

Washington University School of Medicine

Digital Commons@Becker

Open Access Publications

2014

Genetic Analysis Workshop 18: Methods and strategies for analyzing human sequence and phenotype data in members of extended pedigrees

Robert C. Culverhouse
Washington University School of Medicine in St. Louis
et al

Follow this and additional works at: https://digitalcommons.wustl.edu/open_access_pubs

Please let us know how this document benefits you.

Recommended Citation

Culverhouse, Robert C. and et al, "Genetic Analysis Workshop 18: Methods and strategies for analyzing human sequence and phenotype data in members of extended pedigrees." *BMC Proceedings*. 8, S1. S1. (2014).

https://digitalcommons.wustl.edu/open_access_pubs/3554

This Open Access Publication is brought to you for free and open access by Digital Commons@Becker. It has been accepted for inclusion in Open Access Publications by an authorized administrator of Digital Commons@Becker. For more information, please contact vanam@wustl.edu.

PROCEEDINGS

Open Access

Genetic Analysis Workshop 18: Methods and strategies for analyzing human sequence and phenotype data in members of extended pedigrees

Heike Bickeböller^{1*}, Julia N Bailey², Joseph Beyene³, Rita M Cantor⁴, Heather J Cordell⁵, Robert C Culverhouse⁶, Corinne D Engelman⁷, David W Fardo⁸, Saurabh Ghosh⁹, Inke R König¹⁰, Justo Lorenzo Bermejo¹¹, Phillip E Melton¹², Stephanie A Santorico¹³, Glen A Satten¹⁴, Lei Sun¹⁵, Nathan L Tintle¹⁶, Andreas Ziegler^{10,17}, Jean W MacCluer¹⁸, Laura Almasy¹⁸

From Genetic Analysis Workshop 18
Stevenson, WA, USA. 13-17 October 2012

Abstract

Genetic Analysis Workshop 18 provided a platform for developing and evaluating statistical methods to analyze whole-genome sequence data from a pedigree-based sample. In this article we present an overview of the data sets and the contributions that analyzed these data. The family data, donated by the Type 2 Diabetes Genetic Exploration by Next-Generation Sequencing in Ethnic Samples Consortium, included sequence-level genotypes based on sequencing and imputation, genome-wide association genotypes from prior genotyping arrays, and phenotypes from longitudinal assessments. The contributions from individual research groups were extensively discussed before, during, and after the workshop in theme-based discussion groups before being submitted for publication.

Introduction

This supplement to *BMC Proceedings* contains the proceedings of the Genetic Analysis Workshop 18 (GAW18), which was held October 14-17, 2012, in Stevenson, Washington, USA. The Genetic Analysis Workshops (GAWs) were initiated in 1982 and are held in even-numbered years. They provide a discussion forum for developing and evaluating statistical methods aimed at deciphering the architecture of human complex diseases, mainly by identifying genetic risk factors for them. The same data set(s) are provided to all researchers, thus facilitating the discussion and comparison of methods. These data sets are chosen by the GAW Advisory Committee and take into consideration the suggestions and concerns of previous attendees, in particular, those

offered at the discussion meeting held at the end of the previous workshop. Data sets must be well characterized, address urgent needs for analysis tools in genetic epidemiology, and be available upon request before the workshop. After the GAW organizers release the data set (s), researchers analyze the data and prepare a manuscript to submit to the workshop. Co-authors of submitted manuscripts are eligible to attend the workshop. Active participation in group discussions is required, as is attendance at overall presentation and discussion meetings. Individuals who provide data or participate in GAW organization may also attend. More information about the workshops, including upcoming ones, can be found at <http://www.gaworkshop.org>. GAW19 will be held in Vienna, Austria, August 24-27, 2014.

Genetic Analysis Workshop 18

GAW18 was the first GAW to provide whole-genome sequence (WGS) data from a pedigree-based sample.

* Correspondence: hbickeb@gwdg.de

¹Department of Genetic Epidemiology, University Medicine Göttingen, University of Göttingen, Humboldtallee 32, 37073 Göttingen, Germany
Full list of author information is available at the end of the article

Analyses of these data by GAW18 participants were focused primarily on dealing with the high dimensionality of the data, with a special focus on rare variants and accounting for the family structure. These issues are natural, considering the two data sets that were provided. The data sets are described in detail in Almasy et al. [1].

The **Problem 1** data set was provided by the Type 2 Diabetes Genetic Exploration by Next-Generation Sequencing in Ethnic Samples (T2D-GENES) Consortium. It included data from 20 Mexican American families from San Antonio, Texas, with whole-genome sequence information on 464 individuals and dense single-nucleotide polymorphism (SNP) information on 959 individuals. The original study was designed to identify low-frequency variants that influence type 2 diabetes. An early release, the so-called freeze 1 data set, was provided to GAW18. This data set included data from 464 key individuals whose sequences were considered most informative to use in imputing genotype data on the remaining 959 pedigree members for whom only data from earlier genome-wide association (GWA) genotyping chips based on SNPs were available. Genotype data were provided only for odd-numbered autosomes and contained sequence data, data from GWA chips for almost 500,000 SNPs, and variant dosages from imputation of sequence data. The phenotype data were longitudinal measurements of systolic and diastolic blood pressure, sex, age, year of examination, use of antihypertensive medication, and tobacco smoking.

The **Problem 2** data set was a simulated data set of 200 phenotype replicates based closely on the real data of Problem 1. It used the same pedigree structure and individuals as before, except that data were generated only for those 849 individuals who had both phenotype data and imputed sequence data in the real data set. Sex and age were taken directly from the real data. Blood pressure, medication use, and tobacco smoking were generated anew for each replicate, using the distributional structure found in the real data. The simulated values of systolic and diastolic blood pressure were influenced by more than 1000 variants in over 200 genes. The effect of medication on blood pressure was also accounted for in the simulation and was an area of special concern for workshop participants who analyzed these data. In addition, a normally distributed trait, Q1, was simulated that was not influenced by any genotyped SNPs but was correlated between family members. The total heritability for each simulated phenotype was again taken from the original data, and the simulation model for assigning the corresponding variants using gene expression results are described in detail in Almasy et al. [1].

The availability of the GAW18 data was announced by email in the summer of 2012 to roughly 3500 individuals on the GAW mailing list. The number of GAW18 attendees in October was 184. The data set was distributed

fairly late for GAW18, not leaving much time for extensive analyses before the workshop. Thus, in contrast to previous workshops, individuals were allowed to present more analyses at the meetings than had been described in their papers submitted to the workshop. However, each group was still required to report the results of some analyses before the meeting in order to participate. Manuscripts were distributed among participants before the workshop within assigned discussion groups in order to facilitate discussion before and during the workshop. Manuscripts from the other discussion groups were also available for download from the GAW18 online discussion forum or upon request before the workshop. After the workshop 109 individual papers were accepted for publication, and these papers constitute this proceedings volume.

Participants and contributions were from many countries, with the largest numbers of contributions from the United States, Canada, and Germany. Additional contributing participants were from Australia, Denmark, Finland, France, Hong Kong, India, the Netherlands, Singapore, South Korea, Taiwan, and the United Kingdom.

The contributions were subdivided into 16 discussion groups by topic and were only occasionally further subdivided by the two data sets being analyzed because of their close connection. The themes were admixture mapping and adjusting for admixture (Group 1), collapsing methods (Group 2), dropping WGS through families using a genome-wide association studies (GWAS) framework (Group 3), genotype and sample quality control (Group 4), family-based tests of association for rare variants using simulated data (Group 5), family-based tests of association for rare variants using real and simulated data (Group 6), gene-based tests (Group 7), population-based tests of association (Group 8), gene-environment interaction (Group 9), genetic prediction (Group 10), methods for joint association analysis of multiple phenotypes (Group 11), analysis of longitudinal data in GWAS (Group 12), analysis of longitudinal data in sequence and GWAS (Group 13), machine learning and data mining approaches (Group 14), pathway-based approaches for WGS (Group 15), and role of linkage in analysis of WGS (Group 16). The papers in this proceedings volume are presented according to these groupings. Note, however, that group assignment was often not easy, and topics in groups may overlap. The contributed papers are preceded by the data description overview by Almasy et al. [1].

All groups were led by a person with previous GAW experience. This person encouraged and organized the discussion and presentations before, during, and after the workshop. Discussions largely started before the workshop and continued at the workshop within group meetings. Each discussion group, directed by the group leader, was also in charge of preparing a presentation of the issues discussed in the group and the conclusions. These

presentations were made to all GAW18 attendees in plenary sessions. There were also two poster sessions at which individual contributions could be presented. The workshop closed with plenary sessions on what we learned and future workshops. After the GAW18 meetings, the group leader was typically in charge of editing the group's manuscripts and writing the summary paper for the group. To avoid possible conflicts of interest of group editors, articles to which the group editor contributed were reassigned to other groups for the editing process. Summary papers are published in a supplement to *Genetic Epidemiology*, and individual contributions are found in these proceedings.

Overall, GAW18 uncovered many new challenges and unsolved problems with WGS data, and with WGS data from family samples in particular. Some progress was made, and some individual contributions turned out to be extremely useful. However, the discussions highlighted the need for methodological development in almost all areas considered. Accordingly, GAW19 will also focus on WGS, reusing much of the GAW18 data and supplementing it with additional data.

Disclaimer

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

Competing interests

AZ received intramural funding from the University of Lübeck, Germany. All other authors declare that they have no competing interests.

Authors' contributions

HB, JNB, RMC, HJC, RCC, CDE, DWF, SG, IRK, JLB, PEM, SAS, GAS, LS, NLT, AZ, JWM, and LA participated in workshop organization and editing of the GAW18 proceedings. HB drafted the text of this manuscript with contributions from LA. All authors read and approved the final manuscript.

Acknowledgements and declarations

Numerous individuals contributed to GAW18 by helping select workshop topics, providing data sets, conducting simulations, distributing data to the participants, leading discussion groups, overseeing the writing of group summaries, reviewing manuscripts, and preparing everything that needs to be done for the event management of the workshop and for the publishing process afterward.

We are grateful to the T2D-GENES Consortium for allowing GAW18 participants to use the whole-genome sequence and blood pressure data set around which GAW18 was based. The T2D-GENES Consortium is supported by NIH grants U01 DK085524, U01 DK085584, U01 DK085501, U01 DK085526, and U01 DK085545. The other genetic and phenotypic data for GAW18 were provided by the San Antonio Family Heart Study and the San Antonio Family Diabetes/Gallbladder Study, which are supported by NIH grants P01 HL045222, R01 DK047482, and R01 DK053889. The Genetic Analysis Workshops are supported by NIH grant R01 GM031575. The GAW18 discussion groups were led by Julia Bailey, Justo Lorenzo Bermejo, Joseph Beyene, Rita M. Cantor, Heather Cordell, Corinne D. Engelman, David Fardo, Saurabh Ghosh, Jack W. Kent Jr., Inke R. König, Phillip Melton, Stephanie Santorico, Glen A. Satten, Lei Sun, Nathan Tintle, Ellen M. Wijsman, and Andreas Ziegler. We are grateful to them for their work before, during, and after GAW18 in initiating, organizing, and

overseeing pre-workshop communication, group discussions, group presentations, and summary paper writing.

Eighty-one individuals assisted in peer review of the papers in this volume: Andrew S. Allen, Christopher I. Amos, Hugues Aschard, Marie-Claude Babron, Joan E. Bailey-Wilson, M. Michael Barmada, Jenny Barrett, Michael Boehnke, Laurent Briollais, Sharon Browning, Darren Brunner, Shelley Bull, Jenny Chang-Claude, Daniel I. Chasman, Charlie Chen, Gary Chen, Karen Conneally, L. Adrienne Cupples, Mariza de Andrade, Vince Diego, José Dupuis, Robert C. Elston, Michael P. Epstein, France Gagnon, Katrina A. Goddard, David Goldgar, Lynn Goldin, Alisa M. Goldstein, Derek Gordon, Harald H. Göring, Celia T. Greenwood, Jemila Hamid, Elizabeth R. Hauser, Anthony L. Hinrichs, Jeanine Houwing-Duistermaat, Yijian Hu, Rayjean Hung, Joanne Knight, Carl D. Langefeld, Jerry Lawless, Xihong Lin, Jinghua Liu, Douglas Londono, Sharon Lutz, James D. Malley, Lisa J. Martin, Maria Martinez, Braxton D. Mitchell, Andrew Morris, Bertram Müller-Myhsok, Benjamin M. Neale, Nora L. Nock, Kari E. North, Michael Nothnagel, Janne Pitkaniemi, Elizabeth Pugh, Steve Rich, Nancy L. Saccone, Daniel J. Schaid, André Scherag, Claire Simpson, Janet Sinsheimer, Anne Spence, Lisa Strug, Yan Sun, Rinku Sutradhar, Silke Szymczak, Duncan Campbell Thomas, Elizabeth A. Thompson, Timothy A. Thornton, Roula Tsonaka, Michael E. Weale, John C. Whittaker, Marsha Wilcox, Alexander F. Wilson, Ian J. Wilson, Rongling Wu, Yan Yan Wu, Tracy Xu, Wei Xu, and Yildiz Yilmaz. We are grateful to them for their constructive comments, criticisms, and feedback.

Beginning with GAW7 in 1991, Vanessa Olmo has been responsible for major aspects of workshop organization. We are grateful to her for the many things she does that keep the Genetic Analysis Workshops running smoothly. This includes interacting with participants, organizers, editors, and publishers; coordinating data requests and data distribution; facilitating selection of workshop sites and making local arrangements; maintaining the GAW website and mailing list; and preparing many aspects of the GAW proceedings. Selina Flores, Richard Polich, Rene Sandoval, Rudy Sandoval, and Gerry Vest assisted with distribution of data, communication with participants, and preparation of the pre-workshop volume. Ravindranath Duggirala, Sharon Fowler, Thomas Dyer, John Blangero, Juan Peralta, Marcio Almeida, and Jack Kent worked on data simulation and preparation. Sophie Colunga assisted with pre-workshop organization and on-site meeting management. Maria Messenger and Malinda Mann prepared the articles for these proceedings.

The GAW Advisory Committee assists with planning for the workshops, including selection of workshop sites and topics. At the time of GAW18, the committee members were Laura Almasy (chair), Shelly Bull, Adrienne Cupples, Jim Gauderman, Saurabh Ghosh, Elizabeth Hauser, Jeanine Houwing-Duistermaat, Jean MacCluer, Andrew Patterson, Glen Satten, and Ellen Wijsman.

Since 1982, the Genetic Analysis Workshops have been funded by the National Institute of General Medical Sciences (NIGMS) through grant R01 GM31575 to Jean MacCluer and Laura Almasy. This grant also provides scholarship funds to assist graduate students and postdoctoral trainees attending GAW18. We would like to recognize Donna Krasnewich for her ongoing support and for her efforts as program director for the GAW grant at the time of GAW18. These proceedings, as well as the continued work of statistical genetic methods development through the collaborative format of the Genetic Analysis Workshops, would not be possible without her support and that of NIGMS.

We are particularly grateful to Jean MacCluer. Without her there would be no GAW.

As always, we wish to express our gratitude to the GAW participants, whose ongoing, enthusiastic support and vigorous scientific discussions are the very foundation of the Workshop.

This article has been published as part of *BMC Proceedings* Volume 8 Supplement 1, 2014: Genetic Analysis Workshop 18. The full contents of the supplement are available online at <http://www.biomedcentral.com/bmcproc/supplements/8/S1>. Publication charges for this supplement were funded by the Texas Biomedical Research Institute.

Authors' details

¹Department of Genetic Epidemiology, University Medicine Göttingen, University of Göttingen, Humboldtallee 32, 37073 Göttingen, Germany.

²Department of Epidemiology, Fielding School of Public Health, University of California, Los Angeles, CA 90095, USA. ³Department of Clinical Epidemiology and Biostatistics, McMaster University, Hamilton, ON L8S 4K1,

Canada. ⁴David Geffen School of Medicine, University of California, Los Angeles, CA 90095, USA. ⁵Institute of Genetic Medicine, Newcastle University, Newcastle upon Tyne NE1 3BZ, UK. ⁶Department of Medicine and Division of Biostatistics, Washington University School of Medicine, Saint Louis, MO 63110, USA. ⁷Department of Population Health Sciences, School of Medicine and Public Health, University of Wisconsin, Madison, WI 53726, USA. ⁸Department of Biostatistics, University of Kentucky, Lexington, KY 40536, USA. ⁹Indian Statistical Institute, Kolkata 700108, West Bengal, India. ¹⁰Institut für Medizinische Biometrie und Statistik, Universität zu Lübeck, Universitätsklinikum Schleswig-Holstein, Campus Lübeck, 23562 Lübeck, Germany. ¹¹Institute of Medical Biometry and Informatics, University of Heidelberg, 69120 Heidelberg, Germany. ¹²Centre for Genetic Origins of Health and Disease, Statistical Genetics, University of Western Australia, Crawley 6009, Australia. ¹³Department of Mathematical and Statistical Sciences, University of Colorado, Denver, CO 80217, USA. ¹⁴Centers for Disease Control and Prevention, Atlanta, GA 30333, USA. ¹⁵Department of Statistical Sciences, University of Toronto, Toronto, ON M5S 3G3, Canada. ¹⁶Department of Mathematics, Computer Science and Statistics, Dordt College, Sioux Center, IA 51250, USA. ¹⁷Zentrum für Klinische Studien, Universität zu Lübeck, 23562 Lübeck, Germany. ¹⁸Department of Genetics, Texas Biomedical Research Institute, San Antonio, TX 78245, USA.

Published: 17 June 2014

Reference

1. Almasly L, Dyer TD, Peralta JM, Jun G, Wood AR, Fuchsberger C, Almeida MA, Kent JW Jr, Fowler S, Blackwell TW, *et al*: **Data for Genetic Analysis Workshop 18: Human whole genome sequence, blood pressure, and simulated phenotypes in extended pedigrees.** *BMC Proc* 2014, **8**(suppl 2):S2.

doi:10.1186/1753-6561-8-S1-S1

Cite this article as: Bickeböller *et al*: Genetic Analysis Workshop 18: Methods and strategies for analyzing human sequence and phenotype data in members of extended pedigrees. *BMC Proceedings* 2014 **8**(Suppl 1):S1.

**Submit your next manuscript to BioMed Central
and take full advantage of:**

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

Submit your manuscript at
www.biomedcentral.com/submit

