

Resource Summary Report

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ADMIXTURE

RRID:SCR_001263

Type: Tool

Proper Citation

ADMIXTURE (RRID:SCR_001263)

Resource Information

URL: <https://dalexander.github.io/admixture/download.html>

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Description: A software tool for maximum likelihood estimation of individual ancestries from multilocus SNP genotype datasets. It uses the same statistical model as STRUCTURE but calculates estimates much more rapidly using a fast numerical optimization algorithm. It uses a block relaxation approach to alternately update allele frequency and ancestry fraction parameters. Each block update is handled by solving a large number of independent convex optimization problems, which are tackled using a fast sequential quadratic programming algorithm. Convergence of the algorithm is accelerated using a novel quasi-Newton acceleration method., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: ADMIXTURE

Synonyms: ADMIXTURE: fast ancestry estimation

Resource Type: software resource

Defining Citation: [PMID:19648217](#)

Keywords: ancestry, macos x, linux, admixture, allele, genome, single nucleotide polymorphism, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: ADMIXTURE

Resource ID: SCR_001263

Alternate IDs: biotools:admixture, OMICS_02077

Alternate URLs: <http://www.genetics.ucla.edu/software/admixture/>

Record Creation Time: 20220129T080206+0000

Record Last Update: 20261017T202451+0000

Ratings and Alerts

No rating or validation information has been found for ADMIXTURE.

No alerts have been found for ADMIXTURE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.