Resource Summary Report

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Eagle

RRID:SCR_015991
Type: Tool

Proper Citation

Eagle (RRID:SCR_015991)

Resource Information

URL: https://data.broadinstitute.org/alkesgroup/Eagle/

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Description: Software package for statistical estimation of haplotype phase either within a genotyped cohort or using a phased reference panel in large scale sequencing. The package includes Eagle1 (to harness identity-by-descent among distant relatives to rapidly call phase using a fast scoring approach) and Eagle2 (to analyze a full probabilistic model similar to the diploid Li-Stephens model used by previous HMM-based methods.

Synonyms: Bio-eagle, Eagle1, Eagle2

Resource Type: software toolkit, software resource

Defining Citation: PMID:27694958, PMID:27270109

Keywords: hmm, hidden markov model, statistic, estimation, haplotype, phase, reference, panel, sequencing, algorithm, analysis, probability

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NCRR S10 RR028832;
NWO 480-05-003;
Dutch Brain Foundation

Availability: Free, Available for download, Freely available

Resource Name: Eagle

Resource ID: SCR_015991

Alternate IDs: OMICS_14099, SCR_017262

Alternate URLs: https://sources.debian.org/src/bio-eagle/, https://github.com/poruloh/Eagle, https://data.broadinstitute.org/alkesgroup/Eagle/downloads/

License: GNU GPL v3.0

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260810T040657+0000

Ratings and Alerts

No rating or validation information has been found for Eagle.

No alerts have been found for Eagle.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 57 mentions in open access literature.

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

Toda N, et al. (2026) Genetic and Social Determinants of Renin-Angiotensin-Aldosterone System Inhibitor-Induced Angioedema: A Precision Medicine Health Equity Study. medRxiv : the preprint server for health sciences.

Verbitsky M, et al. (2026) Urobiota analysis and genome-wide association study in pediatric recurrent urinary tract infections and vesicoureteral reflux. JCI insight, 11(2).

Kitoh R, et al. (2026) Inflammation and Oxidative-Stress Pathways Are Associated with Idiopathic Sudden Hearing Loss: A Genome-Wide Association Study in 15,494 Japanese Individuals. International journal of molecular sciences, 27(4).

Bassiouni R, et al. (2026) Integrated Single-Cell Whole-Genome Sequencing and Spatial Transcriptomics Reveal Intratumoral Heterogeneity in Ovarian Cancer. Cancer research communications, 6(5), 1020.

Lopera-Maya E, et al. (2026) Effect of ancestry and shared genetic architecture of serious mental illness on symptoms and cognition in an admixed Latin American population. Research square.

Jelcic I, et al. (2025) T-bet+ CXCR3+ B cells drive hyperreactive B-T cell interactions in multiple sclerosis. Cell reports. Medicine, 6(3), 102027.

Wonkam A, et al. (2025) FLT1 and other candidate fetal haemoglobin modifying loci in sickle cell disease in African ancestries. Nature communications, 16(1), 2092.

Kraft J, et al. (2025) Polygenic contributions to lithium augmentation outcomes in antidepressant non-responders with unipolar depression. medRxiv : the preprint server for health sciences.

Zhang Q, et al. (2025) Multi-centric origins and gene flow shape the diversity of ??-thalassemia mutations in Southern East Asia. Nature communications, 16(1), 10220.

Lyu J, et al. (2024) Identification of biomarkers and potential therapeutic targets for pancreatic cancer by proteomic analysis in two prospective cohorts. Cell genomics, 4(6), 100561.

Tamuhla T, et al. (2024) Implementation of a genotyped African population cohort, with virtual follow-up: A feasibility study in the Western Cape Province, South Africa. Wellcome open research, 9, 620.

Kim JJ, et al. (2024) Multi-ancestry genome-wide association meta-analysis of Parkinson's disease. Nature genetics, 56(1), 27.

Tjader NP, et al. (2024) Association of ESR1 Germline Variants with TP53 Somatic Variants in Breast Tumors in a Genome-wide Study. Cancer research communications, 4(6), 1597.

Lennon NJ, et al. (2024) Selection, optimization and validation of ten chronic disease polygenic risk scores for clinical implementation in diverse US populations. Nature medicine, 30(2), 480.

Sulkava S, et al. (2024) Job-related exhaustion risk variant in UST is associated with dementia and DNA methylation. Scientific reports, 14(1), 13668.

Ruotsalainen S, et al. (2024) Inherited infertility: Mapping loci associated with impaired female reproduction. American journal of human genetics, 111(12), 2789.

Dichgans M, et al. (2023) Genetically proxied HTRA1 protease activity and circulating levels independently predict risk of ischemic stroke and coronary artery disease. Research square.

Bhatraju PK, et al. (2023) Genome-wide Association Study for AKI. Kidney360, 4(7), 870.

Lennon NJ, et al. (2023) Selection, optimization, and validation of ten chronic disease polygenic risk scores for clinical implementation in diverse populations. medRxiv : the preprint server for health sciences.

Zhou H, et al. (2023) Multi-ancestry study of the genetics of problematic alcohol use in over 1 million individuals. Nature medicine, 29(12), 3184.