## **Resource Summary Report**

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# **ADMIXTURE**

RRID:SCR\_001263 Type: Tool

**Proper Citation** 

ADMIXTURE (RRID:SCR\_001263)

#### **Resource Information**

URL: http://www.genetics.ucla.edu/software/admixture/

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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.

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

Funding:

Resource Name: ADMIXTURE

Resource ID: SCR\_001263

Alternate IDs: biotools:admixture, OMICS\_02077

Alternate URLs: https://bio.tools/admixture

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250420T014024+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 2351 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

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.

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

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

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

Ding R, et al. (2025) Chromosome-Level Genome Assembly and Whole-Genome Resequencing Revealed Contrasting Population Genetic Differentiation of Black Bream (Megalobrama skolkovii) (Teleostei: Cyprinidae) Allopatric and Sympatric to Its Kin Species. Ecology and evolution, 15(1), e70874.

Gouveia MH, et al. (2025) Subcontinental Genetic Diversity in the All of Us Research Program: Implications for Biomedical Research. bioRxiv : the preprint server for biology.

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.

Pandey N, et al. (2025) Plasma phospho-tau217 as a predictive biomarker for Alzheimer's disease in a large south American cohort. Alzheimer's research & therapy, 17(1), 1.

Hayakawa T, et al. (2025) Genome-scale evolution in local populations of wild chimpanzees. Scientific reports, 15(1), 548.

Yap WS, et al. (2025) High-coverage whole-genome sequencing of a Jakun individual from the "Orang Asli" Proto-Malay subtribe from Peninsular Malaysia. Human genome variation, 12(1), 4.

Mastrangelo AM, et al. (2025) A new wild emmer wheat panel allows to map new loci associated with resistance to stem rust at seedling stage. The plant genome, 18(1), e20413.

Tihagam RD, et al. (2025) The TRIM37 variant rs57141087 contributes to triple-negative breast cancer outcomes in Black women. EMBO reports, 26(1), 245.

Hirase S, et al. (2025) Phenotypic and Genomic Signatures of Latitudinal Local Adaptation Along With Prevailing Ocean Current in a Coastal Goby. Molecular ecology, 34(2), e17599.

Saag L, et al. (2025) North Pontic crossroads: Mobility in Ukraine from the Bronze Age to the early modern period. Science advances, 11(2), eadr0695.

Lei Y, et al. (2025) Population sequencing of cherry accessions unravels the evolution of Cerasus species and the selection of genetic characteristics in edible cherries. Molecular horticulture, 5(1), 6.

Fu M, et al. (2025) The Role of de novo and Ultra-Rare Variants in Hirschsprung Disease (HSCR): Extended Gene Discovery for Risk Profiling of Patients. medRxiv : the preprint server for health sciences.

Derkx I, et al. (2025) The genetic demographic history of the last hunter-gatherer population of the Himalayas. Scientific reports, 15(1), 1505.

Rojas-Barrera IC, et al. (2025) Evolution of sympatric host-specialized lineages of the fungal plant pathogen Zymoseptoria passerinii in natural ecosystems. The New phytologist, 245(4), 1673.

Torrado H, et al. (2025) Evolutionary Genomics of Two Co-occurring Congeneric Fore Reef Coral Species on Guam (Mariana Islands). Genome biology and evolution, 17(1).