

# Resource Summary Report

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## [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 application, software resource

**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:** 20260805T044418+0000

### Ratings and Alerts

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

No alerts have been found for MendelIHT.jl.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [dkNET](#) .

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).