Resource Summary Report

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FlashPCA

RRID:SCR_021680
Type: Tool

Proper Citation

FlashPCA (RRID:SCR_021680)

Resource Information

URL: https://github.com/gabraham/flashpca

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Description: Software tool as fast principal component analysis of large scale genome wide data. FlashPCA performs fast principal component analysis (PCA) of single nucleotide polymorphism (SNP) data. FlashPCA2 used for principal component analysis of biobank scale genotype datasets.

Synonyms: FlashPCA2

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: DOI:10.1093/bioinformatics/btx299, DOI:10.1371/journal.pone.0093766

Keywords: Principal component analysis, large scale genome wide data, single nucleotide polymorphism data, biobank scale genotype datasets

Availability: Free, Available for download, Freely available

Resource Name: FlashPCA

Resource ID: SCR_021680

License: GNU General Public License

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260912T200000+0000

Ratings and Alerts

No rating or validation information has been found for FlashPCA.

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 38 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Maciel BA, et al. (2026) The genetic landscape of human functional brain connectivity. Nature communications, 17(1).

Clifford RE, et al. (2026) Polygenic Contribution to Sensorineural Hearing Loss Implicates Novel Risk Loci and Convergence with Congenital Hearing Loss Genes. Journal of the Association for Research in Otolaryngology : JARO, 27(3), 447.

Schmidt A, et al. (2026) Host control of persistent Epstein-Barr virus infection. Nature, 653(8114), 444.

Kitoh R, et al. (2026) Inflammation and Oxidative-Stress Pathways Are Associated with Idiopathic Sudden Hearing Loss: A Genome-Wide Association Study in 15,494 Japanese Individuals. International journal of molecular sciences, 27(4).

Pan M, et al. (2026) Genetic Susceptibility to Diabetes Subtypes and Risk of Developing Coronary Artery Disease. Diabetes care, 49(5), 843.

Derkx I, et al. (2025) The genetic demographic history of the last hunter-gatherer population of the Himalayas. Scientific reports, 15(1), 1505.

Douville NJ, et al. (2025) Clinical and Genetic Factors Associated with Intraoperative Minimum Alveolar Concentration Ratio: A Single-center Retrospective Cohort and Genome-wide Association Study. Anesthesiology, 143(3), 541.

Katzourou IK, et al. (2025) Contributions of common and rare genetic variation to different measures of mood and anxiety disorder in the UK Biobank. BJPsych open, 11(3), e97.

Nicolas A, et al. (2025) Transferability of European-derived Alzheimer's disease polygenic risk scores across multiancestry populations. Nature genetics, 57(7), 1598.

Beneker O, et al. (2025) Urbanization and genetic homogenization in the medieval Low Countries revealed through a ten-century paleogenomic study of the city of Sint-Truiden. Genome biology, 26(1), 127.

Wang Z, et al. (2025) The APOE ?4 allele affects the survival of patients with Parkinson's disease independent of dementia. Journal of translational medicine, 23(1), 1094.

Milind N, et al. (2025) Buffering and non-monotonic behavior of gene dosage response curves for human complex traits. medRxiv : the preprint server for health sciences.

Bhérer C, et al. (2025) Frequency enrichment of coding variants in a French-Canadian founder population and its implication for inflammatory bowel diseases. medRxiv : the preprint server for health sciences.

Gao Y, et al. (2024) Reconstructing the ancestral gene pool to uncover the origins and genetic links of Hmong-Mien speakers. BMC biology, 22(1), 59.

Venkateswaran V, et al. (2024) Polygenic scores for tobacco use provide insights into systemic health risks in a diverse EHR-linked biobank in Los Angeles. Translational psychiatry, 14(1), 38.

Chia R, et al. (2024) Genome sequence analyses identify novel risk loci for multiple system atrophy. Neuron, 112(13), 2142.

Tissink E, et al. (2023) The Genetic Architectures of Functional and Structural Connectivity Properties within Cerebral Resting-State Networks. eNeuro, 10(4).

Sadler KV, et al. (2023) Genome-wide association analysis identifies a susceptibility locus for sporadic vestibular schwannoma at 9p21. Brain : a journal of neurology, 146(7), 2861.

Walters RG, et al. (2023) Genotyping and population characteristics of the China Kadoorie Biobank. Cell genomics, 3(8), 100361.

Dattani S, et al. (2023) Common and rare variant associations with latent traits underlying depression, bipolar disorder, and schizophrenia. Translational psychiatry, 13(1), 46.