Resource Summary Report

Generated by NIF on Apr 22, 2025

CLUSTAG

RRID:SCR_001816
Type: Tool

Proper Citation

CLUSTAG (RRID:SCR_001816)

Resource Information

URL: http://www.math.hkbu.edu.hk/~mng/CLUSTAG/CLUSTAG.html

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Description: Software application that uses hierarchical clustering and graph methods for selecting tag SNPs (single nucleotide polymorphisms). Cluster and set-cover algorithms are developed to obtain a set of tag SNPs that can represent all the known SNPs in a chromosomal region, subject to the constraint that all SNPs must have a squared correlation R2 > C with at least one tag SNP, where C is specified by the user. The program is implemented with Java, and it can run in Windows platform as well as the Unix environment.

Abbreviations: CLUSTAG

Synonyms: CLUSTAG: Hierarchical Clustering and Graph Methods for Selecting Tag SNPs

Resource Type: software resource, software application

Defining Citation: PMID:15585525

Keywords: gene, genetic, genomic, java, hierarchical clustering, single nucleotide polymorphism, windows, unix

Funding:

Resource Name: CLUSTAG

Resource ID: SCR_001816

Alternate IDs: nlx_154273

Old URLs: http://hkumath.hku.hk/web/link/CLUSTAG/CLUSTAG.html

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250421T053256+0000

Ratings and Alerts

No rating or validation information has been found for CLUSTAG.

No alerts have been found for CLUSTAG.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Khvorykh G, et al. (2021) A Workflow for Selection of Single Nucleotide Polymorphic Markers for Studying of Genetics of Ischemic Stroke Outcomes. Genes, 12(3).