Resource Summary Report

Generated by NIF on May 25, 2025

MultiPhen

RRID:SCR_003498
Type: Tool

Proper Citation

MultiPhen (RRID:SCR_003498)

Resource Information

URL: http://cran.r-project.org/web/packages/MultiPhen/

Proper Citation: MultiPhen (RRID:SCR_003498)

Description: Software package that performs genetic association tests between SNPs (one-at-a-time) and multiple phenotypes (separately or in joint model).

Synonyms: MultiPhen: a package for the genetic association testing of multiple phenotypes

Resource Type: software resource

Defining Citation: PMID:22567092

Keywords: standalone software, r, bio.tools

Funding:

Availability: GNU General Public License, v2

Resource Name: MultiPhen

Resource ID: SCR_003498

Alternate IDs: biotools:multiphen, OMICS_04397

Alternate URLs: https://bio.tools/multiphen

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250525T030755+0000

Ratings and Alerts

No rating or validation information has been found for MultiPhen.

No alerts have been found for MultiPhen.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 27 mentions in open access literature.

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

Cao X, et al. (2024) A novel method for multiple phenotype association studies based on genotype and phenotype network. PLoS genetics, 20(5), e1011245.

Mbye H, et al. (2022) Plasmodium falciparum merozoite invasion ligands, linked antimalarial resistance loci and ex vivo responses to antimalarials in The Gambia. The Journal of antimicrobial chemotherapy, 77(11), 2946.

Liang X, et al. (2022) HCLC-FC: A novel statistical method for phenome-wide association studies. PloS one, 17(11), e0276646.

Vilor-Tejedor N, et al. (2021) Multivariate Analysis and Modelling of multiple Brain endOphenotypes: Let's MAMBO! Computational and structural biotechnology journal, 19, 5800.

De T, et al. (2021) Signatures of TSPAN8 variants associated with human metabolic regulation and diseases. iScience, 24(8), 102893.

Fu L, et al. (2021) A Novel Approach Integrating Hierarchical Clustering and Weighted Combination for Association Study of Multiple Phenotypes and a Genetic Variant. Frontiers in genetics, 12, 654804.

Liu D, et al. (2021) Impact of low-frequency coding variants on human facial shape. Scientific reports, 11(1), 748.

Klimentidis YC, et al. (2020) Phenotypic and Genetic Characterization of Lower LDL Cholesterol and Increased Type 2 Diabetes Risk in the UK Biobank. Diabetes, 69(10), 2194.

van der Meer D, et al. (2020) Understanding the genetic determinants of the brain with MOSTest. Nature communications, 11(1), 3512.

Schmid AB, et al. (2019) Genetic components of human pain sensitivity: a protocol for a

genome-wide association study of experimental pain in healthy volunteers. BMJ open, 9(4), e025530.

Zhang X, et al. (2019) Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing, 24, 272.

Chung J, et al. (2019) Comparison of methods for multivariate gene-based association tests for complex diseases using common variants. European journal of human genetics : EJHG, 27(5), 811.

Truong DT, et al. (2019) Multivariate genome-wide association study of rapid automatised naming and rapid alternating stimulus in Hispanic American and African-American youth. Journal of medical genetics, 56(8), 557.

Ganesamoorthy D, et al. (2018) GtTR: Bayesian estimation of absolute tandem repeat copy number using sequence capture and high throughput sequencing. BMC bioinformatics, 19(1), 267.

Chibnik LB, et al. (2018) Susceptibility to neurofibrillary tangles: role of the PTPRD locus and limited pleiotropy with other neuropathologies. Molecular psychiatry, 23(6), 1521.

Shen X, et al. (2017) Multivariate discovery and replication of five novel loci associated with Immunoglobulin G N-glycosylation. Nature communications, 8(1), 447.

Kaakinen M, et al. (2017) A rare-variant test for high-dimensional data. European journal of human genetics : EJHG, 25(8), 988.

Porter HF, et al. (2017) Multivariate simulation framework reveals performance of multi-trait GWAS methods. Scientific reports, 7, 38837.

Sood RF, et al. (2016) Missense Variant in MAPK Inactivator PTPN5 Is Associated with Decreased Severity of Post-Burn Hypertrophic Scarring. PloS one, 11(2), e0149206.

Restrepo NA, et al. (2016) Shared Genetic Etiology of Autoimmune Diseases in Patients from a Biorepository Linked to De-identified Electronic Health Records. Frontiers in genetics, 7, 185.