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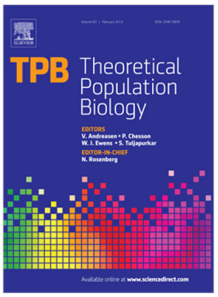

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PII: S0040-5809(18)30066-2
DOI: https://doi.org/10.1016/j.tpb.2018.03.006
Reference: YTPBI 2637

To appear in: *Theoretical Population Biology*

Please cite this article as: Buzbas E.O., Verdu P., Inference on admixture fractions in a mechanistic model of recurrent admixture. *Theoretical Population Biology* (2018), https://doi.org/10.1016/j.tpb.2018.03.006

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Inference on Admixture Fractions in a Mechanistic Model of Recurrent Admixture

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Abstract

Signatures of recent historical admixture are ubiquitous in human populations. We present a mechanistic model of admixture with two source populations, encompassing recurrent admixture periods and study the distribution of admixture fractions for finite but arbitrary genome size. We provide simulation-based methods to estimate the introgression parameters and discuss the implications of reaching stationarity on estimability of parameters when there are recurrent admixture events with different rates.

Keywords: recurrent admixture, introgression parameters, stationary distribution, population genetics, Bayesian computation

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