Resource Summary Report

Generated by NIF on Apr 21, 2025

BIMBAM

RRID:SCR_009129
Type: Tool

Proper Citation

BIMBAM (RRID:SCR_009129)

Resource Information

URL: http://stephenslab.uchicago.edu/software.html

Proper Citation: BIMBAM (RRID:SCR_009129)

Description: Software application (entry from Genetic Analysis Software)

Abbreviations: BIMBAM

Synonyms: Bayesian IMputation-Based Association Mapping

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Funding:

Resource Name: BIMBAM

Resource ID: SCR_009129

Alternate IDs: nlx_154242

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250421T053718+0000

Ratings and Alerts

No rating or validation information has been found for BIMBAM.

No alerts have been found for BIMBAM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 75 mentions in open access literature.

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

Tough RH, et al. (2025) Functionally-informed fine-mapping identifies genetic variants linking increased CHD1L expression and HIV restriction in monocytes. Scientific reports, 15(1), 2325.

Ahmed SR, et al. (2024) Advancing crop improvement through GWAS and beyond in mung bean. Frontiers in plant science, 15, 1436532.

Wang Z, et al. (2024) Refine localizations of functional variants affecting eggshell color of Lueyang black-boned chicken in the SLCO1B3. Poultry science, 103(1), 103212.

Chen Q, et al. (2022) A new molecular mechanism supports that blue-greenish egg color evolved independently across chicken breeds. Poultry science, 101(12), 102223.

Sinclair-Waters M, et al. (2022) Dissecting the loci underlying maturation timing in Atlantic salmon using haplotype and multi-SNP based association methods. Heredity, 129(6), 356.

Vilor-Tejedor N, et al. (2021) Multivariate Analysis and Modelling of multiple Brain endOphenotypes: Let's MAMBO! Computational and structural biotechnology journal, 19, 5800.

Ahluwalia TS, et al. (2021) Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human molecular genetics, 30(5), 393.

Yang Z, et al. (2021) Genome-Wide Association Study Using Whole-Genome Sequencing Identifies a Genomic Region on Chromosome 6 Associated With Comb Traits in Nandan-Yao Chicken. Frontiers in genetics, 12, 682501.

Wang Z, et al. (2021) Research Note: Fine mapping of sequence variants associated with body weight of Lueyang black-boned chicken in the CCKAR gene. Poultry science, 100(11), 101448.

García-Fernández C, et al. (2021) GWAS of pod morphological and color characters in common bean. BMC plant biology, 21(1), 184.

Shang L, et al. (2020) Genetic Architecture of Gene Expression in European and African

Americans: An eQTL Mapping Study in GENOA. American journal of human genetics, 106(4), 496.

Abuga KM, et al. (2020) Interferon-gamma polymorphisms and risk of iron deficiency and anaemia in Gambian children. Wellcome open research, 5, 40.

Xu Z, et al. (2020) Selection signature reveals genes associated with susceptibility loci affecting respiratory disease due to pleiotropic and hitchhiking effect in Chinese indigenous pigs. Asian-Australasian journal of animal sciences, 33(2), 187.

Su M, et al. (2020) Genomic analysis of variability in Delta-toxin levels between Staphylococcus aureus strains. PeerJ, 8, e8717.

Rito T, et al. (2019) Association of Leukotriene A4 Hydrolase with Tuberculosis Susceptibility Using Genomic Data in Portugal. Microorganisms, 7(12).

Chundru VK, et al. (2019) Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. Genetics, 212(3), 577.

Mozaffari SV, et al. (2019) Parent-of-origin effects on quantitative phenotypes in a large Hutterite pedigree. Communications biology, 2, 28.

Morton MJL, et al. (2019) Salt stress under the scalpel - dissecting the genetics of salt tolerance. The Plant journal : for cell and molecular biology, 97(1), 148.

Vieira A, et al. (2019) Genome-Wide Signatures of Selection in Colletotrichum kahawae Reveal Candidate Genes Potentially Involved in Pathogenicity and Aggressiveness. Frontiers in microbiology, 10, 1374.

Park CS, et al. (2019) Hepatocyte gene expression and DNA methylation as ancestry-dependent mechanisms in African Americans. NPJ genomic medicine, 4, 29.