Resource Summary Report

Generated by NIF on Apr 20, 2025

Genetic Analysis Software

RRID:SCR_013155
Type: Tool

Proper Citation

Genetic Analysis Software (RRID:SCR_013155)

Resource Information

URL: http://www.jurgott.org/linkage/ListSoftware.html

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 4th,2023. Listing of computer software for the gene mapping community on the following topics: genetic linkage analysis for human pedigree data, QTL analysis for animal/plant breeding data, genetic marker ordering, genetic association analysis, haplotype construction, pedigree drawing, and population genetics. The inclusion of a program should not be interpreted as an endorsement to that program from us. In the last few years, new technology produces new types of genetic data, and the scope of genetic analyses change dramatically. It is no longer obvious whether a program should be included or excluded from this list. Topics such as next-generation-sequencing (NGS), gene expression, genomics annotation, etc. can all be relevant to a genetic study, yet be specialized topics by themselves. Though programs on variance calling from NSG can be in, those can sequence alignment might be out; programs on eQTL can be in, those on differential expression might be out. This page was created by Dr. Wentian Li, when he was at Columbia University (1995-1996). It was later moved to Rockefeller University (1996-2002), and now takes its new home at North Shore LIJ Research Institute (2002-now). The present copy is maintained by Jurg Ott as a single file. More than 240 programs have been listed by December 2004, more than 350 programs by August 2005, close to 400 programs by December 2006, and close to 480 programs by November 2008, and over 600 programs by October 2012. A version of the searchable database was developed by Zhiliang Hu of Iowa State University, and a recent round of updating was assisted by Wei JIANG of Harbin Medical School. Some earlier software can be downloaded from EBI: ftp://ftp.ebi.ac.uk/pub/software/linkage_and_mapping/ (Linkage and Mapping Software Repository), and http://genamics.com/software/index.htm may contain archived copy of some programs.

Abbreviations: GAS

Synonyms: An Alphabetic List of Genetic Analysis Software

Resource Type: database, software resource, data set, catalog, data or information resource

Keywords: gene mapping, gene, genetic, genomic, model, modeling, software program, genetic linkage analysis, qtl analysis, genetic marker order, genetic association analysis, haplotype construction, pedigree drawing, population genetics

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Genetic Analysis Software

Resource ID: SCR_013155

Alternate IDs: nif-0000-33506

Alternate URLs: http://lab.rockefeller.edu/ott/geneticsoftware

Old URLs: http://linkage.rockefeller.edu/soft/

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250420T014634+0000

Ratings and Alerts

No rating or validation information has been found for Genetic Analysis Software.

No alerts have been found for Genetic Analysis Software.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Ozyurt IB, et al. (2016) Resource Disambiguator for the Web: Extracting Biomedical Resources and Their Citations from the Scientific Literature. PloS one, 11(1), e0146300.

Poletta FA, et al. (2014) Genealogical data in population medical genetics: Field guidelines. Genetics and molecular biology, 37(1 Suppl), 171.

Bennett TM, et al. (2014) Mutation of the melastatin-related cation channel, TRPM3, underlies inherited cataract and glaucoma. PloS one, 9(8), e104000.

Dong B, et al. (2013) Two novel PRP31 premessenger ribonucleic acid processing factor 31 homolog mutations including a complex insertion-deletion identified in Chinese families with retinitis pigmentosa. Molecular vision, 19, 2426.

He Y, et al. (2009) IkappaBalpha gene promoter polymorphisms are associated with hepatocarcinogenesis in patients infected with hepatitis B virus genotype C. Carcinogenesis, 30(11), 1916.

Hu Z, et al. (2009) PROC QTL-A SAS Procedure for Mapping Quantitative Trait Loci. International journal of plant genomics, 2009, 141234.

Salem RM, et al. (2005) A comprehensive literature review of haplotyping software and methods for use with unrelated individuals. Human genomics, 2(1), 39.

Almasy L, et al. (2005) Software for quantitative trait analysis. Human genomics, 2(3), 191.

Fischer G, et al. (2003) Expressionview: visualization of quantitative trait loci and gene-expression data in Ensembl. Genome biology, 4(11), R77.