

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 15, 2025

BEAGLE

RRID:SCR_001789

Type: Tool

Proper Citation

BEAGLE (RRID:SCR_001789)

Resource Information

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

Proper Citation: BEAGLE (RRID:SCR_001789)

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 application, software resource

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: 20250412T054635+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 [FDI Lab - SciCrunch.org](#).

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*.

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.

Malomane DK, et al. (2025) Patterns of population structure and genetic variation within the

Saudi Arabian population. *bioRxiv* : the preprint server for biology.

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.

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.

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

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.

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.

Derkx I, et al. (2025) The genetic demographic history of the last hunter-gatherer population

of the Himalayas. Scientific reports, 15(1), 1505.

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