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Prediction of biogeographical ancestry in admixed individuals

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Highlights

- “All-or-nothing” classifiers are not suitable for ancestry assignment in admixed individuals with multiple contributions
- STRUCTURE and our novel genetic distance algorithm (GDA) are suitable for predicting admixture
- STRUCTURE can be adopted for admixed individuals but accuracy decreases with degree of admixture
- Our GDA is a simpler alternative to STRUCTURE for admixed individuals
- The mean divergence per population per individual differed by a maximum of 10.7% between STRUCTURE and our GDA

ABSTRACT

Estimation of ancestral affiliation for human genotypes is now possible for major geographic populations and has been employed for forensic casework. Prediction algorithms, such as the Snipper Bayesian classifier, have the ability to classify non-admixed BGA in African (AFR), European (EUR), East Asian (EAS), and most Amerindian (NAM) individuals, but are not

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