

## CURRICULUM VITAE

**JASON H. MOORE, Ph.D.**

### Personal

Work Address: 706 Rubin Bldg, HB 7937  
One Medical Center Dr.  
Dartmouth-Hitchcock Medical Center  
Lebanon, New Hampshire 03756

Email: [jason.h.moore@dartmouth.edu](mailto:jason.h.moore@dartmouth.edu)  
Web: [www.epistasis.org](http://www.epistasis.org)  
Blog: [compgen.blogspot.com](http://compgen.blogspot.com)

### Education

1994-1999	University of Michigan Ann Arbor, Michigan Dissertation: "Genetic Analyses of Dynamic Quantitative Traits" Mentor: Dr. Charles F. Sing, Department of Human Genetics	Ph.D. in Human Genetics
1994-1998	University of Michigan Ann Arbor, Michigan Mentor: Dr. Vijay Nair, Department of Statistics	M.A. in Applied Statistics
1993-1994	University of Michigan Ann Arbor, Michigan Mentor: Dr. Charles F. Sing, Department of Human Genetics	M.S. in Human Genetics
1988-1991	Florida State University Tallahassee, Florida Mentor: Dr. Siwo R. deKloet, Department of Biological Sciences	B.S. in Biological Sciences

### Postdoctoral Training

none

### Licensure and Certification

none

### Academic Appointments

- 2007-present Founding Member, Complex Systems Center, University of Vermont, Burlington, Vermont
- 2005-present Adjunct Associate Professor of Computer Science  
University of Vermont, Burlington, Vermont
- 2004-present Affiliate Associate Professor of Computer Science  
University of New Hampshire, Durham, New Hampshire
- 2004-present Adjunct Associate Professor of Biological Sciences  
Dartmouth College, Hanover, New Hampshire
- 2004-present Adjunct Associate Professor of Community and Family Medicine  
Dartmouth Medical School, Lebanon, New Hampshire
- 2004-present Frank Lane Research Scholar in Computational Genetics  
Dartmouth Medical School, Lebanon, New Hampshire
- 2004-present Associate Professor of Genetics  
Member, Norris-Cotton Cancer Center  
Member, Cancer Epidemiology and Chemoprevention Research Program  
Member, Center for Environmental Health Sciences  
Member, Center for Neuroscience  
Member, Graduate Program in Cellular and Molecular Biology (CMB)  
Dartmouth Medical School, Lebanon, New Hampshire
- 2003-2004 Associate Professor (with tenure) of Molecular Physiology and Biophysics  
Ingram Associate Professor of Cancer Research  
Member, Center for Human Genetics Research  
Member, Vanderbilt-Ingram Cancer Center  
Member, Interdisciplinary Graduate Program (IGP)  
Member, Neuroscience Graduate Program  
Member, Chemical and Physical Biology Graduate Program  
Member, Biomedical Informatics Graduate Program  
Vanderbilt University Medical School, Nashville, Tennessee
- 1999-2003 Assistant Professor of Molecular Physiology and Biophysics  
Member, Program in Human Genetics  
Member, Vanderbilt-Ingram Cancer Center  
Member, Interdisciplinary Graduate Program (IGP)  
Member, Neuroscience Graduate Program  
Member, Biomedical Informatics Graduate Program  
Vanderbilt University Medical School, Nashville, Tennessee
- 1993-1998 Graduate Research Assistant with Dr. Charles F. Sing, Department of Human Genetics,  
University of Michigan, Ann Arbor, Michigan
- 1991-1993 Research Assistant with Dr. David G. Beer, Department of Surgery, Thoracic Oncology  
Laboratory, University of Michigan Cancer Center, University of Michigan, Ann  
Arbor, Michigan
- 1989-1991 Undergraduate Research Assistant with Dr. Siwo R. deKloet, Department of Biological  
Sciences, Institute of Molecular Biophysics, Florida State University, Tallahassee,  
Florida

## **Other Professional Positions**

- 1999-2004 Director, Bioinformatics Core, Center for Human Genetics Research, Vanderbilt University Medical School (highlight: expanded core from three to 12 fulltime programmers)
- 2003-2004 Co-Founder and Co-Director, Vanderbilt Advanced Computing Center for Research and Education (ACCRE) (highlight: established a new center with \$8.3 million in competitive funding to provide high-performance computing support to all investigators at Vanderbilt University)
- 2003-2004 Founder and Director, Bioinformatics and Supercomputing Shared Resource, Vanderbilt-Ingram Cancer Center
- 2004-present Founder and Director, Computational Genetics Laboratory, Dartmouth Medical School
- 2004-present Director, Bioinformatics Shared Resource, Norris-Cotton Cancer Center, Dartmouth Medical School (highlight: expanded core from one to five fulltime programmers)
- 2004-present Director of Bioinformatics, Dartmouth Medical School
- 2005-present Founder and Director, The DISCOVERY Resource – Dartmouth Initiative for SuperCOMputing Ventures in Education and REsearch. (highlight: established a shared 300-processor parallel computing resource for Dartmouth College).

## **Honors and Awards**

- 1990 American Cancer Society Summer Research Fellowship, Florida State University
- 1994-1998 American Heart Association Graduate Fellowship, University of Michigan
- 2001 James V. Neel Young Investigator Award, International Genetic Epidemiology Society
- 2002 EvoSolve Best Paper Award for Research towards Biomedical Applications of Biocomputing
- 2003-2004 Endowed Ingram Professorship in Cancer Research, Vanderbilt University
- 2004-present Frank Lane Research Scholar in Computational Genetics, Dartmouth Medical School
- 2004 Best Paper Award, Biological Applications Track of the 2004 Genetic and Evolutionary Computing Conference (GECCO).
- 2007 Nominated to the Institute of Medicine, National Academy of Sciences (election pending – October 2007)

## **Major Committee Assignments and Consultations**

### ***International, National and Regional***

- 1999 Co-Moderator, Session on “Linkage and Polymorphisms II”, 49<sup>th</sup> Annual Meeting of the American Society of Human Genetics, San Francisco, California, October 19 - 23.
- 1999-2000 Treasurer, American Statistical Association, Middle Tennessee Chapter
- 2001 President, American Statistical Association, Middle Tennessee Chapter
- 2001 Scientific Committee, Critical Assessment of Microarray Data Analysis (CAMDA-2001) conference, Duke University, Durham, North Carolina

- 2001 Grant Reviewer, Medical Research Council (MRC), United Kingdom
- 2002-present Scientific Advisory Board, GenoMed Inc., St. Louis, Missouri
- 2002 Grant Reviewer, Genome Canada, Canada
- 2002-2005 Grant Reviewer, "Technology Development for Biomedical Applications: Phased Innovation Award (R21/R33)", PAR-02-091, PAR-03-075, National Center for Research Resources, National Institutes of Health
- 2002-2005 Program Committee for the annual European Workshop on Evolutionary Bioinformatics (EvoBIO)
- 2003 Chair, Session on "Microarray Analysis", 1st European Workshop on Evolutionary Bioinformatics (EvoBIO 2003), Essex, England
- 2003 Grant Reviewer, Special Emphasis Panel, National Institute of Allergy and Infectious Disease, National Institutes of Health
- 2003 Chair, Session on "Real World Applications in Bioinformatics", 2003 Genetic and Evolutionary Computation Conference (GECCO 2003), Chicago, Illinois
- 2003-2005 Scientific Committee, annual workshop on "Grammatical Evolution"
- 2003-2006 Organizer and Chair (with Marylyn Ritchie), annual workshop on "Biological Applications of Genetic and Evolutionary Computation (BioGEC)"
- 2003-present Scientific Committee, Genetic and Evolutionary Computation Conference (GECCO)
- 2004 Grant Reviewer, Idaho Research Center Grant Program, Idaho State Board of Education
- 2004 Grant Reviewer, Special Emphasis Panel for Centers of Biomedical Research Excellence (COBRE), National Center for Research Resources, National Institutes of Health
- 2004 Co-Organizer and Co-Chair, National Cancer Institute (NCI) Think Tank on Cancer Susceptibility and Resistance. (highlight: this was one of eight NCI-sponsored think tanks that were charged with making recommendations to Dr. von Eschenbach, Director of the NCI, about the future of cancer research)
- 2004 Grant Reviewer, WellBeing of Women – The Health Research Charity for Women and Babies, London.
- 2004-2005 Organizer and Chair, Educational Session on "Gene-Gene Interactions in Cancer Etiology", 2005 annual meeting of the American Association of Cancer Research
- 2004-2005 Co-Organizer and Co-Chair, National Cancer Institute (NCI) Conference on "Predictive Models of Cancer Susceptibility: Integrated Strategies", Newport Beach, California.
- 2005 Grant Reviewer, Howard Hughes Medical Institute (HHMI).
- 2005 Grant Reviewer, Special Emphasis Panel on Bioinformatics Tools and Systems, ZRG1 BST-A (10). National Institutes of Health.
- 2005 Grant Reviewer, NIH Director's Roadmap Initiative, National Centers for Biomedical Computing (NCBC), National Institutes of Health.
- 2005 Chair, Session on Structure Activity Relationships, 3rd European Workshop on Evolutionary Bioinformatics (EvoBIO 2005), Lausanne, Switzerland.
- 2005 Chair, Panel Discussion on Advanced Computational Methods in Bioinformatics, 3rd European Workshop on Evolutionary Bioinformatics (EvoBIO 2005), Lausanne, Switzerland.
- 2005 Program Committee, 2005 Graduate Student Workshop on Genetic and Evolutionary Computing, Washington D.C.

- 2005 Consultant, InterGenetics, Inc.
- 2005-present Technical Committee, European Conference on Evolutionary Computing, Machine Learning and Data Mining in Bioinformatics (EvoBIO)
- 2005-2006 Program Chair (with Carlos Cotta), 4<sup>th</sup> European Workshop on Evolutionary Computation and Machine Learning in Bioinformatics (EvoBIO 2006), Budapest, Hungary.  
(highlight: helped transform this workshop to a full conference for 2007)
- 2005-2006 Program Chair (with James Foster), Biological Application Track, 2006 ACM Genetic and Evolutionary Computation Conference (GECCO 2006), Seattle, Washington.
- 2005 Technical Committee, IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology. San Diego, California.
- 2005-present Founding Council Member, International Society of Cancer Informatics.
- 2005-present Head, Working Group on Methodology, Bladder Cancer Consortium
- 2005-present Consultant, Celera Diagnostics, Inc.
- 2005-2006 Education Committee, International Genetic Epidemiology Society (IGES).
- 2005-2006 Program Committee, Workshop on Pattern Recognition in Bioinformatics (PRIB'06), International Association for Pattern Recognition (IAPR), Hong Kong, China.
- 2006 Grant Reviewer, High-End Instrumentation Program (S10), National Center Research Resources (NCRR), National Institutes of Health.
- 2006 Chair, Panel Discussion on Computational Approaches for Pharmacogenetics, Pacific Symposium on Biocomputing (PSB), Wailea, Maui, Hawaii.
- 2006 Grant Reviewer, NHLBI RFA "SCCOR in Pulmonary Vascular Disease," (RFA HL-05-007), National Institutes of Health.
- 2006 Member, Task Force on Statistical Genetics Software Development, International Genetic Epidemiology Society
- 2006 Chair, Panel Discussion on Advanced Computational Methods in Bioinformatics, 4th European Workshop on Evolutionary Computation and Machine Learning in Bioinformatics (EvoBIO 2006), Budapest, Hungary.
- 2006 Chair, Session on Data Mining and Knowledge Discovery, 4th European Workshop on Evolutionary Computation and Machine Learning in Bioinformatics (EvoBIO 2006), Budapest, Hungary.
- 2006-2007 Steering Committee, 5th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EvoBIO 2007), Valencia, Spain.
- 2006-2007 Program Committee, 5th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EvoBIO 2007), Valencia, Spain.
- 2006 Technical Committee, 2006 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (IEEE CIBCB 2006), Toronto, Ontario, Canada.
- 2006 Grant Reviewer, Interdisciplinary Research Consortium (PAR-06-122), NIH Roadmap Initiative, National Institutes of Health.
- 2006-2007 Program Committee, Workshop on Pattern Recognition in Bioinformatics (PRIB'07), International Association for Pattern Recognition (IAPR), Singapore.
- 2006-2007 Program Chair (with Clare Congdon), Biological Applications Track, 2007 ACM

- Genetic and Evolutionary Computation Conference (GECCO 2007), London, England.
- 2006-2007 Founder, Organizer and Chair, 2007 Workshop on Open-Source Software for Applied Genetic and Evolutionary Computation (SoftGEC'07), London, England.
- 2006-present Working Group on Modeling Variation in Gene Networks, National Evolutionary Synthesis Center, Durham, North Carolina.
- 2007 Grant Reviewer, Comparative Biology Elucidation of Environmental Pathways and Susceptibility (RFA-ES-06-004), National Institute of Environmental Health Sciences.
- 2007 Chair, Education Committee, International Genetic Epidemiology Society (IGES).
- 2007 Grant Reviewer, Horizon Program, The Netherlands Genomics Initiative.
- 2007 Chair, Session on "Network Construction and Analysis", 5th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EvoBIO 2007), Valencia, Spain.
- 2007 Grant Reviewer, Interdisciplinary Research Consortium – U54 (RFA-RM-06-008), NIH Roadmap Initiative, National Institutes of Health.
- 2007 Program Committee, IEEE 7<sup>th</sup> International Symposium on Bioinformatics and Bioengineering, Harvard Medical School, Boston, Massachusetts.
- 2007-2008 Internal Advisory Board, 2008 International Conference on Neural Networks and Genetic Algorithms in Materials Science and Engineering (NGMS'08).
- 2007-2008 Steering Committee, 6th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EvoBIO 2008), Naples, Italy.
- 2007-2008 Program Committee, 6th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EvoBIO 2008), Naples, Italy.
- 2007-2008 Program Chair (with Clare Congdon), Biological Applications Track, 2008 ACM Genetic and Evolutionary Computation Conference (GECCO 2008), Atlanta, Georgia.
- 2007-2008 Founder, Organizer and Chair, 2008 Workshop on Open-Source Software for Applied Genetic and Evolutionary Computation (SoftGEC'08), Atlanta, Georgia.

### ***Institutions***

- 1997-1998 Awards Committee, University of Michigan
- 1999-2001 Coordinator, Genetics Interest Group, Vanderbilt University (highlight: invited, scheduled, and introduced speakers for weekly meetings)
- 1999-2004 Core Oversight Board, Center for Human Genetics Research, Vanderbilt University
- 1999-2004 Courtesy seminars in the Departments of Medicine, Biomedical Informatics, Microbiology and Immunology, Physics, Mathematics, and Molecular Physiology and Biophysics, as well as the Center for Human Genetics Research, Genetics Interest Group, Vanderbilt-Ingram Cancer Center, Biomathematics Program, General Clinical Research Center, Biophysics Group, Vanderbilt University
- 2000 Organizer and Moderator, Workshop on Statistical Genomics: Making Sense of

- All the Data, Vanderbilt University
- 2001-2002 Trans-Institutional Bioinformatics Recruiting Team, Vanderbilt University
- 2002 Co-Organizer, Workshop on Sequence Mining, Vanderbilt University
- 2002-2004 Research Advisory Committee for Information Technology, Vanderbilt University
- 2001-2003 Planning Committee for the Vanderbilt Advanced Computing Center for Research and Education (ACCRE), Vanderbilt University (highlight: secured \$8.3 million from the Vanderbilt Academic Venture Capital Fund as a PI)
- 2003-2004 Bioinformatics Search Committee, Vanderbilt University
- 2003-2004 Information Technology Executive Committee, Vanderbilt-Ingram Cancer Center
- 2003-2004 Large Lecture Course Project Taskforce, Vanderbilt University
- 2003-2004 Executive Board for Program in Biomathematics, Vanderbilt University
- 2004 Research Enterprise Taskforce, Vanderbilt University (highlight: appointed by the Associate Vice Chancellor to help plan the future of research at Vanderbilt Medical School)
- 2004-present Courtesy seminars: Departments of Biochemistry, Biological Sciences, Genetics, Medicine, and Pathology, Cardiology Grand Rounds, Cancer Center Grand Rounds, Thayer School of Engineering, Dartmouth Medical School and Dartmouth College
- 2004-present Search Committee for Associate Director of Research Computing, Dartmouth College
- 2004-2006 Search Committee for the Director of the Neukom Institute for Computational Sciences, Dartmouth College
- 2004-2006 Biostatistics Search Committee, Department of Community and Family Medicine, Dartmouth Medical School
- 2005-present Director, Cancer Biomedical Informatics Grid (caBIG), Norris-Cotton Cancer Center, Dartmouth Medical School.
- 2006-present Chair, Research Computing Oversight Subcommittee (RCOS), Council on Computing, Dartmouth College.
- 2006-present Chair, Bioinformatics Committee, Dartmouth Medical School
- 2006-present Search Committee for Director of Biostatistics, Department of Community and Family Medicine, Dartmouth Medical School
- 2006-2007 Cores Planning Committee for the Translational Research Building, Dartmouth Medical School
- 2006-present Information Technology Planning Committee, Dartmouth Medical School
- 2007-present Organizer and Chair (with Craig Tomlinson), Dartmouth Symposium on Integrative Biology

### **Editorial Boards and Positions**

- 2003-present Managing Editor for Frontiers in Biosciences
- 2004-present Writer, Computing Reviews
- 2004-present Founding Member of the Editorial Board for Cancer Informatics
- 2005-present Founding Editor-in-Chief for BioData Mining
- 2006-present Editorial Board for Physiological Genomics
- 2007-present Founding Associate Editor for Journal of Artificial Evolution and Applications

## **Journal Referee Activities**

1999-present referee for American Heart Journal, American Journal of Human Genetics, American Journal of Hypertension, American Journal of Physiology, American Journal of Respiratory and Critical Care Medicine, Annals of Human Genetics, Artificial Life, Atherosclerosis, Bioinformatics, Biophysical Journal, Blood Coagulation and Fibrinolysis, BMC Bioinformatics, BMC Cancer, BMC Medical Genetics, BMC Medical Informatics and Decision Making, Cancer Research, Circulation, Clinical Genetics, Diabetes, European Journal of Human Genetics, Evolutionary Computing, Expert Review of Molecular Diagnostics, Genetic Epidemiology, Genetics, Genetic Programming and Evolvable Machines, Genomics, Human Heredity, Human Molecular Genetics, IEEE Transactions on Evolutionary Computing, Journal of the American Medical Association (JAMA), Journal of the American Medical Informatics Association (JAMIA), Journal of Machine Learning Research, Lecture Notes in Computer Science, Machine Learning, Nature Genetics, Pacific Symposium on Biocomputing, Pharmacogenomics, Proceedings of the National Academy of Sciences USA (PNAS)

## **Memberships in Professional Societies**

1994-present American Statistical Association (ASA)  
1999-present American Society of Human Genetics (ASHG)  
1999-present International Genetic Epidemiology Society (IGES)  
1999-present International Society for Genetic and Evolutionary Computation (ISGEC)  
2000-present International Society of Computational Biology (ISCB)  
2000-present International Society for Psychiatric Genetics (ISPG)  
2004-present Association for Computing Machinery (ACM)  
2007-present American Association for Cancer Research (AACR)

## **Teaching Experience/Current Teaching Responsibilities**

### *Courses and Lectures*

1991 Assistant, Animal Development (PCB 3253C), Florida State University  
1992-1998 Tutor, Student Athlete Support Program, University of Michigan, Biology 130 (Animal Behavior), Biology 152 (Biology), Biology 154 (Biology), Biology 305 (Genetics), Statistics 100 (Statistical Reasoning), Statistics 402 (Statistics and Data Analysis)  
1997-1998 “The Likelihood Method in Genetics I”, lecture for Human Genetics (HG 542), University of Michigan  
1997-1998 “The Likelihood Method in Genetics II”, lecture for Human Genetics (HG 542), University of Michigan  
1999 “Genetics of Alzheimer’s Disease”, lecture for Neuroscience Section of the Interdisciplinary Graduate Program (IGP) first year course, Vanderbilt University

- 2000-2004 “Biostatistics in Genetics”, lecture for Human Genetics (MPB340), Vanderbilt University
- 2000-2004 “Human Population Genetics”, lecture for Human Genetics (MPB340), Vanderbilt University
- 2000-2004 “Quantitative Trait Genetics”, lecture for Human Genetics (MPB340), Vanderbilt University
- 2000-2001 Course Co-Director, Tutorials in Physiology (MPB324), Vanderbilt University
- 2000-2004 Founder and Director of the Vanderbilt Individualized Graduate Program in Applied Statistics (highlight: allows Ph.D. students to obtain an M.S. degree in Applied Statistics concurrent with their doctoral studies – still active)
- 2002-2004 Founder and Director of the Biostatistics Section of the Interdisciplinary Graduate Program (IGP) first year course (6 lectures), Vanderbilt University
- 2002-2004 “Philosophy of Statistics I”, lecture for the Biostatistics Section of the Interdisciplinary Graduate Program (IGP) first year course, Vanderbilt University
- 2002-2004 “Philosophy of Statistics II”, lecture for the Biostatistics Section of the Interdisciplinary Graduate Program (IGP) first year course, Vanderbilt University
- 2002-2004 “Descriptive Statistics”, lecture for the Biostatistics Section of the Interdisciplinary Graduate Program (IGP) first year course, Vanderbilt University
- 2002-2004 “Categorical Data Analysis”, lecture for the Biostatistics Section of the Interdisciplinary Graduate Program (IGP) first year course, Vanderbilt University
- 2002-2004 “T-test and ANOVA”, lecture for the Biostatistics Section of the Interdisciplinary Graduate Program (IGP) first year course, Vanderbilt University
- 2002-2004 “Correlation and Regression”, lecture for the Biostatistics Section of the Interdisciplinary Graduate Program (IGP) first year course, Vanderbilt University
- 2002 “Transmission Disequilibrium Test”, lecture for Fundamentals of Genetics course, Vanderbilt University and Meharry Medical College
- 2002 “Microarray Data Analysis”, lecture for course on Genetic Analysis of Complex Human Diseases, Vanderbilt University
- 2002 “Quantitative Genetics”, lecture for course on Genetic Analysis of Complex Human Diseases, Vanderbilt University
- 2003 “Study Design in Genetics”, lecture for Human Genetics (MPB340), Vanderbilt University
- 2003 “Computational Approaches for Detecting and Characterizing Gene-Gene Interactions”, lecture in short course for Bristol-Myers Squibb, Department of Biomedical Informatics, Vanderbilt University
- 2004 “Low-Penetrance Genes and Gene-Gene Interactions”, lecture for course on Molecular Epidemiology, International Agency on Cancer Research and Vanderbilt University
- 2004 “Emerging Issues in Bioinformatics”, lecture for short course on Molecular Epidemiology, International Agency on Cancer Research and Vanderbilt University
- 2005 “Data Mining in Human Genetics”, lecture for Topics in Computer Science: Data Mining (CS88/188), Dartmouth College.
- 2005 “Logic Regression”, lecture for Computational Biology Journal Club (BIO270), Dartmouth College.
- 2005 Course Director and Lecturer (with Mike Whitfield), Genetics 118, “Genomics and Bioinformatics”, Dartmouth Medical School.

- 2005 “SNPs and Genome Variation”, lecture for Genetics 118, Dartmouth Medical School.
- 2005 “Genotype to Phenotype”, lecture for Genetics 118, Dartmouth Medical School.
- 2005 “Cyber-Genetics”, lecture for Humanities Institute course on “Cyber-Disciplinarity”, Department of Film and Television Studies, Dartmouth College.
- 2006-present Course Director and Lecturer (with Mike Whitfield), Genetics 146, “Molecular and Computational Genomics”, Dartmouth Medical School.
- 2006 “Introduction to Biostatistics and Data Mining”, lecture for Genetics 146, Dartmouth Medical School.
- 2006 “Biostatistics and Data Mining using R”, lecture for Genetics 146, Dartmouth Medical School.
- 2006 “SNPs and Genome Variation”, lecture for Genetics 146, Dartmouth Medical School.
- 2006 “Genotype to Phenotype”, lecture for Genetics 146, Dartmouth Medical School.
- 2006 “Biostatistics I”, lecture for Biochemistry 103, Dartmouth Medical School
- 2006 “Biostatistics II”, lecture for Biochemistry 103, Dartmouth Medical School
- 2006 “Data Mining and Analysis”, lecture for Pharmacology 131, Dartmouth Medical School
- 2006 “Artificial Life”, lecture for Genetics 146, Dartmouth Medical School.
- 2006 “Digital Biology”, lecture for “Genes and Society”, Biology 4, Dartmouth College.
- 2006 “Genetic Analysis of Common Human Diseases”, lecture for Experimental and Molecular Medicine I (PEMM 101), Dartmouth Medical School
- 2007 “Genetics of Complex Diseases”, lecture for 4<sup>th</sup>-year medical students taking Advanced Medical Sciences, Dartmouth Medical School.
- 2007 “Introduction to Biostatistics and Data Mining”, lecture for Genetics 146, Dartmouth Medical School.
- 2007 “Biostatistics and Data Mining using R”, lecture for Genetics 146, Dartmouth Medical School.
- 2007 “SNPs and Genome Variation”, lecture for Genetics 146, Dartmouth Medical School.
- 2007 “Genotype to Phenotype”, lecture for Genetics 146, Dartmouth Medical School.
- 2007 “Biostatistics I”, lecture for Biochemistry 103, Dartmouth Medical School
- 2007 “Biostatistics II”, lecture for Biochemistry 103, Dartmouth Medical School

### ***High School Students Mentored***

- 2007 Delaney Granizo-MacKenzie, Hanover High School, Hanover, NH
- 2007 Daniel Himmelstein, Hanover High School, Hanover, NH

### ***Undergraduate Students Mentored***

- 2005-2007 Adam Chmelynski, class of 2008, Presidential Scholar, Dartmouth College
- 2006-present Ryan Church, class of 2009, Dartmouth College

2006-2007 Kristin Fladseth, class of 2009, Dartmouth College  
2006-present Oleg Seletsky, class of 2009, Presidential Scholar, Dartmouth College  
2007-present Arvis Sulovari, class of 2010, Dartmouth College  
2007-present Elizabeth Weber, class of 2009, Dartmouth College  
2007-present Emmanuel Mensah, class of 2009, Dartmouth College  
2007-present Kevin Mwenda, class of 2009, Dartmouth College  
2007-present Joann Gruber, class of 2010, HHMI Fellow, Dartmouth College

### ***Graduate Rotation Students Mentored***

1999 Don Carpenter, Interdisciplinary Graduate Program (IGP), Vanderbilt University  
2000 Joel Parker, Biomedical Informatics Graduate Program, Vanderbilt University  
2000 Sheng-Ru Shiou, Interdisciplinary Graduate Program (IGP), Vanderbilt University  
2000 Jennifer Lamb, Interdisciplinary Graduate Program (IGP), Vanderbilt University  
2000 Marylyn Ritchie, Interdisciplinary Graduate Program (IGP), Vanderbilt University  
2002 Jian Shi, Chemical and Physical Biology Program, Vanderbilt University  
2002 David Reif, Interdisciplinary Graduate Program (IGP), Vanderbilt University  
2002 Lawrence Fu, Biomedical Informatics Graduate Program, Vanderbilt University  
2002 Ken Stawowy, Interdisciplinary Graduate Program (IGP), Vanderbilt University  
2002 Scott Gruver, Chemical and Physical Biology Program, Vanderbilt University  
2003 Nykolaus Reed, Meharry Medical College, Nashville, Tennessee  
2003 Digna Valez, Interdisciplinary Graduate Program (IGP), Vanderbilt University  
2003 Jana Shirey, Interdisciplinary Graduate Program (IGP), Vanderbilt University  
2003 Will Bush, Chemical and Physical Biology Program, Vanderbilt University  
2004 Alison Motsinger, Interdisciplinary Graduate Program (IGP), Vanderbilt University  
2004 Todd Edwards, Interdisciplinary Graduate Program (IGP), Vanderbilt University  
2005 Kristine Pattin, Molecular and Cellular Biology (MCB), Dartmouth College  
2005 Anna Tyler, Molecular and Cellular Biology (MCB), Dartmouth College  
2005 Chantel Sloan, Molecular and Cellular Biology (MCB), Dartmouth College  
2005 Sarah Pendergrass (Co-mentor with Mike Whitfield), Molecular and Cellular Biology (MCB), Dartmouth College  
2005 Eric Arehart, M.D.-Ph.D. Program, Dartmouth College  
2005 Randy Lambrechts, Molecular and Cellular Biology (MCB), Dartmouth College  
2005 Ryan Urbanowicz, Molecular and Cellular Biology (MCB), Dartmouth College  
2006 Casey Green, Molecular and Cellular Biology (MCB), Dartmouth College  
2006 Amelia Lyman, Molecular and Cellular Biology (MCB), Dartmouth College  
2006 Diyong Xu, Molecular and Cellular Biology (MCB), Dartmouth College

### ***Masters Students Mentored***

2000-2002 Joel Parker, M.S. in Biomedical Informatics, Vanderbilt University, Thesis: "Dynamics Based Pattern Recognition for the Analysis of Multivariate Gene Expression Data".  
2000-2002 Marylyn Ritchie, M.S. in Applied Statistics, Vanderbilt University, Thesis:

“Power of Multifactor Dimensionality Reduction for the Detection of Gene-Gene Interactions in the Presence of Noise Due to Genotyping Error, Missing Data, Phenocopy, and Genetic Heterogeneity”.

2001-2005 Tricia Thornton, M.S. in Biomedical Informatics (Co-Mentor with Jonathan Haines), Vanderbilt University, Thesis: “Comparison of Three Clustering Methods for Dissecting Trait Heterogeneity in Simulated Data”

2003-2005 David Reif, Applied Statistics M.S. Student, Vanderbilt University. Thesis: “Exploratory Visual Analysis of Pharmacogenomic Results”

### ***M.D. Students Mentored***

2003 Robert Thiele, Introduction to Biomedical Research (IBR) Program, Vanderbilt University

2005-present Eric Arehart (Co-Mentor with John Hwa), M.D.-Ph.D. Program, Dartmouth College

### ***Ph.D. Committees Served On***

1999-2003 Holli Hutcheson, Interdisciplinary Graduate Program (IGP), Vanderbilt University

2000-2004 Alecia Willis, Interdisciplinary Graduate Program (IGP), Vanderbilt University

2000-2004 Renee Dawson, Interdisciplinary Graduate Program (IGP), Vanderbilt University

2001-2004 Jake McCauley, Interdisciplinary Graduate Program (IGP), Vanderbilt University

2001-2004 Sarah Schwartz, Interdisciplinary Graduate Program (IGP), Vanderbilt University

2002-2004 Roger Liu, Interdisciplinary Graduate Program (IGP), Vanderbilt University

2003-2004 Elizabeth Rula, Neuroscience Graduate Program, Vanderbilt University

2005-present Gavin Grant, Molecular and Cellular Biology Program, Dartmouth College

2005-present Lacy George, Molecular and Cellular Biology Program, Dartmouth College

2006-present Jennifer Sargent, Molecular and Cellular Biology Program, Dartmouth College

2006-present Darren Bauer, Genome Center, University of New Hampshire

2006-present Viktor Martyanov, Molecular and Cellular Biology Program, Dartmouth College

2007 Catarina Campbell, Genetics, Harvard Medical School

### ***Ph.D. Students Mentored***

2000-2003 Marylyn Ritchie, Interdisciplinary Graduate Program (IGP) Ph.D. Student, Vanderbilt, Dissertation: “Genetic programming neural networks for detecting gene-gene interactions” (highlight: Dr. Ritchie started in 2004 as a tenure-track assistant professor of molecular physiology and biophysics at Vanderbilt University)

2001-2006 Tricia Thornton-Wells (Co-Mentor with Jonathan Haines), Integrative Neuroscience Ph.D. Student, Vanderbilt University, Dissertation: “Confronting complexity: A comprehensive statistical and computational strategy for identifying the missing link between genotype and phenotype” (highlight: Dr. Thornton-Wells is a postdoctoral fellow in neuroimaging at Vanderbilt

University.

2003-2006 David Reif, Interdisciplinary Graduate Program (IGP) Ph.D. Student, Vanderbilt

- University, Dissertation: “Integrated analysis of genetic and proteomics data” (highlight: Dr. Reif is a postdoctoral fellow in the Computational Toxicology program at the Environmental Protection Agency)
- 2005-present Sarah Pendergrass (Co-Mentor with Mike Whitfield), Molecular and Cellular Biology (MCB), Dartmouth College
- 2005-present Chantel Sloan, Molecular and Cellular Biology (MCB), Dartmouth College
- 2005-present Kristine Pattin, Molecular and Cellular Biology (MCB), Dartmouth College
- 2006-present Casey Greene, Molecular and Cellular Biology (MCB), Dartmouth College
- 2006-present Ryan Urbanowicz, Molecular and Cellular Biology (MCB), Dartmouth College
- 2006-present Anna Tyler, Molecular and Cellular Biology (MCB), Dartmouth College
- 2007-present Richard Cowper, Molecular and Cellular Biology (MCB), Dartmouth College

### ***Postdoctoral Students and Non-Tenure Track Faculty Mentored***

- 2003-2005 Brett McKinney, Ph.D., Vanderbilt University (highlight: Dr. McKinney joined the Center for Human Genetics at the University of Alabama Birmingham as a tenure-track Assistant Professor in July of 2006)
- 2004-2006 Tom Chittenden, Ph.D. (Co-Mentor with Mike Simmons), Dartmouth College
- 2005-present David Jewell, Ph.D., Instructor of Genetics, Dartmouth College

### ***Tenure Track Faculty Mentored***

- 2006-present Jiang Gui, Ph.D., Assistant Professor of Community and Family Medicine, Dartmouth College

### **Research Interests**

A central goal of human genetics is to understand how DNA sequence variations increase or decrease susceptibility to common diseases such as sporadic breast cancer or essential hypertension. This endeavor is complicated by the fact that the mapping relationship between genotype and phenotype may be highly nonlinear due, in part, to complex gene-gene interactions (epistasis) and gene-environment interactions (plastic reaction norms). The primary focus of my research program is to develop, evaluate, and apply novel computational and statistical algorithms for identifying combinations of DNA sequence variations along with combinations of environmental factors that are predictive of common disease endpoints. To this end, we have developed the first new methodology and open-source software package designed specifically for detecting and characterizing gene-gene and gene-environment interactions. Our novel multifactor dimensionality reduction (MDR) approach has been validated both empirically and theoretically and has successfully detected nonlinear interactions that are associated with a variety of common diseases including, for example, sporadic breast cancer, essential hypertension, atrial fibrillation, bladder cancer, prostate cancer, schizophrenia, and type II diabetes. Our open-source MDR software has been downloaded more than 7500 times since 2005 via [www.epistasis.org](http://www.epistasis.org) and [sourceforge.net](http://sourceforge.net). Recent work has focused on the implementation of MDR and other methods for detecting interactions in genome-wide association studies using filtering methods such as our novel Tuned ReliefF (TuRF) algorithm and wrapper methods such as genetic programming. The open-source MDR software package is primarily funded by NIH R01 AI59694. Extension of MDR

to genome-wide association studies is supported by NIH R01 LM009012. We are funded to apply MDR to identifying biomarkers of adverse events to smallpox vaccination (R01 AI59694), lung function following traumatic injury (R01 HD047447) and susceptibility to bladder cancer (R01 LM009012).

The future of biomedical research will involve the integrated analysis of genetic, genomic, proteomic, and metabolic data. To this end, we have developed several methods including a flexible machine learning strategy called symbolic discriminant analysis (SDA) that makes no assumptions about the type of data or the functional form of the mathematical model. This is accomplished by providing a list of variables and list of mathematical functions that can be used to construct predictive equations that can take any form. We have successfully applied this new approach to microarray, MALDI-TOF mass spectrometry, and genetic data from a variety of diseases including atrial fibrillation, lung cancer, brain cancer, diabetic nephropathy, autoimmune disease, and adverse events following vaccination to smallpox. We are in the process of developing an integrated strategy for the combined analysis of these data with DNA sequence variations. It is our hypothesis that the joint analysis of multiple data types will be superior to the analysis of any one data type. We are funded by National Institutes of Health grant R01 AI59694 to develop these methods and then apply them to the detection of combinations of genetic and proteomic biomarkers that predict adverse events following vaccination for smallpox.

The detection of gene-gene and gene-environment interactions associated with common diseases is both a computational and a statistical challenge. We will continue to develop, evaluate, and apply new and novel approaches for identifying susceptibility genes, especially in genome-wide association studies. Perhaps an even greater challenge is the interpretation of nonlinear interaction models. That is, how do interactions impact disease susceptibility through a hierarchical network of biochemical, metabolic, and physiological systems? To this end we have developed an Exploratory Visual Analysis (EVA) database and graphic-user interface for storing, managing, and visualizing statistical results in the context of Gene Ontology, biochemical pathways, chromosomal location, protein domain, phenotype, etc. The purpose of EVA is to facilitate exploration of statistical analysis results by biologists and epidemiologists. An open-source EVA software package is in development and will be available in early 2007.

In addition to the methodological work summarized above, I actively participate in subject recruitment and genotyping for our funded studies of several different biomedical endpoints. For example, we have recruited more than 1300 subjects from 2005 to 2006 that were admitted to the intensive care unit following traumatic injury. The goal of this study is to identify genetic predictors of which patients are likely to develop adult respiratory distress syndrome or acute lung injury. This study is funded by NIH R01 HD047447. I have also worked closely with Dr. Scott Williams to recruit more than 3,000 Africans from Sunyani, Ghana for a population-based study of the genetic architecture of plasma levels of tissue plasminogen activator (t-PA) and plasminogen activator inhibitor 1 (PAI-1). DNA and plasma samples are available on all recruited subjects. This study was funded by NIH R01 HL65234 and represents one of the largest population genetics studies in Africa.

In summary, my research program lies at the intersection of genetics, genomics, biostatistics, epidemiology, and computer science. We are pioneering a quantitative biomedical research strategy that embraces, rather than ignores, the complexity of the relationship between biological markers and disease endpoints.

### **Research Funding (dollar amounts are annual direct costs)**

**Completed**

- 1999-2000 American Cancer Society (P.I. – Moore)  
\$15,534  
Genetic Epidemiology of Adenoma Response to Chemoprevention
- 1999-2000 VUMC Discovery Grant (P.I. - Moore)  
\$50,000  
VANPAC: A VANDerbilt PARallel Computer
- 1999-2001 GlaxoSmithKline (P.I. – Haines)  
\$702,846  
A Genetic Epidemiology Center  
  
Role: lead statistical geneticist on the Depression Network (DeNt) project
- 2000-2002 VU Discovery Grant (Co-P.I. – Moore)  
\$75,000  
VAMPIRE Parallel Computing Facility
- 2000-2003 NIH R24 DK58749 (P.I. - George)  
\$336,029  
Vanderbilt NIDDK Biotechnology Center  
  
Role: Co-P.I. of Bioinformatics Core
- 2000-2004 NIH R01 HL65962 (P.I. – Brown)  
\$250,000  
Genes and Fibrinolytic Capacity of Human Endothelium
- 2001-2003 Kleberg Fund (P.I. - Moore)  
\$37,018  
Collaborative Microarray Data Analysis for Cancer Research
- 2001-2004 NIH P50 CA90949 (P.I. – Carbone)  
\$1,655,547  
SPORE in Lung Cancer  
  
Role: Co-investigator to help with data analysis and bioinformatics
- 2001-2004 NIH U01 HL65962 (P.I. - Roden)  
\$1,828,997 (\$220,000 to Moore)  
Pharmacogenomics of arrhythmia therapy  
  
Role: P.I. of Genetic Epidemiology Core

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- 2001-2004 NIH R01 AG19085 (P.I. – Haines)  
\$779,306  
Genetic Studies of Dementia in the Amish  
  
Role: Co-investigator to help with data analysis and bioinformatics
- 2001-2004 NIH R01 CA064277 (P.I. – Zheng)  
\$363,464  
Shanghai Breast Cancer Study  
  
Role: Co-investigator to help with data analysis and bioinformatics
- 2001-2004 NIH U01 HL68744 (P.I. - Hawiger)  
\$1,299,416 (\$50,000 to Moore)  
Functional Genomics of Inflammation  
  
Role: P.I. of Bioinformatics Core
- 2003-2004 Kleberg Fund (P.I. - Moore)  
\$37,005  
Visual Analysis of Microarray Data Analysis Results for Cancer Research
- 2001-2004 NIH U19 DK42502 (P.I. - Magnuson)  
\$1,067,922 (\$50,000 to Moore)  
Genes of Pancreas Function and Development  
  
Role: P.I. of Bioinformatics Core
- 2002-2004 NIH P01 GM31304 (P.I. – Wilkinson)  
\$849,554  
Determinants of Individual Responsiveness to Drugs  
  
Role: Co-investigator to help with data analysis and bioinformatics
- 2002-2004 NIH R01 AG20135 (P.I.- Martin)  
\$468,000 (\$103,005 to Moore)  
Revealing Epistasis in Alzheimer Disease  
  
Role: P.I. of subcontract
- 2002-2004 VUMC Discovery Grant (P.I. - Olsen)  
\$50,000  
Gene Expression in Systemic Lupus Erythmatosus  
  
Role: Co-investigator to help with data analysis and bioinformatics
- 2002-2004 NIH P20 LM07613 (P.I. - Stead)

\$260,270 (\$75,000 to Moore)  
Exploratory Visual Analysis of Genomic and Proteomic Data

Role: P.I. of Project 2

2002-2004 NIH P50 CA95103 (P.I. – Coffey)  
\$1,685,494  
SPORE in GI Cancer

Role: Co-investigator to help with data analysis and bioinformatics

2003-2004 NIH P50 CA098131 (P.I. – Arteaga)  
\$1,698,501  
SPORE in Breast Cancer

Role: Co-investigator to help with data analysis and bioinformatics

2003-2004 VU AVCF (P.I. - Moore, with Sheldon and Schrimpf)  
\$8,300,000 total costs  
A Vanderbilt Scientific Computing Center (SCC) for Multidisciplinary Research

2003-2004 NIH R01 AI057661 (P.I. - Crowe)  
\$250,000  
Cell-Mediated Immune Responses to Vaccinia Viruses

Role: Co-investigator to help with data analysis and bioinformatics

2004 NIH U01 CA084239 (P.I. - Coffey)  
\$725,536  
Prevention and Metastasis: Final Frontier in Colon Cancer

Role: Co-investigator to help with data analysis and bioinformatics

2004-2005 NIH S10 RR017210 (P.I. - Moore)  
\$1,536,000  
Parallel Computer

2000-2006 NIH R01 HL65234 (P.I. – Moore)  
\$250,000  
Genetic Architecture of Plasma t-PA and PAI-1

***Current***

2004-2009 NIH R01 AI59694 (P.I. - Moore)  
\$322,000  
Bioinformatics Strategies for Biodefense Vaccine Research

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- 2004-2009 NIH R01 HD047447 (P.I. - Moore)  
\$368,000  
Genetic Basis of Trauma Recovery
- 2006-2010 NIH R01 LM009012 (P.I. – Moore)  
\$200,000  
Machine Learning Prediction of Cancer Susceptibility  
(highlight: received a 121 priority score, 0.6<sup>th</sup> percentile)
- 2005-2008 NIH P42 ES007373 (P.I. – Hamilton)  
\$1,500,000  
Toxic Metals in the Northeast
- Role: Co-investigator to help with data analysis and bioinformatics
- 2006-2007 NIH R01 (P.I. Ahles)  
\$291,000  
Genetics of Cognitive Decline Post Cancer Chemotherapy
- Role: Co-investigator to help with data analysis and bioinformatics

### ***Pending***

- 2007-2012 NIH P20 RR024475 (P.I. Moore)  
\$1,500,000  
Quantitative Biology Research Institute  
(received a 203 priority score)
- 2007-2010 NIH R01 HL090573 (P.I. Moore)  
\$200,000  
Bioinformatics Strategies for the Analysis of Gene-Environment Interactions
- 2009-2014 NIH P42 ES007373 (P.I. – Hamilton)  
\$1,798,000  
Toxic Metals in the Northeast
- Role: PI of Integrative Biology Core (Core E)

### **Invited Presentations**

- 1997 “Association of variation in the *ACE* and *ATR* Genes with interindividual variation in linear dynamic features of ambulatory blood pressure”, 4<sup>th</sup> International Conference on Preventive Cardiology. Montréal, Québec, Canada, June 29 - July 3.
- 1997 “Genetic linkage analysis”, Breast Cancer: Genetics and Risk Evaluation Workshop. University of Michigan Cancer Center, Ann Arbor, Michigan, July 8 - 13. (Host: Diane Baker)

- 1998 “Genetic analyses of dynamic quantitative traits”, Vanderbilt University Medical School, Nashville, Tennessee, March 9. (Host: Jonathan Haines)
- 1998 “Genetic studies of blood pressure dynamics improve the identification of genes influencing blood pressure regulation”, 48<sup>th</sup> Annual Meeting of the American Society of Human Genetics, Denver, Colorado, October 27 – 31.
- 1999 “Genetics of quantitative traits”, Genetic Analysis Methods for Medical Researchers Workshop, Duke University, Durham, North Carolina, March 13 – 17. (Host: Margaret Pericak-Vance)
- 1999 “New traits for genetic studies of blood pressure regulation”, Department of Microbiology, Meharry Medical College, Nashville, Tennessee, November 2. (Host: Scott Williams)
- 1999 “Simulation of gene expression patterns in cDNA microarray data”, American Statistical Association, Middle Tennessee Chapter, Nashville, Tennessee, November 19. (Host: Yu Shyr)
- 2000 “Analysis of quantitative traits”, Workshop on the Genetic Analysis of Complex Human Diseases, Duke University, Durham, North Carolina, April 2-5. (Host: Marcy Speer)
- 2000 “Analytical issues associated with SNPs”, Workshop on the Genetic Analysis of Complex Human Diseases, Duke University, Durham, North Carolina, April 2-5. (Host: Marcy Speer)
- 2000 “What are we going to do with 300,000 SNPs?”, Glaxo-Wellcome, London, England, April 19. (Host: Lefkos Middleton)
- 2000 “A cellular automata approach to identifying gene-gene and gene-environment interaction effects on complex traits”, 8<sup>th</sup> World Congress on Psychiatric Genetics, Versailles, France, August 27-31.
- 2000 “A cellular automata-based pattern recognition approach to identifying gene-gene and gene-environment interactions” 50<sup>th</sup> Annual Meeting of the American Society of Human Genetics, Philadelphia, Pennsylvania, October 3-7.
- 2000 “Combinatorial partitioning reveals interactive effects of the *ACE I/D* and *PAI-1 4G/5G* polymorphisms on plasma PAI-1 levels” 50<sup>th</sup> Annual Meeting of the American Society of Human Genetics, Philadelphia, Pennsylvania, October 3-7.
- 2000 “A cellular automata-based pattern recognition approach to identifying gene-gene and gene-environment interactions”, James V. Neel New Investigator Award Finalist Presentation, 2000 International Genetic Epidemiology Society meeting, San Antonio, Texas, October 27-29.
- 2000 “Symbolic discriminant analysis for mining gene expression patterns”. Critical Assessment of Techniques for Microarray Data Analysis (CAMDA’00) meeting, Duke University Durham, North Carolina, December 18-19, 2000.
- 2001 “Data reduction and pattern recognition approaches to the genetics of complex diseases”. Center for Human Genetics, Duke University Medical School, Durham, North Carolina, January 17. (Host: Margaret Pericak-Vance).
- 2001 “Data reduction and pattern recognition approaches to the genetics of complex diseases”. GlaxoSmithKline, Durham, North Carolina, February 7. (Host: Chris Foster).
- 2001 “Genetics of quantitative traits”, Workshop on the Genetic Analysis of Complex Human Diseases, Duke University, Durham, North Carolina, May 5-9. (Host: Marcy Speer).

- 2001 “Future directions and major unsolved problems in genetic epidemiology”, Workshop on the Genetic Analysis of Complex Human Diseases, Duke University, Durham, North Carolina, May 5-9. (Host: Marcy Speer)
- 2001 “Introduction to biostatistics”, Workshop on the Genetic Analysis of Complex Human Diseases, Duke University, Durham, North Carolina, May 5-9. (Host: Marcy Speer).
- 2001 “The role of interactions among ACE and PAI-1 polymorphisms in risk of myocardial infarction”, Division of Cardiology, Yale University Medical School, New Haven, Connecticut, August 23, 2001 (Host: Pat Hebert).
- 2001 “Symbolic discriminant analysis for mining gene expression patterns”, James V. Neel New Investigator Award Presentation, 2001 International Genetic Epidemiology Society meeting, Garmisch-Partenkirchen, Germany, September 2-4, 2001.
- 2001 “Power of multifactor dimensionality reduction (MDR) for identifying gene-gene and gene-environment interactions”, 2001 International Genetic Epidemiology Society meeting, Garmisch-Partenkirchen, Germany, September 2-4, 2001.
- 2001 “Symbolic discriminant analysis for mining gene expression patterns”, European Conference on Machine Learning, Freiberg, Germany, September 5-7, 2001
- 2001 “Power of cellular automata for identifying gene-gene and gene-environment interactions”, 9<sup>th</sup> World Congress on Psychiatric Genetics, St. Louis, Missouri, October 6-10, 2001.
- 2001 “Machine learning optimization of neural network architecture improves the identification of gene-gene and gene-environment interactions”, 9<sup>th</sup> World Congress on Psychiatric Genetics, St. Louis, Missouri, October 6-10, 2001.
- 2001 “Computational approaches to the analysis of microarray data”, Department of Biology, California State University, San Marcos, California, October 18, 2001 (Host: Thomas Wahlund).
- 2001 “New paradigms for the analysis of high-dimensional genetic data”, Department of Mathematics, University of Tennessee, Chattanooga, Tennessee, November 6, 2001 (Host: John Graef).
- 2002 “A cellular automata approach to detecting interactions among single-nucleotide polymorphisms in complex multifactorial diseases”, Pacific Symposium on Biocomputing 2002, Kaua’i, Hawaii, January 5, 2002 (Host: Russ Altman).
- 2002 “New strategies for identifying combinations of single-nucleotide polymorphisms associated with common multifactorial diseases”, Department of Biostatistics and Epidemiology, University of Pennsylvania, Philadelphia, Pennsylvania, January 31, 2002 (Host: Tim Rebbeck).
- 2002 “symbolic discriminant analysis for mining gene expression patterns”, Division of Nephrology, Department of Pediatrics, University of Minnesota, Minneapolis, Minnesota, February 15, 2002 (Host: Mike Mauer).
- 2002 “New strategies for identifying gene-gene interactions in common multifactorial diseases”, Department of Biostatistics, University of Alabama, Birmingham, Alabama, March 4, 2002 (Host: Hemant Tiwari).
- 2002 “New strategies for identifying gene-gene interactions in common multifactorial diseases”, Clinical Diabetes and Nutrition Section, NIDDK, National Institutes of Health, Phoenix, Arizona, March 8, 2002 (Host: Johanna Wolford).
- 2002 “Application of genetic algorithms to the discovery of complex genetic models for simulation studies in human genetics”, 2002 Genetic and Evolutionary Algorithm Conference (GECCO’02), New York, New York, July 12, 2002.

- 2002 “Strategies for identifying gene-gene interactions in cardiovascular disease”, Department of Clinical Pharmacology and Cardiology, University of Groningen, Groningen, The Netherlands, August 8, 2002 (Host: Wiek van Gilst).
- 2002 “Non-traditional statistical approaches for the analysis of high-dimensional genetic data”, Invited Session at the 2002 Joint Statistical Meetings, New York, New York, August 15, 2002 (Host: Dan Weeks).
- 2002 “Symbolic discriminant analysis for mining gene expression patterns: The Importance of cross-validation consistency”, Workshop on Evolutionary and Neural Computation in Bioinformatics, Granada, Spain, September 7, 2002 (Host: David Corne).
- 2002 “Cellular automata and genetic algorithms for parallel problem solving in human genetics”, EvoSolve Best Paper Award Presentation at the Seventh International Conference on Parallel Problem Solving from Nature (PPSN), Granada, Spain, September 10, 2002.
- 2002 "Genetic architecture of intermediate traits for arterial thrombosis in Africa and The Netherlands". Third Annual Vanderbilt-Meharry Genetics Symposium, Vanderbilt University, Nashville, Tennessee, September 20, 2002.
- 2002 “Multifactor dimensionality reduction is an ideal discriminator of discrete clinical endpoints using multilocus genotypes”, Xth World Congress for Psychiatric Genetics, Brussels, Belgium, October 10, 2002.
- 2002 “Concordant results of microarray and gene mapping studies in human autoimmune Disease”, 52nd Annual Meeting of the American Society of Human Genetics, Baltimore, Maryland, October 17, 2002.
- 2002 “A novel strategy for selecting optimal subsets of SNPs for the analysis of gene-gene interactions”, 2002 Annual Meeting of the International Genetic Epidemiology Society, New Orleans, Louisiana, November 16, 2002.
- 2003 “Computational approaches for detecting and characterizing gene-gene interactions”, Invited Tutorial at the Pacific Symposium on Biocomputing, Kaua’i, Hawaii, January 3, 2003 (Host: Russ Altman).
- 2003 "Symbolic discriminant analysis of proteomics data", 2nd Annual Conference on Protein Informatics: From Database to Prediction, San Diego, California, January 14, 2003.
- 2003 "Computational approaches for detecting gene-gene interactions", Oberwolfach Conference on Medical Statistics: Current Developments in Statistics Methodology for Genetic Architecture of Complex Diseases, Oberwolfach, Germany, February 4, 2003. (Hosts: Christopher Amos, Max Bauer, Helmut Schafer).
- 2003 “Computational approaches for detecting and characterizing gene-gene interactions in multifactorial diseases”, 2003 University of Tennessee - Oak Ridge National Laboratory Bioinformatics Summit, Pikeville, Tennessee, March 28, 2003. (Host: Jay Snoddy).
- 2003 "Cross validation consistency for the assessment of genetic programming results in microarray studies", 1st European Workshop on Evolutionary Computation and Bioinformatics (EvoBio), Essex, England, April 14, 2003. (Hosts: David W. Corne and Elena Marchiori).
- 2003 “Computational approaches for detecting and characterizing gene-gene interactions”, Department of Cancer Biology, Wake Forest University School of Medicine, Winston-Salem, North Carolina, May 1, 2003 (Host: Jennifer Hu).
- 2003 “Computational approaches for detecting and characterizing gene-gene interactions”, Invited Tutorial at the 11th International Conference on Intelligent Systems in Molecular

- Biology (ISMB), Brisbane, Australia, June 29, 2003 (Presented by Marylyn Ritchie on my behalf).
- 2003 "A grammar for petri net modeling in human genetics", 2nd Workshop on Grammatical Evolution, Chicago, Illinois, July 12, 2003. (Host: Conor Ryan).
- 2003 "Complex systems strategies for cancer bioinformatics", Fred Hutchinson Cancer Research Center. Seattle, Washington, November 13, 2003. (Host: Ross Prentice)
- 2003 "The importance of epistasis for understanding breast cancer", NCI/NIH Breast SPORE Roundtable. Cambridge, Massachusetts, November 20, 2003. (Host: Dirk Iglehart).
- 2003 "Complex Systems Strategies for Cancer Bioinformatics", Lombardi Cancer Center, Georgetown University, Washington D.C., December 8, 2003. (Host: Ed Gelman).
- 2004 "Biocomputing strategies for the study of complex biological systems", Dartmouth College, Hanover, New Hampshire, January 19, 2004. (Host: Dan Rockmore).
- 2004 "Biocomputing strategies for the study of complex biological systems", University of North Carolina, Chapel Hill, North Carolina, January 28, 2004. (Host: Terry Magnuson).
- 2004 "Biocomputing strategies for the study of complex biological systems", Department of Computer Science, Colby College, Waterville, Maine, March 19, 2004. (Host: Clare Congdon)
- 2004 "Computational analysis of gene-gene interactions in cancer epidemiology", Invited session presentation for the 2004 meeting of the American Association for Cancer Research, Orlando, Florida, March 30, 2004. (Host: Tim Rebbeck).
- 2004 "Biocomputing strategies for the study of complex biological systems", University of Texas Southwestern Medical Center, Dallas, Texas, April 28, 2004. (Host: Steve Crozier).
- 2004 "Systems biology thought experiments for interpreting epistasis models", Invited session presentation at the 36<sup>th</sup> Symposium on the Interface: Computing Science and Statistics, Baltimore, Maryland, May 28, 2004. (Host: Bill Shannon).
- 2004 "Petri nets for modeling high-order genetic systems", 2004 SIAM Conference on Discrete Mathematics, Nashville, Tennessee, June 13, 2004. (Host: Chun Li).
- 2004 "Systems biology modeling in human genetics using Petri nets and grammatical evolution". 2004 Genetic and Evolutionary Computation Conference (GECCO 2004), Seattle, Washington, June 29, 2004 (Host: James Foster).
- 2004 "Epistasis and human biology", Marshfield Clinic, Marshfield, Wisconsin, August 9th, 2004 (Host: Russell Wilke).
- 2004 "Systems biology thought experiments in human genetics using artificial life and grammatical evolution", Ninth International Conference on the Simulation and Synthesis of Living Systems (ALIFE IX), Boston, Massachusetts, September 12, 2004.
- 2004 "Systems biology thought experiments in human genetics", invited session presentation for the 2004 Scientific Sessions of the American Heart Association (AHA), New Orleans, Louisiana, November 7, 2004.
- 2004 "Bioinformatics", Colby-Sawyer College, New Hampshire, November 16, 2004 (Host: Bill Thomas).
- 2004 "Machine learning analysis of attribute interactions in human genetics", University of New Hampshire, Durham, New Hampshire, December 10, 2004 (Host: Phil Hatcher).
- 2005 "Data mining in human genetics using multifactor dimensionality reduction", Celera Diagnostics, San Francisco, California, February 3, 2005 (Host: David Ross).
- 2005 "Gene-gene interactions in cancer etiology", invited session presentation for the 2005

- meeting of the American Association for Cancer Research (AACR), Anaheim, California, April 16, 2005.
- 2005 “Interpreting gene-gene interactions”, invited session presentation for the 2005 meeting of the American Association for Cancer Research (AACR), Anaheim, California, April 16, 2005.
- 2005 “Epistasis and human diseases”, New England Complex Systems Institute, Cambridge, Massachusetts, May 3, 2005 (Host: Yaneer Bar-Yam).
- 2005 “Bioinformatics: genotype to phenotype”, invited tutorial presentation for the 2005 Genetic and Evolutionary Computation Conference (GECCO), Washington, D.C., June 25, 2005 (Host: James Foster).
- 2005 “Computational human genetics”, keynote speaker for the 2005 Computer Science Research Day, Department of Computer Science, University of Vermont, Burlington, Vermont, August 26, 2005 (Host: Xindong Wu).
- 2005 “A complete BNF grammar for systems biology thought experiments in human genetics using artificial life and biologically inspired computing”, 2005 Congress on Evolutionary Computing (CEC), Edinburgh, Scotland, September 3, 2005.
- 2005 “A flexible framework for data mining and knowledge discovery in psychiatric genetics”, 2005 World Congress on Psychiatric Genetics (WCPG), Boston, Massachusetts, October 15, 2005.
- 2005 “A flexible framework for data mining and knowledge discovery in human genetics”, 2005 Annual Meeting of the International Genetic Epidemiology Society (IGES), Park City, Utah, October 23, 2005.
- 2005 “Traversing the conceptual divide between biological and statistical epistasis: Systems biology and a more modern synthesis”, Department of Biology, University of Idaho, Moscow, Idaho, November 4, 2005. (Host: James Foster).
- 2005 “A global view of epistasis”, Keynote speaker for the 2005 Annual Conference of the Portuguese Society of Human Genetics, Cascais, Portugal, November 10, 2005. (Host: Joao Lavinha).
- 2005 “Population biology: new concepts for modeling risk”, Predictive Models of Cancer Susceptibility: Integrated Strategies meeting, Newport Beach, California, December 6, 2005 (Host: Hoda Anton-Culver).
- 2005 “Epistasis and cancer risk: A data mining approach”, Predictive Models of Cancer Susceptibility: Integrated Strategies meeting, Newport Beach, California, December 6, 2005 (Host: Hoda Anton-Culver).
- 2006 “Combinatorial pharmacogenetics”, Pacific Symposium on Biocomputing, Wailea, Maui, Hawaii, January 4, 2006 (Host: Marylyn Ritchie).
- 2006 “Detecting and interpreting epistasis in epidemiologic studies of common human diseases”, Department of Epidemiology and Population Sciences, Albert Einstein College of Medicine, New York, New York, January 19, 2006 (Host: Sylvia Wassertheil-Smoller).
- 2006 “Genome-wide analysis of epistasis”, Department of Statistics, Oxford University, Oxford, United Kingdom, February 7, 2006 (Host: Jonathan Marchini).
- 2006 “Genome-wide analysis of epistasis”, The Wellcome Trust Centre for Human Genetics, Oxford University, Oxford, United Kingdom, February 9, 2006 (Host: Lon Cardon).
- 2006 “Detecting and interpreting epistasis in epidemiologic studies of common human diseases”, Department of Epidemiology, M.D. Anderson Cancer Center, Houston, Texas, March 16, 2006 (Host: Margaret Spitz).

- 2006 “Genome-wide genetic analysis using genetic programming: the critical need for expert knowledge”, Workshop on Genetic Programming Theory and Practice (GPTP-2006), Center for the Study of Complex Systems, University of Michigan, Ann Arbor, Michigan, May 10, 2006 (Host: Bill Worzerl and Rick Riolo).
- 2006 “Bioinformatics strategies for human genetics”, Invited keynote speaker for the Bioinformatics Session of the 2006 Annual Conference on the Mathematics of Information Technology and Complex Systems (MITACS), Toronto, Canada, June 19, 2006 (Host: Shelley Bull).
- 2006 “Bioinformatics”, invited tutorial presentation for the 2006 Genetic and Evolutionary Computation Conference (GECCO), Seattle, Washington, July 8, 2006.
- 2006 “Quantitative biology approaches to the study of gene-environment interaction in environmental health and toxicology”, National IDEA Symposium of Biomedical Research Excellence (NISBRE), Washington, D.C., July 22, 2006.
- 2006 “Genome-wide analysis of epistasis: Finding epistatic needles in a genomic haystack”, Celera Diagnostics, San Francisco, California, August 14, 2006 (Host: David Ross).
- 2006 “Symbolic modeling of epistasis using competent genetic programming”, Celera Diagnostics, San Francisco, California, August 15, 2006 (Host: David Ross).
- 2006 “Symbolic modeling of epistasis”, Department of Computer Science, University of Amsterdam, Amsterdam, The Netherlands, September 8, 2006 (Host: Elena Marchiori).
- 2006 “Exploiting expert knowledge in genetic programming for genome-wide genetic analysis”, Parallel Problem Solving from Nature IX Conference, Reykjavik, Iceland, September 9, 2006.
- 2006 “Symbolic modeling of gene-gene interactions using genetic programming”, Workshop on Bio-inspired Computing in Computational Biology, Parallel Problem Solving from Nature IX Conference, Reykjavik, Iceland, September 12, 2006.
- 2006 “Genome-wide genetic analysis using computational intelligence: The importance of expert knowledge”, Invited keynote speaker for the 2006 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology, Toronto, Canada, September 28, 2006 (Host: Dan Ashlock).
- 2006 “Feature selection using random forests for the integrated analysis of multiple data types”, 2006 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology, Toronto, Canada, September 30, 2006 (Host: Dan Ashlock).
- 2006 “Exploiting expert knowledge for genome-wide genetic analysis”, Invited speaker for the Session on Physiological Genomics and Proteomics of Lung Diseases, 2006 Conference of the American Physiological Society, Ft. Lauderdale, Florida, November 3, 2006.
- 2006 “Detecting, characterizing, and interpreting epistasis using multifactor dimensionality reduction”, Invited speaker for the Workshop on Statistical Genetics, Mayo Clinic, Rochester, Minnesota, November 29, 2006 (host: Jean-Pierre Kocher).
- 2007 “Detecting, characterizing, and interpreting epistasis”, Department of Physics, University of Georgia, Athens, Georgia, March 22, 2007 (Host: Rob Geller).
- 2007 “Solving Complex Problems in Human Genetics using Genetic Programming”, 5<sup>th</sup> European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EvoBIO), Valencia, Spain, April 11<sup>th</sup>, 2007 (Host: Elena Marchiori).
- 2007 “Tuning ReliefF for genome-wide genetic analysis”, 5<sup>th</sup> European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EvoBIO), Valencia, Spain, April 12<sup>th</sup>, 2007.

- 2007 “Genetic analysis using multifactor dimensionality reduction”, Department of Epidemiology, University Medical Center, Groningen, The Netherlands, April 16, 2007 (Host: Harold Snieder).
- 2007 “Genome-wide analysis of epistasis”, Department of Epidemiology, University Medical Center, Groningen, The Netherlands, April 16, 2007 (Host: Harold Snieder).
- 2007 “Open-source software for applied genetic programming in the domain of human genetics: challenges and opportunities”, Invited Speaker for the Workshop on Genetic Programming Theory and Practice (GPTP-2007), Center for the Study of Complex Systems, University of Michigan, Ann Arbor, Michigan, May 17, 2007 (Hosts: Bill Worzel and Rick Riolo).
- 2007 “Genome-wide analysis of epistasis using computational intelligence and biological knowledge”, Invited speaker for the American Association of Cancer Research conference on Approaches to Complex Pathways in Molecular Epidemiology, Albuquerque, New Mexico, May 31, 2007 (Host: Duncan Thomas).
- 2007 “Integrated Human and Mouse Systems Genetics”, Invited speaker for the Board of Scientific Advisors, National Cancer Institute, Bethesda, Maryland, June 29, 2007 (Host: Cheryl Marks).
- 2007 “Symbolic Modeler: Open-source software for applied genetic programming in human genetics”, Invited Speaker for the Workshop on Open-Source Software for Applied Genetic and Evolutionary Computing (SoftGEC-2007), London, England, July 7, 2007.
- 2007 “Bioinformatics”, invited tutorial presentation for the 2007 Genetic and Evolutionary Computation Conference (GECCO), London, England, July 8, 2007.
- 2007 “Exploratory visual analysis of statistical and computational results”, invited presentation for the Northeast Regional IDEa Meeting, Burlington, Vermont, August 17, 2007 (Host: Karl Steiner).
- 2007 “Cyber-infrastructure in New Hampshire”, invited presentation for the Workshop on Cyber-Infrastructure, Northeast Regional IDEa Meeting, Burlington, Vermont, August 17, 2007 (Host: Karl Steiner).
- 2007 “New strategies for MDR analysis of epistasis”, Celera Diagnostics, Alameda, California, August 27, 2007 (Host: David Ross).
- 2007 “A role for high-performance computing in the genetic analysis of common human Diseases”, Lawrence Livermore National Laboratory, Livermore, California, August 28, 2007 (Host: Ed Turano).
- 2007 “Genome-wide genetic analysis using computational intelligence”, New England Biolabs, August 30, 2007. *to be presented*
- 2007 “Detecting, characterizing, and interpreting epistasis”, James Graham Brown Cancer Center, University of Louisville, Louisville, Kentucky, September 18, 2007 (Host: La Creis Kidd). *to be presented*
- 2007 “A role for computational intelligence and expert knowledge in genome-wide association studies”, Center for Bioinformatics and Computational Biology, University of Indiana, Indianapolis, Indiana, November, 2007 (Host: Sean Mooney). *to be presented*

## Bibliography

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