Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 23, 2025

Eigensoft

RRID:SCR_004965
Type: Tool

Proper Citation

Eigensoft (RRID:SCR_004965)

Resource Information

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

Proper Citation: Eigensoft (RRID:SCR_004965)

Description: EIGENSOFT package combines functionality from our population genetics methods (Patterson et al. 2006) and our EIGENSTRAT stratification method (Price et al. 2006). The EIGENSTRAT method uses principal components analysis to explicitly model ancestry differences between cases and controls along continuous axes of variation; the resulting correction is specific to a candidate marker''s variation in frequency across ancestral populations, minimizing spurious associations while maximizing power to detect true associations. The EIGENSOFT package has a built-in plotting script and supports multiple file formats and quantitative phenotypes. Source code, documentation and executables for using EIGENSOFT 3.0 on a Linux platform can be downloaded. New features of EIGENSOFT 3.0 include supporting either 32-bit or 64-bit Linux machines, a utility to merge different data sets, a utility to identify related samples (accounting for population structure), and supporting multiple file formats for EIGENSTRAT stratification correction.

Abbreviations: EIGENSOFT

Synonyms: EIGENSOFT Software

Resource Type: software resource, software toolkit

Defining Citation: PMID:17194218, DOI:10.1038/ng1847

Keywords: population genetics, genetics, stratification, variation

Funding:

Availability: Free, Freely available

Resource Name: Eigensoft

Resource ID: SCR_004965

Alternate IDs: OMICS_07868, nlx_93059

Alternate URLs: https://sources.debian.org/src/eigensoft/

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

Record Creation Time: 20220129T080227+0000

Record Last Update: 20250422T055216+0000

Ratings and Alerts

No rating or validation information has been found for Eigensoft.

Warning: Warning: PCA results may be sensitive to the sample size, population composition, and the number of columns, in which case the results will not be reliable, robust, nor replicable and should not be used to draw conclusions.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1108 mentions in open access literature.

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

Aizpurua-Iraola J, et al. (2025) A reduction in effective population size has not relaxed purifying selection in the human population of Eivissa (Balearic Islands). Scientific reports, 15(1), 660.

Hovhannisyan A, et al. (2025) Demographic history and genetic variation of the Armenian population. American journal of human genetics, 112(1), 11.

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

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.

Yap WS, et al. (2025) High-coverage whole-genome sequencing of a Jakun individual from the "Orang Asli" Proto-Malay subtribe from Peninsular Malaysia. Human genome variation, 12(1), 4.

Saag L, et al. (2025) North Pontic crossroads: Mobility in Ukraine from the Bronze Age to the early modern period. Science advances, 11(2), eadr0695.

Tough RH, et al. (2025) Functionally-informed fine-mapping identifies genetic variants linking increased CHD1L expression and HIV restriction in monocytes. Scientific reports, 15(1), 2325.

Xia X, et al. (2025) Orogeny and High Pollen Flow as Driving Forces for High Genetic Diversity of Endangered Acer griseum (Franch.) Pax Endemic to China. International journal of molecular sciences, 26(2).

Zhu K, et al. (2024) Protocol for a comprehensive pipeline to study ancient human genomes. STAR protocols, 5(2), 102985.

Bai F, et al. (2024) Ancient genomes revealed the complex human interactions of the ancient western Tibetans. Current biology : CB, 34(12), 2594.

Du P, et al. (2024) Ancient genome of the Chinese Emperor Wu of Northern Zhou. Current biology : CB, 34(7), 1587.

Liu Z, et al. (2024) Multiomics analyses of Jining Grey goat and Boer goat reveal genomic regions associated with fatty acid and amino acid metabolism and muscle development. Animal bioscience, 37(6), 982.

Gill H, et al. (2024) Reconstructing the Genetic Relationship between Ancient and Present-Day Siberian Populations. Genome biology and evolution, 16(4).

Li J, et al. (2024) Genome-wide association research on the reproductive traits of Qianhua Mutton Merino sheep. Animal bioscience, 37(9), 1535.

Vilà-Valls L, et al. (2024) Understanding the genomic heterogeneity of North African Imazighen: from broad to microgeographical perspectives. Scientific reports, 14(1), 9979.

Wu Z, et al. (2024) Human pangenome analysis of sequences missing from the reference genome reveals their widespread evolutionary, phenotypic, and functional roles. Nucleic acids research, 52(5), 2212.

Mentzer AJ, et al. (2024) High-resolution African HLA resource uncovers HLA-DRB1 expression effects underlying vaccine response. Nature medicine, 30(5), 1384.

de la Fuente Castro C, et al. (2024) The Genomic and Cultural Diversity of the Inka Qhapaq Hucha Ceremony in Chile and Argentina. Genome biology and evolution, 16(9).

Yao M, et al. (2024) Commonly used genomic arrays may lose information due to imperfect coverage of discovered variants for autism spectrum disorder. Journal of neurodevelopmental disorders, 16(1), 54.

Higgins OA, et al. (2024) Life history and ancestry of the late Upper Palaeolithic infant from Grotta delle Mura, Italy. Nature communications, 15(1), 8248.