

Resource Summary Report

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

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

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: 20260829T182516+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 [dkNET](#) .

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.