

Resource Summary Report

Generated by [NIF](#) on Aug 1, 2026

Eigensoft

RRID:SCR_004965

Type: Tool

Proper Citation

Eigensoft (RRID:SCR_004965)

Resource Information

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

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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

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: 20260801T042552+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 1225 mentions in open access literature.

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

Tang J, et al. (2026) Social Stratification Without Genetic Differentiation at the Xisima Site in the Late Shang Dynasty. *Molecular biology and evolution*, 43(1).

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Zou Y, et al. (2025) Ancient genomes from the Yellow River Bend reveal long-distance population interactions between the Central Plains, Steppe, and southern China. *Cell reports*, 44(8), 116034.

Ran J, et al. (2025) Ancient genomes reveal basal Asian ancestries and dynamic population interactions over time on the southern Tibetan Plateau. *iScience*, 28(11), 113676.

Light-Maka I, et al. (2025) Bronze Age *Yersinia pestis* genome from sheep sheds light on hosts and evolution of a prehistoric plague lineage. *Cell*.

Fang H, et al. (2025) Dynamic history of the Central Plain and Haidai region inferred from Late Neolithic to Iron Age ancient human genomes. *Cell reports*, 44(2), 115262.

Xiong J, et al. (2025) The genomic history of East Asian Middle Neolithic millet- and rice-agricultural populations. *Cell genomics*, 100976.

- Purnomo GA, et al. (2025) Benchmarking Imputed Low Coverage Genomes in a Human Population Genetics Context. *Molecular ecology resources*, 25(8), e70007.
- Roca-Rada X, et al. (2025) The genetic history of Portugal over the past 5,000 years. *Genome biology*, 26(1), 248.
- Petersen ME, et al. (2025) Health and Aging Brain Study-Health Disparities (HABS-HD) methods and partner characteristics. *Alzheimer's & dementia (New York, N. Y.)*, 11(3), e70140.
- Geng F, et al. (2025) Genome Assembly and Winged Fruit Gene Regulation of Chinese Wingnut: Insights from Genomic and Transcriptomic Analyses. *Genomics, proteomics & bioinformatics*, 22(6).
- Fortes-Lima CA, et al. (2025) Population history and admixture of the Fulani people from the Sahel. *American journal of human genetics*, 112(2), 261.
- 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.
- Shi X, et al. (2025) Selection Increases Mitonuclear DNA Discordance but Reconciles Incompatibility in African Cattle. *Molecular biology and evolution*, 42(2).
- Yan T, et al. (2025) Genomic-based revelation of genetic structure and adaptive characterization of *Schizopygopsis malacanthus* in the Jinsha River and Yalong River. *BMC genomics*, 26(1), 870.
- Gyuris B, et al. (2025) Long shared haplotypes identify the southern Urals as a primary source for the 10th-century Hungarians. *Cell*, 188(21), 6064.
- Wingo AP, et al. (2025) Multiancestry brain pQTL fine-mapping and integration with genome-wide association studies of 21 neurologic and psychiatric conditions. *Nature genetics*, 57(9), 2156.
- Tao Y, et al. (2025) Genetic diversity and evolutionary insights of Dali tea (*Camellia taliensis*) in the Lancang River Basin: Implications for tea breeding and resource conservation. *PloS one*, 20(7), e0328658.
- Helmerson C, et al. (2025) A century of anthropogenic perturbations impact genomic signatures of the iconic migratory Atlantic cod. *Science advances*, 11(31), eadp3342.
- Mariño-Ramírez L, et al. (2025) The Consortium for Genomic Diversity, Ancestry, and Health in Colombia (CÓDIGO): building local capacity in genomics and bioinformatics. *Communications biology*, 8(1), 1062.