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

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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 51 mentions in open access literature.

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

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.

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.

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.

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.

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.

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

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.

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.

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.

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.

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.

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.

Martinez-Carrasco A, et al. (2023) Genetic meta-analysis of levodopa induced dyskinesia in Parkinson's disease. NPJ Parkinson's disease, 9(1), 128.

Rodríguez-Fernández B, et al. (2022) Genetically predicted telomere length and Alzheimer's disease endophenotypes: a Mendelian randomization study. Alzheimer's research & therapy, 14(1), 167.

Ruiz-Arenas C, et al. (2022) Identification of autosomal cis expression quantitative trait methylation (cis eQTMs) in children's blood. eLife, 11.

Wang L, et al. (2022) Performance of polygenic risk scores for cancer prediction in a racially diverse academic biobank. Genetics in medicine : official journal of the American College of Medical Genetics, 24(3), 601.

Cerqueira JXM, et al. (2021) Independent and cumulative coeliac disease-susceptibility loci are associated with distinct disease phenotypes. Journal of human genetics, 66(6), 613.