Resource Summary Report

Generated by NIF on May 21, 2025

ADMIXTOOLS

RRID:SCR_018495
Type: Tool

Proper Citation

ADMIXTOOLS (RRID:SCR_018495)

Resource Information

URL: https://github.com/DReichLab/AdmixTools

Proper Citation: ADMIXTOOLS (RRID:SCR_018495)

Description: Software package that supports formal tests of whether admixture occurred, and makes it possible to infer admixture proportions and dates.

Resource Type: software resource, software toolkit

Defining Citation: PMID:22960212

Keywords: Formal test support, admixture, infer admixture proportion, infer admixture date, bio.tools

Funding: U.S. National Science Foundation HOMINID ;
NIGMS GM100233

Availability: Free, Available for download, Freely available

Resource Name: ADMIXTOOLS

Resource ID: SCR_018495

Alternate IDs: biotools:admixtools

Alternate URLs: http://genetics.med.harvard.edu/reich/Reich_Lab/Software.html., https://bio.tools/admixtools

Record Creation Time: 20220129T080340+0000

Record Last Update: 20250519T205013+0000

Ratings and Alerts

No rating or validation information has been found for ADMIXTOOLS.

No alerts have been found for ADMIXTOOLS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 176 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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

Yan Z, et al. (2024) A time-resolved multi-omics atlas of transcriptional regulation in response to high-altitude hypoxia across whole-body tissues. Nature communications, 15(1), 3970.

Yavuz OE, et al. (2024) Biomolecular analysis of the Epigravettian human remains from Riparo Tagliente in northern Italy. Communications biology, 7(1), 1415.

Wang C, et al. (2024) Genome-wide analysis tracks the emergence of intraspecific polyploids in Phragmites australis. npj biodiversity, 3(1), 29.

Michel M, et al. (2024) Ancient Plasmodium genomes shed light on the history of human malaria. Nature, 631(8019), 125.

Wang B, et al. (2024) Population expansion from central plain to northern coastal China inferred from ancient human genomes. iScience, 27(12), 111405.

Tims AR, et al. (2024) Museum Genomics Reveals the Hybrid Origin of an Extinct Crater Lake Endemic. Systematic biology, 73(3), 506.

Zhang L, et al. (2024) Genomic adaptation to small population size and saltwater consumption in the critically endangered Cat Ba langur. Nature communications, 15(1),

8531.

Lin H, et al. (2024) Genomic data provides insights into the evolutionary history and adaptive differentiation of two tetraploid strawberries. Horticulture research, 11(9), uhae194.

Varga GIB, et al. (2024) Archaeogenetic analysis revealed East Eurasian paternal origin to the Aba royal family of Hungary. iScience, 27(10), 110892.

Ketchum RN, et al. (2024) Rapid speciation in the holopelagic ctenophore Mnemiopsis following glacial recession. bioRxiv : the preprint server for biology.

Gnecchi-Ruscone GA, et al. (2024) Network of large pedigrees reveals social practices of Avar communities. Nature, 629(8011), 376.

Zhu K, et al. (2024) Protocol for a comprehensive pipeline to study ancient human genomes. STAR protocols, 5(2), 102985.

Lyu B, et al. (2024) Genomic analysis reveals deep population divergence in the water snake Trimerodytes percarinatus (Serpentes, Natricidae). Ecology and evolution, 14(4), e11278.

Salojärvi J, et al. (2024) The genome and population genomics of allopolyploid Coffea arabica reveal the diversification history of modern coffee cultivars. Nature genetics, 56(4), 721.

Scheib CL, et al. (2024) Low Genetic Impact of the Roman Occupation of Britain in Rural Communities. Molecular biology and evolution, 41(9).

Henschel A, et al. (2024) Human migration from the Levant and Arabia into Yemen since Last Glacial Maximum. Scientific reports, 14(1), 31704.

Yamamoto K, et al. (2024) Genetic legacy of ancient hunter-gatherer Jomon in Japanese populations. Nature communications, 15(1), 9780.

Kaptan D, et al. (2024) The Population History of Domestic Sheep Revealed by Paleogenomes. Molecular biology and evolution, 41(10).