

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: 20260725T190459+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 found 2679 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#).

Alves da Quinta D, et al. (2025) Genetic Ancestry, Intrinsic Tumor Subtypes, and Breast Cancer Survival in Latin American Women. Cancer research communications, 5(7), 1070.

Chen H, et al. (2025) Chromosome-level genome assembly of Pinus massoniana provides insights into conifer adaptive evolution. GigaScience, 14.

Garsmeur O, et al. (2025) The genomic footprints of wild Saccharum species trace domestication, diversification, and modern breeding of sugarcane. Cell, 188(25), 7252.

Xiong J, et al. (2025) The genomic history of East Asian Middle Neolithic millet- and rice-agricultural populations. Cell genomics, 100976.

Saoud C, et al. (2025) Germline pathogenic variants in DNA repair pathways: a key feature in a significant subset of translocation-associated sarcomas. NPJ precision oncology, 9(1), 133.

Hu K, et al. (2025) Development and Application of MiMouse, a Comprehensive Genomic Profiling Panel for Credentialing Mouse Tumor Models. Cancer research communications, 5(10), 1910.

Elias R, et al. (2025) Clear-Cell Renal Cell Carcinoma Molecular Subtypes Differ by African and European Genetic Similarity. Cancer research communications, 5(5), 743.

Zou Y, et al. (2025) Ancient genomes from the Yellow River Bend reveal long-distance population interactions between the Central Plains, Steppe, and southern China. Cell reports, 44(8), 116034.

Wang ZF, et al. (2025) Chromosome-scale assemblies of three Ormosia species: repetitive sequences distribution and structural rearrangement. GigaScience, 14.

Ran J, et al. (2025) Ancient genomes reveal basal Asian ancestries and dynamic population interactions over time on the southern Tibetan Plateau. *iScience*, 28(11), 113676.

Arshad F, et al. (2025) A comprehensive water buffalo pangenome reveals extensive structural variation linked to population-specific signatures of selection. *GigaScience*, 14.

Siu JHY, et al. (2025) Early lymph node T follicular helper cell signalling hub drives influenza vaccine response in an ancestrally diverse cohort. *EBioMedicine*, 122, 106036.

Monteiro JPC, et al. (2025) Expression patterns of melanin-related genes are linked to crypsis and conspicuousness in a pumpkin toadlet. *Molecular ecology*, 34(15), e17458.

Hovhannisyan A, et al. (2025) Demographic history and genetic variation of the Armenian population. *American journal of human genetics*, 112(1), 11.

Kim J, et al. (2025) Genetic analysis of a Yayoi individual from the Doigahama site provides insights into the origins of immigrants to the Japanese Archipelago. *Journal of human genetics*, 70(1), 47.

Yao Y, et al. (2025) Whole-genome sequencing identifies novel loci for keratoconus and facilitates risk stratification in a Han Chinese population. *Eye and vision (London, England)*, 12(1), 5.

Barquera R, et al. (2025) Ancient genomes reveal a deep history of *Treponema pallidum* in the Americas. *Nature*, 640(8057), 186.

Uhdre R, et al. (2025) Association study of crude seed protein and fat concentration in a USDA pea diversity panel. *The plant genome*, 18(1), e20485.

Malomane DK, et al. (2025) Patterns of population structure and genetic variation within the Saudi Arabian population. *bioRxiv : the preprint server for biology*.

Britto GSG, et al. (2025) Genome-Wide Insights into Internalizing Symptoms in Admixed Latin American Children. *Genes*, 16(1).