

Resource Summary Report

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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

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

Synonyms: Mach2dat: Association with MACH output

Resource Type: software application, software resource

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: 20260821T042844+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 [NIF](#) .

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

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

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.

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

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.

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.

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.