Resource Summary Report

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PLINK

RRID:SCR_001757
Type: Tool

Proper Citation

PLINK (RRID:SCR_001757)

Resource Information

URL: http://www.nitrc.org/projects/plink

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Description: Open source whole genome association analysis toolset, designed to perform range of basic, large scale analyses in computationally efficient manner. Used for analysis of genotype/phenotype data. Through integration with gPLINK and Haploview, there is some support for subsequent visualization, annotation and storage of results. PLINK 1.9 is improved and second generation of the software.

Synonyms: PLINK 1.9, PLINK/SEQ, plink - Whole genome association analysis toolset

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

Defining Citation: PMID:17701901, DOI:10.1086/519795

Keywords: gene, genetic, genomic, genotype, phenotype, copy number variant, whole-genome association, population, linkage analysis, whole-genome association study, data management, summary statistics, population stratification, association analysis, identity-by-descent estimation

Funding:

Availability: Free, Available for download, Freely Available

Resource Name: PLINK

Resource ID: SCR_001757

Alternate IDs: nlx_154200, OMICS_00206, SCR_021271

Alternate URLs: https://zzz.bwh.harvard.edu/plink/, https://www.cog-genomics.org/plink/1.9/general_usage#cite, https://sources.debian.org/src/plink/

Old URLs: http://pngu.mgh.harvard.edu/~purcell/plink/

License: GPLv3

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250417T065057+0000

Ratings and Alerts

No rating or validation information has been found for PLINK.

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 13420 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Al-Mamun HA, et al. (2025) Exploring genomic feature selection: A comparative analysis of GWAS and machine learning algorithms in a large-scale soybean dataset. The plant genome, 18(1), e20503.

Annis AC, et al. (2025) Genetic Associations of Persistent Opioid Use After Surgery Point to OPRM1 but Not Other Opioid-Related Loci as the Main Driver of Opioid Use Disorder. Genetic epidemiology, 49(1), e22588.

Zhou J, et al. (2025) Deep learning predicts DNA methylation regulatory variants in specific brain cell types and enhances fine mapping for brain disorders. Science advances, 11(1), eadn1870.

Opmeer Y, et al. (2025) Polymyositis in Kooiker dogs is associated with a 39 kb deletion upstream of the canine IL21/IL2 locus. PLoS genetics, 21(1), e1011538.

Wang C, et al. (2025) Integrating electronic health records and GWAS summary statistics to predict the progression of autoimmune diseases from preclinical stages. Nature communications, 16(1), 180.

Husami SF, et al. (2025) Corporate genome screening India (CoGsI) identified genetic variants association with T2D in young Indian professionals. Scientific reports, 15(1), 506.

Kim H, et al. (2025) Effects of Genetic Risk and Lifestyle Habits on Gout: A Korean Cohort Study. Journal of Korean medical science, 40(2), e1.

Jiang X, et al. (2025) The whole-genome dissection of root system architecture provides new insights for the genetic improvement of alfalfa (Medicago sativa L.). Horticulture research, 12(1), uhae271.

Manullang C, et al. (2025) Slight thermal stress exerts genetic diversity selection at coral (Acropora digitifera) larval stages. BMC genomics, 26(1), 36.

Laffranchi M, et al. (2025) Neutrophils restricted contribution of CCRL2 genetic variants to COVID-19 severity. Heliyon, 11(1), e41267.

Chaddock NJM, et al. (2025) Genetic proxies for clinical traits are associated with increased risk of severe COVID-19. Scientific reports, 15(1), 2083.

Shi Y, et al. (2025) Genetic Commonalities Between Metabolic Syndrome and Rheumatic Diseases Through Disease Interactome Modules. Journal of cellular and molecular medicine, 29(1), e70329.

Huang YJ, et al. (2025) A semi-empirical Bayes approach for calibrating weak instrumental bias in sex-specific Mendelian randomization studies. medRxiv : the preprint server for health sciences.

Hytönen MK, et al. (2025) IP3 receptor depletion in a spontaneous canine model of Charcot-Marie-Tooth disease 1J with amelogenesis imperfecta. PLoS genetics, 21(1), e1011328.

Tedja MS, et al. (2025) A genome-wide scan of non-coding RNAs and enhancers for refractive error and myopia. Human genetics, 144(1), 67.

Domínguez M, et al. (2025) Genomics Reveal Population Structure and Intergeneric Hybridization in an Endangered South American Bird: Implications for Management and Conservation. Ecology and evolution, 15(1), e70820.

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

Bellou E, et al. (2025) Benchmarking Alzheimer's disease prediction: personalised risk assessment using polygenic risk scores across various methodologies and genome-wide studies. Alzheimer's research & therapy, 17(1), 6.

Higashino A, et al. (2025) Population Genomics of Japanese Macaques (Macaca fuscata): Insights Into Deep Population Divergence and Multiple Merging Histories. Genome biology and evolution, 17(1).

Li R, et al. (2025) Whole genome sequence-based association analysis of African American individuals with bipolar disorder and schizophrenia. medRxiv : the preprint server for health sciences.