

Resource Summary Report

Generated by [RRID](#) on Sep 11, 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: 20260905T133234+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 1299 mentions in open access literature.

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

Zhang G, et al. (2026) Ancient genomes provide insight into the Paleolithic-to-Neolithic transition in northern East Asia. *Current biology* : CB, 36(6), 1399.

Xu Y, et al. (2026) Reconstructing the west-east genetic division in Indonesia using ancient genomes. *iScience*, 29(6), 115974.

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).

Chotiprasidhi P, et al. (2026) Lower Allele Frequency of TERT-rs2242652 in Sub-Saharan African Populations Compared With American Populations and Hepatocellular Carcinoma Risk. *JCO global oncology*, 12(3), e2500446.

Lv X, et al. (2026) Population history and subsistence of farming communities in an agro-pastoral transition zone of northern China: ancient DNA and isotopic evidence from the Erdaojingzi site. *Scientific reports*, 16(1).

Miyazawa S, et al. (2026) Peculiar pigment pattern and population profile of a poisonous pufferfish. *PeerJ*, 14, e21378.

Jain R, et al. (2026) Layers in the sand: The genetic imprint of migration, culture, and Indus craft in the Thar Desert. *HGG advances*, 7(3), 100623.

Jin M, et al. (2026) Genomic insights into the population history of fat-tailed sheep and identification of two mutations that contribute to fat tail adipogenesis. *Journal of advanced research*, 80, 725.

Hu JY, et al. (2026) Pangolin museum genomics reveal the dynamic genetic consequences and extinction risk of the critically endangered Chinese pangolin. *Molecular biology and evolution*, 43(5).

Tao L, et al. (2026) Genetic formation and regional disparities of Kra-Dai and Hmong-Mien speakers inferred from ancient genomes of cave burial populations in southwest China. *Molecular biology and evolution*, 43(2).

Mandla R, et al. (2026) Statistical uncertainty explains the poor agreement in polygenic scoring for type 2 diabetes. *medRxiv : the preprint server for health sciences*.

Rai N, et al. (2026) Ancient human genomes from Ladakh reveal Tibetan, South Asian, and Central Asian admixture over the last three millennia. *bioRxiv : the preprint server for biology*.

An D, et al. (2026) Sweet Potato Gene Clusters Control Anthocyanin Biosynthesis and Leaf Morphology. *Plant biotechnology journal*, 24(7), 4500.

Marsh WA, et al. (2026) Dogs were widely distributed across western Eurasia during the Palaeolithic. *Nature*, 651(8107), 995.

McHugo GP, et al. (2026) Integrative Genomics Identifies Candidate Genes Underlying Trypanotolerance in Hybrid African Cattle. *Evolutionary applications*, 19(6), e70274.

Font-Porterias N, et al. (2026) Signatures of pathogen-driven selection and Austronesian gene flow of Papua New Guinea HLA alleles. *American journal of human genetics*, 113(6), 1175.

Dobrose MM, et al. (2026) Molecular analysis and immunological characterization of a founder mutation causing ARPC1B deficiency. *Genes and immunity*, 27(1), 69.

Zeng W, et al. (2026) Ancient Yellow River ancestry and divergent admixture histories in the Qiang people. *Science advances*, 12(3), eady6667.

Romeyer-Dherbey JH, et al. (2026) Ancient DNA study provides clues to leprosy susceptibility in medieval Europe. *Genome biology*, 27(1), 4.

Kim J, et al. (2026) Ancient genomes reveal early-stage admixture and genetic diversity in the Northwestern Kyushu Yayoi. *Scientific reports*, 16(1), 4833.