Resource Summary Report

Generated by NIF on May 23, 2025

MendelIHT.jl

RRID:SCR_018292
Type: Tool

Proper Citation

MendelIHT.jl (RRID:SCR_018292)

Resource Information

URL: https://github.com/OpenMendel/MendelIHT.jl

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Description: Software Julia package that implements iterative hard thresholding as multiple regression model for GWAS. Built-in support for handling PLINK and VCF files, parallel computing, fits a variety of GLM models, and handles grouping/weighting SNPs.

Synonyms: Mendel Iterative Hard Thresholding.jl, Mendel Iterative Hard Thresholding, MendelIHT

Resource Type: software application, software resource

Defining Citation: DOI:10.1101/697755

Keywords: GWAS, iterative hard thresholding, multiple regression, GLM model, feature selection, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: MendelIHT.jl

Resource ID: SCR_018292

Alternate IDs: biotools:mendeliht.jl

Alternate URLs: https://bio.tools/mendeliht.jl

License: MIT

Record Creation Time: 20220129T080339+0000

Record Last Update: 20250522T061201+0000

Ratings and Alerts

No rating or validation information has been found for MendelIHT.jl.

No alerts have been found for MendelIHT.jl.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Chu BB, et al. (2023) Multivariate genome-wide association analysis by iterative hard thresholding. Bioinformatics (Oxford, England), 39(4).

Chu BB, et al. (2020) Iterative hard thresholding in genome-wide association studies: Generalized linear models, prior weights, and double sparsity. GigaScience, 9(6).