Resource Summary Report

Generated by NIF on May 14, 2025

MACH 1.0

RRID:SCR_001759
Type: Tool

Proper Citation

MACH 1.0 (RRID:SCR_001759)

Resource Information

URL: http://csg.sph.umich.edu//abecasis/MACH/index.html

Proper Citation: MACH 1.0 (RRID:SCR_001759)

Description: A Markov Chain based software tool for haplotyping, genotype imputation and disease association analysis that can resolve long haplotypes or infer missing genotypes in samples of unrelated individuals.

Synonyms: MArkov Chain Haplotyper MINIMAC, MArkov Chain Haplotyping

Resource Type: software resource, data analysis software, software application, data processing software

Defining Citation: PMID:21058334, PMID:19715440

Keywords: gene, genetic, genomic, haplotype, genotype, genomic analysis, imaging genomics, imputation, snp, gene, haplotyping, sequence

Funding:

Availability: Free, Non-commercial, Acknowledgement requested, Registration requested

Resource Name: MACH 1.0

Resource ID: SCR_001759

Alternate IDs: nlx_154202, OMICS_00064

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250514T061209+0000

Ratings and Alerts

No rating or validation information has been found for MACH 1.0.

No alerts have been found for MACH 1.0.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 58 mentions in open access literature.

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

Akiyama M, et al. (2023) Genome-wide association study reveals BET1L associated with survival time in the 137,693 Japanese individuals. Communications biology, 6(1), 143.

Akiyama M, et al. (2019) Characterizing rare and low-frequency height-associated variants in the Japanese population. Nature communications, 10(1), 4393.

Bhatnagar V, et al. (2016) Analysis of ABCG2 and other urate transporters in uric acid homeostasis in chronic kidney disease: potential role of remote sensing and signaling. Clinical kidney journal, 9(3), 444.

Finkel TH, et al. (2016) Variants in CXCR4 associate with juvenile idiopathic arthritis susceptibility. BMC medical genetics, 17, 24.

Keaton JM, et al. (2016) Genome-Wide Interaction with Insulin Secretion Loci Reveals Novel Loci for Type 2 Diabetes in African Americans. PloS one, 11(7), e0159977.

Lu AT, et al. (2016) Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. Nature communications, 7, 10561.

Chahal HS, et al. (2016) Genome-wide association study identifies novel susceptibility loci for cutaneous squamous cell carcinoma. Nature communications, 7, 12048.

Chahal HS, et al. (2016) Genome-wide association study identifies 14 novel risk alleles associated with basal cell carcinoma. Nature communications, 7, 12510.

van Nistelrooij AM, et al. (2015) Single nucleotide polymorphisms in CRTC1 and BARX1 are associated with esophageal adenocarcinoma. Journal of carcinogenesis, 14, 5.

Cao S, et al. (2015) Genome-wide Association Study on Platinum-induced Hepatotoxicity in Non-Small Cell Lung Cancer Patients. Scientific reports, 5, 11556.

Huang T, et al. (2015) Genetic Predisposition to Central Obesity and Risk of Type 2 Diabetes: Two Independent Cohort Studies. Diabetes care, 38(7), 1306.

Corvol H, et al. (2015) Genome-wide association meta-analysis identifies five modifier loci of lung disease severity in cystic fibrosis. Nature communications, 6, 8382.

Kim YJ, et al. (2015) A new strategy for enhancing imputation quality of rare variants from next-generation sequencing data via combining SNP and exome chip data. BMC genomics, 16, 1109.

Michailidou K, et al. (2015) Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature genetics, 47(4), 373.

Nakano M, et al. (2014) Novel common variants and susceptible haplotype for exfoliation glaucoma specific to Asian population. Scientific reports, 4, 5340.

Cai Q, et al. (2014) Genome-wide association analysis in East Asians identifies breast cancer susceptibility loci at 1q32.1, 5q14.3 and 15q26.1. Nature genetics, 46(8), 886.

Orozco G, et al. (2014) Novel rheumatoid arthritis susceptibility locus at 22q12 identified in an extended UK genome-wide association study. Arthritis & rheumatology (Hoboken, N.J.), 66(1), 24.

Rafiq S, et al. (2014) A genome wide meta-analysis study for identification of common variation associated with breast cancer prognosis. PloS one, 9(12), e101488.

Wang Y, et al. (2014) Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. Nature genetics, 46(7), 736.

Gialluisi A, et al. (2014) Genome-wide screening for DNA variants associated with reading and language traits. Genes, brain, and behavior, 13(7), 686.