Resource Summary Report

Generated by T1D on Aug 2, 2026

Mach2dat

RRID:SCR_009599
Type: Tool

Proper Citation

Mach2dat (RRID:SCR_009599)

Resource Information

URL: http://genome.sph.umich.edu/wiki/Mach2dat:_Association_with_MACH_output

Proper Citation: Mach2dat (RRID:SCR_009599)

Description: Software that performs logistic regression, using imputed SNP dosage data and adjusting for covariates.

Synonyms: Mach2dat: Association with MACH output

Resource Type: software resource, software application

Defining Citation: PMID:21058334, PMID:19715440

Keywords: genetic association, genomic analysis, imaging genomics, snp, gene, imputation

Availability: Free, Non-commercial, Acknowledgement requested

Resource Name: Mach2dat

Resource ID: SCR_009599

Alternate IDs: nlx_155801

Alternate URLs: http://www.nitrc.org/projects/mach2dat

Record Creation Time: 20220129T080253+0000

Record Last Update: 20260801T191052+0000

Ratings and Alerts

No rating or validation information has been found for Mach2dat.

No alerts have been found for Mach2dat.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 40 mentions in open access literature.

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

Li J, et al. (2022) Limb development genes underlie variation in human fingerprint patterns. Cell, 185(1), 95.

Masuda T, et al. (2020) GWAS of five gynecologic diseases and cross-trait analysis in Japanese. European journal of human genetics : EJHG, 28(1), 95.

Spracklen CN, et al. (2020) Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 582(7811), 240.

Mehta SD, et al. (2020) Host Genetic Factors Associated with Vaginal Microbiome Composition in Kenyan Women. mSystems, 5(4).

Shah S, et al. (2020) Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature communications, 11(1), 163.

Cha PC, et al. (2020) Genome-wide association study identifies zonisamide responsive gene in Parkinson's disease patients. Journal of human genetics, 65(8), 693.

Low SK, et al. (2019) Identification of two novel breast cancer loci through large-scale genome-wide association study in the Japanese population. Scientific reports, 9(1), 17332.

Kou I, et al. (2019) Genome-wide association study identifies 14 previously unreported susceptibility loci for adolescent idiopathic scoliosis in Japanese. Nature communications, 10(1), 3685.

Ogura Y, et al. (2018) An international meta-analysis confirms the association of BNC2 with adolescent idiopathic scoliosis. Scientific reports, 8(1), 4730.

Taira M, et al. (2018) A variant within the FTO confers susceptibility to diabetic nephropathy in Japanese patients with type 2 diabetes. PloS one, 13(12), e0208654.

Shah RL, et al. (2018) A genome-wide association study of corneal astigmatism: The CREAM Consortium. Molecular vision, 24, 127.

Salem JE, et al. (2017) GENomE wide analysis of sotalol-induced IKr inhibition during ventricular REPOLarization, "GENEREPOL study": Lack of common variants with large effect sizes. PloS one, 12(8), e0181875.

Gao G, et al. (2017) Trans-ethnic predicted expression genome-wide association analysis identifies a gene for estrogen receptor-negative breast cancer. PLoS genetics, 13(9), e1006727.

Einarsdottir E, et al. (2017) CELSR2 is a candidate susceptibility gene in idiopathic scoliosis. PloS one, 12(12), e0189591.

Li Y, et al. (2016) Genome-wide association study identifies 8p21.3 associated with persistent hepatitis B virus infection among Chinese. Nature communications, 7, 11664.

Sailer A, et al. (2016) A genome-wide association study in multiple system atrophy. Neurology, 87(15), 1591.

Shiraishi K, et al. (2016) Association of variations in HLA class II and other loci with susceptibility to EGFR-mutated lung adenocarcinoma. Nature communications, 7, 12451.

Zanetti D, et al. (2016) Analysis of Genomic Regions Associated With Coronary Artery Disease Reveals Continent-Specific Single Nucleotide Polymorphisms in North African Populations. Journal of epidemiology, 26(5), 264.

Ferrari R, et al. (2015) A genome-wide screening and SNPs-to-genes approach to identify novel genetic risk factors associated with frontotemporal dementia. Neurobiology of aging, 36(10), 2904.e13.

Acosta-Herrera M, et al. (2015) Common variants of NFE2L2 gene predisposes to acute respiratory distress syndrome in patients with severe sepsis. Critical care (London, England), 19(1), 256.