Genetic Analysis Workshop 7
Issues in Gene Mapping and Detection of Major Genes

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Table of Contents
Preface
MacCluer JW, Chakravarti A, Cox DR, Bishop DT, Bale SJ, Skolnick MH 71
Acknowledgements 72
Resolution of Physical and Genetic Maps — Chromosome 21
Summary
Genetic Analysis Workshop 7: Radiation hybrid and somatic cell hybrid mapping of chromosome 21
Boehnke M 74

Genetic Analysis Workshop 7: Mapping chromosome 21 linkage markers
Green P 77

The Data
Radiation hybrid mapping
Cox DR 80

The role of somatic cell hybrids in physical mapping
Gardiner K, Patterson D 82

Chromosome 21 genetic linkage data set based on CEPH pedigrees
Warren AC, Antonarakis SE, Chakravarti A 86

Chromosome 21 genetic linkage data set based on the Venezuelan reference pedigree
Haines JL, Trofatter JA, Tanzi RE, Watkins P, Wexler NS, Conneally PM, Gusella JF 88

Contributions
Analyses of Radiation Hybrid Data
The gene order problem when using somatic cell hybrids
Aston CE, Chakravarti A 90

Comparisons of radiation hybrid mapping and linkage mapping
Bishop DT, Crockford GP 93

Radiation hybrid mapping by minimization of the number of obligate chromosome breaks
Boehnke M 96

A theory for radiation hybrid (Goss-Harris) mapping: Application to proximal 21q markers
Chakravarti A, Reefer JE 99

Order of markers on chromosome 21
Goldstein DR 102

A Bayesian analysis for mapping from radiation hybrid data
Guerra R, McPeek MS, Speed TP, Stewart PM 104

Physical mapping by multiple pairwise analysis
Lawrence S, Morton N 107

A statistical and numerical view of the chromosome 21 physical map data
Wilson SR 110

Analyses of Family Data
An application of empirical Bayes methods to updating linkage information on chromosome 21
Bonney GE, Amfoh KK, Sherman SL, Keats BJB 112

Mapping of chromosome 21 markers in the Venezuelan pedigree
Goldin LR 114

Using recombinant chromosomes to map new markers
Maestri NE, King TM, Colyer CR, Mellen BG, Chase GA, Meyers DA 116
Analyses of All Data Sets
Multilocus mapping strategies on chromosome 21 data sets:
Comparison of results from family data, radiation
hybrids and somatic cell hybrids
Falk CT  119
Construction and comparison of chromosome 21 radiation
hybrid and linkage maps using CRI-MAP
Green P  122
Preliminary ranking procedures for multilocus ordering based on radiation hybrid data
Weeks DE, Lehner T, Ott J  125
Disequilibrium on chromosome 21 in some Utah families
Weir BS  128
Statistical Genetic Methods Summary
Genetic Analysis Workshop 7: Recent progress in statistical
methods
Bishop DT  131
Contributions
A novel pedigree plotting algorithm
Round AP  133
Compilation for fast calculation over pedigrees
Szolovits P  136
68
Table of Contents
ELODS for three loci
Lewis CM  139
A multisample bootstrap approach to the estimation of maximized-over-models likelihood score
Terwilliger JD, Ott J  142
Linkage analysis of two-locus diseases under single-locus and two-locus analysis models
Vieland V, Greenberg DA, Hodge SE, Ott J  145
Quantitative Precursors of Complex Diseases — Melanoma
Summary-Genetic Analysis Workshop 7: Summary of the melanoma workshop
Risch N, Sherman S  148
The Data
Description of the National Cancer Institute melanoma families
Bale SJ, Goldstein AM, Tucker MA  159
The Dutch FAMMM family material: Clinical and genetic data
Bergman W, Gruis NA, Frants RR  161
The study of nevi in British twins: Study design and description of the data set
Easton DF, Cox GM, Macdonald AM, Ponder BAJ  165
Number, size, and histopathology of nevi in Utah kindreds
Meyer LJ, Goldgar DE, Cannon-Albright LA, Piepkorn
MW, Zone JJ, Risman MB, Skolnick MH  167
Clinical aspects of hereditary melanoma in Australia
Salmon JA, Rivers JK, Donald JA, Shaw HM, McCarthy
Contributions

Preliminary evaluation of linkage between chromosome lp markers and nevus densities in the Utah data
Amos CI, Murigande C

Sib-pair linkage analysis applied to pedigrees with melanoma and dysplastic nevi
Bailey-Wilson JE, Dobbins TE

Multivariate genetic analysis of nevus measurements and melanoma
Blangero J, Williams-Blangero S, Kammerer CM, Towne B, Konigsberg LW

Linkage analysis of malignant melanoma with the chromosome 1 markers D1S47 and PND
Blossey H, Guo SW, McKnight B, Tierney C, Thompson E, Wijsman E

Analysis of nevus count data from twins
Cantor RM

Genetic relationship between nevus count or nevus density and cutaneous malignant melanoma
Claus EB, Giuffra L, Rogers J, and Risch N

Regressive logistic models in linkage analysis of the cutaneous malignant melanoma-dysplastic nevus syndrome
Demenais FM, Martinez MM, Laing AE

Is the genetics of moliness simply the genetics of sun exposure? A path analysis of nevus counts and risk factors in British twins
Duffy DL, Macdonald AM, Easton DF, Ponder BAJ, Martin NG

Segregation analysis of total nevus density and estimation of lifetime risk and average onset age of melanoma
Farrer LA, Myers RH, Cupples LA

Inheritance of nevus number and size in melanoma/DNS kindreds
Goldgar DE, Cannon-Albright LA, Meyer LJ, Piepkorn

MW, Zone JJ, Skolnick MH

Linkage analysis of melanoma alone and chromosome lp markers PND, D1S47, and LMYC
Goldstein AM, Bale SJ, Tucker MA

Genetic linkage and affected pedigree member analysis in malignant melanoma
Haines J, Trofatter JA

Linkage analysis with adjustment for covariates: A method combining peeling with Gibbs sampling
Kong A, Frigge M, Cox N, Wong WH

Multivariate analysis of nevus counts in twins
Mendell NR, Yuan

Genetic analysis of cutaneous melanoma and dysplastic nevi under varying phenotypic definitions
Neuman R, Van Eerdewegh P, Moldin S, Rochberg N

Genetic analysis of nevus density in melanoma families
Petersen GM, Elashoff JD
Estimated power to detect linkage in three CM/DN data sets
Prenger VL, Colyer CR, Mellen BG, Harris EL, Beaty TH, Meyers DA  220
Investigation of major gene and covariate effects using a new Poisson process model
Province MA, Borecki IB, Rice T, Vogler GP  223
Segregation analysis in cutaneous malignant melanoma/dysplastic nevus syndrome families
Speer MC, Haynes CS, Pericak-Vance MA  225
Fitting genetic data using Gibbs sampling: An application to nevus counts in 38 Utah kindreds
Thomas DC  228
Table of Contents
69
PEDSCORE analysis of identical by descent (IBD) marker allele distributions among family members with cutaneous melanoma
Weitkamp LR, Lewis RA  231
Contributors and Participants  234
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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
the mailing list to receive further information about the Genetics Analysis Workshops, please contact:
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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:
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.

Acknowledgements

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.