

Resource Summary Report

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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

Availability: Free, Available for download, Freely available

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>

License: GNU General Public License, v3 or newer

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260731T042616+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 2197 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Yang W, et al. (2026) Multi-omics reveals co-regulation of hepatic bile acid metabolism in laying hens by host genetics and the cecal Anaerostipes. Poultry science, 105(3), 106388.

Lan T, et al. (2025) Enhancing inbreeding estimation and global conservation insights through chromosome-level assemblies of the Chinese and Malayan pangolin. GigaScience, 14.

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within Salmonella enterica serovar Dublin. eLife, 13.

Arshad F, et al. (2025) A comprehensive water buffalo pangenome reveals extensive structural variation linked to population-specific signatures of selection. GigaScience, 14.

Ni A, et al. (2025) Identifying candidate genetic variants for egg number by analyzing over 1,000 fully sequenced layers. GigaScience, 14.

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.

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.

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.

Bui TH, et al. (2025) Factors Associated With Type 2 Diabetes in Older Japanese With Similar Genetic Risk Scores: The Bunkyo Health Study. *Journal of the Endocrine Society*, 9(2), bvaf019.

Kri??anac AM, et al. (2025) Sequence-based GWAS in 180,000 German Holstein cattle reveals new candidate variants for milk production traits. *Genetics, selection, evolution : GSE*, 57(1), 3.

Li X, et al. (2025) Genomic Insights into Post-Domestication Expansion and Selection of Body Size in Ponies. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(16), e2413023.

Ahmad SF, et al. (2025) Dissecting genomes of multiple yak populations: unveiling ancestry and high-altitude adaptation through whole-genome resequencing analysis. *BMC genomics*, 26(1), 214.

Mitchell J, et al. (2025) Assessing the contribution of rare protein-coding germline variants to prostate cancer risk and severity in 37,184 cases. *Nature communications*, 16(1), 1779.

He K, et al. (2025) Leveraging Automated Machine Learning for Environmental Data-Driven Genetic Analysis and Genomic Prediction in Maize Hybrids. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(17), e2412423.

Peng W, et al. (2025) Investigation of selection signatures of dairy goats using whole-genome sequencing data. *BMC genomics*, 26(1), 234.

Singh A, et al. (2025) Local ancestry informed GWAS of warfarin dose requirement in African Americans identifies a novel CYP2C19 splice QTL. *medRxiv : the preprint server for health sciences*.

Vitale P, et al. (2025) Improving wheat grain yield genomic prediction accuracy using historical data. *G3 (Bethesda, Md.)*, 15(4).

Perez LJ, et al. (2025) Climate, inter-serotype competition and arboviral interactions shape dengue dynamics in Thailand. *Communications biology*, 8(1), 601.

Guo X, et al. (2025) KBeagle: An Adaptive Strategy and Tool for Improving Imputation Accuracy and Computation Time. *International journal of molecular sciences*, 26(12).