

Resource Summary Report

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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: 20260725T191306+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 205 mentions in open access literature.

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

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.

Ferraretti G, et al. (2025) Convergent evolution of complex adaptive traits modulates angiogenesis in high-altitude Andean and Himalayan human populations. *Communications biology*, 8(1), 377.

Krettek KL, et al. (2025) A 6000-year-long genomic transect from the Bogotá Altiplano reveals multiple genetic shifts in the demographic history of Colombia. *Science advances*, 11(22), eads6284.

Liu J, et al. (2025) Reference genome and population genomic analyses reveal insight into herbicide tolerance in *Avena fatua* L. *Nature communications*, 16(1), 9851.

Bretos Ezcurra M, et al. (2025) Genomic insights from a final Bronze Age community buried in a collective tumulus in an Urnfield settlement in Northeastern Iberia. *Communications biology*, 8(1), 1299.

Roca-Rada X, et al. (2025) The genetic history of Portugal over the past 5,000 years. *Genome biology*, 26(1), 248.

Chen G, et al. (2025) Population Genomic Analysis Provides Insights Into the Evolution and Conservation of Two Critically Endangered Musk Deer Species. *Evolutionary applications*, 18(8), e70134.

Amjadi MA, et al. (2025) Ancient DNA indicates 3,000 years of genetic continuity in the Northern Iranian Plateau, from the Copper Age to the Sassanid Empire. *Scientific reports*, 15(1), 16530.

Scarsbrook L, et al. (2025) A 120-y time series of genomes reveals the consequences of closed breeding in German Shepherd Dogs. *Proceedings of the National Academy of Sciences of the United States of America*, 122(48), e2421755122.

Chen Z, et al. (2025) Ancient DNA from Shimao city records kinship practices in Neolithic China. *Nature*, 648(8094), 659.

- Szécsényi-Nagy A, et al. (2025) Ancient DNA reveals diverse community organizations in the 5th millennium BCE Carpathian Basin. *Nature communications*, 16(1), 5318.
- Liu J, et al. (2025) East Asian Gene flow bridged by northern coastal populations over past 6000 years. *Nature communications*, 16(1), 1322.
- Hovhannisyan A, et al. (2025) Demographic history and genetic variation of the Armenian population. *American journal of human genetics*, 112(1), 11.
- Beneker O, et al. (2025) Urbanization and genetic homogenization in the medieval Low Countries revealed through a ten-century paleogenomic study of the city of Sint-Truiden. *Genome biology*, 26(1), 127.
- Kong Y, et al. (2025) Genetic traceability, conservation effectiveness, and selection signatures analysis based on ancestral information: a case study of Beijing-You chicken. *BMC genomics*, 26(1), 402.
- 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.
- Liu S, et al. (2025) Admixture and selection offer insights for the conservation and breeding of Guyuan cattle. *BMC biology*, 23(1), 128.
- Wen J, et al. (2025) Sex-Biased Admixture Followed by Isolation and Adaptive Evolution Shaped the Genomic and Blood Pressure Diversity of the LopNur People. *Molecular biology and evolution*, 42(4).
- Salem N, et al. (2025) Ancient DNA from the Green Sahara reveals ancestral North African lineage. *Nature*, 641(8061), 144.
- Dehasque M, et al. (2025) Genomic and morphological analysis reveals long-term mammoth hybridization in British Columbia, Canada. *Biology letters*, 21(9), 20250305.