

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

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 toolkit, software resource

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: 20260729T044108+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 [kravitz2](#) .

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.

Han J, et al. (2025) Genomic insights into the genetic diversity and genetic basis of body height in endangered Chinese Ningqiang ponies. *BMC genomics*, 26(1), 292.

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.

Shi X, et al. (2025) Selection Increases Mitonuclear DNA Discordance but Reconciles Incompatibility in African Cattle. *Molecular biology and evolution*, 42(2).

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.

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).

Gong L, et al. (2025) Haplotype-resolved genome assembly and genome-wide association study identifies the candidate gene closely related to sugar content and tuber yield in *Solanum tuberosum*. *Horticulture research*, 12(6), uhaf075.

Xu J, et al. (2025) Genomic Diversity and Selection Signatures for Zaosheng Cattle. *Biology*, 14(6).

Sun L, et al. (2025) The demic expansion of Yangshao culture inferred from ancient human genomes. *BMC biology*, 23(1), 186.

DePaolo J, et al. (2025) Genome-First Approach to Rare and Common Variant Risk of Thoracic Aortic Aneurysm and Dissection. *medRxiv : the preprint server for health sciences*.

Roca-Rada X, et al. (2025) The genetic history of Portugal over the past 5,000 years. *Genome biology*, 26(1), 248.

Long Z, et al. (2025) Evolutionary Genomics Unravels the Responses and Adaptation to Climate Change in a Key Alpine Forest Tree Species. *Molecular biology and evolution*, 42(7).

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.

Purnomo GA, et al. (2025) Benchmarking Imputed Low Coverage Genomes in a Human Population Genetics Context. *Molecular ecology resources*, 25(8), e70007.