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ANNOUNCEMENT
GENETIC ANALYSIS WORKSHOP 8
Issues in the Analysis of Complex Diseases and Their Risk Factors
GAW8 will be held from 6-8 November 1992 in Watsonville, CA, USA
Genetic Analysis Workshop 8 (GAW8) will focus on two current problems in genetic epidemiology, both of which require novel approaches to statistical genetic analysis: (1) analysis of family data for Alzheimer’s disease, for which apparent genetic heterogeneity has led to disagreement in results of previous analyses; and (2) methods for genetic analysis of the multiple quantitative risk factors for coronary heart disease (CHD).
The data sets distributed to participants will include (1) data for 803 members of 59 families from the Duke-Boston Collaborative Alzheimer Disease Linkage Study, including markers on chromosomes 19 and 21; and (2) data from several genetic studies of lipoproteins and other CHD risk factors, including phenotypic information from a single 195-member pedigree, from a collection of smaller pedigrees, and from a large twin study. Data for GAW8 will be distributed in March 1992.
Genetic Analysis Workshop 8 is open to individuals who analyze GAW8 data and submit a summary of their analyses for presentation at the workshop, or who submit a summary of a theoretical or methodological paper relevant to one of the topics. If you wish to be placed on
Preface

This issue of Cytogenetics and Cell Genetics is devoted to the proceedings of Genetic Analysis Workshop 7 (GAW7), which was held October 14-16, 1990, at the Bergamo Conference Center near Dayton, Ohio. The Genetic Analysis Workshops focus on statistical genetic analysis of family and population data, to identify the genetic contribution to common diseases and their risk factors. The purpose of these workshops is to learn how conclusions concerning the role of genetic factors are influenced by different methodologies and assumptions. GAW7, like previous Genetic Analysis Workshops, provided investigators with the opportunity to evaluate and compare different methods of analysis, and led to the development of some new analytical approaches to current problems in genetic epidemiology. GAW7 was devoted to two subject areas: resolution of physical and genetic maps and analysis of quantitative precursors of complex diseases. These problems were chosen because they represent the types of analyses that we anticipate will become more necessary and important if we are to understand genetic effects on disease susceptibility.

More than a year before GAW7, data sets were solicited which were appropriate for each of the two topics. For the resolution of physical and genetic maps, four sets of chromosome 21 marker data were assembled. These were from hamster-human radiation hybrids, from a chromosome 21 hybrid clone panel, from a single large Venezuelan pedigree, and from 40 CEPH families. For the analysis of quantitative precursors of complex disease, five melanoma data sets were solicited: four sets of family data and one set of twin data plus cases and their relatives. Each melanoma data set included quantitative or categorical data on regional or total body nevus counts as well as genetic marker data.

Seven months before GAW7, a memo describing the workshop topics and announcing the availability of the data sets was sent to more than 350 investigators. The chromosome 21 data were requested by 37 groups and the melanoma data, by 52 groups. One month before GAW7, participants submitted 46 contributions summarizing their analyses of one or more of these data sets. These contributions were made available to all participants two weeks before GAW7.

The 80 participants in GAW7 were investigators who had provided data, contributed analyses, or been responsible for workshop organization. At the workshop, a brief description was given of each of the data sets, contributors summarized their analyses, the various analytical approaches were compared, and methodological issues were debated. There was considerable discussion and controversy during the portion of the workshop devoted to melanoma. It became apparent that for melanoma, as for any complex disease, uncertainties concerning diagnosis can have a substantial impact on subsequent analyses and interpretation. The manuscripts included here are derived from the GAW7 presentations. All have been reviewed for inclusion in these proceedings. The format of the proceedings is as follows:

the mailing list to receive further information about the Genetics Analysis Workshops, please contact:
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There are three sections, one devoted to each of the two subject areas, and one to a group of papers that did not utilize the GAW7 data sets, but that addressed relevant statistical genetic methods. Each section includes a paper summarizing the topic and discussing the conclusions reached by the contributors to that topic. The two sections devoted to analyses of the GAW7 data sets include descriptions of each data set. Also included are brief papers by each contributing group.

W. MacCluer, A. Chakravarti, D.R. Cox, D.T. Bishop, S.J. Bale, and M.H. Skolnick

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The success of the Genetic Analysis Workshops depends upon the generosity of investigators who provide their data for analysis by workshop participants. We are grateful to the following individuals who provided data for Genetic Analysis Workshop 7:

The organization of GAW7 involved the contributions of many people who helped in obtaining the data, led workshop discussions, made presentations at the meeting of the American Society of Human Genetics, and prepared summary papers. GAW7 would not have been possible without the considerable efforts of these organizers. Special thanks are due to Roger Siervogel, who selected the site for GAW7, and Faye Kesner, who was responsible for the many tasks involved in local organization.

We also would like to thank the following individuals who served as scientific reviewers for this publication: George Bonney, Kenneth Buetow, Christopher Cannings, Lisa Cannon-Albright, Ranajit Chakraborty, Douglas Easton, Robert Elston, David Goldgar, Lynn Goldin, Jonathan Haines, Bronya Keats, Mary-Claire King, Deborah Meyers, Jurg Ott, Margaret Pericak-Vance, Lodewijk Sandkuijl, Elizabeth Thompson, and Dan Weeks.

Jo Fletcher was responsible for directing the editing and typesetting of the proceedings. She was assisted in typesetting by Jeanette Morales, Dolores Olivo, and Harriet Smith. Vanessa Olmo provided invaluable assistance with proofreading and maintaining contacts with reviewers and authors.

Overall planning for the Genetic Analysis Workshops is the responsibility of the GAW Advisory Committee, whose members include Max Baur, Tim Bishop, Irene Eckstrand, Cathy Falk, Sue Hodge, Jean MacCluer, and Anne Spence. As always, we are especially grateful to Irene Eckstrand of the National Institute of General Medical Sciences, who has been an enthusiastic proponent of the workshops since their inception, and to the NIGMS for their continuing interest and support. Genetic Analysis Workshop 7 and this volume were supported by NIH grant GM31575.