Resource Summary Report

Generated by dkNET on Apr 17, 2025

PAP

RRID:SCR_009083
Type: Tool

Proper Citation

PAP (RRID:SCR_009083)

Resource Information

URL: http://hasstedt.genetics.utah.edu/

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Description: Software application that can (1) compute the likelihood of specified parameter values; (2) compute the probability of each genotype for pedigree members; (3) simulate phenotypes for output into files; (4) maximize the likelihood over specified parameters (with or without standard errors); (5) compute the standard errors of parameters for unknown estimates; (6) simulate phenotypes and estimate parameter values; (7) estimate expected lod score; (8) compute a grid of likelihood over one or two parameters. New additions to V5: assortative mating; TDT; additive multi-locus models (entry from Genetic Analysis Software)

Abbreviations: PAP

Synonyms: Pedigree Analysis Package

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, fortran 77, unix

Funding:

Resource Name: PAP

Resource ID: SCR_009083

Alternate IDs: nlx_154094

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250416T063536+0000

Ratings and Alerts

No rating or validation information has been found for PAP.

No alerts have been found for PAP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Hasstedt SJ, et al. (2013) Five linkage regions each harbor multiple type 2 diabetes genes in the African American subset of the GENNID Study. Journal of human genetics, 58(6), 378.

Hasstedt SJ, et al. (2011) Pleiotropy of type 2 diabetes with obesity. Journal of human genetics, 56(7), 491.

Kosta K, et al. (2007) A Bayesian approach to copy-number-polymorphism analysis in nuclear pedigrees. American journal of human genetics, 81(4), 808.

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

Elston RC, et al. (2004) A review of the 'Statistical Analysis for Genetic Epidemiology' (S.A.G.E.) software package. Human genomics, 1(6), 456.

Goode EL, et al. (2003) Multiple genome-wide analyses of smoking behavior in the Framingham Heart Study. BMC genetics, 4 Suppl 1(Suppl 1), S102.

Xu J, et al. (2002) Major recessive gene(s) with considerable residual polygenic effect regulating adult height: confirmation of genomewide scan results for chromosomes 6, 9, and 12. American journal of human genetics, 71(3), 646.