

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: 20260801T191037+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 [RRID](#) .

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.

Buso P, et al. (2025) Parallel Selection in Domesticated Atlantic Salmon from Divergent Founders Including on Whole-Genome Duplication-derived Homeologous Regions. Genome biology and evolution, 17(4).

Yu W, et al. (2025) Optimization and application of genome prediction model in rapeseed: flowering time, yield components, and oil content as examples. *Horticulture research*, 12(8), uhaf115.

Guinat C, et al. (2025) Poultry farm density and proximity drive highly pathogenic avian influenza spread. *Communications biology*, 8(1), 1306.

Ma W, et al. (2025) DeepAnnotation: A novel interpretable deep learning-based genomic selection model that integrates comprehensive functional annotations. *GigaScience*, 14.

Gretzinger J, et al. (2025) Ancient DNA connects large-scale migration with the spread of Slavs. *Nature*, 646(8084), 384.

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

Ottensmann L, et al. (2025) Examining the link between 179 lipid species and 7 diseases using genetic predictors. *EBioMedicine*, 114, 105671.

Wen J, et al. (2025) Sex-Biased Admixture Followed by Isolation and Adaptive Evolution Shaped the Genomic and Blood Pressure Diversity of the LopNur People. *Molecular biology and evolution*, 42(4).

Chaudhary VB, et al. (2025) TraitAM, a global spore trait database for arbuscular mycorrhizal fungi. *Scientific data*, 12(1), 588.

G??mbaro F, et al. (2025) Navigating Sampling Bias in Discrete Phylogeographic Analysis: Assessing the Performance of an Adjusted Bayes Factor. *Molecular biology and evolution*, 42(11).

Abner E, et al. (2025) Characterization of prevalent genetic variants in the Estonian Biobank body-mass index GWAS. *Nature communications*, 16(1), 8956.

Gill MS, et al. (2025) Infinite Mixture Models for Improved Modeling of Across-Site Evolutionary Variation. *Molecular biology and evolution*, 42(8).

Tan HZ, et al. (2025) High Imputation Accuracy Can Be Achieved Using a Small Reference Panel in a Natural Population With Low Genetic Diversity. *Molecular ecology resources*, 25(8), e70024.

Zhou X, et al. (2025) Genomic selection for growth and wood properties in multi-generation hybrid populations of *Populus deltoides*. *Horticulture research*, 12(9), uhaf165.

Gagnon M, et al. (2025) Rare variants and founder effect in the Beauce region of Quebec. *Communications biology*, 8(1), 1184.