Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 8, 2025

IMPUTE

RRID:SCR_009245
Type: Tool

Proper Citation

IMPUTE (RRID:SCR_009245)

Resource Information

URL: https://mathgen.stats.ox.ac.uk/impute/impute.html

Proper Citation: IMPUTE (RRID:SCR_009245)

Description: Software application for estimating (imputing) unobserved genotypes in SNP association studies. The program is designed to work seamlessly with the output of the genotype calling program CHIAMO and the population genetic simulator HAPGEN, and it produces output that can be analyzed using the program SNPTEST. (entry from Genetic Analysis Software)

Abbreviations: IMPUTE

Resource Type: software application, software resource

Keywords: gene, genetic, genomic

Funding:

Resource Name: IMPUTE

Resource ID: SCR_009245

Alternate IDs: nlx_154411

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250508T065223+0000

Ratings and Alerts

No rating or validation information has been found for IMPUTE.

No alerts have been found for IMPUTE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 610 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Shealy EP, et al. (2025) DNA methylation-based age prediction and sex-specific epigenetic aging in a lizard with female-biased longevity. Science advances, 11(5), eadq3589.

Power GM, et al. (2025) The role of body image dissatisfaction in the relationship between body size and disordered eating and self-harm: complimentary Mendelian randomization and mediation analyses. Molecular psychiatry, 30(2), 521.

Tan H, et al. (2025) Genetic predisposition to Behcet's disease mediated by a IL10RA enhancer polymorphism. Heliyon, 11(1), e41529.

Arellano Spano M, et al. (2024) Genetic associations of risk behaviours and educational achievement. Communications biology, 7(1), 435.

Koyanagi YN, et al. (2024) Genetic architecture of alcohol consumption identified by a genotype-stratified GWAS and impact on esophageal cancer risk in Japanese people. Science advances, 10(4), eade2780.

Zhang J, et al. (2024) A transcriptome-wide association study identified susceptibility genes for hepatocellular carcinoma in East Asia. Gastroenterology report, 12, goae057.

Melas K, et al. (2024) Blood-derived microRNAs are related to cognitive domains in the general population. Alzheimer's & dementia : the journal of the Alzheimer's Association, 20(10), 7138.

Young WJ, et al. (2024) Genome-Wide Interaction Analyses of Serum Calcium on Ventricular Repolarization Time in 125?393 Participants. Journal of the American Heart Association, 13(17), e034760.

Jang MJ, et al. (2024) Identification of interactions between genetic risk scores and dietary patterns for personalized prevention of kidney dysfunction in a population-based cohort. Nutrition & diabetes, 14(1), 62.

Imtiaz MA, et al. (2024) Genome-Wide Association Study Meta-Analysis Uncovers Novel

Genetic Variants Associated with Olfactory Dysfunction. medRxiv : the preprint server for health sciences.

Brouwer JMJL, et al. (2024) Association of CYP2D6 and CYP2C19 metabolizer status with switching and discontinuing antidepressant drugs: an exploratory study. BMC psychiatry, 24(1), 394.

Xicota L, et al. (2024) Whole genome-wide sequence analysis of long-lived families (Long-Life Family Study) identifies MTUS2 gene associated with late-onset Alzheimer's disease. Alzheimer's & dementia : the journal of the Alzheimer's Association, 20(4), 2670.

Chen L, et al. (2024) Genetic Susceptibility to Astrovirus Diarrhea in Bangladeshi Infants. Open forum infectious diseases, 11(3), ofae045.

Salgado I, et al. (2024) Deep Learning Techniques to Characterize the RPS28P7 Pseudogene and the Metazoa-SRP Gene as Drug Potential Targets in Pancreatic Cancer Patients. Biomedicines, 12(2).

Han L, et al. (2024) Exercise may delay cognitive decline in Chinese older adults: a causal inference for ordered multi-categorical exposures with a Mendelian randomization approach. Scientific reports, 14(1), 13007.

Downie CG, et al. (2024) Genome-wide association study reveals shared and distinct genetic architecture underlying fatty acid and bioactive oxylipin metabolites in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). medRxiv : the preprint server for health sciences.

Talevi V, et al. (2024) Peripheral whole blood microRNA expression in relation to vascular function: a population-based study. Journal of translational medicine, 22(1), 670.

Hodel F, et al. (2024) Prevalence of actionable pharmacogenetic variants and high-risk drug prescriptions: A Swiss hospital-based cohort study. Clinical and translational science, 17(9), e70009.

Wang M, et al. (2024) DNA methylation variations of DNA damage response correlate survival and local immune status in melanomas. Immunity, inflammation and disease, 12(9), e1331.

Abbondanza F, et al. (2024) A GWAS for grip strength in cohorts of children-Advantages of analysing young participants for this trait. Genes, brain, and behavior, 23(5), e70003.