

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

Relate

RRID:SCR_010794

Type: Tool

Proper Citation

Relate (RRID:SCR_010794)

Resource Information

URL: <http://www.popgen.dk/software/index.php/Relate>

Proper Citation: Relate (RRID:SCR_010794)

Description: Software providing a method that estimates the probability of sharing alleles identity by descent (IBD) across the genome and can also be used for mapping disease loci using distantly related individuals.

Abbreviations: Relate

Resource Type: software resource

Defining Citation: [PMID:19025785](#)

Keywords: bio.tools

Resource Name: Relate

Resource ID: SCR_010794

Alternate IDs: biotools:relateadmix, OMICS_00207

Alternate URLs: <https://bio.tools/relateadmix>

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260801T190416+0000

Ratings and Alerts

No rating or validation information has been found for Relate.

No alerts have been found for Relate.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 44 mentions in open access literature.

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

Moreau J, et al. (2025) Contrast quality control for segmentation task based on deep learning models-Application to stroke lesion in CT imaging. *Frontiers in neurology*, 16, 1434334.

Peng D, et al. (2025) Evaluating ARG-estimation methods in the context of estimating population-mean polygenic score histories. *Genetics*, 229(4).

Alam O, et al. (2025) Evolutionary histories of functional mutations during the domestication and spread of japonica rice in Asia. *Proceedings of the National Academy of Sciences of the United States of America*, 122(43), e2514614122.

Tjia J, et al. (2025) A Novel Communication Rating Scale to Mitigate the Effect of Implicit Bias. *JAMA network open*, 8(9), e2532319.

Ishigohoka J, et al. (2025) High-recombining genomic regions affect demography inference based on ancestral recombination graphs. *Genetics*, 229(3).

Zhang Q, et al. (2025) Multi-centric origins and gene flow shape the diversity of β -thalassemia mutations in Southern East Asia. *Nature communications*, 16(1), 10220.

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

Fakhraldein SA, et al. (2024) Shotgun metagenomics reveals the interplay between microbiome diversity and environmental gradients in the first marine protected area in the northern Arabian Gulf. *Frontiers in microbiology*, 15, 1479542.

Whitehouse LS, et al. (2024) Tree sequences as a general-purpose tool for population genetic inference. *bioRxiv : the preprint server for biology*.

Martiniano R, et al. (2024) Ancient genomes illuminate Eastern Arabian population history and adaptation against malaria. *Cell genomics*, 4(3), 100507.

Yermakovich D, et al. (2024) Denisovan admixture facilitated environmental adaptation in Papua New Guinean populations. *Proceedings of the National Academy of Sciences of the United States of America*, 121(26), e2405889121.

Masbi M, et al. (2024) Challenges of providing of special care services in hospitals during emergencies and disasters: a scoping review. *BMC emergency medicine*, 24(1), 238.

André M, et al. (2024) Positive selection in the genomes of two Papua New Guinean populations at distinct altitude levels. *Nature communications*, 15(1), 3352.

Whitehouse LS, et al. (2024) Tree Sequences as a General-Purpose Tool for Population Genetic Inference. *Molecular biology and evolution*, 41(11).

Ma X, et al. (2024) Adaptive Evolution of Two Distinct Adaptive Haplotypes of Neanderthal Origin at the Immunoglobulin Heavy-chain Locus in East Asian and European Populations. *Molecular biology and evolution*, 41(7).

Jeffers K, et al. (2024) Non-family Living Arrangements Among Young Adults in the United States. *European journal of population = Revue europeenne de demographie*, 40(1), 10.

Peng D, et al. (2024) Evaluating ARG-estimation methods in the context of estimating population-mean polygenic score histories. *bioRxiv : the preprint server for biology*.

Neto C, et al. (2023) Genetic Architecture of Flowering Time Differs Between Populations With Contrasting Demographic and Selective Histories. *Molecular biology and evolution*, 40(8).

Pope NS, et al. (2023) The expansion of agriculture has shaped the recent evolutionary history of a specialized squash pollinator. *Proceedings of the National Academy of Sciences of the United States of America*, 120(15), e2208116120.

Li Z, et al. (2023) Gender Effects of Dioecious Plant *Populus cathayana* on Fungal Community and Mycorrhizal Distribution at Different Arid Zones in Qinghai, China. *Microorganisms*, 11(2).