Resource Summary Report

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Eagle

RRID:SCR_017262
Type: Tool

Proper Citation

Eagle (RRID:SCR_017262)

Resource Information

URL: https://github.com/poruloh/Eagle

Proper Citation: Eagle (RRID:SCR_017262)

Description: Open source software tool for haplotype phasing. Estimates haplotype phase either within genotyped cohort or using phased reference panel.

Synonyms: Eagle1, Eagle2

Resource Type: software application, data analysis software, data processing software, software resource

Defining Citation: PMID:27694958

Keywords: haplotype, phasing, estimate, genotype, cohort, reference, panel

Funding: NHGRI R01 HG006399;
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Wellcome Trust ;
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NHGRI HG007022;
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Fannie and John Hertz Foundation ;
NCRR S10 RR028832;
Netherlands Scientific Organization ;
Dutch Brain Foundation ;
VU University Amsterdam

Availability: Free, Available for download, Freely available

Resource Name: Eagle

Resource ID: SCR_017262

Alternate URLs: https://data.broadinstitute.org/alkesgroup/Eagle/, https://www.hsph.harvard.edu/alkes-price/software/

License: GNU GPLv3

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260903T235420+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 13 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

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.

Rajan S, et al. (2023) Structurally Complex Osteosarcoma Genomes Exhibit Limited Heterogeneity within Individual Tumors and across Evolutionary Time. Cancer research communications, 3(4), 564.

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.

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.

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

Chia R, et al. (2021) Genome sequencing analysis identifies new loci associated with Lewy body dementia and provides insights into its genetic architecture. Nature genetics, 53(3), 294.

Keys KL, et al. (2020) On the cross-population generalizability of gene expression prediction models. PLoS genetics, 16(8), e1008927.

Ueno K, et al. (2020) Integrated GWAS and mRNA Microarray Analysis Identified IFNG and CD40L as the Central Upstream Regulators in Primary Biliary Cholangitis. Hepatology communications, 4(5), 724.

Lam M, et al. (2019) Comparative genetic architectures of schizophrenia in East Asian and European populations. Nature genetics, 51(12), 1670.

Delaneau O, et al. (2019) Accurate, scalable and integrative haplotype estimation. Nature communications, 10(1), 5436.

Duijvesteijn N, et al. (2018) Genomic prediction of the polled and horned phenotypes in Merino sheep. Genetics, selection, evolution : GSE, 50(1), 28.

Mostafavi H, et al. (2017) Identifying genetic variants that affect viability in large cohorts. PLoS biology, 15(9), e2002458.