

Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

[MendelIHT.jl](#)

RRID:SCR_018292

Type: Tool

Proper Citation

MendelIHT.jl (RRID:SCR_018292)

Resource Information

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

Proper Citation: MendelIHT.jl (RRID:SCR_018292)

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 resource, software application

Defining Citation: [DOI:10.1101/697755](https://doi.org/10.1101/697755)

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

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: 20260801T191110+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 [ASWG](#) .

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).