Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 11, 2025

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

Funding:

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: 20250410T070021+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 38 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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

Fakhraldeen 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.

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).

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

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. Molecular biology and evolution, 41(11).

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

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.

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.

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.

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.

Link V, et al. (2023) Tree-based QTL mapping with expected local genetic relatedness matrices. bioRxiv : the preprint server for biology.

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).

Elfarargi AF, et al. (2023) Genomic Basis of Adaptation to a Novel Precipitation Regime. Molecular biology and evolution, 40(3).

Fulgione A, et al. (2022) Parallel reduction in flowering time from de novo mutations enable evolutionary rescue in colonizing lineages. Nature communications, 13(1), 1461.

Fulford RS, et al. (2022) In situ differences in nitrogen cycling related to presence of submerged aquatic vegetation in a Gulf of Mexico estuary. Ecosphere (Washington, D.C), 13(12), 1.

Alam MR, et al. (2022) Metal(loid) accumulation in the leaves of the grey mangrove (Avicennia marina): Assessment of robust sampling requirements and potential use as a bioindicator. Environmental research, 211, 113065.

Kreiner JM, et al. (2022) Repeated origins, widespread gene flow, and allelic interactions of target-site herbicide resistance mutations. eLife, 11.