Resource Summary Report

Generated by NIF on May 7, 2025

Ancestrymap

RRID:SCR_004353
Type: Tool

Proper Citation

Ancestrymap (RRID:SCR_004353)

Resource Information

URL: https://reich.hms.harvard.edu/software

Proper Citation: Ancestrymap (RRID:SCR_004353)

Description: Software application that finds skews in ancestry that are potentially associated with disease genes in recently mixed populations like African Americans. It can be downloaded for either UNIX or Linux.

Abbreviations: ANCESTRYMAP

Resource Type: software resource, software application, source code

Defining Citation: PMID:15088269

Keywords: disease gene, ancestry, gene, genomic, unix, linux, admixture mapping, admixture, genome, linkage disequilibrium, population

Funding: Burroughs Wellcome Fund ;
NHGRI K-01 HG002758-01

Availability: Restricted

Resource Name: Ancestrymap

Resource ID: SCR_004353

Alternate IDs: nlx_39116, biotools:ancestrymap, OMICS_02083

Alternate URLs: https://reich.hms.harvard.edu/software, https://bio.tools/ancestrymap

Old URLs: http://genepath.med.harvard.edu/~reich/Software.htm,

http://genetics.med.harvard.edu/reich/Reich_Lab/Software.html

Record Creation Time: 20220129T080224+0000

Record Last Update: 20250507T060239+0000

Ratings and Alerts

No rating or validation information has been found for Ancestrymap.

No alerts have been found for Ancestrymap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Cole BS, et al. (2021) The Role of Genetic Ancestry as a Risk Factor for Primary Open-angle Glaucoma in African Americans. Investigative ophthalmology & visual science, 62(2), 28.

Qin P, et al. (2021) Pan-genome analysis of 33 genetically diverse rice accessions reveals hidden genomic variations. Cell, 184(13), 3542.

Nakatsuka N, et al. (2020) Two genetic variants explain the association of European ancestry with multiple sclerosis risk in African-Americans. Scientific reports, 10(1), 16902.

Liu H, et al. (2020) Evolution and Domestication Footprints Uncovered from the Genomes of Coix. Molecular plant, 13(2), 295.

Nam BH, et al. (2019) Whole genome sequencing reveals the impact of recent artificial selection on red sea bream reared in fish farms. Scientific reports, 9(1), 6487.

Yang C, et al. (2018) Clinical Implication and the Hereditary Factors of NM23 in Hepatocellular Carcinoma Based on Bioinformatics Analysis and Genome-Wide Association Study. Journal of oncology, 2018, 6594169.

Kim J, et al. (2017) The genome landscape of indigenous African cattle. Genome biology, 18(1), 34.

Guo T, et al. (2017) Genome-Wide Association Study to Find Modifiers for Tetralogy of Fallot in the 22q11.2 Deletion Syndrome Identifies Variants in the GPR98 Locus on 5q14.3. Circulation. Cardiovascular genetics, 10(5), e001690.

Keaton JM, et al. (2016) Genome-Wide Interaction with Insulin Secretion Loci Reveals Novel Loci for Type 2 Diabetes in African Americans. PloS one, 11(7), e0159977.

Kassahun Y, et al. (2015) Admixture mapping of tuberculosis and pigmentation-related traits in an African-European hybrid cattle population. Frontiers in genetics, 6, 210.

Jin G, et al. (2015) Low-frequency coding variants at 6p21.33 and 20q11.21 are associated with lung cancer risk in Chinese populations. American journal of human genetics, 96(5), 832.

Gusev A, et al. (2014) Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases. American journal of human genetics, 95(5), 535.