Resource Summary Report

Generated by NIF on Aug 21, 2026

FBAT

RRID:SCR_009178
Type: Tool

Proper Citation

FBAT (RRID:SCR_009178)

Resource Information

URL: http://www.biostat.harvard.edu/~fbat/fbat.htm

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Description: Software application that allows the user to test for association/linkage between disease phenotypes and haplotypes by utilizing family-based controls. The method extends the approach for testing described in Rabinowitz and Laird (2000) to handle multiple tightly linked markers. It is robust to population admixture, yet efficient in the sense that it utilizes data from families where phase cannot be completely resolved in all individuals by using weights, which are estimated from the sample. However, the method remains robust to population stratification and population admixture. The method can handle any type of phenotype, including multiple phenotypes and missing parents, marker data, and/or phase, and provides both bi-allelic and multi-allelic tests. PowerFBAT is a tool for power simulation of association analysis using FBAT with binary outcomes. XWXW is an extension to the Haseman-Elston method for non-parametric linkage test with quantitative traits. XDT is a software that performs classical TDT, SDT and Rabinowitz TDT for nuclear families (not supported anymore). (entry from Genetic Analysis Software)

Abbreviations: FBAT

Synonyms: (haplotype) Family Based Association Test PBAT

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, unix, solaris, linux, ms-windows, mac, macos x, darwin

Resource Name: FBAT

Resource ID: SCR_009178

Alternate IDs: nlx_154315

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260821T042825+0000

Ratings and Alerts

No rating or validation information has been found for FBAT.

No alerts have been found for FBAT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 82 mentions in open access literature.

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

Salvo MA, et al. (2026) Alzheimer's disease-linked ACE variants increase ACE1 catalytic activity and production of angiotensin II. The Journal of biological chemistry, 302(3), 111171.

Justice CM, et al. (2026) Combined family-based association and linkage analyses in families affected by attention-deficit hyperactivity disorder. Human genetics, 145(1).

Pilat DJ, et al. (2026) The gain-of-function TREM2-T96K mutation increases risk for Alzheimer's disease by impairing microglial function. Neuron, 114(1), 46.

Lee S, et al. (2025) On the analysis of metabolite quantitative trait loci: Impact of different data transformations and study designs. Science advances, 11(15), eadp4532.

Gauron MC, et al. (2025) Protein kinase C eta enhances Golgi-localized signaling and is associated with Alzheimer's disease using a recessive mode of inheritance. medRxiv : the preprint server for health sciences.

Yu A, et al. (2025) The regulatory role of ACP5 in the diesel exhaust particle-induced AHR inflammatory signaling pathway in a human bronchial epithelial cell line. Scientific reports, 15(1), 8826.

Uittenbogaard P, et al. (2024) FCGR2/3 polymorphisms are associated with susceptibility to Kawasaki disease but do not predict intravenous immunoglobulin resistance and coronary artery aneurysms. Frontiers in immunology, 15, 1323171.

Lin F, et al. (2024) Replication of previous autism-GWAS hits suggests the association between NAA1, SORCS3, and GSDME and autism in the Han Chinese population. Heliyon, 10(1), e23677.

Cruz-Leite VRM, et al. (2023) Proteomics of Paracoccidioides lutzii: Overview of Changes Triggered by Nitrogen Catabolite Repression. Journal of fungi (Basel, Switzerland), 9(11).

Mewamba EM, et al. (2023) Association between polymorphisms of IL4, IL13, IL10, STAT6 and IFNG genes, cytokines and immunoglobulin E levels with high burden of Schistosoma mansoni in children from schistosomiasis endemic areas of Cameroon. Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases, 111, 105416.

Prokopenko D, et al. (2022) Region-based analysis of rare genomic variants in whole-genome sequencing datasets reveal two novel Alzheimer's disease-associated genes: DTNB and DLG2. Molecular psychiatry, 27(4), 1963.

de Souza AF, et al. (2021) Interacting with Hemoglobin: Paracoccidioides spp. Recruits hsp30 on Its Cell Surface for Enhanced Ability to Use This Iron Source. Journal of fungi (Basel, Switzerland), 7(1).

Wang Z, et al. (2021) Family-based association study identifies SNAP25 as a susceptibility gene for autism in the Han Chinese population. Progress in neuro-psychopharmacology & biological psychiatry, 105, 109985.

Prokopenko D, et al. (2021) Whole-genome sequencing reveals new Alzheimer's disease-associated rare variants in loci related to synaptic function and neuronal development. Alzheimer's & dementia : the journal of the Alzheimer's Association, 17(9), 1509.

Fageera W, et al. (2021) Sex-dependent complex association of TPH2 with multiple dimensions of ADHD. Progress in neuro-psychopharmacology & biological psychiatry, 110, 110296.

Cervantes-Henriquez ML, et al. (2021) ADGRL3, FGF1 and DRD4: Linkage and Association with Working Memory and Perceptual Organization Candidate Endophenotypes in ADHD. Brain sciences, 11(7).

Alumasa L, et al. (2021) Hospital-based evidence on cost-effectiveness of brucellosis diagnostic tests and treatment in Kenyan hospitals. PLoS neglected tropical diseases, 15(1), e0008977.

Daneshpour MS, et al. (2021) Chromosomal regions strongly associated with waist circumference and body mass index in metabolic syndrome in a family-based study. Scientific reports, 11(1), 6082.

Witten A, et al. (2020) ADAMTS12, a new candidate gene for pediatric stroke. PloS one, 15(8), e0237928.

Prokopenko D, et al. (2020) Identification of Novel Alzheimer's Disease Loci Using Sex-Specific Family-Based Association Analysis of Whole-Genome Sequence Data. Scientific reports, 10(1), 5029.