Resource Summary Report

Generated by dkNET on Apr 18, 2025

GCHAP

RRID:SCR_009186
Type: Tool

Proper Citation

GCHAP (RRID:SCR_009186)

Resource Information

URL: http://episun7.med.utah.edu/~alun/gchap/index.html

Proper Citation: GCHAP (RRID:SCR_009186)

Description: THIS RESOURCE IS NO LONGER IN SERVCE, documented September 22, 2016. Software application that finds maximum likelihood estimates of haplotype frequencies from a sample of genotyped individuals. By excluding haplotypes with zero MLE at an early stage, this implementation uses many orders of magnitude less space and time than naive implementations. A second program, ApproxGCHap, is provided to give alternate estimates for data sets with large numbers of loci or large amounts of missing genotypes.

Abbreviations: GCHAP

Synonyms: Gene Counting method for HAPlotype analysis. GENEPI.JAR

Resource Type: software resource, software application

Defining Citation: PMID:14555636

Keywords: gene, genetic, genomic, java

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GCHAP

Resource ID: SCR_009186

Alternate IDs: nlx_154325

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250416T063539+0000

Ratings and Alerts

No rating or validation information has been found for GCHAP.

No alerts have been found for GCHAP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Lu Y, et al. (2024) Pangenome characterization and analysis of the NAC gene family reveals genes for Sclerotinia sclerotiorum resistance in sunflower (Helianthus annuus). BMC genomic data, 25(1), 39.

Zhang J, et al. (2024) Genome-wide identification of rice CXE gene family and mining of alleles for potential application in rice improvement. Frontiers in plant science, 15, 1435420.

Wang X, et al. (2023) Identification of the CNGC Gene Family in Rice and Mining of Alleles for Application in Rice Improvement. Plants (Basel, Switzerland), 12(24).

Li S, et al. (2023) Genetic Dissection of Salt Tolerance and Yield Traits of Geng (japonica) Rice by Selective Subspecific Introgression. Current issues in molecular biology, 45(6), 4796.

Shi Y, et al. (2022) Comprehensive Analysis of Glutamate Receptor-like Genes in Rice (Oryza sativa L.): Genome-Wide Identification, Characteristics, Evolution, Chromatin Accessibility, gcHap Diversity, Population Variation and Expression Analysis. Current issues in molecular biology, 44(12), 6404.

Zhang F, et al. (2021) The landscape of gene-CDS-haplotype diversity in rice: Properties, population organization, footprints of domestication and breeding, and implications for genetic improvement. Molecular plant, 14(5), 787.

Zhang LJ, et al. (2017) Phylogeographic patterns of Lygus pratensis (Hemiptera: Miridae): Evidence for weak genetic structure and recent expansion in northwest China. PloS one,

12(4), e0174712.