Resource Summary Report

Generated by RRID on Apr 11, 2025

MaCH-Admix

RRID:SCR_009598
Type: Tool

Proper Citation

MaCH-Admix (RRID:SCR_009598)

Resource Information

URL: http://www.unc.edu/~yunmli/MaCH-Admix/

Proper Citation: MaCH-Admix (RRID:SCR_009598)

Description: A genotype imputation software that is an extension to MaCH for faster and more flexible imputaiton, especially in admixed populations. It has incorporated a novel piecewise reference selection method to create reference panels tailored for target individual(s). This reference selection method generates better imputation quality in shorter running time. MaCH-Admix also separates model parameter estimation from imputation. The separation allows users to perform imputation with standard reference panels + pre-calibrated parameters in a data independent fashion. Alternatively, if one works with study-specific reference panels, or isolated target population, one has the option to simultaneously estimate these model parameters while performing imputation. MaCH-Admix has included many other useful options and supports VCF input files. All existing MaCH documentation applies to MaCH-Admix.

Synonyms: MaCH-Admix: Genotype Imputation Software

Resource Type: software resource, software application

Defining Citation: PMID:23074066

Keywords: genomic analysis, imaging genomics, imputation, snp, gene, bio.tools

Funding:

Availability: Free, Non-commercial, Acknowledgement requested

Resource Name: MaCH-Admix

Resource ID: SCR_009598

Alternate IDs: nlx_155800, biotools:mach-admix

Alternate URLs: http://www.nitrc.org/projects/mach-admix, https://bio.tools/mach-admix

Record Creation Time: 20220129T080253+0000

Record Last Update: 20250411T055345+0000

Ratings and Alerts

No rating or validation information has been found for MaCH-Admix.

No alerts have been found for MaCH-Admix.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

de Zeeuw EL, et al. (2020) Intergenerational Transmission of Education and ADHD: Effects of Parental Genotypes. Behavior genetics, 50(4), 221.

Gong Y, et al. (2020) ABTB2 Regulatory Variant as Predictor of Epirubicin-Based Neoadjuvant Chemotherapy in Luminal A Breast Cancer. Frontiers in oncology, 10, 571517.

Baselmans BML, et al. (2019) A Genetic Investigation of the Well-Being Spectrum. Behavior genetics, 49(3), 286.

Sariya S, et al. (2019) Rare Variants Imputation in Admixed Populations: Comparison Across Reference Panels and Bioinformatics Tools. Frontiers in genetics, 10, 239.

de Zeeuw EL, et al. (2019) The moderating role of SES on genetic differences in educational achievement in the Netherlands. NPJ science of learning, 4, 13.

Fan Z, et al. (2018) DLGAP1 and NMDA receptor-associated postsynaptic density protein genes influence executive function in attention deficit hyperactivity disorder. Brain and behavior, 8(2), e00914.

Qin X, et al. (2017) Risk alleles for IgA nephropathy-associated SNPs conferred completely

opposite effects to idiopathic membranous nephropathy in Chinese Han. Immunologic research, 65(5), 1059.

Zhu W, et al. (2017) Genome-wide association analysis of secondary imaging phenotypes from the Alzheimer's disease neuroimaging initiative study. NeuroImage, 146, 983.

Smith CE, et al. (2016) Associations of the MCM6-rs3754686 proxy for milk intake in Mediterranean and American populations with cardiovascular biomarkers, disease and mortality: Mendelian randomization. Scientific reports, 6, 33188.

Sun C, et al. (2016) High-density genotyping of immune-related loci identifies new SLE risk variants in individuals with Asian ancestry. Nature genetics, 48(3), 323.

Wijsman EM, et al. (2016) Family-based approaches: design, imputation, analysis, and beyond. BMC genetics, 17 Suppl 2(Suppl 2), 9.

Adeyemo AA, et al. (2015) Evaluation of Genome Wide Association Study Associated Type 2 Diabetes Susceptibility Loci in Sub Saharan Africans. Frontiers in genetics, 6, 335.

Buchkovich ML, et al. (2015) Removing reference mapping biases using limited or no genotype data identifies allelic differences in protein binding at disease-associated loci. BMC medical genomics, 8, 43.

Peck BC, et al. (2015) MicroRNAs Classify Different Disease Behavior Phenotypes of Crohn's Disease and May Have Prognostic Utility. Inflammatory bowel diseases, 21(9), 2178.

Zhu Z, et al. (2015) Genome-wide association study identifies new susceptibility loci for adolescent idiopathic scoliosis in Chinese girls. Nature communications, 6, 8355.

Bentley AR, et al. (2014) Gene-based sequencing identifies lipid-influencing variants with ethnicity-specific effects in African Americans. PLoS genetics, 10(3), e1004190.

Ye H, et al. (2013) Genetic associations with coronary heart disease: meta-analyses of 12 candidate genetic variants. Gene, 531(1), 71.

Hancock DB, et al. (2012) Assessment of genotype imputation performance using 1000 Genomes in African American studies. PloS one, 7(11), e50610.