Resource Summary Report

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Michigan Imputation Server

RRID:SCR_017579
Type: Tool

Proper Citation

Michigan Imputation Server (RRID:SCR_017579)

Resource Information

URL: https://imputationserver.sph.umich.edu/

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Description: Web server to implement whole genotype imputation workflow for efficient parallelization of computationally intensive tasks. Service for imputation that facilitates access to new reference panels and greatly improves user experience and productivity. Used to find haplotype segments and reference panel of sequenced genomes, assign genotypes at untyped markers, improve genome coverage, facilitate comparison and combination of studies that use different marker panels, increase power to detect genetic association, and guide fine mapping.

Synonyms: Next Generation Genotype Imputation Service

Resource Type: software resource, data access protocol, service resource, web service

Defining Citation: PMID:27571263

Keywords: Whole, genotype, imputation, workflow, parallelization, task, find, haplotype, segment, reference, panel, sequence, genome, mapping

Funding: NHGRI HG007022;
NHLBI HL117626;
NHGRI HG000376;
NIDA R01 DA037904;
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European Community Seventh Framework Programme ;
NIA

Availability: Restricted

Resource Name: Michigan Imputation Server

Resource ID: SCR_017579

Alternate URLs: https://github.com/genepi/imputationserver

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260801T042820+0000

Ratings and Alerts

No rating or validation information has been found for Michigan Imputation Server.

No alerts have been found for Michigan Imputation Server.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 156 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Ruiz M, et al. (2025) Exploring the Impact of Mitonuclear Discordance on Disease in Latin American Admixed Populations. Genes, 16(6).

de Santana MBR, et al. (2025) Chromosome 21 variants tied to severe asthma exacerbations: A genome-wide association study in a Brazilian population. The journal of allergy and clinical immunology. Global, 4(3), 100507.

Hoffmann TJ, et al. (2025) Genome-wide association study of prostate-specific antigen levels in 392,522 men identifies new loci and improves prediction across ancestry groups. Nature genetics, 57(2), 334.

Ding K, et al. (2025) Admixture Mapping of Lipid Traits in Hispanic Americans. Journal of the American Heart Association, 14(21), e036650.

Li Y, et al. (2025) UDA-seq: universal droplet microfluidics-based combinatorial indexing for massive-scale multimodal single-cell sequencing. Nature methods, 22(6), 1199.

Tekola-Ayele F, et al. (2025) Sex-differentiated placental methylation and gene expression regulation has implications for neonatal traits and adult diseases. Nature communications, 16(1), 4004.

Pratt T, et al. (2025) Distinct glial functions are associated with Alzheimer's disease based on cell-type- and pathway-specific polygenic risk score analysis. Journal of Alzheimer's disease : JAD, 107(2), 755.

Lou J, et al. (2025) Genetic and striatal structural connection linking behavioral inhibition/activation system to adolescent anxiety and depression. Translational psychiatry, 15(1), 451.

Zhu JD, et al. (2025) Mapping Genetic Associations With Functional Brain Area Alterations in Schizophrenia and Implications for Cortical Development. Brain and behavior, 15(7), e70688.

Chase BA, et al. (2025) Lipid trajectories improve risk models for Alzheimer's disease and mild cognitive impairment. Journal of lipid research, 66(1), 100714.

Das S, et al. (2025) Genetic regulation of exosome biogenesis pathway in human adipose and muscle tissue and association with obesity and insulin resistance. Research square.

Duggan MR, et al. (2025) Proteomic signatures of corona and herpes viral antibodies identify IGDCC4 as a mediator of neurodegeneration. Science advances, 11(22), eadt7176.

May AK, et al. (2025) Predictors of Environmental Sensitivity in Syrian refugee children. Journal of child psychology and psychiatry, and allied disciplines, 66(11), 1688.

Gaviria-Sabogal CC, et al. (2025) Refining rare disease variant discovery in an isolated Andean community through imputation-enhanced IBD and kinship inference from whole exome sequencing data. Human molecular genetics, 34(20), 1733.

Rout M, et al. (2025) Excess of rare noncoding variants in several type 2 diabetes candidate genes among Asian Indian families. Communications medicine, 5(1), 47.

Toikumo S, et al. (2025) Gene discovery and pleiotropic architecture of Chronic Pain in a Genome-wide Association Study of >1.2 million Individuals. medRxiv : the preprint server for health sciences.

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Huang SY, et al. (2025) Genome-wide association study unravels mechanisms of brain glymphatic activity. Nature communications, 16(1), 626.

Chakraborty S, et al. (2025) Genome-wide study links cardiometabolic factors to cognition via APOA4-APOA5-ZPR1-BUD13 and other loci in rural Indians. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(7), e70429.

Ivie JJ, et al. (2025) Myeloid cell genome-wide screen identifies variants associated with Mycobacterium tuberculosis-induced cytokine transcriptional responses. The Journal of clinical investigation, 135(14).