Eigensoft
RRID:SCR_004965
Type: Tool

Proper Citation

Eigensoft (RRID:SCR_004965)

Resource Information

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

Description: Software for population genetics analysis. The 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.

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Resource Type: Resource, software resource, source code, software application

Keywords: population genetics, genetics, stratification, variation

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Parent Organization: Harvard Medical School; Massachusetts; USA

Website Status: Last checked up
Ratings and Alerts

No rating or validation information has been found for Eigensoft.

No alerts have been found for Eigensoft.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 481 mentions in open access literature.

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


Font-Porterias N, et al. (2019) European Roma groups show complex West Eurasian
admixture footprints and a common South Asian genetic origin. PLoS genetics, 15(9), e1008417.


Chen J, et al. (2019) Genomic data provide new insights on the demographic history and the extent of recent material transfers in Norway spruce. Evolutionary applications, 12(8), 1539-1551.


Cruz PRS, et al. (2019) Genetic comparison of sickle cell anaemia cohorts from Brazil and the United States reveals high levels of divergence. Scientific reports, 9(1), 10896.