

Resource Summary Report

Generated by T1D on Aug 1, 2026

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 SERVICE, 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

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: 20260731T042814+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 [T1D](#).

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.

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.

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.