by phylogenetic treeness 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 treeness may be considered as auxiliary. The Brownian-like trajectory depicted from $b$ to $j$ is

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**The Geometry Of Population Genetics:**

The Geometry of Population Genetics Ethan Akin,1979-11-01    Information Geometry and Population Genetics Julian Hofrichter,Jürgen Jost,Tat Dat Tran,2017-02-23 The present monograph develops a versatile and profound mathematical perspective of the Wright Fisher model of population genetics This well known and intensively studied model carries a rich and beautiful mathematical structure which is uncovered here in a systematic manner In addition to approaches by means of analysis combinatorics and PDE a geometric perspective is brought in through Amari s and Chentsov s information geometry This concept allows us to calculate many quantities of interest systematically likewise the employed global perspective elucidates the stratification of the model in an unprecedented manner Furthermore the links to statistical mechanics and large deviation theory are explored and developed into powerful tools Altogether the manuscript provides a solid and broad working basis for graduate students and researchers interested in this field    **Information Geometry and the Wright-Fisher Model of Mathematical Population Genetics** Tat Dat Tran,2012    **Population Genetics, Molecular Evolution, and the Neutral Theory** Motoo Kimura,1994 One of this century s leading evolutionary biologists Motoo Kimura revolutionized the field with his random drift theory of molecular evolution the neutral theory and his groundbreaking theoretical work in population genetics This volume collects 57 of Kimura s most important papers and covers forty years of his diverse and original contributions to our understanding of how genetic variation affects evolutionary change Kimura s neutral theory first presented in 1968 challenged the notion that natural selection was the sole directive force in evolution Arguing that mutations and random drift account for variations at the level of DNA and amino acids Kimura advanced a theory of evolutionary change that was strongly challenged at first and that eventually earned the respect and interest of evolutionary biologists throughout the world This volume includes the seminal papers on the neutral theory as well as many others that cover such topics as population structure variable selection intensity the genetics of quantitative characters inbreeding systems and reversibility of changes by random drift Background essays by Naoyuki Takahata examine Kimura s work in relation to its effects and recent developments in each area    Population Genetics in Forestry Hans-Rolf Gregorius,2013-03-13 When we consider the main object of forestry the tree it immediately becomes clear why experimental population geneticists have been so hesitant in making this object a primary concern of their research Trees are very long living organisms with generation intervals frequently exceeding those of their investigators by multiples They virtually exclude therefore application of the classical methods of population genetics since these are based on observing genetic structures over generations This situation where the limits set to observation are so severe particularly requires close cooperation between theory and experiment It also requires careful consideration of results obtained for organisms other than trees in order to gain additional insights by comparing the results for trees with those for other organisms Yet the greatest challenge to population and ecological genetics probably originates from the fact that forests are very likely to be

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     **Mathematical Reviews** ,1994     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     Current Index to Statistics, Applications, Methods and Theory ,1990 The Current Index to Statistics CIS is a bibliographic index of publications in statistics probability and related fields     **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 coverge of both elementary and advanced topics that are essential to those interested in evolutionary biology ecology animal behavior sociobiology and paleobiology     Proceedings of the National Academy of Sciences of the United States of America National Academy of Sciences (U.S.),1926     Current Advances in Genetics ,1980     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     **An Author and Permuted Title Index to Selected Statistical Journals** Brian L. Joiner,1970 All articles notes queries corrigenda and obituaries appearing in the following journals during the indicated years are indexed Annals of mathematical statistics 1961 1969 Biometrics 1965 1969 3 Biometrics 1951 1969 Journal of the American Statistical Association 1956 1969 Journal of the Royal Statistical Society Series B 1954 1969 2 South African statistical journal 1967 1969 2 Technometrics 1959 1969 p iv     **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     **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     Acta Botanica Academiae Scientiarum Hungaricae ,1983     **Foundations of Biology** Paul Weingartner,Georg Dorn,1986     The Mathematical Theory of Selection, Recombination, and Mutation R. Bürger,2000-11-02 It is close to being a masterpiece could well be the classic presentation of the area Warren J Ewens University of Pennsylvania USA Population genetics is concerned with the study of the genetic ecological and evolutionary factors that influence and change the genetic composition of populations The emphasis here is on models that have a direct bearing on evolutionary quantitative genetics Applications concerning the maintenance of genetic variation in quantitative traits and their dynamics under selection are treated in detail Provides a unified self contained and in depth study of the theory of multilocus systems Introduces the basic population genetic models Explores the dynamical and equilibrium properties of the distribution of quantitative traits under

selection Summarizes important results from more demanding sections in a comprehensible way Employs a clear and logical presentation style Following an introduction to elementary population genetics and discussion of the general theory of selection at two or more loci the author considers a number of mutation selection models and derives the dynamical equations for polygenic traits under general selective regimes The final chapters are concerned with the maintenance of quantitative genetic variation the response to directional selection the evolutionary role of deleterious mutations and other topics Graduate students and researchers in population genetics evolutionary theory and biomathematics will benefit from the in depth coverage This text will make an excellent reference volume for the fields of quantitative genetics population and theoretical biology

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**Table of Contents The Geometry Of Population Genetics**

1. Understanding the eBook The Geometry Of Population Genetics
    - The Rise of Digital Reading The Geometry Of Population Genetics
    - Advantages of eBooks Over Traditional Books
2. Identifying The Geometry Of Population Genetics
    - Exploring Different Genres
    - Considering Fiction vs. Non-Fiction
    - Determining Your Reading Goals
3. Choosing the Right eBook Platform
    - Popular eBook Platforms
    - Features to Look for in an The Geometry Of Population Genetics
    - User-Friendly Interface
4. Exploring eBook Recommendations from The Geometry Of Population Genetics
    - Personalized Recommendations
    - The Geometry Of Population Genetics User Reviews and Ratings
    - The Geometry Of Population Genetics and Bestseller Lists
5. Accessing The Geometry Of Population Genetics Free and Paid eBooks

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