Resource Summary Report

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Genetic Analysis Workshop

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Type: Tool

Proper Citation

Genetic Analysis Workshop (RRID:SCR_008350)

Resource Information

URL: http://www.gaworkshop.org/

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Description: The Genetic Analysis Workshops (GAWs) are a collaborative effort among genetic epidemiologists to evaluate and compare statistical genetic methods. For each GAW, topics are chosen that are relevant to current analytical problems in genetic epidemiology, and sets of real or computer-simulated data are distributed to investigators worldwide. Results of analyses are discussed and compared at meetings held in even-numbered years. The GAWs began in 1982 were initially motivated by the development and publication of several new algorithms for statistical genetic analysis, as well as by reports in the literature in which different investigators, using different methods of analysis, had reached contradictory conclusions. The impetus was initially to determine the numerical accuracy of the algorithms, to examine the robustness of the methodologies to violations of assumptions, and finally, to compare the range of conclusions that could be drawn from a single set of data. The Workshops have evolved to include consideration of problems related to analyses of specific complex traits, but the focus has always been on analytical methods. The Workshops provide an opportunity for participants to interact in addressing methodological issues, to test novel methods on the same well-characterized data sets, to compare results and interpretations, and to discuss current problems in genetic analysis. The Workshop discussions are a forum for investigators who are evolving new methods of analysis as well as for those who wish to gain further experience with existing methods. The success of the Workshops is due at least in part to the focus on specific problems and data sets, the informality of sessions, and the requirement that everyone who attends must have made a contribution. Topics are chosen and a small group of organizers is selected by the GAW Advisory Committee. Data sets are assembled, and six or seven months before each GAW, a memo is sent to individuals on the GAW mailing list announcing the availability of the GAW data. Included with the memo is a short description of the data sets and a form for requesting data. The form contains a statement to be signed by any investigator requesting the data, acknowledging that the data are confidential and agreeing not to use them for any purpose other than the Genetic Analysis Workshop without written permission from the data provider(s). Data are

distributed by the ftp or CD-ROM or, most recently, on the web, together with a more complete written description of the data sets. Investigators who wish to participate in GAW submit written contributions approximately 6-8 weeks before the Workshop. The GAW Advisory Committee reviews contributions for relevance to the GAW topics. Contributions are assembled and distributed to all participants approximately two weeks before the Workshop. Participation in the GAWs is limited to investigators who (1) submit results of their analyses for presentation at the Workshop, or (2) are data providers, invited speakers or discussants, or Workshop organizers. GAWs are held just before the meetings of the American Society of Human Genetics or the International Genetic Epidemiology Society, at a meeting site nearby. We choose a location that will encourage interaction among participants and permit an intense period of concentrated work. The proceedings of each GAW are published. Proceedings from GAW16 were published in part by Genetic Epidemiology 33(Suppl 1), S1-S110 (2009) and in part by Biomed Central (BMC Proceedings, Volume 3, Supplement 7, 2009). Sponsors: GAW is funded by the Southwest Foundation for Biomedical Research.

Synonyms: GAW

Resource Type: training resource, workshop

Keywords: epidemiologist, epidemiology, genetic, algorithm, analysis, method, statistical

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Ratings and Alerts

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

No alerts have been found for Genetic Analysis Workshop.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Chi J, et al. (2023) Association detection between multiple traits and rare variants based on family data via a nonparametric method. PeerJ, 11, e16040.

Zhou J, et al. (2021) A two-stage testing strategy for detecting genes??environment interactions in association studies. G3 (Bethesda, Md.), 11(10).

Khodayari Moez E, et al. (2019) Longitudinal linear combination test for gene set analysis. BMC bioinformatics, 20(1), 650.

Zou QL, et al. (2018) A powerful parent-of-origin effects test for qualitative traits on X chromosome in general pedigrees. BMC bioinformatics, 19(1), 8.

Xu SQ, et al. (2018) A statistical measure for the skewness of X chromosome inactivation based on family trios. BMC genetics, 19(1), 109.

Tintle NL, et al. (2018) GAW20: methods and strategies for the new frontiers of epigenetics and pharmacogenomics. BMC proceedings, 12(Suppl 9), 26.

Li JL, et al. (2017) Generalized disequilibrium test for association in qualitative traits incorporating imprinting effects based on extended pedigrees. BMC genetics, 18(1), 90.

Engelman CD, et al. (2016) Genetic Analysis Workshop 19: methods and strategies for analyzing human sequence and gene expression data in extended families and unrelated individuals. BMC proceedings, 10(Suppl 7), 67.

Cantor RM, et al. (2016) Genetic complexity at expression quantitative trait loci. BMC proceedings, 10(Suppl 7), 85.

Xu J, et al. (2016) A powerful score-based test statistic for detecting gene-gene co-association. BMC genetics, 17, 31.

Gola D, et al. (2016) Identification of interactions using model-based multifactor dimensionality reduction. BMC proceedings, 10(Suppl 7), 135.

Guo X, et al. (2014) Cloud computing for detecting high-order genome-wide epistatic interaction via dynamic clustering. BMC bioinformatics, 15, 102.

Blackburn AN, et al. (2014) Imputation in families using a heuristic phasing approach. BMC proceedings, 8(Suppl 1 Genetic Analysis Workshop 18Vanessa Olmo), S16.

Ghosh S, et al. (2011) Identifying rare variants from exome scans: the GAW17 experience. BMC proceedings, 5 Suppl 9(Suppl 9), S1.

Zhang L, et al. (2010) A towards-multidimensional screening approach to predict candidate genes of rheumatoid arthritis based on SNP, structural and functional annotations. BMC medical genomics, 3, 38.

Cupples LA, et al. (2009) Genetic Analysis Workshop 16: Strategies for genome-wide association study analyses. BMC proceedings, 3 Suppl 7(Suppl 7), S1.

Peng B, et al. (2007) Forward-time simulations of human populations with complex diseases. PLoS genetics, 3(3), e47.

Cordell HJ, et al. (2007) Genetic Analysis Workshop 15: gene expression analysis and approaches to detecting multiple functional loci. BMC proceedings, 1 Suppl 1(Suppl 1), S1.

Zhao JH, et al. (2006) Integrated analysis of genetic data with R. Human genomics, 2(4), 258.

Bailey-Wilson JE, et al. (2005) Genetic Analysis Workshop 14: microsatellite and single-nucleotide polymorphism marker loci for genome-wide scans. BMC genetics, 6 Suppl 1(Suppl 1), S1.