BEAGLE

RRID:SCR_001789
Type: Tool

Proper Citation

BEAGLE (RRID:SCR_001789)

Resource Information

URL: http://faculty.washington.edu/browning/beagle/beagle.html

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Description: Software package for analysis of large-scale genetic data sets with hundreds of thousands of markers genotyped on thousands of samples. BEAGLE can * phase genotype data (i.e. infer haplotypes) for unrelated individuals, parent-offspring pairs, and parent-offspring trios. * infer sporadic missing genotype data. * impute ungenotyped markers that have been genotyped in a reference panel. * perform single marker and haplotypic association analysis. * detect genetic regions that are homozygous-by-descent in an individual or identical-by-descent in pairs of individuals. Beagle can also be used in conjunction with PRESTO, a program for fast and flexible permutation testing. PRESTO can compute empirical distributions of order statistics, analyze stratified data, and determine significance levels for one-stage and two-stage genetic association studies. BEAGLE is written in Java and runs on any computing platform with a Java version 1.6 interpreter (e.g. Windows, Unix, Linux, Solaris, Mac).

Abbreviations: BEAGLE

Synonyms: BEAGLE Genetic Analysis Software Package

Resource Type: software resource, software application

Defining Citation: PMID:17924348, PMID:17326099, PMID:21310274, DOI:10.1086/521987

Keywords: gene, genetic, genomic, java, ms-windows, linux, unix, solaris, macos, identity by descent, genotype, haplotype

Funding:

Availability: Acknowledgement requested, Free, Public

Resource Name: BEAGLE

Resource ID: SCR_001789

Alternate IDs: nlx_154238, OMICS_00052, OMICS_00201

Alternate URLs: https://sources.debian.org/src/beagle/

Old URLs: https://www.stat.auckland.ac.nz/%7Ebrowning/beagle/beagle.html

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250519T204855+0000

Ratings and Alerts

No rating or validation information has been found for BEAGLE.

No alerts have been found for BEAGLE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1963 mentions in open access literature.

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

Rubino E, et al. (2025) Exome sequencing reveals a rare damaging variant in GRIN2C in familial late-onset Alzheimer's disease. Alzheimer's research & therapy, 17(1), 21.

Masaki N, et al. (2025) Mean gene conversion tract length in humans estimated to be 459 bp from UK Biobank sequence data. bioRxiv : the preprint server for biology.

Malomane DK, et al. (2025) Patterns of population structure and genetic variation within the Saudi Arabian population. bioRxiv : the preprint server for biology.

Yang K, et al. (2025) Genetic diversity of highly pathogenic avian influenza H5N6 and H5N8 viruses in poultry markets in Guangdong, China, 2020-2022. Journal of virology, 99(1), e0114524.

Patil A, et al. (2025) Looking back into the Hepatitis C Virus epidemic dynamics from Unnao,

India through phylogenetic approach. PloS one, 20(1), e0317705.

Lagutkin D, et al. (2025) Revisiting the Link Between HLA-DRB1 Alleles and Autoantibodies in Rheumatoid Arthritis: Association of non-Shared Epitope Alleles *09 and *15 With High Levels of Anti-Citrullinated Peptide/Protein Antibodies. ACR open rheumatology, 7(1), e11767.

Tihagam RD, et al. (2025) The TRIM37 variant rs57141087 contributes to triple-negative breast cancer outcomes in Black women. EMBO reports, 26(1), 245.

Arantes I, et al. (2025) Rapid spread of the SARS-CoV-2 Omicron XDR lineage derived from recombination between XBB and BA.2.86 subvariants circulating in Brazil in late 2023. Microbiology spectrum, 13(1), e0119324.

Oh S, et al. (2025) Genome-wide association studies in lettuce reveal the interplay of seed age, color, and germination under high temperatures. Scientific reports, 15(1), 733.

Sasa N, et al. (2025) Blood DNA virome associates with autoimmune diseases and COVID-19. Nature genetics, 57(1), 65.

Xu X, et al. (2025) Redefining the accumulated temperature index for accurate prediction of rice flowering time in diverse environments. Plant biotechnology journal, 23(1), 302.

Assis BA, et al. (2025) Genomic signatures of adaptation in native lizards exposed to human-introduced fire ants. Nature communications, 16(1), 89.

Tian Y, et al. (2025) Population Genomics Reveals Elevated Inbreeding and Accumulation of Deleterious Mutations in White Raccoon Dogs. Biology, 14(1).

Guo H, et al. (2025) Natural variation of CTB5 confers cold adaptation in plateau japonica rice. Nature communications, 16(1), 1032.

Ye H, et al. (2025) Improvement of the accuracy of breeding value prediction for egg production traits in Muscovy duck using low-coverage whole-genome sequence data. Poultry science, 104(2), 104812.

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.

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

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.

McBreen J, et al. (2025) Enhancing genomic-based forward prediction accuracy in wheat by integrating UAV-derived hyperspectral and environmental data with machine learning under heat-stressed environments. The plant genome, 18(1), e20554.

Sun C, et al. (2024) Mechanisms of hepatic steatosis in chickens: integrated analysis of the host genome, molecular phenomics and gut microbiome. GigaScience, 13.