

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

simplePHENOTYPES

RRID:SCR_022523

Type: Tool

Proper Citation

simplePHENOTYPES (RRID:SCR_022523)

Resource Information

URL: <https://CRAN.R-project.org/package=simplePHENOTYPES>

Proper Citation: simplePHENOTYPES (RRID:SCR_022523)

Description: Software R package that simulates pleiotropy, partial pleiotropy, and spurious pleiotropy in wide range of genetic architectures, including additive, dominance and epistatic models. Used to simulate multiple traits controlled by loci with varying degrees of pleiotropy.

Synonyms: Simulation of Pleiotropic, Linked and Epistatic Phenotypes

Resource Type: software resource, software toolkit

Defining Citation: [PMID:33129253](#)

Keywords: Multiple traits simulation, pleiotropy, partial pleiotropy, spurious pleiotropy, causal mutations affecting multiple traits

Funding: NSF 1733606

Availability: Free, Available for download, Freely available

Resource Name: simplePHENOTYPES

Resource ID: SCR_022523

Alternate URLs: <https://github.com/samuelbfernandes/simplePHENOTYPES>

License: MIT License

Record Creation Time: 20220628T050153+0000

Record Last Update: 20260905T133310+0000

Ratings and Alerts

No rating or validation information has been found for simplePHENOTYPES.

No alerts have been found for simplePHENOTYPES.

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 [Kravitz](#) .

Dwivedi SL, et al. (2024) Epistasis and pleiotropy-induced variation for plant breeding. Plant biotechnology journal, 22(10), 2788.

Farooq M, et al. (2022) Genomic prediction in plants: opportunities for ensemble machine learning based approaches. F1000Research, 11, 802.