

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 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: 20260808T185936+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 47 mentions in open access literature.

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

Riser MM, et al. (2026) Genomic information increases prediction accuracy of behavior traits of Labrador Retrievers used as guide dogs. Genetics, selection, evolution : GSE, 58(1).

Miwa H, et al. (2026) Polygenic and single-locus selection on BMI during Polynesian expansion. Journal of human genetics, 71(5), 293.

Jaratlerdsiri W, et al. (2026) A catalogue of early diverged contemporary human genome variation reveals distinct Khoe-San populations. Nature communications, 17(1).

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.

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

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

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

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

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.

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.

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).

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.

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.

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*.

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.

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).