

Resource Summary Report

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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 application, software resource

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

Resource Name: PAP

Resource ID: SCR_009083

Alternate IDs: nlx_154094

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260805T044218+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 [RRID](#) .

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.