Resource Summary Report

Generated by NIF on May 25, 2025

PhenoSpD

RRID:SCR_016359
Type: Tool

Proper Citation

PhenoSpD (RRID:SCR_016359)

Resource Information

URL: https://github.com/MRCIEU/PhenoSpD

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Description: Software toolkit for phenotypic correlation estimation and multiple testing correction (Spectral Decomposition, SpD) for human phenome using genome-wide association study (GWAS) summary statistics. It is a command line R based tool.

Abbreviations: PSD

Synonyms: Pheno Spectral Decomposition, PhenoSpD

Resource Type: software application, software toolkit, data analysis software, data processing software, software resource

Keywords: spectral, decomposition, matrice, phenotypic, correlation, estimation, multiple, testing, correction, human, phenome, genome, summary, statistic, decomposition, matrice, genomics

Funding:

Availability: Free, Available for download, Freely available

Resource Name: PhenoSpD

Resource ID: SCR_016359

License: GNU GPL v3

Record Creation Time: 20220129T080330+0000

Record Last Update: 20250525T031445+0000

Ratings and Alerts

No rating or validation information has been found for PhenoSpD.

No alerts have been found for PhenoSpD.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Zhu X, et al. (2022) A hypothesis-driven study to comprehensively investigate the association between genetic polymorphisms in EPHX2 gene and cardiovascular diseases: Findings from the UK Biobank. Gene, 822, 146340.

Perrot N, et al. (2021) A trans-omic Mendelian randomization study of parental lifespan uncovers novel aging biology and therapeutic candidates for chronic diseases. Aging cell, 20(11), e13497.

Barbitoff YA, et al. (2020) A Data-Driven Review of the Genetic Factors of Pregnancy Complications. International journal of molecular sciences, 21(9).

Song J, et al. (2019) Genetic polymorphisms of long noncoding RNA RP11-37B2.1 associate with susceptibility of tuberculosis and adverse events of antituberculosis drugs in west China. Journal of clinical laboratory analysis, 33(5), e22880.

Zheng J, et al. (2018) PhenoSpD: an integrated toolkit for phenotypic correlation estimation and multiple testing correction using GWAS summary statistics. GigaScience, 7(8).

Zheng J, et al. (2017) Recent Developments in Mendelian Randomization Studies. Current epidemiology reports, 4(4), 330.