Darlene R. Goldstein

École Polytechnique Fédérale de Lausanne (EPFL)
Institut de Mathématiques
Bâtiment MA, Station 8
CH-1015 Lausanne, Switzerland

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web: http://ludwig-sun2.unil.ch/~darlene/

RESEARCH INTERESTS

Statistical and computational methods for molecular data analysis

Computer-intensive statistical methods

Integration of heterogeneous biological data types

EDUCATION

Ph.D. in Statistics, University of California, Berkeley, 1993

Dissertation: *Statistical Problems in Linkage Mapping*
Committee: Terence P. Speed, Chair; Steven N. Evans; Glenys J. Thomson

M.A. in Statistics, University of California, Berkeley, 1985
Advisor: Elizabeth L. Scott

A.B. in Statistics and also in Applied Mathematics (double major), University of California, Berkeley, 1983

AWARDS AND FELLOWSHIPS

Fellow, *Program in Functional Genomics*, Institute of Pure and Applied Mathematics, University of California, Los Angeles, Fall 2000

- Directed group of 10 – 15 postdoctoral researchers analyzing genomic data

Research Fellow, United States National Institutes of Health/National Institute of General Medical Sciences, *Statistical Methods for Gene Mapping*, 1999 – 2001

- Researched properties of a new score test for genetic linkage
- Implemented the score test in a computer program

Postdoctoral Fellowship, United States National Institutes of Health/National Institute of Diabetes and Digestive and Kidney Diseases, *Genetics of Diabetes*, 1997

Postdoctoral Travel Grant, Program in Mathematics and Molecular Biology, 1997

Postdoctoral Fellowship, United States National Institutes of Health/National Center for Human Genome Research, *Gene Mapping*, 1994 – 1996

Affirmative Action Research Assistantship/Mentorship Award, 1988 – 1989
Mentor: Elizabeth L. Scott

Outstanding Graduate Student Instructor Award, 1987

PROFESSIONAL EXPERIENCE

Statistician (50%), June 2006 – present
DNA Array Faciliity, Centre Intégratif de Genomique, Université de Lausanne, 1015 Lausanne
Responsibilities include:

- Design of microarray experiments
- Statistical data analysis for microarray gene expression studies
- Implementation of analysis methods for new array-based technologies
- Methodological research in bioinformatics

Première Assistante (20%), April 2002 – present
Chaire de Statistique, Institut de Mathématiques, EPFL, 1015 Lausanne

- Research in statistical methods for genomic data, including microarrays
- Teaching undergraduate and graduate courses to students from EPFL, UniL, Swiss Institute of Bioinformatics and graduate students enrolled in the NCCR – Plant Survival
- Supervision of doctoral student (jointly with Prof. Anthony Davison)

Statistician (50%), June 2002 – March 2004
ISREC, Bioinformatics Core Facility (BCF), 1066 Epalinges

- Design and analysis of microarray experiments carried out for the SNF-funded NCCR in Molecular Oncology
- Statistical data analysis for microarray gene expression studies
- Creation of educational materials
- Teaching and practical training in bioinformatics for biologists and BCF data analysts
- Grant proposal preparation

Adjunct Assistant Professor, 1997 – 2001
Statistics Department, University of California, Los Angeles

- Teaching of statistics courses to students of statistics, mathematics, engineering, computer science, economics, business administration
- Created and taught new courses in statistics for the life and health sciences (both undergraduate and graduate level)
- Consultant with the Statistical Consulting Service
- Statistical advisor in monthly Genetics Roundtable brainstorming sessions (Human Genetics Department, UCLA), in which genetics investigators seek counsel for problems arising in their research
- Statistical supervisor and consultant for the Department of Cancer Prevention and Control Research, Jonsson Comprehensive Cancer Center, UCLA
- Participation in the UCLA Center for Teaching Statistics
- Mentor for UCLA Catalyst Program to increase the participation of women in science and mathematics

Research Biostatistician, 1996 – 1997
Department of Medical Genetics, Cedars-Sinai Medical Center, Los Angeles, California

- Linkage studies of coronary artery disease in African Americans
- Genetic linkage and association studies of insulin-dependent and noninsulin-dependent diabetes in Mexican Americans
- Study design for population-specific genetic studies of hypertension (Caucasian, African American and Mexican American)
- Developed empirical familial risk profiles for osteoporosis

Postdoctoral Researcher (50%), 1994 – 1996
United States National Institutes of Health/National Center for Human Genome Research, University of California, Berkeley

- Statistical research in gene mapping in humans and experimental organisms

GRADUATE STUDENT EXPERIENCE

Statistical Software Consultant, 1991 – 1992
Mathematical Sciences Research Institute, Berkeley, California

- Advised visiting mathematicians and statisticians on use of statistical software and local computing logistics

Computer Teaching Assistant, 1990 – 1992
Statistics Department, University of California, Berkeley

- Designed and implemented the introduction of computer labs to undergraduate statistics courses
- Trained and supervised teaching assistants
- Created computer-based learning exercises for students

Statistical Consultant, Fall 1990
Statistical Consulting Service, University of California, Berkeley

- Provided statistical consulting to researchers
- Projects involved Department of Genetics, Department of Integrative Biology, School of Optometry, School of Business

CONSULTING

Nestlé, S. A.

Serono Pharmaceutical Research Institute, S. A.

University of California, Los Angeles (UCLA), Statistics Department Consulting Center

Human Genetics Department, UCLA

Department of Cancer Prevention and Control Research, UCLA

University of California, Berkeley, Consulting Service of the Statistics Department

ACTIVE COLLABORATIVE RESEARCH PROJECTS

Human, mouse and rat genomic studies of Huntington's disease
Collaborator: Ruth Luthi-Carter, Laboratoire de neurogénomique fonctionnelle, EPFL

Bayesian methods for molecular data integration
Collaborator: Terry Speed, Statistics Department, UC Berkeley and WEHI, Melbourne

Meta-analysis methods for genomic data
Collaborators: Mauro Delorenzi and Pratyaksha Wirapati, ISREC Bioinformatics Core Facility and Swiss Institute of Bioinformatics

Comparison of microarray, PCR and digital gene expression technologies
Collaborators: Mauro Delorenzi and Eugenia Migliavacca, ISREC Bioinformatics Core Facility and Swiss Institute of Bioinformatics

Methodology and software development for gene expression in large data sets
Collaborators: Li Long, Swiss Institute of Bioinformatics, VITAL-IT Project; and Francois Collin, Affymetrix

Atlas of gene expression in Arabidopsis thaliana
Collaborators: Lars Hennig, Institute of Plant Sciences, ETH Zürich; and Mauro Delorenzi, ISREC Bioinformatics Core Facility and Swiss Institute of Bioinformatics

Computational methods for large-scale microarray quality assessment
Collaborators: Lars Hennig, Institute of Plant Sciences, ETH Zürich; and Francois Collin, Affymetrix

Methodologies for quality assessment of Affymetrix GeneChips
Collaborators: Gareth Hughes, Julia Thomas and Angela Hodges, Departments of Psychological Medicine and Medical Genetics, Wales College of Medicine and School of Biosciences, Cardiff University; and Francois Collin, Affymetrix

Statistical modeling of quantitative RT-PCR data
Collaborator: Rolf Jaggi, Department of Clinical Research, University of Bern

REFEREED PUBLICATIONS

D. R. Goldstein (2006). Partition Resampling and Extrapolation Averaging: Approximation Methods for Quantifying Gene Expression in Large Numbers of Short Oligonucleotide Arrays. *Bioinformatics*, in press.

D. Bhowmick, A. C. Davison, **D. R. Goldstein** and Y. Ruffieux (2006). A Laplace Mixture Model for Identification of Differential Expression in Microarray Experiments. *Biostatistics*, in press.

O. Menzel, M. Migliaccio, **D. R. Goldstein**, S. Dahoun, M. Delorenzi and N. Rufer (2006). Mechanisms regulating the proliferative potential of human CD8+ T lymphocytes over-expressing hTERT. *Journal of Immunology*, 177: 3657–3668.

C. U. Riedel, F. Foata, **D. R. Goldstein**, S. Blum and B. J. Eikmanns (2006). Interaction of bifidobacteria with intestinal epithelial cells – adhesion and impact on expression profiles. *International Journal of Food Microbiology*, 110:62–68.

L. Jones, **D. R. Goldstein**, G. P. Hughes, A. Strand, F. Collin, S. B Dunnett, C. L. Kooperberg, A. Aragaki, J. M. Olson, S. J. Augood, R. L. M. Faull, R. Luthi-Carter, V. Moskvina, A. K. Hodges (2006). Assessment of the relationship between prechip and post-chip quality measures for Affymetrix GeneChip expression data. *BMC Bioinformatics* 7:211.

A. Hodges, A. D. Strand, A. K. Aragaki, A. Kuhn, T. Sengstag, G. Hughes, L. A. Elliston, C. Hartog, **D. R. Goldstein**, D. Thu, Z. R. Hollingsworth, F. Collin, B. Synek, P. A. Holmans, A. B. Young, N. S. Wexler, M. Delorenzi, C. Kooperberg, S. J. Augood, R. L. M. Faull, J. M. Olson, L. Jones, R. Luthi-Carter (2006). Gene expression changes in human Huntington's disease brain. *Human Molecular Genetics*, 15:965–977.

J. Antonov, **D. R. Goldstein**, A. Oberli, A. Baltzer, M. Pirotta, A. Fleischmann, H. J. Altermatt, R. Jaggi (2005). Gene Expression Measurements by Quantitative Real-time PCR Depends on Short Amplicons and a Proper Normalization. *Laboratory Investigation* 85:1040–1050.

P. Farmer, H. Bonnefoi, V. Becette, M. Tubiana-Hulin, P. Fumoleau, D. Larsimont, G. Macgrogan, J. Bergh, D. Cameron, **D. R. Goldstein**, S. Duss, A. L. Nicoulaz, C. Brisken, M. Fiche, M. Delorenzi, R. Iggo (2005). Identification of molecular apocrine breast tumours by microarray analysis. *Oncogene* 24:4660–4671.

S. Dudoit and **D. R. Goldstein** (2003). Extensions to a score test for genetic linkage with identity by descent data. In D. R. Goldstein (ed.), *Science and Statistics: A Festschrift for Terry Speed*, Vol. 40 of *Institute of Mathematical Statistics, Lecture Notes – Monograph Series*, p. 307–319.

B. A. Berman, G. C. Wong, R. Bastani, T. Hoang, C. Jones, **D. R. Goldstein**, J. T. Bernert, K. S. Hammond, D. Tashkin and M. A. Lewis (2003). Household smoking behavior and ETS exposure among children with asthma in low-income, minority households. *Addictive Behaviors* 28:111–28.

D. R. Goldstein, D. Ghosh and E. M. Conlon (2002). Statistical issues in the clustering of gene expression data. *Statistica Sinica* 12:219–240.

C. M. Greenwood, A. Bureau, J. C. Loredo-Osti, N. M. Roslin, M. J. Crumley, C. G. Brewer, T. M. Fujiwara, **D. R. Goldstein** and K. Morgan (2001). Identity-by-descent sharing using Markov chain Monte Carlo in subsets of the asthma Hutterite pedigree. *Genetic Epidemiology* 21, Suppl:244–251.

D. R. Goldstein, S. Dudoit and T. P. Speed (2001). Power and robustness of a score test for linkage analysis of quantitative traits using identity by descent data on sib pairs. *Genetic Epidemiology* 20:415–431.

D. R. Goldstein, S. Dudoit and T. P. Speed (2000). Power of a score test for quantitative trait linkage analysis of relative pairs. *Genetic Epidemiology* 19:S85–S91.

L. B. Henderson, J. S. Adams, **D. R. Goldstein**, G. D. Braunstein, J. I. Rotter and M. T. Scheuner (2000). A familial risk profile for osteoporosis. *Genetics in Medicine* 2:222–225.

D. R. Goldstein, S. R. Sain, R. Guerra and C. J. Etzel (1999). Meta-analysis by combining parameter estimates: simulated linkage studies. In L. Goldin, C. I. Amos, G. A. Chase, A. M. Goldstein, G. P. Jarvik, M. M. Martinez, B. K. Suarez, D. E. Weeks, E. M. Wijsman and J. W. MacCluer. Genetic Analysis Workshop 11: Analysis of genetic and environmental factors in common diseases. *Genetic Epidemiology* 17:S581–S586.

R. Guerra, C. J. Etzel, **D. R. Goldstein** and S. R. Sain (1999). Meta-analysis by combining p-values: simulated linkage studies. In L. Goldin, C. I. Amos, G. A. Chase, A. M. Goldstein, G. P. Jarvik, M. M. Martinez, B. K. Suarez, D. E. Weeks, E. M. Wijsman and J. W. MacCluer. Genetic Analysis Workshop 11: Analysis of genetic and environmental factors in common diseases. *Genetic Epidemiology* 17:S605–609.

D. R. Goldstein, H. Zhao and T. P. Speed (1997). The effects of genotyping errors and interference on estimation of genetic distance. *Human Heredity* 47:86–100.

H. Yang, Y. Wang, **D. R. Goldstein**, Z. Li, H. Vora and R. M. Cantor (1997). Factors influencing the identification of major genes in a complex disease genome scan. *Genetic Epidemiology* 14:933–938.

M. Marron, L. J. Raffel, H. J. Garchon, C. Jacob, M. Serrano-Rios, M. T. Martinez Larrad, W. P. Teng, Y. Park, Z. X. Zhang, **D. R. Goldstein**, Y. W. Tao, G. Beaurain, J. F. Bach, H. S. Huang, D. F. Luo, A. Zeidler, J. I. Rotter, M. C. K. Yang, T. Modilevshy, N. K. Maclaren, J. X. She (1997). Insulin-dependent diabetes mellitus (IDDM) is associated with CTLA4 polymorphisms in multiple ethnic groups. *Human Molecular Genetics* 6:1275–1282.

D. R. Goldstein, H. Zhao and T. P. Speed (1994). Relative efficiencies of chi-square models of recombination for exclusion mapping and gene ordering. *Genomics* 27:265–273.

D. R. Goldstein (1994a). Asymptotic distributions of polylocus test statistics. *Genetic Epidemiology* 12:195–202.

D. R. Goldstein (1994b). A combined test of linkage heterogeneity. *American Journal of Human Genetics* 55:841–848.

D. R. Goldstein (1992). Order of markers on chromosome 21. *Cytogenetics and Cell Genetics* 59:102–103.

BOOK CHAPTERS and INVITED PAPERS

D. R. Goldstein, M. Delorenzi, R. Luthi-Carter and T. Sengstag (2006). Comparison of Meta-analysis to Combined Analysis of a Replicated Microarray Study. To appear in R. Guerra, D. B. Allison and D. R. Goldstein (eds.), *Meta-analysis and Combining Information in Genetics*, Boca Raton, FL: Chapman&Hall/CRC.

D. R. Goldstein (2005). Book review of G. J. McLachlan, K-A. Do and C. Ambroise: *Analyzing Microarray Gene Expression Data. Journal of the American Statistical Association* 100:1464–1465.

D. R. Goldstein and M. Delorenzi (2004). Statistical Design and Data Analysis for Microarray Experiments. In A. Berger and M. A. Roberts (eds.), *Unraveling Lipid Metabolism with Microarrays*, New York: Dekker.

D. R. Goldstein (2003). A brief introduction to genetics. In D. R. Goldstein (ed.), *Science and Statistics: A Festschrift for Terry Speed*, Vol. 40 of *Institute of Mathematical Statistics, Lecture Notes – Monograph Series*, p. 231–236.

D. R. Goldstein (2002). Discussion of K. W. Broman and T. P. Speed: *A model selection approach for the identification of quantitative trait loci in experimental crosses* and G. Parmigiani, E. S. Garrett, R. Anbazhagan, E. Gabrielson: *A statistical framework for expressionbased molecular classification in cancer. Journal of the Royal Statistical Society* 64:744.

BOOK

D. R. Goldstein (ed.), *Science and Statistics: A Festschrift for Terry Speed*, Vol. 40 of *Institute of Mathematical Statistics, Lecture Notes – Monograph Series* (2003). Beachwood, Ohio: Institute of Mathematical Statistics.

BOOK IN PREPARATION

R. Guerra, D. B. Allison and **D. R. Goldstein** (eds.), *Meta-analysis and Combining Information in Genetics*, Boca Raton, FL: Chapman&Hall/CRC.

SOFTWARE

D-test: A test for genetic linkage under heterogeneity (FORTRAN program supporting the publication Goldstein 1994b)

ST-rels: Score test for genetic linkage based on identity by descent data on relative pairs (C program supporting publications Goldstein, Dudoit, Speed 2000, 2001)

MIST-rels: Multiple imputation score test for genetic linkage with missing data on relative pairs (C program in development supporting the publication Dudoit and Goldstein 2003)

affyLS: Methods for multichip quantification of gene expression for high density short oligonucleotide arrays in large data sets (R package, in development for the BioConductor Project, supported by the life science informatics initiative VITAL-IT (http://www.vital-it.ch/vitalit-projects-new/vitalit-current.html))

SUBMITTED FOR PUBLICATION

D. R. Goldstein. Linkage mapping of lethal recessive traits (I): statistical information for ordering loci.

D. R. Goldstein. Linkage mapping of lethal recessive traits (II): statistical information for recombination fraction estimation.

D. R. Goldstein. Value of genotype classification of dominant offspring in a lethal recessive intercross.

WORKING PAPERS

E. Migliavacca, **D. R. Goldstein**, C. Iseli, O. Hagenbüchle, J. Wyniger, R. Lyle, C. Gehrig, S. E. Antonarakis, M. Docquier, P. Descombes, B. Stevenson, C. V. Jongeneel, M. Delorenzi. A Comparison of RNA Abundance Quantification Methods.

AtGenExpress Consortium (a very large international group which includes **D. R. Goldstein**; the consortium is examining gene expression in *Arabidopsis thaliana*). AtGeneExpress: The dynamic transcriptome of *Arabidopsis thaliana.*

D. R. Goldstein, L. Long and F. Collin. *affyLS* – Software for Quantifying Gene Expression in Large Sets of Affymetrix GeneChips.

D. R. Goldstein, P. Wirapati and M. Delorenzi. Joint analysis of genomic data from heterogeneous sources.

OTHER PROFESSIONAL ACTIVITIES

Grant Proposal Review

Swiss National Science Foundation

European Heads Of Research Councils, EURYI proposal

Member of Conference Organizing Committee

Statistics for Biomolecular Data Integration and Modeling, Ascona, Switzerland, 10 – 15 June 2007

Statistics in Functional Genomics, Ascona, Switzerland, 27 June – 2 July 2004

Program in Functional Genomics, First Reunion Meeting, Institute for Pure and Applied Mathematics, UCLA, Los Angeles, CA, 17 – 21 June 2002

Examination Committee

External examiner, EPFL, December 2001

External thesis examiner, University of Melbourne, April 2004

Editorial Duties

Western Journal of Medicine, Editorial Committee, 1999 – 2001

Referee Service

American Journal of Human Genetics

Bioinformatics

Biometrics

Biostatistics

Cancer Letters

CRC Press

Comparative and Functional Genomics

European Conference on Computational Biology

European Journal of Human Genetics

Functional and Integrative Genomics

Genetic Epidemiology

Journal of Biomedical Informatics

Journal of the American Statistical Society

Methods of Information in Medicine

Pharmacogenomics

Springer – Verlag

Statistics in Medicine

Statistica Sinica

Wiley

PRESENTATIONS

Invited Presentations

Workshop on MicroRNA in Development and Cancer, Mathematical Biosciences Institute, The University of Ohio, Columbus, OH, USA, 12–13 April 2007
Invited presenter and discussant

High Level Analysis, Applied Techniques Workshop, European Bioinformatics Institute, Cambridge, UK, 25 September 2006
Bayesian and Empirical Bayesian Methods for Identifying Differentially Expressed Genes in Microarray Experiments

Joint Meeting of the Chinese Society of Probability and Statistics and the Institute of Mathematical Statistics, Beijing, China, 9 July 2005
Meta-analysis in Genetics and Genomics

ISREC Bioinformatics Core Facility, University of Lausanne, 21 June 2005
Comparison of meta-analysis to combined analysis of a replicated microarray study

Workshop on Emerging Genomic Technologies and Data Integration Problems, Mathematical Biosciences Institute, The University of Ohio, Columbus, OH, USA, 21–24 February 2005
Invited discussant

DNA Array Facility, University of Lausanne, 27 October 2004
Strategies for quantifying GeneChip expression for large studies

Workshop on Analysis of Gene Expression Data, Mathematical Biosciences Institute, The University of Ohio, Columbus, OH, USA, 12 October 2004
Strategies for quantifying GeneChip expression for large studies

International Conference on Analysis of Genomic Data, Harvard University, Boston, MA, USA, 10 May 2004
Strategies for quantifying GeneChip expression for large studies

DNA Array Facility, University of Lausanne, 28 April 2004
Quality Assessment for Affymetrix GeneChips

IMS Workshop on Statistical Methods in Microarray Analysis, National University of Singapore, 7 January 2004
A Comparison of Microarray Platforms

ISREC Chip Data Club, Epalinges, Switzerland, 17 December 2003
Literate Programming and Reproducible Research

Computational Molecular Biology Program, EURANDOM, Eindhoven, Netherlands, 6 June 2003
Statistical Issues in the Clustering of Gene Expression Data

Swiss Array Consortium Meeting, University of Lausanne, 21 May 2003
Microarray data analysis

Swiss Institute of Bioinformatics, Epalinges, Switzerland, 29 January 2003
ROC Curves

ISREC Chip Data Club, Epalinges, Switzerland, 20 November 2002
Pitfalls in cluster analysis

Institute for Pure and Applied Mathematics UCLA, Los Angeles, CA, 20 June 2002
Multiple hypothesis testing with microarray gene expression data

Swiss Institute of Bioinformatics, Epalinges, Switzerland, 8 October 2001

Statistical issues in the clustering of gene expression data

Institute for Pure and Applied Mathematics UCLA, Lake Arrowhead, CA December 2000
Statistical issues in the clustering of gene expression data

Society for the Advancement of Chicanos and Native Americans in Science, Atlanta, GA, USA, October 2000
Statistical Methods for Gene Mapping

Department of Pediatrics, College of Medicine, University of California, Irvine, March 2000
Power and robustness of a score test for genetic linkage using identity by descent data on relative pairs

Department of Statistics, Southern Methodist University, March 1999
Power and robustness of a score test for genetic linkage using identity by descent data on sibling pairs

Départment de mathématiques, Ecole Polytechnique Fédérale de Lausanne, Switzerland, 7 December 1998
A score test for genetic linkage using identity by descent data on sibling pairs

Department of Statistics, University of California, Los Angeles, 18 March 1997
Effects of genotyping errors and interference on estimates of genetic distance

Department of Statistics, University of California, Berkeley, November 1996
Genetic analysis of simulated common disease data

Department of Statistics, University of California, Berkeley, February 1996
Chi-square models of crossover interference with genotyping errors for multipoint data

National Institutes of Health, Bethesda, MD, USA, January 1996
A combined test of linkage heterogeneity

Department of Statistics, Edinburgh University, December 1995
Chi-square models of crossover interference with genotyping errors

Department of Biomathematics, University of California, Los Angeles, May 1995
Effects of genotyping errors and interference on estimates of genetic distance

Department of Statistics, University of California, Berkeley, December 1994
Chi-square models of crossover interference with genotyping errors

Department of Preventive Medicine, University of Southern California, April 1994
A combined test of linkage heterogeneity

Contributed Presentations

Bioconductor User and Developer Conference, Seattle, WA, August 2006
Poster: *Partition Resampling and Extrapolation Averaging: Approximate Gene Expression for Large Numbers of Short Oligo Arrays*

World Congress on Huntington's Disease, Manchester, UK September 2005
Poster: *Integrating behaviour and brain gene expression in Huntington's disease using*

the R6/1 HD mouse model

All-Wales Bioinformatics Workshop, Aberystwyth, UK, March 2005
Poster: *Assessing pre- and post chip integrity measures in differential gene expression using the Affymetrix GeneChip system*

12th Annual Congress of Immunology, Montreal, Canada, July 2004
Poster: *Host:microbial adaptation and the role of Bifidobacterium longum NCC2705 in the control of mucosal inflammation*

Statistics in Functional Genomics, Ascona, Switzerland, June 2004
Poster: *Robust and rapid molecular profiling of human breast cancer with Low Density Arrays (LDAs)*

CHUV Research Day, Lausanne, Switzerland, January 2004
Poster: *Quantification of RNA Abundance: A Comparison of Methods*

Affymetrix GeneChip Microarray Low-Level Workshop, University of California, Berkeley, August 2003
Poster: *Comparison of Expression Measures and Quantitative RT-PCR Results for Affymetrix GeneChips*

Royal Statistical Society meeting on Statistical Genetics and Bioinformatics. Limburgs Universitair Centrum, Belgium, July 2003
Poster: *Identifying Differentially Expressed Genes in cDNA Microarrays*

American Statistical Association Annual Meeting, New York, NY, August 2002
Oral presentation: *Multiple imputation in genetic linkage analysis*

European Society of Human Genetics Annual Meeting, Vienna, Austria, May 2002
Poster: *Multiple testing in the survival analysis of microarray data*

International Interdisciplinary Conference on Hypertension in Blacks, Toronto, Canada, July 1999
Poster: *Diastolic blood pressure is linked to the MnSOD locus on chromosome 6in African American families with CAD*

American Statistical Association Annual Meeting, Dallas, TX, August 1998
Oral presentation: *Linkage testing of genome mismatch scanning data (GMS) with allowance for interference*

Genetic Analysis Workshop, Arcachon, France, September 1998
Oral presentation: *Meta-analysis of linkage studies*

American Heart Association, Orlando, FL, November 1997
Poster: *Triglyceride levels are linked to chromosome 16q13-22 in African American families with coronary artery disease (CAD)*

American Society for Human Genetics, Baltimore, MD, October 1997
Poster: *Multilocus Determination of Body Mass Index in African Americans*

American Society for Human Genetics, Baltimore, MD, October 1997
Poster: *Conjoint Genetic Regulation of Apolipoproteins AI and AII and Free Fatty Acids: Evidence from African American families*

American Society for Human Genetics, Baltimore, MD, October 1997
Poster: *Familial Risk Characteristics of Osteoporosis*

American Federation for Clinical Research Western Regional Meeting, Carmel, CA, February 1997
Poster: *Empiric Risk Estimates for Osteoporosis*

Program in Mathematics and Molecular Biology Meeting V, Santa Fe, NM, January 1997
Poster: *Addressing questions on interference and recombination in the mouse*

Genetic Analysis Workshop, Monterey, CA, November 1996
Poster: *Genetic analysis of simulated common disease data*

Genetic Analysis Workshop, Dayton, OH, October 1992
Oral presentation: *Order of markers on chromosome 21*

TEACHING

Invited Short Course Organizer and Instructor, March 2007
Statistics for Affymetrix GeneChips, NCCR-Plant Survival

Invited Short Course Organizer and Instructor, March 2007
Statistics for cDNA Microarrays, NCCR-Plant Survival

Invited Lecturer, November 2006
RNA Expression Profiling with DNA Microarrays, Schweizerische Kommission für Molekularbiologie

Invited Lecturer, March 2006
Statistical Methods in Bioinformatics, Swiss EMBnet node, Schweizerische Kommission für Molekularbiologie

Invited Lecturer, December 2005
Genomic Data Analysis, Biotechnology lab (pour SV), EPFL

Invited Lecturer, November 2005
RNA Expression Profiling with DNA Microarrays, Schweizerische Kommission für Molekularbiologie

Invited Short Course Organizer and Instructor, January 2005
Statistics for Affymetrix GeneChips, NCCR-Plant Survival

Invited Short Course Organizer and Instructor, January 2005
Statistics for cDNA Microarrays, NCCR-Plant Survival

Instructor (Responsible), October 2004 – February 2005
Statistics for Genomic Data Analysis, EPFL

Instructor, October 2004 – December 2004
Experimental Design, University of Lausanne

Instructor (Responsible), October 2003 – February 2004
Statistics Module (4), Swiss Institute of Bioinformatics, DEA in Bioinformatics

Invited Lecturer, December 2002
Microarray Data Preprocessing, lecture and practical for Institute of Biochemistry, University of Lausanne

Instructor (Responsible), October 2002 – February 2003
Statistics Module (4), Swiss Institute of Bioinformatics, DEA in Bioinformatics

Course Organizer and Instructor, October 2002 – December 2002
Statistics for Microarray Analysis with R, ISREC, Epalinges, Switzerland

Invited Short Course, 26 June – 3 July 2002
Statistics for microarrays, Forschungsinstitut für Mathematik ETH Zürich

Instructor (Responsible), March – June 2002
Statistics for Microarrays, optional 3ème cycle course in Statistics, EPFL and required part of Transcriptome Module, Swiss Institute of Bioinformatics, DEA in Bioinformatics

Instructor (Responsible), 1997 – 2001
Department of Statistics, University of California, Los Angeles

- Introduction to Statistical Reasoning
- Statistical Methods for Business and Economics
- Applied Statistics
- Statistical Methods for the Life and Health Sciences

Teaching Assistant/Graduate Student Instructor, 1985 – 1990
Statistics Department, University of California, Berkeley

- Introduction to Probability and Statistics
- Introductory Probability and Statistics for Business
- Introduction to Probability and Statistics for Engineers
- Bayesian Statistics
- Introduction to Probability and Statistics at an Advanced Level
- Analysis of Discrete Observations
- Sole responsible for summer course Introduction to Statistics

COMPUTING EXPERIENCE

Operating Systems: UNIX/Linux, Windows

Computer Languages and Statistical Software: FORTRAN, C, R/S/S-PLUS, Emacs Speaks Statistics (ESS), SAS, Mathematica, Perl, LaTeX, HTML

Genetics and Genomics Software: BioConductor (R-based open source software for bioinformatics), MAPMAKER, GENEHUNTER, LINKAGE, Pedigree Analysis Package, Statistical Analysis for Genetic Epidemiology (SAGE)

LANGUAGES

English (mother tongue); French (average); Japanese (some familiarity)

PERSONAL

Married to Thomas Mountford

3 Children: Aneurin (1994), Tavis (1995), Ian (1998)

Interests: Running, classical music, singing

ADMINISTRATIVE

Citizenship: US

Swiss Residence Permit: C