Resource Summary Report

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HAPGEN

RRID:SCR_009221
Type: Tool

Proper Citation

HAPGEN (RRID:SCR_009221)

Resource Information

URL: http://www.stats.ox.ac.uk/~marchini/software/gwas/hapgen.html

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Description: Software application that simulates case control datasets at SNP markers and can output data in the FILE FORMAT used by IMPUTE, SNPTEST and GTOOL. The approach can handle markers in LD and can simulate datasets over large regions such as whole chromosomes. Hapgen simulates haplotypes by conditioning on a set of population haplotypes and an estimate of the fine-scale recombination rate across the region. The disease model is specified through the choice of a single SNP as the disease causing variant together with the relative risks of the genotypes at the disease SNP. The program is designed to work with publically available files that contain the haplotypes estimated as part of the HapMap project and the estimated fine-scale recombination map derived from that data. Hapgen is computationally tractable. On a modern desktop HAPGEN can simulate several thousand case and control data on a whole chromosome at Hapmap Phase 2 marker density within minutes. This program has been used to assess the power of several different commercially available genotyping chips, in the design stage of the 7 genome-wide association studies carried out by the Wellcome Trust Case-Control Consortium (WTCCC) and for evaluating the power of different methods for detecting association in genome-wide studies. (entry from Genetic Analysis Software)

Abbreviations: HAPGEN

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c++

Funding:

Resource Name: HAPGEN

Resource ID: SCR_009221

Alternate IDs: nlx_154377

Record Creation Time: 20220129T080251+0000

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Ratings and Alerts

No rating or validation information has been found for HAPGEN.

No alerts have been found for HAPGEN.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Huang M, et al. (2023) A gene-based association test of interactions for maternal-fetal genotypes identifies genes associated with nonsyndromic congenital heart defects. Genetic epidemiology, 47(7), 475.

Bao F, et al. (2020) Explaining the Genetic Causality for Complex Phenotype via Deep Association Kernel Learning. Patterns (New York, N.Y.), 1(6), 100057.

Ullah E, et al. (2019) Comparison and assessment of family- and population-based genotype imputation methods in large pedigrees. Genome research, 29(1), 125.

Sinoquet C, et al. (2018) A method combining a random forest-based technique with the modeling of linkage disequilibrium through latent variables, to run multilocus genome-wide association studies. BMC bioinformatics, 19(1), 106.

Herzig AF, et al. (2018) Detecting the dominance component of heritability in isolated and outbred human populations. Scientific reports, 8(1), 18048.

Chun S, et al. (2017) Limited statistical evidence for shared genetic effects of eQTLs and autoimmune-disease-associated loci in three major immune-cell types. Nature genetics, 49(4), 600.

Bertrand J, et al. (2015) Integrating dynamic mixed-effect modelling and penalized regression to explore genetic association with pharmacokinetics. Pharmacogenetics and genomics, 25(5), 231.

Wang YT, et al. (2015) A multi-SNP association test for complex diseases incorporating an optimal P-value threshold algorithm in nuclear families. BMC genomics, 16(1), 381.

Mourad R, et al. (2011) A hierarchical Bayesian network approach for linkage disequilibrium modeling and data-dimensionality reduction prior to genome-wide association studies. BMC bioinformatics, 12, 16.

Spencer C, et al. (2011) Quantifying the underestimation of relative risks from genome-wide association studies. PLoS genetics, 7(3), e1001337.

Liu Y, et al. (2008) A survey of genetic simulation software for population and epidemiological studies. Human genomics, 3(1), 79.