Resource Summary Report

Generated by NIF on May 2, 2025

ADMIXMAP

RRID:SCR_009035
Type: Tool

Proper Citation

ADMIXMAP (RRID:SCR_009035)

Resource Information

URL: http://www.homepages.ed.ac.uk/pmckeigu/admixmap/index.html

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Description: General-purpose program for modelling admixture, using marker genotypes and trait data on a sample of individuals from an admixed population (such as African-Americans), where the markers have been chosen to have extreme differentials in allele frequencies between two or more of the ancestral populations between which admixture has occurred. The main difference between ADMIXMAP and classical programs for estimation of admixture such as ADMIX is that ADMIXMAP is based on a multilevel model for the distribution of individual admixture in the population and the stochastic variation of ancestry on hybrid chromosomes. This makes it possible to model the associations of ancestry between linked marker loci, and the association of a trait with individual admixture or with ancestry at a linked marker locus. (entry from Genetic Analysis Software)

Abbreviations: ADMIXMAP

Synonyms: Admixture mapping

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, c++, linux, ms-windows, bio.tools

Funding:

Resource Name: ADMIXMAP

Resource ID: SCR_009035

Alternate IDs: nlx_153999, biotools:admixmap

Alternate URLs: https://bio.tools/admixmap

Record Creation Time: 20220129T080250+0000

Record Last Update: 20250502T055834+0000

Ratings and Alerts

No rating or validation information has been found for ADMIXMAP.

No alerts have been found for ADMIXMAP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Llibre-Guerra JJ, et al. (2024) Social determinants of health but not global genetic ancestry predict dementia prevalence in Latin America. Alzheimer's & dementia : the journal of the Alzheimer's Association, 20(7), 4828.

Kizil C, et al. (2022) Admixture Mapping of Alzheimer's disease in Caribbean Hispanics identifies a new locus on 22q13.1. Molecular psychiatry, 27(6), 2813.

Chen TK, et al. (2020) Association of APOL1 Genotypes With Measures of Microvascular and Endothelial Function, and Blood Pressure in MESA. Journal of the American Heart Association, 9(17), e017039.

Caro-Gomez MA, et al. (2018) Association of Native American ancestry and common variants in ACE, ADIPOR2, MTNR1B, GCK, TCF7L2 and FTO genes with glycemic traits in Colombian population. Gene, 677, 198.

Yao S, et al. (2018) Genetic ancestry and population differences in levels of inflammatory cytokines in women: Role for evolutionary selection and environmental factors. PLoS genetics, 14(6), e1007368.

Uribe-Salazar JM, et al. (2018) Admixture mapping and fine-mapping of type 2 diabetes susceptibility loci in African American women. Journal of human genetics, 63(11), 1109.

Cahua-Pablo JÁ, et al. (2017) Analysis of admixture proportions in seven geographical regions of the state of Guerrero, Mexico. American journal of human biology : the official journal of the Human Biology Council, 29(6).

de Jesús Ascencio-Montiel I, et al. (2017) Characterization of Large Copy Number Variation in Mexican Type 2 Diabetes subjects. Scientific reports, 7(1), 17105.

Chen TK, et al. (2017) Association Between APOL1 Genotypes and Risk of Cardiovascular Disease in MESA (Multi-Ethnic Study of Atherosclerosis). Journal of the American Heart Association, 6(12).

Muñoz AM, et al. (2017) Examining for an association between candidate gene polymorphisms in the metabolic syndrome components on excess weight and adiposity measures in youth: a cross-sectional study. Genes & nutrition, 12, 19.

Ruiz-Narváez EA, et al. (2016) Birth weight modifies the association between central nervous system gene variation and adult body mass index. Journal of human genetics, 61(3), 193.

Ruiz-Narváez EA, et al. (2016) Admixture Mapping of African-American Women in the AMBER Consortium Identifies New Loci for Breast Cancer and Estrogen-Receptor Subtypes. Frontiers in genetics, 7, 170.

Muñoz AM, et al. (2016) Cardio-metabolic parameters are associated with genetic admixture estimates in a pediatric population from Colombia. BMC genetics, 17(1), 93.

Zhao J, et al. (2016) Preferential association of a functional variant in complement receptor 2 with antibodies to double-stranded DNA. Annals of the rheumatic diseases, 75(1), 242.

Mersha TB, et al. (2015) Mapping asthma-associated variants in admixed populations. Frontiers in genetics, 6, 292.

Cardona-Castro N, et al. (2015) Human Genetic Ancestral Composition Correlates with the Origin of Mycobacterium leprae Strains in a Leprosy Endemic Population. PLoS neglected tropical diseases, 9(9), e0004045.

Zhang K, et al. (2015) Admixture mapping of genetic variants for uterine fibroids. Journal of human genetics, 60(9), 533.

Vaughn SE, et al. (2014) Lupus risk variants in the PXK locus alter B-cell receptor internalization. Frontiers in genetics, 5, 450.

Willig AL, et al. (2009) Uncoupling protein 2 Ala55Val polymorphism is associated with a higher acute insulin response to glucose. Metabolism: clinical and experimental, 58(6), 877.