

## Curriculum Vitae

**Veronica J. Vieland, Ph.D.**  
**Battelle Chair in Quantitative and Computational Biology**  
**Director, Battelle Center for Mathematical Medicine**  
**Vice-President for Computational Research**  
**The Research Institute at Nationwide Children's Hospital**  
**&**  
**Professor, Departments of Pediatrics & Statistics**  
**The Ohio State University**

### Contact Information

Battelle Center for Mathematical Medicine  
 WB5129  
 575 Children's Crossroad  
 Columbus OH 43215

*Phone* (614) 355-5651  
*Fax* (614) 355-6671  
*Email* [Veronica.Vieland@Nationwidechildrens.org](mailto:Veronica.Vieland@Nationwidechildrens.org)

### Areas of Research Interest

Statistical genetics  
 Genetic architecture of psychiatric and other complex human disorders  
 Genetic modifiers of Mendelian disorders  
 Computational methods in biology  
 Measurement theory in biology  
 Foundations of statistical inference  
 Intersection of thermodynamics, information theory and statistical inference  
 Philosophy of statistics

### Education

<u>Year</u>	<u>Degree, field</u>	<u>Institution</u>
1979	B.A., Philosophy	Barnard College, New York, New York
1981	M.A., Philosophy (Mathematical Logic and Philosophy of Science)	Columbia University, Department of Philosophy New York, New York
1986	Ph.D., Philosophy (Mathematical Logic and Philosophy of Science)	Columbia University, Department of Philosophy New York, New York
1988	M.S., Biostatistics	Columbia University, Department of Biostatistics New York, New York
1988-90	Postdoctoral Research Fellow Biostatistics/Child psychiatry	Columbia University, Department of Child Psychiatry New York, New York

### Academic Appointments

<u>Year</u>	<u>Position</u>	<u>Institution</u>
1981-84	Instructor	Columbia University, New York, NY
1984-86	Graduate Research Assistant	Columbia University
1986	Instructor	Marymount Manhattan College, New York, NY
1986-88	Graduate Research Assistant	Columbia University, School of Public Health, New York, NY

1988-90	Research Scientist	New York State Psychiatric Institute, New York, NY
1990-95	Assistant Professor	Departments of Psychiatry and Biostatistics, Columbia University
1991	Visiting Scholar	Department of Biomathematics, University of California Los Angeles
1995-99	Associate Professor	Department of Preventive Medicine & Environmental Health, Division of Biostatistics, College of Medicine The University of Iowa, Iowa City, IA (primary appointment)
1995-00	Associate Professor	Department of Psychiatry, College of Medicine The University of Iowa (secondary appointment)
1996-00	Associate Professor	Interdepartmental Ph.D. Program in Genetics The University of Iowa
1999-00	Associate Professor	Department of Biostatistics, College of Public Health (founded 1999) The University of Iowa (primary appointment)
2000-03	Professor	Department of Biostatistics, College of Public Health The University of Iowa (primary appointment)
2000-06	Professor	Department of Psychiatry, College of Medicine The University of Iowa (secondary appointment)
2000-06	Professor	Interdepartmental Ph.D. Program in Genetics The University of Iowa
2000-03	Director	Division of Statistical Genetics, Department of Biostatistics College of Public Health The University of Iowa
2000-06	Director	Center for Statistical Genetics Research College of Public Health & Carver College of Medicine The University of Iowa
2003-06	Professor & Head	Department of Public Health Genetics College of Public Health The University of Iowa
2006-07	Dwight E. Peters and Juanita R. Curran Professor of Pediatric Research	The Research Institute at Nationwide Children's Hospital
2006-07	Director, Center for Quantitative and Computational Biology	The Research Institute at Nationwide Children's Hospital
2007-	Battelle Chair in Quantitative and Computational Biology	The Research Institute at Nationwide Children's Hospital

2007-	Director, Battelle Center for Mathematical Medicine (formerly known as Center for Quantitative and Computational Biology)	The Research Institute at Nationwide Children's Hospital
2006-	Professor (Primary)	Department of Pediatrics College of Medicine The Ohio State University
2007-	Professor (Secondary)	Department of Statistics The Ohio State University
2007-10	Adjunct Professor	Department of Genetics Rutgers University
2011-	Vice-President for Computational Research	The Research Institute at Nationwide Children's Hospital

### Honors and Awards

Elected Fellow, American Association for the Advancement of Science (AAAS), 2013.

Elected Fellow, American PsychoPathological Association (APPA, founded in 1910), 2012.

National Institute of Mental Health Career Development Award, 1997-2002

Myers Center Award for the Study of Human Rights in North America (awarded to Get Smart!), 1994

World Congress on Psychiatric Genetics Junior Investigator Travel Award, Oct. 1993

National Institute of Mental Health Scientist Development Award, 1990-1995

Columbia University President's Fellowship, 1979-1982

Graduated cum laude with Honors, Barnard College, Columbia University, 1979

William Pepperell Montague Prize for Promise of Distinction in Philosophy, Barnard College, Columbia University, 1979

### Professional Affiliations

Member, Society for Women in Philosophy, 1981-1986

President, New York Chapter of the Society for Women in Philosophy, 1983-1984

American Society of Human Genetics, 1990-

International Genetic Epidemiology Society, founding member, 1991-

Member, American Association for the Advancement of Science (AAAS), 2008-

Member, Society for Philosophy of Science in Practice, 2009-

Member, Genetics Society of America, 2012-

Member, American PsychoPathological Association (APPA), 2012-

Member, The Philosophy of Science Association, 2013 –

### Classroom Teaching

<u>Year</u>	<u>Course Title and Number</u>
-------------	--------------------------------

1981	Formal Logic
1982	Epistemology
1982-84	Contemporary Civilization
1985	Mathematical Logic
1986	Mathematical Logic
1994	Probability Theory with Statistical Applications
1996	Risk and Protective Factors in Childhood Psychopathology (Child Psychiatry Residents' Lecture)
1996	Independent Study in Statistical Genetics (Susan Slager)
1996	Summer Student Seminar Series in Human Genetics
1996	Statistical Genetics
1997	Independent Study (Terry Braun, Genetics Ph.D. Rotation)
1997	Advanced Topics in Genetic Data Analysis
1997	Biostatistics Preceptorship (Kim Williamson)
1998	Risk and Protective Factors in Childhood Psychopathology (Child Psychiatry Residents' Lecture)
1999	Statistical Genetics
1999	Advanced Biostatistics Seminar
1999	Advanced Topics in Genetic Data Analysis
1999	Biostatistics Preceptorship (Wen Huang)
2001	Statistical Genetics I
2001	Advanced Topics in Genetic Data Analysis
2002	Statistical Genetics I: Dichotomous Traits
2002	Biostatistics Preceptorship (Deli Wang)
2002	Statistical Genetics Preceptorship (Jackie Bartlett)
2002	Statistical Genetics Preceptorship (LaVonne Mangin)
2003	Statistical Genetics I: Dichotomous Traits
2003	Advanced Topics in Genetic Data Analysis
2003	Biostatistics Preceptorship (Xinqun Yang)
2003	Statistical Genetics Preceptorship (Huaming Tan)
2004	Statistical Genetics Preceptorship (Min Shi)
2005	Statistical Genetics Preceptorship (Diana Istook)
2005	Clinical Genetics Practicum (Instructor of record for genetics clinic/journal club rotation)
2006	Theory of Statistical Genetics
2006	Clinical Genetics Practicum (Instructor of record for genetics clinic/journal club rotation)
2006	Independent Study in Statistical Genetics (Yungui Huang)

### Doctoral Thesis Committees

Thesis Committee Member for Daniel Nettleton

Department of Statistics & Actuarial Science, The University of Iowa, Ph.D. awarded, 1996.

Dissertation title: Order-restricted inference for interval mapping of quantitative trait loci

Thesis Co-director for Kai Wang

Department of Statistics & Actuarial Science, The University of Iowa, Ph.D. awarded, 1998.

Dissertation title: A Bayesian approach to replication of linkage studies

Oral Examination Committee for Maria Mendoza

Department of Biostatistics, University of Iowa, Ph.D. awarded, 1999

Thesis Co-Director for Susan Slager

Department of Biostatistics, The University of Iowa, Ph.D. awarded, 1999

Dissertation title: Linkage disequilibrium mapping of complex disorders: Investigating statistical power to detect linkage.

Thesis Co-Director for Elizabeth Ludington

Department of Biostatistics, The University of Iowa, Ph.D. awarded, 2000

Dissertation title: Sex-specific recombination in linkage analysis

Thesis Director for Mark Logue

Department of Statistics & Actuarial Science, The University of Iowa, Ph.D. awarded, 2001  
Dissertation title: Bayesian linkage detection under an unknown genetic model

Thesis Committee Member for Terry Braun

Interdisciplinary Genetics Ph.D. Program, The University of Iowa, Ph.D. awarded, 2001  
Dissertation title: A Software Tool Architecture to Assist Disease Gene Identification

Thesis Committee Member for Todd Scheetz

Interdisciplinary Genetics Ph.D. Program, The University of Iowa, Ph.D. awarded, 2001

Thesis Committee Member for Christopher Bartlett

Center for Molecular & Behavioral Neuroscience, Rutgers University, Newark NJ, Ph.D. awarded, 2003  
Dissertation title: Localization of genes negatively influencing language development in specific language impairment with applications to autism.

Thesis Co-Director for Xinqun Yang

Department of Biostatistics, Division of Statistical Genetics, The University of Iowa, Ph.D. awarded, 2005  
Dissertation title: A New Bayesian Approach to Disequilibrium Mapping

Thesis Co-Director for Manika Govil

Program in Public Health Genetics (Statistical Genetics), College of Public Health, The University of Iowa, Ph.D. awarded, 2005

Dissertation Title: Extensions of the Posterior Probability of Linkage: Distributed Computing, Incorporation of Genetic Map Information, an Application to Cleft Lip and/or Palate

Thesis Committee Member for Kwang-Youn Kim

Department of Biostatistics, Division of Statistical Genetics, College of Public Health, The University of Iowa, Ph.D. awarded, 2006

Thesis Director for Yungui Huang

Program in Public Health Genetics (Statistical Genetics), College of Public Health, The University of Iowa, Ph.D. awarded, 2000

Dissertation Title: Association Statistics Under the PPL Framework

### **Postdoctoral Fellows Supervised**

Co-Mentor for Linda Brzustowicz, M.D., Principal Investigator

NIMH Mentored Career Development Award

"Phenotype Definition in Familial Schizophrenia," 1997-2002

Department of Genetics, Rutgers University

Primary Mentor for Jian Huang, Ph.D., Principal Investigator

NIMH Mentored Research Scientist Development Award

"Statistical Models of Genetic Anticipation in Psychiatry," 1998-2003

Department of Statistics, The University of Iowa

Co-Mentor for Peggy C. Nopoulos, M.D., Principal Investigator

NIDR Mentored Patient Oriented Career Development Award

"Brain Structure/Function in Orofacial Clefting Disorders," 1999-2004

Department of Psychiatry, The University of Iowa

Co-Mentor for Thomas Wassink, M.D., Principal Investigator

NIMH Mentored Career Development Award

"A Multi-faceted Search for Autism Disease Genes," 2000-2005

Department of Psychiatry, The University of Iowa

Co-Mentor for Vicki L. Ellingrod, M.D., Principal Investigator  
 NIMH Mentored Scientist Development Award  
 "Genetics of Antipsychotic Metabolism," 2001-2006  
 Department of Psychiatry, The University of Iowa

Primary Mentor for Mark Logue, Ph.D., Postdoctoral Research Fellow  
 NIMH Psychiatric Genetics Training Program (R Crowe, PI)  
 Department of Psychiatry, The University of Iowa, 2002

Co-Mentor for Robert Philibert, M.D., Principal Investigator  
 NIMH Mentored Career Development Award  
 "A Thyroid Receptor Co-Activator Hypothesis for Psychosis," 2002-2006  
 Department of Psychiatry, The University of Iowa

Primary Mentor for Christopher Bartlett, Ph.D., Postdoctoral Research Fellow  
 Center for Statistical Genetics Research, University of Iowa, 2003- 2006

Primary Mentor for Hongling Wang, Ph.D., Postdoctoral Research Fellow  
 Center for Statistical Genetics Research, University of Iowa, 2005-2006; Center for Quantitative and Computational  
 Biology, Columbus Children's Research Institute, 2006-2007.

Primary Mentor for Sang-Cheol Seok, Ph.D., Postdoctoral Research Fellow  
 Battelle Center for Mathematical Medicine, The Research Institute at Nationwide Children's Hospital, 2007-2009.

Co-Mentor for Manika Govil, Ph.D., Principal Investigator  
 NIDCR Translation to Independence Award  
 "Statistical Genetic Analysis of Complex Craniofacial and Dental Genetic Disorders", 2008-2013  
 Center for Craniofacial and Dental Genetics, University of Pittsburgh

Primary Mentor for Kimberly Walters, Ph.D., Postdoctoral Research Fellow  
 Battelle Center for Mathematical Medicine, The Research Institute at Nationwide Children's Hospital, 2009 –2015

Member, Mentorship Committee for Jennifer Trittman, M.D., Assistant Professor of Pediatrics  
 Neonatal-Perinatal Medicine and the Center for Perinatal Research, The Research Institute at  
 Nationwide Children's Hospital 2012-2015

### **Administrative Committees**

<u>Year</u>	<u>Committee</u>
1995-96	Department of Preventive Medicine and Environmental Health, University of Iowa Resource and Space Committee
1996-97	Department of Preventive Medicine and Environmental Health, University of Iowa Computer Committee
1996-01	Department of Preventive Medicine and Environmental Health, University of Iowa NIMH Training Grant Steering Committee
1996-01	Department of Preventive Medicine and Environmental Health, University of Iowa Chair, NIMH Training Grant Pre-Doctoral Recruitment Committee
1997	Department of Preventive Medicine and Environmental Health, University of Iowa Environmental Health Science Research Center, Pilot Project Review Committee
1997-98	Department of Preventive Medicine and Environmental Health, University of Iowa

## Biostatistics Curriculum Review Committee

1997-98	Department of Preventive Medicine and Environmental Health, University of Iowa Student Evaluation Committee
Fall 1998	Department of Preventive Medicine and Environmental Health, University of Iowa Faculty Organizer, M.S. Specialty and Ph.D. Qualifying Exam in Biostatistics
1999	Ad Hoc Committee to Design a Biostatistics Track For the Undergraduate Mathematics Major, University of Iowa
1999-00	Department of Preventive Medicine and Environmental Health, University of Iowa Master's Examination Committee
1999-01	College of Public Health, Department of Biostatistics, University of Iowa Co-chair, Statistical Genetics Search Committee
2000-01	Offices of the Vice President for Research and Provost, University of Iowa Member, Informatics Study Committee
2000-01	College of Public Health & College of Medicine, University of Iowa Research Week Planning Committee
2000-02	Interdisciplinary Genetics Ph.D. Program, University of Iowa Planning Committee for new Bioinformatics and Computational Biology Track
2000-02	College of Medicine, Department of Psychiatry, University of Iowa Statistical Genetics/Psychiatry Search Committee
2000- 06	College of Public Health, University of Iowa CPH Research Advisory Council
2001-02	College of Public Health, Department of Biostatistics, University of Iowa Chair, Statistical Genetics Search Committee
2001-02	College of Public Health, Department of Biostatistics, University of Iowa Biostatistics Department Head Search Committee
2001-02	College of Public Health, University of Iowa Merck Fellowship Committee
2001-02	College of Public Health, University of Iowa New Investigator Research Award Review Committee
2001-02	Offices of the Vice President for Research and Dean of the Graduate College, University of Iowa Informatics Initiative Steering Committee
2002-05	College of Public Health, University of Iowa Chair, Computation and Informatics Committee
2002-03	College of Public Health, University of Iowa Chair, Admissions Committee, Department of Biostatistics
2002-05	Health Informatics Program Steering Committee
2003	College of Public Health, Department of Biostatistics, University of Iowa Chair, Statistical Genetics Subtrack Comprehensive Exam Committee

2003-04	College of Public Health, Program in Public Health Genetics, University of Iowa Chair, Strategic Planning Committee
2003-06	College of Public Health, University of Iowa Executive Committee
2003-05	College of Public Health, University of Iowa Alumni Relations Council
2003-05	Co-Chair, Offices of the Vice President for Research and Dean of the Graduate College, University of Iowa Informatics Steering Committee
2003-06	Interdisciplinary PhD Program in Genetics, University of Iowa Computational Genetics Subtrack Committee
2004	Graduate College, University of Iowa Collegiate Consulting Group
2010-2011	Member, Research Information Technology Advisory Council, The Research Institute at Nationwide Children's Hospital
2011-2014	Chair, Research Information Technology Advisory Council, The Research Institute at Nationwide Children's Hospital
2010-	Member, Research Conflict of Interest Committee, The Research Institute at Nationwide Children's Hospital
2011-12	Member, Research Strategic Planning Committee, The Ohio State University
2011-	Member, Enterprise Data Strategy Committee, Nationwide Children's Hospital
2012	Chair, The Chief Research Information Officer Search Committee, The Research Institute at Nationwide Children's Hospital
2013-2014	Member, The Chief Research Information Officer Search Committee, The Research Institute at Nationwide Children's Hospital
2013-2014	Chair, Research Computing Executive Committee, The Research Institute at Nationwide Children's Hospital
2014	Member, Director of Genomics Search Committee, Nationwide Children's Hospital
2014	Member and Affirmative Action Advocate, Center for Gene Therapy Faculty Member Search Committee, Nationwide Children's Hospital
2014-	Member, Internal Advisory Board for the Center for Genomic Medicine & Pharmacogenomics, The Ohio State University College of Medicine
2016	Member, Research Retreat Planning Committee, The Research Institute at Nationwide Children's Hospital
2016-2017	Member, Biostatistical Core Director Search Committee
2016-2017	Member, Biobehavioral Health Faculty Search Committee
2017	Member, Bremer Lecture Selection Committee



## Other Professional Activities

<u>Year</u>	<u>Activity</u>
1991	Invited Participant, Genetics Training Workshop, MacArthur Foundation Mental Health Research Network
1990 -	Participant in Genetic Analysis Workshops 7, 9, 10, 11, 12, 13, 15
1994-	Referee for <i>American Journal of Epidemiology</i> , <i>American Journal of Human Genetics</i> , <i>American Journal of Public Health</i> , <i>Annals of Human Genetics</i> , <i>Archives of General Psychiatry</i> , <i>European Journal of Human Genetics</i> , <i>Genomics</i> , <i>Neuropsychiatric Genetics</i> , <i>Nature Genetics</i> , <i>Thyroid et al.</i>
1995	NIMH Ad Hoc Genetics Review Committee
1996, 2000	Referee for Genetic Analysis Workshop 10 publication submissions
1996-2001	Consultant, NIH-NIDCD Grant R01 DC01654, Family Genetic Studies of Language Impairment. PI: P Tallal
1997	NIMH Genetics and Epidemiology Initial Review Group
1998	NIMH, Chair, Special Initial Review Group
1998, 2000	Co-chair, Psychiatric Genetics Chromosome 5 Workshops
1997-2005	Member of International Board of Scientific Advisors, Canadian Medical Research Grant GR-14501, The Genetics of Complex Disorders: An Integrated Approach To the Study of Bipolar Disorder, Schizophrenia, Alcoholism and Autism. PI's: M Maziade, R Palmour, MA Roy, P Szatmari
1998	Organizer and Chair, Iowa Workshop in Statistical Genetics in Public Health, June 15-17, 1998, The University of Iowa
2001	Associate Editor, Genetic Analysis Workshop (Genet Epidem)
2002	Session Co-Moderator, Haplotype blocks and linkage disequilibrium mapping. American Society of Human Genetics, Baltimore MD
2002	NIH Special Review Panel
2002	NCI Biostatistics Program, External Review Committee
2002-2005	Psychiatric Genetics editorial board
2002	American Society of Human Genetics, Abstract Reviewer for 2002 Annual Meeting
2003	NIH Mammalian Genetics Review Committee, Ad Hoc Member
2003	Judge, Poster Session, College of Medicine/College of Public Health Research Week
2004	Invited Participant and Presenter, NIH Forum on "Gene Discovery in Mental Disorders: How to Proceed?", Laguna Beach CA
2004	Judge, Poster Session, College of Medicine/College of Public Health Research Week
2004	Group Leader, Genetic Analysis Workshop 14, Noordwijkerhout, The Netherlands

2004-2006 Collaborator, Gerontological Nursing Interventions Research Center, UI College of Nursing

2005 Associate Editor, Genetic Analysis Workshop 14 (Biomed Central)

2006-2011 Scientific Consultant to Genome Canada's Autism Genome Project (Steve Scherer, PI)

2006 Participant, Committee on Institutional Cooperation (CIC) Professional Development Seminar for Department Heads and Chairs, Park Ridge, Illinois February 9-11

2006 Invited Participant, "A Critical Assessment of Autism Genetics" and Chair, Session 5 Statistical Genetics, Banbury Center, Cold Spring Harbor Laboratory NY, March 12-14

2006 Invited Workshop Participant, "Systems Genetics and Complex Phenotypes." National Institute of General Medical Sciences, Bethesda MD, September 7-9

2006 Group Leader, Genetic Analysis Workshop 15, St. Pete Beach, FL

2006-2011 Consultant, Molecular Genetic Study of Autism and Related Phenotypes In Extended Pedigrees, CIHR, Szatmari PI

2007-2008 Scientific Consultant to NIH 1R01DK-077510-01  
 'Genome-wide association of common alleles with long-term diabetic complications'  
 Period: 09/30/2006 08/31/2009  
 PI: AD Paterson.

2007 Associate Editor, Genetic Analysis Workshop 15, (Biomed Central)

2005-2007 Member, NIH Center for Inherited Disease Research Access Committee

2007 -2008 Chair, NIH Center for Inherited Disease Research Access Committee

2008 Chair, NIH Center for Inherited Disease Research Ad hoc Review

2008 Session Co-Moderator, Neuropsychiatric Disorders and Neurodevelopment. American Society of Human Genetics, Philadelphia, PA

2008-2013 Consultant, "Genome-Wide Association Study of Hypoplastic Left Heart and Related Defects" RO1 HL090506, McBride PI

2010-2012 Member, Steering Committee, NIMH Rutgers University Cell and DNA Repository U24 MH068457, Tischfield, PI

2010 Member, NIA Special Emphasis Panel (U01: Alzheimer's Disease Neuroimaging Initiative)

2010- Member, College of CSR Reviewers, National Institutes of Health Center for Scientific Review

2010-2016 Associate Editor, Human Heredity

2011-2016 Editorial Board, G3:Genes|Genomes|Genetics, International Conference on Mathematical and Computational Medicine

2012 Co-Organizer (with Gunter Wagner, Yale University), Workshop on Measure Theoretic Issues in Biology, Columbus, Ohio, June 10-12.

2013 Member, Advisory Panel, "Foundations of Quantification and Measurement in the Biological Science", Templeton Foundation, New York, NY, February.

- 2014 Ad Hoc Grant Reviewer, Natural Sciences and Engineering Research Council of Canada
- 2015 Organizer, American Association for the Advancement of Science Symposium “Extracting Evidence from Biological Data: Multiple Disciplines Get In on the Act,” San Jose, CA, February 14.
- 2016 Organizer, Society for Philosophy of Science in Practice Symposium, “Replication and Evidence: A Tenuous Relationship,” Glassboro, NJ, June 17-19.
- 2017 Invited Symposium participant, “Evidence: An Interdisciplinary Conversation about Knowing and Certainty,” Center for Science and Society and the Institute for Social and Economic Research and Policy, Columbia University, New York, NY, April 21-22. (See also Scientific Presentations and Invited Lectures, below.)
- 2017 Invited Symposium participant, “Unraveling Genetic Modifiers of Muscular Dystrophy” Eccles Institute of Human Genetics, University of Utah, Salt Lake City, UT, May 24. (See also Scientific Presentations and Invited Lectures, below.)
- 2017 Invited Workshop participant, “How do we decide what to measure?” Centre for Biodiversity Dynamics, Norwegian University of Science and Technology, Trondheim, Norway, June 6-10. (See also Scientific Presentations and Invited Lectures, below.)

### Research Grants

<u>Title &amp; Agency</u>	<u>Role</u>	<u>Dates</u>
Post-doctoral Fellowship in Psychiatric Genetics NIMH Training Grant MH14620 (Raymond Crowe, PI)	Faculty Member	1989-2002
Genetic Modeling of Child Psychopathology NIH Mentored Career Development Award K01 MH00884	PI	1990-1995
Psychiatric Genetics and Family Studies: Robust Methods NIH R01 MH48858 (Susan E. Hodge, PI)	Co-I	1992-1997
Sampling Models & Methods for Complex Genetic Diseases NIMH Shannon Award	PI	1994-1995
Family Study of Obsessive Compulsive Disorder NIH R01 MH44175 (Abby Fyer, PI)	Co-I	1994-1998
Sampling Models & Methods for Complex Genetic Diseases NIH R01 MH2841	PI	1995-2004
Pre- and Post-doctoral Fellowships in Psychiatric Epidemiology and Biometry NIMH Training Grant MH15168 (Robert Woolson, PI)	Faculty Member	1996-2001
Genetic Modeling of Psychopathy NIMH Career Development Award K02 MH01432	PI	1997-2002
Linkage Study of Panic Disorder NIMH R01 MH 34728 (Raymond Crowe, PI)	Co-I	1997-2000
Collaborative Linkage Study of Autism NIH R01 MH5528401 (Joseph Piven, PI)	Co-I	1999-2004
Molecular Genetics of Autism NIMH R01 NS43550 (Thomas Wassink, PI)	Co-I	2002-2006

Gene-Brain-Behavior Relationships in Autism NIMH STAART Center U54 MH066418 (Joseph Piven, PI)	Co-I	2002-2007
Infrastructure to Facilitate Discovery of Autism Genes NINDS R01 NS42165-01 (Joachim Hallmeyer, PI)	Co-PI	2002-2009
Autism Genome Project National Alliance for Autism Research (NAAR) PI for Data Coordination Site	Co-PI	2004-2006
Integrated Statistical and Computational Methods for Isolating Genes for Non-Syndromic Cleft Lip with or without Cleft Palate Roy J Carver Charitable Trust	PI	2005-2007
Identification and Functional Assessment of Autism Susceptibility Genes NIMH R01 MH76433 Linked to separate R01s to L. Bruzstowicz and J. Millonig	PI	2005-2011
Molecular Genetic Study of Autism and Related Phenotypes In Extended Pedigrees NIMH RO1 MH076028 (Joseph Piven, PI)	Co-I	2005-2010
Bayesian Reanalysis of a Multi-Site Gene-Mapping Study of Cleft Lip/Cleft Palate NIDCR R03 DE017167	PI	2006-2008
Autism Genome Project Autism Speaks PI for Data Coordinating Site	Co-PI	2007-2012
Autism Trio Collection Consortium Autism Speaks PI for Data Coordinating Site	Co-PI	2007-2009
Coalescent Modeling for Genetic Mapping in Population-Based Samples IPR and Population & Health TIE Seed Grant, The Ohio State University	Co-PI	2008-2009
The Psychiatric GWAS Consortium: Integrated and Coordinated GWAS Meta-Analyses NIH U01 MH085515 (Mark Daly, PI)	Co-I	2008-2009
Combining Epidemiologic Designs to Model Genetic Risks for Psychiatric Disorders NIMH RO1 MH086117	PI	2009-2012
Combining Epidemiologic Designs to Model Genetic Risks for Psychiatric Disorders (Supplement) NIMH RO1 MH086117 S1	PI	2010-2012
A Molecular Genetic Study of Autism and Related Phenotypes In Extended Pedigrees Canadian Institutes of Health Research (Peter Szatmari, PI)	Co-I	2011-2016
NIMH Center for Collaborative Genetic Studies (CCGS) Combined Analysis of Psychiatric Studies (CAPS) NIH U24MH068457 (Jay Tischfield, PI)	PI (CAPS)	2012-2018

Quantitative determination of Ecological Niches for Polymicrobial Colonization in OM NIH RO1 GM 103612 (Jayajit Das, PI)	Co-I	2013-2017
Genetic Modifiers of Duchenne Muscular Dystrophy NIH R01 NS 085238 (Kevin Flanigan, PI)	Co-I	2014-2018
A National Pediatric Learning Health System Patient-Centered Outcomes Research Institute (Chris Forrest, PI)	Site PI (NCH)	2014-2015
Uncovering Basic Signaling Mechanisms in NK Cells in Mice And Humans NIH R56 AI 108880 (Jayajit Das, PI)	Co-I	2014-2016
Measuring the Evidence in Evidence-Based Medical Research W. M. Keck Foundation	PI	2015-2019

## Bibliography

### Peer-reviewed Publications

1. Shaffer D, **Vieland V**, Garland A, Rojas M, Underwood M, and Busner C. Adolescent suicide attempters: Response to suicide-prevention programs. *JAMA* 264:3151-3155, 1990.
2. Shaffer D, Garland A, **Vieland VJ**, Underwood M, and Whittle B. The impact of curriculum-based suicide prevention programs for teenagers. *J Am Acad Child Adolesc Psychiatry* 30:588-596, 1991.
3. **Vieland VJ**, Whittle B, Garland A, Hicks R, and Shaffer D. The impact of curriculum-based suicide prevention programs for teenagers: And 18-month follow-up. *J Am Acad Child Adolesc Psychiatry* 30:811-815, 1991.
4. Shaffer D, **Vieland VJ**, Garland A, et al. Adolescents who attempt suicide – reply. *JAMA – Journal of the American Medical Association* 265(21):2805-2806, 1991.
5. **Vieland VJ**, Greenberg DA, Hodge SE, and Ott J. Linkage analysis of two-locus diseases under single-locus and two-locus analysis models. *Cytogen Cell Genet* 59:145-146, 1992.
6. **Vieland VJ**, Hodge SE, and Greenberg DA. The adequacy of single-locus approximations for linkage analysis of oligogenic traits. *Genet Epi* 9:45-59, 1992.
7. Knowles JA, **Vieland VJ**, and Gilliam TC. Perils of gene mapping with microsatellite markers. *Am J Hum Genet* 31:905-909, 1992.
8. Hodge SE, Durner M, **Vieland VJ**, and Greenberg DA. Better data analysis through data exploration. Letter, *Am J Hum Genet* 53:775-776, 1993.
9. **Vieland VJ**, Hodge SE, Lish J, Adams P, and Weissman MM. Segregation analysis of panic disorder. *Psychiat Genet* 3:63-71, 1993.
10. **Vieland VJ**, Greenberg DA, and Hodge SE. Adequacy of single-locus linkage analysis for oligogenic traits: Extension to multigenerational pedigree structures. *Hum Heredity* 43:329-336, 1993.
11. **Vieland VJ**. A cautionary note regarding the interpretation of heritabilities. *Psychol Med* 24:259-260, 1994.
12. **Vieland VJ**, Knowles J, Fyer A, Stefanovich M, Freimer NF, Lish J, Adams P, Woodley K, Rassnick H, Heiman G, White P, Das K, Klein J, Ott J, Weissman MM, and Gilliam TC. Linkage study of panic disorders: A preliminary report. In *Genetic Approaches to Mental Disorders*, Gershon ES, Cloninger CR eds. Washington, DC: Amer Psychiatric Press, 1994.

13. **Vieland VJ**, and Hodge SE. Inherent intractability of the problems of ascertainment for pedigree data: A general likelihood approach. *Am J Hum Genet*, 56:33-43, 1995.
14. **Vieland VJ**, Merette C, Goodman D, Rouillard E. Identification and mapping of Mendelian subtypes of disease. *Genet Epidem* 12:819-824, 1995.
15. Greenberg DA, Hodge SE, **Vieland VJ**, Spence MA. Affecteds-only linkage methods are not a panacea. Letter, *Am J Hum Genet* 58(4):892-895, 1996.
16. **Vieland VJ**, Goodman DW, Chapman T, Fyer AJ. A new segregation analysis of panic disorder. *Am J Med Genet (Neuropsychiat Genet)* 67(2):147-153, 1996.
17. **Vieland VJ**, Hodge SE. The problem of ascertainment for linkage analysis. *Am J Hum Genet* 58(5):1072-1084, 1996.
18. Hodge SE, **Vieland VJ**. The essence of single ascertainment. *Genetics* 144(3):1215-1223, 1996.
19. Huang J, **Vieland VJ**. A new statistical test for age-of-onset anticipation: Application to bipolar disorder. *Genet Epidem (Genetic Analysis Workshop 10)* 14(6):1091-1096, 1997.
20. Slager SL, **Vieland VJ**. Investigating the numerical effects of ascertainment bias in linkage analysis: Development of methods and preliminary results. *Genet Epidem (Genetic Analysis Workshop 10)* 14(6):1119-1124, 1997.
21. Greenberg DA, Hodge SE, **Vieland VJ**, Spence MA. Power, mode of inheritance, and type I error in lod scores and affecteds-only methods: Reply to Kruglyak. Letter, *Am J Hum Genet* 62(1):202-204, 1998.
22. Knowles JA, Fyer AJ, **Vieland VJ**, Weissman MM, Hodge SE, Heiman GA, Haghighi F, de Jesus GM, Rassnick H, Preud'homme-Rivelli X, Austin T, Cunjak J, Mick S, Fine LD, Woodley KA, Das K., Maier W, Adams PB, Freimer NB, Klein DF, and Gilliam TC. Results of a genome-wide genetic screen for panic disorder. *Am J Med Genet (Neuropsychiat Genet)* 81(2):139-147, 1998.
23. **Vieland VJ**, Huang J. Statistical evaluation of age-at-onset anticipation: A new test and evaluation of its behavior in realistic applications. *Am J Hum Genet* 62(5):1212-1227, 1998.
24. **Vieland VJ**. Bayesian linkage analysis, or: How I learned to stop worrying and love the posterior probability of linkage. *Am J Hum Genet* 63(4):947-954, 1998.
25. Durner M, **Vieland VJ**, Greenberg DA. Further evidence for increased power of lod scores compared with nonparametric methods. *Am J Hum Genet*, 64(1):281-289, 1999.
26. Wang K, **Vieland VJ**, Huang J. A Bayesian approach to replication of linkage findings. In Goldin L, Amos CI, Chase GA, Goldstein AM, Jarvik GP, Martinez MM, Suarez BK, Weeks DE, Wijsman EM, and MacCluer JW: Genetic Analysis Workshop 11: Analysis of genetic and environmental factors in common diseases. *Genet Epidem* 17 (Suppl 1):S749-S754, 1999.
27. Collaborative Linkage Study of Autism (CLSA). An autosomal genomic screen for autism. *Am J Med Genet (Neuropsychiat Genet)* 88:609-615, 1999.
28. Slager SL, Huang J, **Vieland VJ**. The effect of allelic heterogeneity on the power of the transmission disequilibrium test. *Genet Epidem (Suppl)* 18(2):143-156, 2000.
29. Goedken R, Ludington E, Crowe R, Fyer AJ, Hodge SE, Knowles JA, **Vieland VJ**, Weissman MM. Drawbacks of GENEHUNTER for larger pedigrees: Application to panic disorder. *Am J Med Genet (Neuropsychiat Genet)* 96(6):781-783, 2000.
30. Wang K, Huang J, **Vieland VJ**. The consistency of the posterior probability of linkage. *Annals Hum Genet* 64(Pt 6):533-553, 2000.

31. **Vieland VJ**, Wang K, Huang J. Power to detect linkage based on multiple sets of data in the presence of locus heterogeneity: Comparative evaluation of model-based linkage methods for affected sib pair data. *Hum Hered* 51(4):199-208, 2001.
32. Huang J, **Vieland VJ**. Comparison of 'model-free' and 'model-based' linkage statistics in the presence of locus heterogeneity: Single data set and multiple data set applications. *Hum Hered* 51(4):217-225, 2001.
33. Slager SL, Huang J, **Vieland VJ**. Power comparisons between the TDT and two likelihood-based methods for complex traits. *Genet Epidemiol* 20(2):192-209, 2001.
34. Wassink TH, Piven J, **Vieland VJ**, Huang J, Swiderski RE, Pietila J, Braun T, Beck G, Folstein SE, Haines JL, Sheffield VC. Evidence supporting WNT2 as an autism susceptibility gene. *Am J Med Genet (Neuropsychiat Genet)* 105(5):406-413, 2001.
35. Collaborative Linkage Study of Autism (CLSA). Incorporating language phenotypes strengthens evidence of linkage to autism. *Am J Med Genet (Neuropsychiat Genet)* 105(6):539-547, 2001.
36. Wang K, Huang J, Logue M, **Vieland VJ**. Combined multipoint analysis of multiple asthma data sets based on the posterior probability of linkage. In: Wijsman EM, Almasy L, Amos CI, Borecki I, Falk CT, King TM, Martinez MM, Meyers D, Neuman R, Olson JM, Rich S, Spence MA, Thomas DC, Vieland VJ, Witte JS, MacCluer JW. *Analysis of complex genetic traits: Applications to asthma and simulated data*. *Genet Epidemiol* 21 (Suppl 1):S1-S853, 2001.
37. **Vieland VJ**. The replication requirement. *Nature Genet* 29(3):244-245, 2001.
38. Huang J, Wang K, **Vieland VJ**. Nonparametric estimation of marginal distributions under bivariate truncation with application to testing for age-of-onset anticipation. *Statistica Sinica* 11(4):1047-1068, 2001.
39. Huang J, **Vieland VJ**. The null distribution of the heterogeneity lod score does depend on the assumed genetic model for the trait. *Hum Hered* 52(4):217-222, 2001.
40. **Vieland VJ**, Logue M. HLODs, trait models, and ascertainment: Implications of admixture for parameter estimation and linkage detection. *Hum Hered* 53:23-35, 2002.
41. Hodge SE, **Vieland VJ**, Greenberg DA. HLODs remain powerful tools for detection of linkage in the presence of genetic heterogeneity. *Am J Hum Genet* 70(2):556-559, 2002.
42. Bartlett CW, Flax JF, Logue MW, **Vieland VJ**, Bassett AS, Tallal P, Brzustowicz LM. A major susceptibility locus for specific language impairment is located on 13q21. *Am J Hum Genet* 71:45-55, 2002. (*Selected as a "Top Ten" Research Paper of the Year by the Canadian Centre of Excellence for Early Childhood Development.*)
43. Wassink TH, Piven J, **Vieland VJ**, Pietila J, Goedken RJ, Folstein SE, Sheffield VC. Evaluation of FOXP2 as an autism susceptibility gene. *Am J Med Genet (Neuropsychiat Genet)* 114:566-569, 2002.
44. Bassett AS, Chow EWC, **Vieland VJ**, Brzustowicz LM. Is schizophrenia linked to chromosome 1q? Letter, *Science* 298:2277a, 2002.
45. Spence MA, Greenberg DA, Hodge SE, **Vieland VJ**. The emperor's new methods. *Am J Hum Genet* 72:1084-1087, 2003.
46. Logue MW, Goedken RJ, **Vieland VJ**. A model-integrated multipoint Bayesian analysis of hypertension in the Framingham data finds little evidence of linkage. In Almasy L, Amos CI, Bailey-Wilson JE, Cantor RM, Jaquish CE, Martinez M, Neuman RJ, Olson JM, Palmer LJ, Rich SS, Spence MA, MacCluer JW (eds). *Genetic Analysis Workshop 13: Analysis of Longitudinal Family Data for Complex Diseases and Related Risk Factors*, *BMC Genet*, 4(Suppl 1):S75, 2003.
47. Yang X, Wang K, Huang J, **Vieland VJ**. Genome-wide linkage analysis of blood pressure under locus heterogeneity. *BMC Genet* 4(Suppl 1) S78, 2003.

48. Logue MW, **Vieland VJ**, Goedken RJ, Crowe RR. Bayesian analysis of a previously published genome screen for panic disorder reveals new and compelling evidence for linkage to chromosome 7. *Am J Med Gen, Neuropsych Genet* 121B:95-99, 2003.
49. **Vieland VJ**, Huang J. Two-locus heterogeneity cannot be distinguished from two-locus epistasis based on affected sib-pair data. *Am J Hum Genet* 73:223-232, 2003.
50. Bartlett CW, Flax JF, Logue MW, Smith BJ, **Vieland VJ**, Tallal P, Brzustowicz LM. Examination of potential overlap in autism and language loci on Chromosomes 2, 7, and 13 in two independent samples ascertained for specific language impairment. *Hum Hered* 57:10-20, 2004.
51. Logue MW, **Vieland VJ**. A new method for computing the multipoint posterior probability of linkage. *Hum Hered* 57:90-99, 2004.
52. Wassink TH, Piven J, **Vieland VJ**, Pietila J, Goedken RJ, Folstein SE, Sheffield VC. Examination of AVPR1a as an autism susceptibility gene. *Mol Psych* 9(10):968-972, 2004.
53. **Vieland VJ**, Hodge SE. Ascertainment bias in linkage analysis: Comments on Ginsburg et al. Letter, *Genet Epidem* 28:283-285, 2005.
54. Wassink TH, Piven J, **Vieland VJ**, Jenkins L, Frantz R, Bartlett CW, Goedken RJ, Childress D, Spence MA, Smith M, Sheffield VC. Evaluation of the chromosome 2q37.3 gene CENTG2 as an autism susceptibility gene. *Am J Med Genet (Neuropsychiat Genet)* 136:36-44, 2005.
55. Wassink TH, Losh M, Frantz RS, **Vieland VJ**, Goedken R, Piven J, Sheffield VC. A case of autism and uniparental disomy of chromosome 1. *Hum Genet*, 117:200-206, 2005.
56. Bartlett CW, Goedken RJ, **Vieland VJ**. Effects of updating evidence across subsets of data: Reanalysis of autism genetic resource exchange dataset. *Am J Hum Genet* 76:688-695, 2005.
57. George AW, Mangin LA, Bartlett CW, Logue MW, Segre AM, **Vieland VJ**. Calculation of multipoint likelihoods using flanking marker data: A simulation study. *BMC Genetics* 6 (Suppl 1): S44, 2005.
58. Logue MW, George AW, Spence MA, **Vieland VJ**. Performance comparison of 2-point linkage methods using microsatellite markers flanking known disease locations. *BMC Genetics* 6 (Suppl 1): S141, 2005.
59. Bartlett CW, **Vieland VJ**. Two novel quantitative trait linkage analysis statistics based on the posterior probability of linkage: Application to the COGA families. *BMC Genetics* 6 (Suppl 1): S121, 2005.
60. **Vieland VJ**. Heterogeneity: GAW Group 15. *Genet Epidem Supp* S110-S115, 2005.
61. Yang X, Huang J, Logue MW, **Vieland VJ**. The posterior probability of linkage allowing for linkage disequilibrium and a new estimate of disequilibrium between a trait and a marker. *Human Hered* 59:210-219, 2005.
62. Logue MW, **Vieland VJ**. The incorporation of prior genomic information does not necessarily improve the performance of Bayesian linkage methods: An example involving sex-specific recombination and the two-point PPL. *Human Hered*, 60:96-205, 2005.
63. Park JW, Logue M, Ni J, Cremer J, Segre A, **Vieland VJ**. Scientific Visualization of Multidimensional Data: Genetic Likelihood Visualization. In Current Trends in High Performance Computing and Its Applications: Proceedings of the International Conference on High Performance Computing and Applications, Zhang W, Chen, Z, Glowinski, R, Tong, W. (Eds.). Springer Verlag pages 157-162, 2005.
64. **Vieland VJ**. Thermometers: Something for statistical geneticists to think about. *Human Hered*, 61:144-156, 2006.
65. Logue MW, Brzustowicz LM, Bassett AS, Chow EWC, **Vieland VJ**. A posterior probability of linkage (PPL) based re-analysis of schizophrenia data yields evidence of linkage to chromosomes 1 and 17. *Hum Hered*, 62:47-54, 2006.



66. Park JW, Cremer JF, Segre AM, Logue MW, **Vieland VJ**. Visual Exploration of Genetic Likelihood Space. Proceedings of the ACM Symposium on Applied Computing 2006.
67. Segre AM, Wildenberg A, **VielandVJ**, Zhang Y. Privacy-preserving data set union. In Privacy in Statistical Databases, Domingo-Ferrer J, Franconi L (eds.). Springer-Verlag: Berlin, p. 266-276, 2006.
68. Wang H, Segre AM, Huang Y, O'Connell J, **Vieland VJ**. Fast computation of human genetic linkage. Proceedings of IEEE 7<sup>th</sup> Symposium on Bioinformatics and Bioengineering (BIBE 2007), pages 857-863, 2007. (*Honorary Mention for Best Paper Award.*)
69. Wang H, Segre AM, Huang Y, O'Connell J, **VielandVJ**. Rapid Computation of Large Numbers of LOD Scores in Linkage Analysis through Polynomial Expression of Genetic Likelihoods", Proceedings of IEEE Workshop on High-Throughput Data Analysis for Proteomics and Genomics (Silicon Valley), pages 197-204, 2007.
70. Bartlett CW, **Vieland VJ**. Accumulating quantitative trait linkage evidence across multiple datasets using the posterior probability of linkage. *Genet Epidem*, 31(2):91-102, 2007.
71. Autism Genome Project. Mapping autism risk loci using genetic linkage and chromosomal rearrangements. *Nature Genet*, 39(3):319-328, 2007.
72. Bartlett CW, **Vieland VJ**, on behalf of Group 7. Discussing gene-gene interaction: Warning - translating equations to English may result in jabberwocky. *Genet Epidem*, 31(Supplement 1):S61-S67, 2007.
73. Huang Y, Bartlett CW, Segre AM, O'Connell JR, Mangin L, **Vieland VJ**. Exploiting gene x gene interaction in linkage analysis. *BMC Proceedings* 1:S64, 2007.
74. Govil M, Segre AM, **Vieland VJ**. MLIP: A multiprocessor linkage analysis system. Second International Multisymposium on Computer and Computational Sciences (IMCCS), pages 17-24, 2007.
75. Wassink TH, **Vieland VJ**, Sheffield VC, Bartlett CW, Goedken R, Childress D, Piven J. Posterior probability of linkage analysis of autism dataset identifies linkage to chromosome 16. *Psychiatric Genet*, 18(2):85-91, 2008.
76. Govil M, Segre AM, **Vieland VJ**. MLIP: Using multiple processors to compute the posterior probability of linkage. *BMC Bioinformatics* 9(Suppl 6):S2, 2008.
77. **Vieland VJ**, Huang Y, Bartlett CW, Davies TF, Tomer Y. A multilocus model of the genetic architecture of Autoimmune Thyroid Disorder with clinical implications. *Am J Hum Genet*, 82:1349-1356, 2008. (Featured Article).
78. Govil M, **Vieland VJ**. Practical considerations for dividing data into subsets prior to PPL analysis. *Hum Hered*, 66:223-237, 2008.
79. Liu XQ, Paterson AD, Szatmari P, Autism Genome Project Consortium. Genome-wide linkage analyses of quantitative and categorical autism subphenotypes. *Biol Psychiatry*, 64(7):561-570, 2008.
80. Wratten NS, Memoli H, Huang Y, Dulencin AM, Matteson PG, Cornacchia MA, Azaro MA, Messenger J, Hayter JE, Bassett AS, Buyske S, Millonig JH, **Vieland VJ**, Brzustowicz LM. Identification of a schizophrenia associated functional non-coding variant in NOS1AP. *Amer J Psychiatry*, 166:434-441, Mar 2, 2009. (*Accompanied by special Editor's commentary highlighting the statistical methods, 166:392-394, 2009.*)
81. Nouanesengsy B, Seok S-C, Shen H-W, **Vieland VJ**. Using projection and 2D plots to visually explore multidimensional genetic likelihood spaces. In proceedings of IEEE Symposium on Visual Analytics Science and Technology (IEEE VAST 2009).
82. Weiss LA, Arking DE; Gene Discovery Project of Johns Hopkins & the Autism Consortium, Daly MJ, Chakravarti A. A genome-wide linkage and association scan reveals novel loci for autism. *Nature* Oct 8; 461(7265):802-808, 2009.

83. Seok S, Evans M, **Vieland VJ**. Fast and accurate calculation of a computationally intensive statistic for mapping disease genes. *J Comput Biol*, 16(5):659-676, 2009.
84. Psychiatric GWAS Consortium Coordinating Committee. Genomewide association studies: history, rationale, and prospects for psychiatric disorders. *Am J Psychiatry*, 166(5):540-556, 2009.
85. Hodge SE, **Vieland VJ**. Expected Monotonicity – A desirable property for evidence measures? *Hum Hered*, 70(3):151-166, 2010.
86. Pinto D, Pagnamenta AT, Klei L, et al for the Autism Genome Project. Functional impact of global rare copy number variation in autism spectrum disorders. *Nature*, 466(7304):368-372, 2010.
87. Anney R, Lambertus K, Pinto D, et al for the Autism Genome Project. A genomewide scan for common alleles affecting risk for autism. *Human Molecular Genetics*, 19(20):4072-4082, 2010.
88. Huang Y, **Vieland VJ**. Association statistics under the PPL framework. *Genet Epidemiol*, 34(8):835-845, 2010.
89. Flax JF, Hare A, Azaro MA, **Vieland VJ**, Brzustowicz LM. Combined linkage and linkage disequilibrium analysis of a motor speech phenotype within families ascertained for autism risk loci. *J Neurodevelopmental Disorders*, 2(4):210-223, 2010.
90. Pagnamenta AT, Khan H, et al for the Autism Genome Project. Rare familial 16q21 microdeletions under a linkage peak implicate cadherin 8 (CDH8) in susceptibility to autism and learning disability. *J of Medical Genetics*, 48(1):48-54, online citation 10.1136/jmg.2010.079426, 2010.
91. Noor A, Whibley A, Marshall, CR, et al for the Autism Genome Project. Disruption at the PTCHD1 Locus on Xp22.11 in Autism Spectrum Disorder and Intellectual Disability. *Sci Transl Med* 15 September 2010, 2:49ra68.
92. Anney R, Kenny EM, O'Dushlaine C, Yaspan BL, Parkhomenka E, The Autism Genome Project (AGP), Buxbaum JD, Sutcliffe J, Gill M and Gallagher L. Gene-ontology enrichment analysis in two independent family-based samples highlights biologically plausible processes for autism spectrum disorders. *European J of Hum Genetics* 19(10):1082-1089, Oct 2011.
93. **Vieland VJ**. Where's the evidence? *Hum Hered*, 71(1):59-66, 2011.
94. **Vieland VJ**, Hodge SE. Measurement of evidence and evidence of measurement. *Stat Applications in Genet & Molec Biol*, 10(1), Article 35, 2011.
95. **Vieland VJ**, Hallmayer J, Huang Y, Pagnamenta AT, Pinto D, Khan H, Monaco AP, Paterson AD, Scherer SW, Sutcliffe JS, Szatmari P; The Autism Genome Project (AGP). Novel method for combined linkage and genome-wide association analysis finds evidence of distinct genetic architecture for two subtypes of autism. *J Neurodev Disord* 3(2):113-123, 2011.
96. **Vieland VJ**, Huang Y, Seok S-C, Burian J, Catalyurek U, O'Connell J, Segre A, Valentine-Cooper W. Kelvin: A software package for rigorous measurement of statistical evidence in human genetics. *Hum Hered* 72(4):276-288, 2011.
97. Casey JP, Magalhaes T, Conroy JM, et al for the Autism Genome Project (AGP). A novel approach of homozygous haplotype sharing identifies candidate genes in autism spectrum disorder. *Hum Genet* (4):565-579, 2012.
98. Anney R, Klei L, Pinto D for the Autism Genome Project (AGP). Individual common variants exert weak effects on risk for autism spectrum disorders. *Hum Molec Genet* 21(21):4781-4792, 2012.
99. **Vieland VJ**, Das J, Hodge SE, Seok S-C. Measurement of statistical evidence on an absolute scale following thermodynamic principles. *Theory in Biosciences* 132(3):181-194, 2013.
100. He H, Bronisz A, Liyanarachchi S, Nagy R, Li W, Huang Y, Akagi K, Saji M, Kula D, Wojcicka A, Sebastian N, Wen B, Puch Z, Kalembe M, Stachlewska E, Czetwertynska M, Dlugosinska J, Dymecka K, Ploski R, Krawczyk M,

- Morrison PJ, Ringel MD, Kloos RT, Jazdzewski K, Symer DE, **Vieland VJ**, Ostrowski M, Jarzab B, de la Chapelle A. SRGAP1 is a candidate gene for papillary thyroid carcinoma susceptibility. *J Clinical Endocrinology & Metabolism* 98(5):E973-E980, March 28, 2013.
101. Huang Y, Thomas A, **Vieland VJ**. Employing MCMC under the PPL framework to analyze sequence data in large pedigrees. *Frontiers in Applied Genetic Epidemiology* 4:59, 2013.
102. Cross-Disorder Group of the Psychiatric Genomics Consortium. Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nature Genet* 45(9):984-994, Aug 2013.
103. Piven J, **Vieland VJ**, Parlier M, Thompson A, O'Conner I, Woodbury-Smith M, Huang Y, Walters KA, Ba F, Szatmari P. A molecular genetic study of autism and related phenotypes in extended pedigrees. *J Neurodev Disord* 5(1):30, 2013.
104. Mukherjee S, Seok S-C, **Vieland VJ**, Das J. Data-driven quantification of the robustness and sensitivity of cell signaling networks. *Phys Biol* 10(6):066002, 2013.
105. Mukherjee S, Seok S-C, **Vieland VJ**, Das J. Cell responses only partially shape cell-to-cell variations in protein abundances in *Escherichia coli* chemotaxis. *Proc Nat Acad Sci*, 110(46):18531-18536, (Nov) 2013.
106. Mukherjee S, Riquaud S, Seok S-C, Fu G, Prochenka A, Dworkin m, Gascoigne NR, **Vieland VJ**, Sauer K, Das J. *In silico* modeling of Itk activation kinetics in thymocytes suggests competing positive and negative IP<sub>4</sub> mediated feedbacks increase robustness. *PLoS One* Jan 6, 9(1), 2014.
107. Walters KA, Huang Y, Azaro M, Tobin K, Lehner T, Brzustowicz LM, **Vieland VJ**. Meta-analysis of repository data: Impact of data regularization on NIMH schizophrenia linkage results. *PLoS One*, Jan 14;9(1):e84696, 2014.
108. **Vieland VJ**, Walters KA, Lehner T, Azaro M, Tobin K, Huang Y, Brzustowicz LM. Revisiting schizophrenia linkage data in the NIMH repository: Reanalysis of regularized data across multiple studies. *Am J Psychiatry*, 171(3):350-359, 2014.
109. Pinto D, Delaby E, Merico D, et al (Autism Genome Project). Convergence of genes and cellular pathways dysregulated in autism spectrum disorders. *Am J Hum Genet* 94(5):677-694, 2014.
110. Oikkonen J, Huang Y, Onkamo P, Ukkola-Vuoti L, Raijas P, Karma K, **Vieland VJ**, Järvelä I. A genome-wide linkage and association study of musical aptitude identifies loci containing genes related to inner ear development and neurocognitive functions. *Mol Psychiatry*, March 11, 2014.
111. Forrest CB, Margolis PA, Bailey LC, Marsolo K, Del Beccaro MA, Finkelstein JA, Milov DE, **Vieland VJ**, Wolf BA, Yu FB, Kahn MG. PEDSnet: a national pediatric learning health system. *J Am Med Inform Assoc* 21(4):602-606, 2014.
112. **Vieland VJ**, Walters KA, Azaro M, Brzustowicz LM, Lehner T. The value of re-genotyping older linkage data sets with denser marker panels. *Hum Hered* 78(1):9-16, 2014.
113. Buxbaum JD, Bolshakova N, Brownfield JM, Anney R, Bender P, Bernier R, Cook EH, Coon H, Cuccaro M, Freitag CM, Hallmayer J, Geshwind D, Klauck SB, Lehner T, Burnberger JI, Oliveira G, Pinto D, Poustka F, Scherer S, Shih A, Sutcliffe JS, Szatmari P, Vicente AM, **Vieland VJ**, Gallagher L. The Autism Simplex Collection: An international, expertly phenotyped autism sample for genetic and phenotypic analyses. *Molec Autism* 5(34), 2014.
114. Stewart WCL, Huang Y, Greenberg DA, **Vieland VJ**. Next generation linkage and association methods applied to hypertension: A multifaceted approach to the analysis of sequence data. *BMC Proceedings* 8(Supp 1):S111, 2014.
115. Hadley D, Wu Z, Kao C, et al (Autism Genome Project). The impact of the metabotropic glutamate receptor and other gene family interaction networks on the autism spectrum disorders. *Nature communications* 5:4074, 2014.
116. **Vieland VJ**. Evidence, temperature and the laws of thermodynamics. *Hum Hered* 78(3):153-163, 2014.

117. Mukherjee S, Weimer KE, Seok S-C, Ray WC, Jayaprakash C, **Vieland VJ**, Swords WE, Das J. Host-to-host variation of ecological interactions in polymicrobial infections. *Phys Biol* 12(1), 2014. (*Selected for Physical Biology Highlights of 2015.*)
118. Trittman JK, Nelin LD, Zmuda EJ, Gastier-Foster JM, Chen B, Backes CH, Frick J, Vaynshtok P, **Vieland VJ**, Klebanoff MA. Arginase I gene single nucleotide polymorphism is associated with decreased risk of pulmonary hypertension in bronchopulmonary dysplasia. *Acta Paediatr* 103(10), 2014.
119. Maier R, Moser G, Chen G-B, Ripke S, Cross-Disorder Working Group of the Psychiatric Genomics Consortium, et al. Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder, and major depressive disorder. *Am J Hum Genet* 96:283-294, 2015.
120. Woodbury-Smith M, Paterson AD, Thiruvahindrapduram B, Lionel AC, Marshall CR, Merico D, Fernandez BA, Duku E, Sutcliffe JS, O'Conner I, Chrysler C, Thompson A, Kellam B, Tammimies K, Walker S, Yuen R, Uddin M, Howe JL, Parlier M, Whitten K, Szatmari P, **Vieland VJ**, Piven J, Scherer SW. Using extended pedigrees to identify novel autism spectrum disorder (ASD) candidate genes. *Hum Genet* 134(2):191-201, 2015.
121. **Vieland VJ**, Seok S-C. Statistical evidence measured on a properly calibrated scale across nested and non-nested hypothesis comparison. *Entropy* 17:5333-5352, 2015.
122. Network and Pathway Analysis Subgroup of Psychiatric Genomics Consortium. Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. *Nat Neurosci* 18(2):199-209, 2015.
123. Trittman JK, Gastier-Foster JM, Zmuda EJ, Frick J, Rogers LK, **Vieland VJ**, Chicoine LG, Nelin LD. A single nucleotide polymorphism in the dimethylarginine dimethylaminohydrolase gene is associated with lower risk of pulmonary hypertension in bronchopulmonary dysplasia. *Acta Paediatr* 105(4):e170-e175, 2016.
124. **Vieland VJ**, Seok SC. Statistical evidence measured on a properly calibrated scale for multinomial hypothesis comparisons. *Entropy* 18(4):114, 2016.
125. **Vieland VJ**. Measurement of Statistical Evidence: Picking up Where Hacking (et al.) Left Off. *Philosophy of Science*, *In press*.
126. Hodge SE, **Vieland VJ**. Information Loss in Binomial Data Due to Data Compression. *Entropy* 19(2):75, 2017.
127. The Autism Spectrum Disorders Working Group of The Psychiatric Genetics Consortium. Meta-analysis of GWAS of over 16,000 individuals with autism spectrum disorder highlights a novel locus at 10q24.32 and a significant overlap with schizophrenia. *Molecular Autism* 8:21, 2017.

#### Books, Chapters, Letters and Reviews

1. Shaffer D, Bacon K, Garland A, Fisher D, and **Vieland VJ**. Suicide Crisis Centers. In *Prevention of Mental Health Disturbance in Childhood*, FE Goldston, CM Heinicke, RS Pynoos and T Yager, Eds. APA Press, 1988.
2. Katz M, **Vieland VJ**. Get Smart! A Woman's Guide to Equality on Campus. The Feminist Press at City University of New York, 1988.
3. Katz M, **Vieland VJ**. Get Smart! Everything you should know but won't learn in class about sexual harassment and sex discrimination (2nd edition). The Feminist Press at the City University of New York, 1993.
4. Katz M, **Vieland VJ**. Uni Knigge fur Frauen (Walmot Moller-Falkenberg, Trans.). Campus Verlag, Frankfurt Germany, 1993.
5. **Vieland VJ**, Susser E, and Weissman MM. Genetic Epidemiology in Psychiatric Research. In Genetics of Mental Disorders, Part I: Theoretical Aspects, GN Papadimitriou, J Mendlewicz, Eds. Baillier's Clinical Psychiatry, International Practice and Research series, Baillier Tindal: London, 1995.
6. Greenberg DA, Hodge SE, **Vieland VJ**, Spence MA. Reply to Dr. Farrall. Letter, *Am J Hum Genet* 60:738, 1997.

7. **Vieland VJ**. Pedigrees, Sequential Sampling. In Encyclopedia of Biostatistics Vol. 4:3315-3316, Wiley: London, 1998.
8. **Vieland VJ**, Hodge SE. Review of Statistical Evidence: A Likelihood Paradigm, by R Royall. *Am J Hum Genet* 63:283-289, 1998.
9. **Vieland VJ**, Hodge SE. Reply to Karunaratne and Elston. Letter, *Am J Hum Genet* 62:739-740, 1998.
10. Crowe RR, **Vieland VJ**. Report of the chromosome 5 workshop of the fifth World Congress on Psychiatric Genetics. *Psychiat Genet*, 8(2):73-78, 1998.
11. Crowe RR, **Vieland VJ**. Report of the chromosome 5 workshop of the sixth World Congress on Psychiatric Genetics. *Am J Med Genet (Neuropsychiat Genet)* 88(3):229-232, 1999.
12. Wijnsman EM, Almasy L, Amos CI, Borecki I, Falk CT, King TM, Martinez MM, Meyers D, Neuman R, Olson JM, Rich S, Spence MA, Thomas DC, **Vieland VJ**, Witte JS, MacCluer JW. Analysis of complex genetic traits: Applications to asthma and simulated data. *Genet Epidemiol* 21 (Suppl 1):S1-S853, 2001.
13. Wassink TH, Sutcliffe JS, **Vieland VJ**, Piven J. The Molecular and Cellular Genetics of Autism. In Neuropsychopharmacology: The Fifth Generation of Progress. Lippincott, Williams & Wilkins: Baltimore, MD, Section 5:549-563, 2002.
14. **Vieland VJ**, Huang J. Reply to Cordell and Farrall. Letter, *Am J Human Genetics* 73:1471-1473, 2003.
15. **Vieland VJ**. Pedigrees, Sequential Sampling. In Encyclopedia of Human Genetics and Genetic Epidemiology, R Elston, J Olson, L Palmer, Eds. Wiley: London, DOI: 10.1002/0470011815.b2a05073, 2005.
16. **Vieland VJ**. Pedigrees, Sequential Sampling. In Encyclopedia of Biostatistics 2<sup>nd</sup> Edition, P. Armitage, T. Colton, Eds. Wiley: Chichester, 2005.
17. Bailey-Wilson JE, Almasy L, de Andrade M, Bailey J, Bickeböller H, Cordell HJ, Warwick Daw E, Goldin L, Goode EL, Gray-McGuire C, Hening W, Jarvik G, Maher BS, Mendell N, Paterson AD, Rice J, Satten G, Suarez B, **Vieland VJ**, Wilcox M, Zhang H, Ziegler A and MacCluer JW. Genetic Analysis Workshop 14: microsatellite and single-nucleotide polymorphism marker loci for genome-wide scans. *BMC Genetics* 6(Suppl 1):S1, 2005.
18. Cordell HJ, de Andrade M, Babron MC, Bartlett CW, BEyene J, Bickeböller H, Culverhouse R, Cupples LA, Daw EW, Dupuis J, Galk CT, Ghosh S, Goddard KA, Goode EL, Hauser ER, Martin LJ, Martinez M, North KE, Saccone NL, Schmidt S, Tapper W, Thomas D, Trichler D, **Vieland VJ**, Wijnsman EM, Wilcox MA, Witte JS, Yang Q, Ziegler A, Almasy L, MacCluer JW. Genetic Analysis Workshop 15: gene expression analysis and approaches to detecting multiple functional loci. *BMC Proceedings* 1:S1, 2007.
19. **Vieland VJ**, Devoto M, Eds. Human Heredity Special Issue: Next generation linkage analysis. *Hum Hered* 72(4):227, 2011.
20. Spence MA, **Vieland VJ**. Genetic epidemiology. *Wiley StatsRef-Statistics Reference Online* (stat05300.pub2), Feb., 2015.
21. Huang Y, Thomas A, **Vieland VJ**. Employing MCMC under the PPL framework to analyze sequence data in large pedigrees (Orig. *Frontiers in Applied Genetic Epidemiology* 4:59, 2013). In Novel Approaches to the Analysis of Family Data in Genetic Epidemiology (ebook), X. Sun, J. S. Barnhotz-Sloan, N Morris, R.C. Elston Eds. *Frontiers in Genetics* 2016.

#### Papers on arXiv

1. **Vieland VJ**. An evidential interpretation of the 1<sup>st</sup> and 2<sup>nd</sup> laws of thermodynamics. arXiv:1301.2150, 2013.

2. Mukherjee S, Weimer KE, Seok S-C, Ray WC, Jayaprakash C, **Vieland VJ**, Swords WE, Das J. Host-to-host variation of ecological interactions in polymicrobial infections. arXiv:1404.6668, 2013.
3. Mukherjee S, Rigaud S, Seok S-C, Fu G, Prochenka A, Dworkin M, Gascoigne NRJ, **Vieland VJ**, Sauer K, Das J. In silico modeling of itk activation kinetics in thymocytes suggests competing positive and negative IP4 mediated feedbacks increase robustness. arXiv:1307.7084, 2013.
4. Mukherjee S, Seok S-C, **Vieland VJ**, Das J. Cell responses only partially shape cell-to-cell variations in protein abundances in *Escherichia coli* chemotaxis. arXiv:1306.2605, 2013.
5. Mukherjee S, Seok S-C, **Vieland VJ**, Das J. Data-driven quantification of robustness and sensitivity of cell signaling networks. arXiv:1305.3902, 2013.
6. **Vieland VJ**, Das J, Hodge SE, Seok S-C. Measurement of statistical evidence on an absolute scale following thermodynamic principles. arXiv:1206.3543, 2013.
7. **Vieland VJ**, Seok S-C. Statistical evidence measured on a properly calibrated scale across nested and non-nested hypothesis comparisons. arXiv:1506.04989, 2015.

#### Selected Abstracts

1. Adams P, Lish J, Freimer NF, Brzustowicz L., and Vieland VJ. Pedigree and DNA marker management: Integrated data management system for molecular and family-genetic studies. Am J Hum Genet Supplement 47:674, 1990.
2. Freimer NF, Fyer A, Stefanovich M, Knowles J, Hodge S, Vieland V, Lish J, Adams P, Klein DF, Ott J, Weissman MM, Gilliam TC. Genetic linkage analysis of panic disorder. Psychiat Genet 2:59, 1991.
3. Knowles J, Fyer A, Stefanovich M, Freimer NF, Vieland VJ, Lish J, Adams P, Klein DF, Gilliam TC, Weissman MM, Ott J. Genetic linkage analysis of panic disorder. Am J Hum Genet Supplement 49:1944, 1991.
4. Adams PB, Vieland VJ, Straub RE, Lenher T, Knowles J. Data management of linkage data - allele typings to lod scores. Am J Hum Genet Supplement 51:1410, 1992.
5. Knowles JA, Vieland VJ, Fyer A, Stefanovich M, Freimer NF, Woodley K, White P, Heiman G, Rassnick H, Lish J, Adams P, Klein J, Ott J, Weissman MM, Gilliam TC. Genetic linkage analysis of panic disorder. Am J Hum Genet Supplement 51:1439, 1992.
6. Cantor RM, Hanna G, Spence MA, Vieland VJ. Familial aggregation of childhood/adolescent onset obsessive-compulsive disorders. Am J Hum Genet Supplement 51:1324, 1992.
7. Knowles JA, Vieland VJ, Fyer A, Heiman G, Rassnick H, Fine L, Austin TL, Adams P, Hodge SE, Klein DF, Ott J, Weissman MM, Gilliam TC. Genetic linkage analysis of panic disorder. Am J Hum Genet Supplement 53:1023, 1993.
8. Vieland VJ, Hodge SE, Lish JD, Adams P, Mannuzza S, Chapman TAF, Goodman D, Fyer A, Weissman MM. Segregation analysis of panic disorder. Psychiat Genet 3:155, 1993.
9. Vieland VJ. Hazards of conditioning on probands in extended pedigrees under multiple ascertainment. Am J Hum Genet Supplement 53:875, 1993.
10. Vieland VJ, Hodge SE. A problem with conditioning likelihoods on observed pedigree structure in segregation analysis. Am J Hum Genet Supplement 55:970, 1994.
11. Knowles JA, Vieland VJ, Fyer AJ, Heiman G, de Jesus G, Judenberg A, Cunjak J, Mick S, Adams P, Hodge SE, Klein DF, Weissman MM, Gilliam TC. Panic disorder is unlikely to be a homogeneous autosomal dominant disorder: results of a genome-wide genetic screen. Am J Hum Genet Supplement 57:1123, 1995.
12. Hodge SE, Vieland VJ. The essence of single ascertainment. Am J Hum Genet Supplement 57:937, 1995.

13. Vieland VJ, Huang J. Statistical evaluation of age-of-onset anticipation in human genetics may not be feasible. *Am J Hum Genet Supplement* 61:235, 1997.
14. Durner M, Vieland VJ, Greenberg DA. Increased power of lod scores of ASP methods. *Am J Hum Genet Supplement* 61:1594, 1997.
15. Weissman MM, Fyer AJ, Haghghi F, Hodge SE, Heiman GA, de Jesus G, Vieland VJ, Cunjak J, Mick S, Adams PB, Klein DR, Gilliam TC, Knowles JA. Progress in the second state of a genome search for genetic factors for panic disorder. *Am J Med Genet (Neuropsychiat Genet)* 74:4, 649, 1997.
16. Wang K, Huang J, Vieland VJ. Combining results in linkage studies: an empirical Bayes approach. *Am J Hum Genet Supplement* 61:1749, 1997.
17. Vieland VJ for the Collaborative Linkage Study of Autism. Results of a genomic screen for autism include strong evidence of linkage to chromosome 13. *Am J Hum Genet Supplement* 63:77, 1998.
18. Slager SL, Huang J, Vieland VJ. The effect of allelic heterogeneity on the power of transmission/disequilibrium tests and affected sib-pair linkage tests. *Genet Epidem* 15:41, 1998.
19. Slager SL, Huang J, Vieland VJ. Power comparisons between the TDT to two likelihood-based tests for complex traits. *Genet Epidem* 17:196, 1999.
20. Goedken R, Crowe R, Deng Z, Fyer AJ, Haghghi V, Heiman G, Hodge SE, Knowles JA, Vieland VJ, Wang K, Weissman MM. Drawbacks of Genehunter for large pedigrees: application to panic disorder. *Molecular Psych* 4 Supplement 1: S10, 1999.
21. Vieland VJ, Wang K, Huang J. A new linkage analysis method for complex disorders based on multiple sets of data. *Am J Hum Genet Supplement* 65:2554, 1999.
22. Folstein S, Santangelo S for Collaborative Linkage Study of Autism. Autism lod on chromosome 7 increased by subset analysis of language. *International Society of Psychiatric Genetics*, 2000.
23. Santangelo S for CLSA, Ashley-Koch A, Pericak-Vance M, Silverman J, Smith CJ, Buxbaum J. Combined analysis of data on chromosome 7q from three autism genome scans. *International Society of Psychiatric Genetics*, 2000.
24. Ludington EA, Vieland VJ, Huang J. Power to detect linkage using sex-averaged vs. sex-specific lod scores. *Genet Epidem* 19, 2000.
25. Santangelo S for CLSA, Ashley-Koch A, Pericak-Vance M, Buxbaum J for SARC. Confirmatory evidence of linkage to 7q for autism based on combined analysis of three independent data sets. *Genet Epidem* 19, 2000.
26. Huang J, Vieland VJ, Wang K. The null distribution of the heterogeneity lod score does depend on the assumed genetic model for the trait. *Genet Epidem* 19:253 2000.
27. Logue M, Vieland VJ. The heterogeneity lod cannot be used to estimate the population proportion of linked families. *Genet Epidem* 19:259, 2000.
28. Vieland VJ, Huang J, Wang K. Summed vs. averaged lod scores: Which represents the true evidence for linkage based on multiple independent data sets? *Genet Epidem* 19:275, 2000.
29. Folstein S, Santangelo S for the Collaborative Linkage Study of Autism. Autism lod on chromosome 7 increased by subset analysis of language. *Am J Hum Genet (Suppl 2)*67, 2000.
30. Santangelo S for CLSA, Ashley-Koch A, Pericak-Vance M, Silverman J, Smith CJ, Buxbaum J. Confirmatory evidence of linkage to chromosome 7q from three autism genome scans. *Am J Hum Genet (Suppl 2)*67, 2000.

31. Logue M, Vieland VJ. Accurate estimation of the recombination fraction for complex disorders using lod scores. *Am J Human Genet (Suppl 2)*67:226, 2000.
32. Huang J, Wang K, Vieland VJ. The use of summed maximum lods as a simple and approximate measure of evidence for linkage based on multiple independent data sets. *Am J Hum Genet (Suppl 2)*67:324, 2000.
33. Vieland VJ, Ludington EA, Wang K, Huang J. The posterior probability of linkage (PPL) incorporating prior genomic information is efficient for detection of linkage and estimation of male/female recombination rates for complex disorders. *Am J Hum Genet (Suppl 2)*67:328, 2000.
34. Ludington EA, Vieland VJ, Huang J. Using ordinary linkage analysis to detect imprinting in general pedigrees. *Am J Hum Genet (Suppl 2)*67:1766, 2000.
35. Wang D, Wassink TH, Huang J, Pietila J, Sheffield VC, Goedken RJ, Vieland VJ, Piven J. Further evaluation of an autism candidate gene on 7q31-33 via linkage disequilibrium. *Genet Epidem* 23, 2002.
36. Logue, MW, Vieland VJ, Goedken RJ, Chow EWC, Bassett AS, Brzustowicz LM. PPL based re-analysis of a genome screen for schizophrenia. *Genet Epidem* 23:293, 2002.
37. Vieland VJ, Sheffield VC, Wassink TH, Beck J, Goedken RJ, Childress D, Piven J. A new genome screen for autism based on the posterior probability of linkage (PPL) and incorporating language-based phenotypes finds evidence of linkage to several genomic locations, each supported by independent sources of information. *Am J Hum Genet* 73(5) Suppl:174, 2003.
38. Bartlett CW, Flax JF, Li W, Reaple-Bonilla T, Hayter J, Hirsch LS, Logue MW, Zimmerman R, Vieland VJ, Tallal P, Brzustowicz LM. A genome scan of specific language impairment loci in families from the United States. *Am J Hum Genet* 73(5) Suppl:1884, 2003.
39. Wassink TH, Piven J, Vieland VJ, Jenkins L, Goedken RJ, Spence MA, Smith M, Sheffield VC. Evidence supporting CENTG2 as an autism susceptibility gene. *Am J Hum Genet* 73(5) Suppl:2011, 2003.
40. Goedken RJ, Piven J, Sheffield VC, Wassink TH, Beck J, Vieland VJ. How multiple data sets are combined affects autism genome screen results: 'Pooled' compared to 'sequentially updated' linkage analyses. *Am J Hum Genet* 73(5) Suppl:2572, 2003.
41. Logue MW, Vieland VJ. A new method for computing a multipoint Bayesian posterior probability of linkage. *Am J Hum Genet* 73(5) Suppl:2618, 2003.
42. Govil M, Segre AM, Logue MW, Vieland VJ. MLIP: Parallel computation of LOD scores enabling full exploration of the trait-parameter space. *Am J Hum Genet* 73(5) Suppl:2621, 2003.
43. Bartlett CW, Logue MW, Vieland VJ. Accurate localization information from the two-point posterior probability of linkage. IGES 13<sup>th</sup> annual meeting proceedings, International Genetic Epidemiology Society, 13, 2004.
44. Vieland VJ, Yang X, Shi M, Bassett A, Brzustowicz LM. Measurement of linkage disequilibrium (LD) parameter D' for complex traits via the posterior probability of LD (PPL-LD) changes the LD picture within CAPON, a large candidate gene for schizophrenia. ASHG 54<sup>th</sup> annual meeting, American Society of Human Genetics, 232, 2004.
45. Yang X, Brzustowicz LM, Bassett AS, Vieland VJ. LD-PPL: The posterior probability of linkage (PPL) with linkage disequilibrium (LD). ASHG 54<sup>th</sup> annual meeting, American Society of Human Genetics, 1933, 2004.
46. Bartlett CW, Vieland VJ. A novel quantitative trait (QT) posterior probability of linkage (PPL) with specific adaptations for QT analysis of autism. ASHG 54<sup>th</sup> annual meeting, American Society of Human Genetics, 2898, 2004.
47. Logue MW, Park J, Ni J, Cremer J, Segre AM, Knosp B, Beck S, Vieland VJ. Interactive visualization tools for genetic data. ASHG 54<sup>th</sup> annual meeting, American Society of Human Genetics, 2957, 2004.



48. Govil M, Murray JC, Marazita ML, Lidral A, Field LL, Arcos-Burgos M, Moreno L, Valencia C, Risk J, Hecht JT, Doheny K, Pugh E, Boehm C, Vieland VJ. Bayesian genome scan for cleft lip with or without cleft palate (CL/P). ASHG 55<sup>th</sup> annual meeting, American Society of Human Genetics 1516, 2005.
49. Bartlett CW, Vieland VJ. Is localization for complex disease genes via linkage analysis really that bad? ASHG 55<sup>th</sup> annual meeting, American Society of Human Genetics 2361, 2005.
50. Logue MW, Vieland VJ. Incorporation of sex-specific recombination information fails to improve PPL performance. ASHG 55<sup>th</sup> annual meeting, American Society of Human Genetics 2407, 2005.
51. Bartlett CW, Vieland VJ. Defining the relationship between a categorical trait and a quantitative endophenotype at a linked locus. *Genet Epidem* 29:237 #12, 2005.
52. Govil M, Vieland VJ. Evaluation of alternative sequential updating procedures for computing the posterior probability of linkage (PPL) across clinically defined data subsets. *Genet Epidem* 29:252-253 #65, 2005.
53. Logue MW, Li Y, Vieland VJ. The importance of "uninformative" models in Bayesian linkage analysis. *Genet Epidem* 29:266 #108, 2005.
54. Govil M, Marazita ML, Murray JC, Field LL, Vieland VJ. Multipoint PPL analysis of cleft lip with/out cleft palate (CL/P) provides compelling evidence in favor of linkage. ASHG 56<sup>th</sup> annual meeting, American Society of Human Genetics 1491/B, 2006.
55. Logue MW, Park JW, Cremer JF, Segre A, Vieland VJ. Exploiting genetic model information to identify homogenous pedigrees. ASHG 56<sup>th</sup> annual meeting, American Society of Human Genetics 1496/A, 2006.
56. Huang Y, Segre A, O'Connell J, Wang H, Vieland VJ. KELVIN: a 2<sup>nd</sup> generation distributed multiprocessor linkage and linkage disequilibrium analysis program. ASHG 56<sup>th</sup> annual meeting, American Society of Human Genetics 1556/A, 2006.
57. Wang H, Segre A, Huang Y, O'Connell J, Vieland VJ. Fast computation of large numbers of LOD scores for genetic linkage analysis via a novel "polynomial" implementation. ASHG 56<sup>th</sup> annual meeting, American Society of Human Genetics 2308/C, 2006.
58. Bartlett CW, Vieland VJ. Why does increasing sample size often dim rather than illuminate: A question of locus heterogeneity. ASHG 56<sup>th</sup> annual meeting, American Society of Human Genetics 118, 2006.
59. Goedken R. on behalf of the AGC. Autism genetics cooperative: preliminary results of a combined linkage genome scan. ASHG 56<sup>th</sup> annual meeting, American Society of Human Genetics 1490/A, 2006.
60. Mostowska A, Vieira AR, Govil M, Lidral AC, Vieland VJ, Mansilla MA, Marazita ML, Murray JC. Association of chromosomal region 6q14-6q16.3 with non-syndromic cleft lip and palate. 29<sup>th</sup> annual meeting, The Society of Craniofacial Genetics, October 9, 2006.
61. Govil M, Logue MW, Vieland VJ. Map-misspecification and an unknown genetic model in multipoint linkage analysis: An evaluation of the sex-specific multipoint PPL, HMOD and MMLS. 15<sup>th</sup> annual meeting, The International Genetic Epidemiology Society, abstract #83, November 16-17, 2006.
62. Mostowska A, McHenry TH, Cooper ME, Govil M, FitzPatrick DR, Vieland VJ, Marazita ML, Murray JC. Evidence for BACH2 in chromosomal region 6q14-6q16.3 with non-syndromic cleft lip and palate. ASHG 57<sup>th</sup> annual meeting, American Society of Human Genetics 1148, 2007.
63. Govil M, Daack-Hirsch S, Lidral AC, Vieland VJ, Murray JC, Marazita ML. Non-syndromic cleft lip with or without cleft palate (CL/P): multipoint posterior probability of linkage (PPL) analysis sequentially updated over phenotypic subgroups reveals a Philippines-specific linkage to a region on chromosome 6q. ASHG 57<sup>th</sup> annual meeting, American Society of Human Genetics 1163, 2007.

64. Benayed R, Choi J, Matteson PG, Gharani N, Kamdar S, Vieland VJ, Brzustowicz L, Millonig JH. Autism associated alleles affect the regulation of the homeobox gene, ENGRAILED. 7<sup>th</sup> Annual International Meeting for Autism Research (IMFAR), 2008.
65. Huang Y, Segre A, O'Connell J, Valentine-Cooper W, Seok SC, Vieland VJ. Kelvin: A 2<sup>nd</sup> generation software package for computation of the PPL framework, ASHG 58<sup>th</sup> annual meeting, American Society of Human Genetics, poster #2336/w, 2008.
66. Stein O for the Autism Genome Project. Data coordinating infrastructure for the Autism Genome Project. ASHG 58<sup>th</sup> annual meeting, American Society of Human Genetics, 900/t, 2008.
67. Seok SC, Huang Y, Evans M, Vieland VJ. Using adaptive numerical integration for multidimensional genetic problems. ASHG 58<sup>th</sup> annual meeting, American Society of Human Genetics, poster #2346/w, 2008.
68. Nouanesengsy B, Seok SC, Vieland VJ. Visualization of multidimensional genetic likelihoods. ASHG 58<sup>th</sup> annual meeting, American Society of Human Genetics, poster #2345/w, 2008.
69. Chen F, Gharani N, Dong C, Wang Y, Gordon D, Huang Y, Millonig JH, Vieland VJ, Wang H, Tischfield J, Matise T, Yu L, Huang W, Brzustowicz L. A posterior probability of linkage and association study of 111 autism candidate genes. ASHG 58<sup>th</sup> annual meeting, American Society of Human Genetics, poster #1709/w, 2008.
70. Bartlett CW, Garavito P, Gharani N, Azaro MA, Flax JF, Stein O, Goedken R, Di-Cicco Bloom E, Millonig JH, Vieland VJ, Brzustowicz LM. Phenotypically homogeneous autism families yields evidence for epistasis between engrailed 2 and loci on 13q13 and 13q14. ASHG 58<sup>th</sup> annual meeting, American Society of Human Genetics, poster #1640/t, 2008.
71. Garavito P, Gharani N, Azaro MA, Bartlett CW, Stein O, Goedken R, Millonig J, Di-Cicco Bloom E, Vieland VJ, Brzustowicz LM. Fine mapping an autism susceptibility locus on chromosome 1q23-24. ASHG 58<sup>th</sup> annual meeting, American Society of Human Genetics, poster #1673/t, 2008.
72. Saviouk V, Huang Y, Azaro MA, Bassett AS, Vieland VJ, Brzustowicz LM. Posterior probability of linkage genome scan in NIMH Chinese schizophrenia sample. ASHG 58<sup>th</sup> annual meeting, American Society of Human Genetics, poster #1746/w, 2008.
73. Brzustowicz LM, Huang Y, Saviouk V, Bassett AS, Vieland VJ. Strong evidence of epistatic interactions involving NOS1AP in schizophrenia. ASHG 58<sup>th</sup> annual meeting, platform presentation, American Society of Human Genetics, #18, 2008.
74. Sutcliffe JS for the Autism Genome Project. The autism genome project: Dissecting the genetic and genomic etiology of autism. ASHG 58<sup>th</sup> annual meeting, platform presentation, American Society of Human Genetics, #220, 2008.
75. Vieland VJ, Autism Genetics Cooperative and Autism Genome Project. New linkage analysis by the Autism Genome Project (AGP) reveals strong evidence of linkage to multiple loci as well as gene-gene interactions. ASHG 58<sup>th</sup> annual meeting, platform presentation, American Society of Human Genetics, #224, 2008.
76. Nouanesengsy, B.; Sang-Cheol Seok; Han-Wei Shen; Vieland, V.J.; , "Using projection and 2D plots to visually reveal genetic mechanisms of complex human disorders," *Visual Analytics Science and Technology*, 2009. VAST 2009. *IEEE Symposium on* , vol., no., pp.171-178, 12-13 Oct. 2009
77. Buxbaum J for the Autism Genome Project. A two-stage genomewide scan for common alleles affecting risk for autism. ASHG 60<sup>th</sup> annual meeting, platform presentation, American Society of Human Genetics, #295, 2010.
78. Pinto D for the Autism Genome Project. Functional impact of global rare copy number variation in autism spectrum disorders. ASHG 60<sup>th</sup> annual meeting, platform presentation, American Society of Human Genetics, #310, 2010.

79. Hare A, Azaro M, Vieland VJ, Flax J, Brzustowicz LM. Using ingenuity pathway analysis to study gene relationships under linkage peaks of interest in autism spectrum disorders. ASHG 60<sup>th</sup> annual meeting, American Society of Human Genetics, #2535/w, 2010.
80. Brzustowicz LM, Huang Y, Seok SC, Hayter JE, Messenger JS, Zimmerman RA, Bassett AS, Vieland VJ. Strong evidence that multiple genes involved in glutamate neurotransmission interact to modulate risk of schizophrenia. ASHG 60<sup>th</sup> annual meeting, American Society of Human Genetics, #2565/w, 2010.
81. Vieland VJ for the Autism Genome Project. Novel statistical methods for combining genome-wide linkage and association analyses provide evidence of different genetic architecture for autism in the presence or absence of intellectual disability. ASHG 60<sup>th</sup> annual meeting, American Society of Human Genetics, #2870/t, 2010.
82. Seok SC, Huang Y, Vieland VJ. Extension of the PPL framework to allow Lander-Green based computation. ASHG 60<sup>th</sup> annual meeting, American Society of Human Genetics, #2979/f, 2010.
83. Walters KA, Vieland VJ. Handling hierarchical phenotypes in the PPL framework. ASHG 60<sup>th</sup> annual meeting, American Society of Human Genetics, #2984/f, 2010.
84. Huang Y, Seok SC, Valentine-Cooper W, Burian J, Mangin L, Nouanesensy B, Modi A, Vieland VJ. KELVIN 2.1: A tool for modeling genetic architecture for complex disorders. ASHG 60<sup>th</sup> annual meeting, American Society of Human Genetics, #3013/f, 2010.
85. Nouanesensy B, Seok SC, Vieland VJ. Visualizing multidimensional support intervals for genetic models. ASHG 60<sup>th</sup> annual meeting, American Society of Human Genetics, #3023/f, 2010.
86. Valentine-Cooper W, Huang Y, Seok S, Veronica VJ. Poster: High-Performance Computing for Mapping Disease-Related Genes. Computational Advances in Bio and Medical Sciences (ICCABS), 2011, *IEEE 1st International Conference on* , vol., no., pp.263, 3-5 Feb. 2011
87. Huang Y, Tomer Y, Vieland VJ. Modeling HLA epistatic interactions using a unified GWAS and linkage analytical method maps new putative genes for Type 1 Diabetes. ASHG 61<sup>st</sup> annual meeting, American Society of Human Genetics, Poster 694W, 2011.
88. Seok SC, Nouanesensy B, Vieland VJ. KELVIZ: A Graphing and Annotating Tool for Statistical Evidence in Human Genetics. ASHG 61<sup>st</sup> annual meeting, American Society of Human Genetics, Poster 674W, 2011.
89. Walters KA, Tobin K, Azaro M, Lehner T, Brzustowicz LM, Vieland VJ. Review and re-analysis of all schizophrenia multiplex families in the NIMH repository substantially alters overall linkage findings. ASHG 61<sup>st</sup> annual meeting, American Society of Human Genetics, Poster 646T, 2011.
90. Vieland VJ, Walters KA, Tobin K, Azaro M, Lehner T, Brzustowicz LM. Combined linkage and genome-wide association analysis of multiple schizophrenia (SZ) and bipolar data (BP) sets from public repositories reveals striking new evidence of distinct and overlapping genes. ASHG 61<sup>st</sup> annual meeting, American Society of Human Genetics, Poster 551F, 2011.
91. Govil M, Mukhopadhyay N, Huang Y, Valentine-Cooper W, Field LL, Lidral A, Murray J, Marazita ML, Vieland VJ. CL/P: Utilizing Advanced Analytic Approaches to Identify Etiologic Genes. AADR Annual Meeting, March 2012.
92. Thompson A, Szatmari P, Vieland VJ, Piven J, Fernandez BA, Walters K, Parlier MC, O'Conner I, Whitten K. Sex differences in extended pedigrees with ASD. International Society for Autism Research (INSAR), Toronto, Canada, May 17, 2012.
93. Oikkonen J, Huang Y, Ukkola-Vuoti L, Raijas P, Vieland VJ, Onkamo P, Järvelä I. Biological pathways of musical aptitude. Poster HGM2013-ICG-1338; HGM/ICG Conference (HGM2013/21<sup>st</sup> International Congress of Genetics), Singapore, April 13-18, 2013.

94. White P, Vieland VJ, Greenberg DA, Hodge SE. Combine and conquer: An integrated software suite for finding causal relationships between sequence variants and clinical phenotypes. Nationwide Children's Hospital and The Ohio State University Genetics Collaboration Symposium, Columbus, OH, May 20, 2014.
95. Trittman JK, Gastier-Foster JM, Vieland VJ, Klebanoff MA, Chicoine LG, Nelin LD. Bronchopulmonary dysplasia-associated pulmonary hypertension and mutations in the *DDAH1* gene. The American Physiological Society, Experimental Biology Conference, 2015.
96. Seok SC, Vieland VJ. A Quest for a Calibrated Statistical Evidence Measure: Multinomial Hypotheses. The Third International Mathematical and Computational Conference, Columbus, OH, May 15-18, 2016.

### Media Attention for Work on Statistical Evidence

"Medicine needs a sensible way to measure weight of the evidence" Tom Siegfried, Science News Prime, December 19, 2011

"Making Data Work: Researchers pursue analogy between statistical evidence and thermodynamics" Tom Siegfried, Science News, September 8, 2012

"An overdependence on p-values". Proceedings of the National Academy Sciences podcast interview, November 13, 2014

"Top 10 scientific mysteries for the 21st century," includes measurement of evidence as mystery #7 with link to Vieland et al. paper. Science News, February 1, 2015.

### Scientific Presentations and Invited Lectures

1. Statistical Inference in the Absence of Sampling. Invited presentation, Bernice Ryerson-MacEvoy Child Psychiatry Research Colloquium, New York State Psychiatric Institute, January 1989.
2. Adequacy of single-locus linkage models for analysis of multilocus traits. Columbia University Seminar in Genetic Epidemiology, February 1992.
3. Data management in molecular genetic studies – from pedigrees to lod scores. American Psychopathological Association, 1992.
4. Genetic linkage analysis of panic disorder. American Psychopathological Association, 1992.
5. Segregation analysis of panic disorder. International Genetic Epidemiology Society, 1992.
6. Evidence for a major gene for obsessive-compulsive disorder. Behavioral Genetic Association, 1992.
7. Why haven't we found any genes for psychiatric disorders? Child Psychiatry Grand Rounds, St. Lukes-Roosevelt Hospital, New York, September 1993.
8. A robust approach to ascertainment correction. Columbia University seminar in genetic epidemiology, December 1993.
9. How many models should we use in linkage analysis of genetically complex disorders? Invited presentation, National Institutes of Health, Molecular Epidemiology and Disease Indicators Branch, February 1994.
10. Ascertainment bias: An intractable problem for segregation analysis. Invited presentation, National Institutes of Mental Health Mentored Awardees Conference, June 1994.
11. Simple linkage analysis of complex traits. Invited presentation, Division of Genetics Seminar, Department of Pediatrics, University of Pennsylvania, November 1994.

12. A likelihood solution to a classical problem in human genetics: ascertainment corrections for sequentially and nonsequentially sampled pedigrees. Invited presentation, Department of Preventive Medicine Seminar, University of Iowa, November 1994.
13. A likelihood solution to a classical problem in human genetics: Ascertainment corrections for sequentially and nonsequentially sampled pedigrees. Invited presentation, Department of Biostatistics Seminar, Columbia University, April 1994.
14. Did you know that maximizing the lod score yields asymptotically biased estimates of the recombination fraction? Invited presentation, Workshop on Statistical Methods in Genetic Mapping, Tarrytown, NY, November 1995.
15. Statistical Genetics and Genetic Epidemiology, Epidemiology Student Meeting, The University of Iowa, November 1995.
16. Families: A problem for genetic linkage studies. Division of Biostatistics Seminar, The University of Iowa, April 1996.
17. A new statistical test of age-of-onset anticipation: With application in bipolar disorder. Invited presentation, Genetic Analysis Workshop 10, 1996.
18. Model fitting in human genetics: How hard can it be. Invited presentation, Statistical Society of Canada Annual Meeting, Fredericton, Canada, June 1997.
19. Design for a genetic linkage study of pulmonary fibrosis. Pulmonary Research Conference, The University of Iowa, June 1997.
20. A new test for age-of-onset anticipation in human genetics. The University of Iowa, 1997.
21. Statistical evaluation of age-of-onset anticipation in human genetics may not be feasible. Platform presentation, American Society of Human Genetics, October 1997.
22. A new statistical test for genetic anticipation. Invited presentation, Department of Biostatistics Seminar, Johns Hopkins School of Public Health, Baltimore MD, October 1997.
23. How hard can it be to find a difference between two means? Division of Biostatistics Seminar, The University of Iowa, November 1997.
24. Results of a genomic screen for autism include strong evidence of linkage to chromosome 13. Vieland VJ, for the Collaborative Linkage Study of Autism (CLSA). Platform presentation, American Society of Human Genetics, October 1998.
25. A Bayesian approach to replication of linkage studies. Genetic Analysis Workshop 11, Arachon, France, 1998.
26. The effect of allelic heterogeneity on the power of transmission-disequilibrium tests and affected sib-pair linkage tests. International Genetic Epidemiology Society, Arachon, France, 1998.
27. A novel Bayesian approach to linkage analysis based on multiple sets of data. Invited presentation, University Seminar in Genetic Epidemiology, Columbia University, November 1998.
28. A novel approach to genetic linkage analysis based on multiple sets of data. Invited presentation, Department of Genetics Seminar, Rutgers University, September 1999.
29. Statistical genetics: is it part of bioinformatics? University of Iowa and Iowa State Joint Workshop on Bioinformatics, The University of Iowa, Iowa City IA, 2000.
30. Combined multipoint analysis of multiple asthma data sets based on the posterior probability of linkage. Genetic Analysis Workshop, San Antonio TX, 2000.

31. Measuring the strength of statistical evidence for or against linkage based on multiple sets of data. Invited presentation, Callaway Gardens Conference on Autism Research GA, March 2001.
32. HLODs, trait models, and ascertainment. Invited presentation, Columbia University, New York NY, March 2001.
33. How many ASPs does it take to tell the heterogeneity from epistasis? Invited presentation, Columbia University, NY, October 2002.
34. Quantitative methods for mapping human disease-genes: Ongoing work in the UI Center for Statistical Genetics Research. Applied Mathematical and Computational Sciences Seminar, The University of Iowa, November 2002.
35. How many ASPs does it take to tell heterogeneity from epistasis? Invited presentation, Mayo Clinic, Rochester MN, December 2002.
36. Center for Statistical Genetics Research (CSGR). Invited presentation, International Autism Conference, Zurich, Switzerland, May 2003.
37. Mapping Genes for Autism: Ongoing Work at the University of Iowa. Dept. of Psychiatry Research Seminar, University of Iowa, 2003.
38. A new genome screen for autism based on the posterior probability of linkage (PPL). Platform Presentation, American Society of Human Genetics, Los Angeles CA, November 2003.
39. Measurement of linkage disequilibrium (LD) parameter  $D'$  for complex traits via the posterior probability of LD (PPL-LD) changes the LD picture with CAPON, a large candidate gene for schizophrenia. Platform Presentation, American Society of Human Genetics, Toronto, Ontario, Canada, October 2004.
40. Current challenges in autism genetics research: A statistical geneticist's perspective. Invited presentation, Columbus Children's Hospital, Columbus OH, August 2005.
41. Statistical paradigms, genetic complexity, and computation: A statistical pragmatist's approach to gene mapping for complex disorders. Invited presentation, Dept. of Epidemiology & Biostatistics, Case Western Reserve University, Cleveland OH, September 2005.
42. Statistical paradigms and statistical genetics. Seminar presentation, Program in Public Health Genetics, Univ. of Iowa, Iowa City IA, September 2005.
43. Statistical paradigms and the search for autism genes. Invited presentation, Dept. of Epidemiology, Biostatistics, & Occupational Health, McGill University, Montreal CA, November 2005.
44. The incredible shrinking LOD: How increasing the sample size can actually obscure true linkage peaks, and what we can do about this. Invited presentation, Banbury Center meeting, "A critical assessment of autism genetics." Cold Spring Harbor Laboratory, Cold Spring Harbor NY, March 2006.
45. Measurement of statistical evidence in genetic research. Invited presentation, Columbus Children's Research Institute Annual Research Retreat, Granville OH, April 2006.
46. Genetics of autism: Common pitfalls in interpretation. Invited Educational Symposium, International Meeting for Autism Research, Montreal CA, June 2006.
47. Understanding genetic studies of autism: Common pitfalls in interpretation. Invited presentation, Educational Session, International Meeting for Autism Research (IMFAR). Montreal, CA, May 31 – June 3, 2006.
48. Measuring statistical evidence in the age of a million SNPs. Second Annual Canadian Genetic Epidemiology & Statistical Genetics Meeting, Toronto CA, April 2007.

49. More is known than is: How what we know (about gene mapping for complex diseases) can hurt us. Invited presentation, Department of Genetics, Rutgers, The State University of New Jersey, Piscataway, New Jersey, September 2007.
50. PPLD: extension of the PPL framework to detect trait-marker LD and estimate  $D'$  in general pedigree structures. Platform Presentation (VJV presenter), American Society of Human Genetics, San Diego, CA, October 2007.
51. And now for something completely different: How philosophy of measurement can help us find genes for autism. Invited presentation, Cincinnati Children's Hospital, Cincinnati, Ohio, May 2008.
52. New linkage analysis by the Autism Genome Project (AGP) reveals strong evidence of linkage to multiple loci as well as gene-gene interactions. Platform Presentation, American Society of Human Genetics, Philadelphia, PA, October 2008.
53. What does it mean to measure statistical evidence? Invited presentation, Columbia University, New York, New York, February 2009.
54. Disease mapping via the coalescent. Hoffman L (presenting author), Kubatko L, Vieland VJ, Huang Y. Joint Statistical Meeting, Washington DC, August 2009.
55. Copy number variation discovery in autism spectrum disorder. Pagnamenta AT (presenting author), Pinto D, Khan H, Vieland VJ, Le Couteur A, Scherer SW, Monaco AP, for the Autism Genome Project (AGP). Platform Presentation, American Society of Human Genetics, Philadelphia, PA, October 2009.
56. Kelvin: Computer Program or Way of Life? A brief history of a piece of statistical genetics software. Invited presentation, Columbia University, New York, New York, November 2009.
57. Theory and practice of evidence measurement in statistical genetics: The PPL framework in its current incarnation. Invited presentation, University of Alabama at Birmingham, January 2010.
58. Measurement of evidence and evidence of measurement. Invited presentation, Offord Centre, McMaster University, Hamilton Ontario, December 2010.
59. Association statistics in the PPL framework. Invited Rounds, Population Genomics Program, McMaster University, Hamilton Ontario, December 2010.
60. The importance of being accurate: Measurement in psychiatric genetic research, Child Psychiatry Grand Rounds, Columbia University, New York, NY, November 2011.
61. Searching for a good measure of evidence: A work in progress, Genetic Epidemiology Seminar, Columbia University, New York, NY, November 2011.
62. Calibration of statistical evidence using principles of thermodynamics. Invited presentation, University of Toronto, Toronto, Ontario, April 2012.
63. Calibration of statistical evidence using principles of thermodynamics. Invited presentation, Johns Hopkins University, Baltimore, MD, May 2012.
64. Measurement of evidence: What's the problem? Workshop on Measure Theoretic Issues in Biology, Columbus, OH, June 2012.
65. Measurement of evidence on an absolute scale using thermodynamic principles. Workshop on Measure Theoretic Issues in Biology, Columbus, OH, June 2012.
66. Measurement of evidence in biomedical (and other) applications. Invited talk at "Foundations of Quantification and Measurement in the Biological Science", Templeton Foundation, New York, NY, February 2013.

67. Is the universe made of information? Plenary Speaker, MidSouth Computational Biology and Bioinformatics Society (MCBIOS) X Conference, Columbia, MO, April 2013.
68. Is the universe made of information? Invited presentation, Mathematical Biosciences Institute, The Ohio State University, Columbus, OH, April 2013.
69. Genomic Medicine: The view from genetics. Invited talk, “Road to Collaboration: NCH and OSU Human Genetics Community”, Columbus, OH, May 2014.
70. P-values are not measures of evidence, in session “The Perils of P Values: How to Be Smart When Writing about Stats”. Invited talk, National Association of Science Writers, Columbus, OH, October 2014.
71. Replication, measurement and biological evidence, with Hasok Chang, part of the symposium “Quantifying Life”. Invited talk, Philosophy of Science Association, Chicago, IL, November 8, 2014.
72. An information-dynamic framework for measuring statistical evidence. Plenary speaker, The Second Annual Zing Conference on Mathematical and Computational Medicine, Cancun, Mexico, December, 2014.
73. Towards a new information-dynamic framework for measuring evidence in biology. American Association for the Advancement of Science, San Jose, CA, February 14, 2015.
74. Measuring statistical evidence in biological research. Invited talk, Department of Biological Sciences, Columbia University, New York, NY, March 2015.
75. Guest speaker, Columbia University Biological Sciences SCNC W3920 (Ignorance, S Firestein Instructor), New York, NY, March 11, 2015.
76. Is rigorous measurement of statistical evidence possible? Invited speaker, Society for Philosophy of Science in Practice, Aarhus, Denmark, June 24, 2015.
77. Measurement of evidence in theory and in practice. Invited speaker, Making of Measurement, Cambridge, UK, July 23, 2015.
78. Reproducibility, Replication and Scientific Evidence. Invited speaker, Sickkids Centre for Brain and Mental Health and Child Health, Toronto, CAN, December 9, 2015.
79. Measurement of Statistical Evidence in Scientific Applications. Invited speaker, Department of Statistical Sciences, University of Toronto, Toronto, CAN, December 10, 2015.
80. How to Know When We Are (or Are Not) Measuring Statistical Evidence. Invited speaker. The Third International Conference on Mathematical and Computational Medicine, Columbus, OH, May 18, 2016.
81. Replication, Evidence, and Statistical Practice. Platform presentation, Society for Philosophy of Science in Practice (SPSP) Biennial Conference, Glassboro NJ, June 17-19, 2016.
82. Measurement of Statistical Evidence: Picking up Where Hacking (et al.) Left Off. Platform presentation, Philosophy of Science Biennial meeting, Atlanta, GA, November 2016.
83. What the History of Age-of-Onset Anticipation Studies Can Teach Us About Reproducibility and Evidence. Invited lecture at Symposium: “Evidence: An Interdisciplinary Conversation about Knowing and Certainty,” Center for Science and Society and the Institute for Social and Economic Research and Policy, Columbia University, New York, NY, April 21-22, 2017. (See also Other Professional Activities, above.)
84. The Relationship Between Replication and Statistical Evidence: To Be Clear, It’s Very Confusing. Invited lecture, Department of Biostatistics (graduate seminar on Likelihood, Professor Lisa Strug, Instructor). University of Toronto, Toronto, CA, May 15, 2017.



85. Statistical Modeling of Genetic Modifiers. Invited lecture at Symposium: “Unraveling Genetic Modifiers of Muscular Dystrophy” Eccles Institute of Human Genetics, University of Utah, Salt Lake City, UT, May 24, 2017. (See also Other Professional Activities, above.)
86. Some Topics in Statistical Measurement. Invited lecture at Workshop: “How do we decide what to measure?” Centre for BiodiversityDynamics, Norwegian University of Science and Technology, Trondheim, Norway, June 6-10. (See also Other Professional Activities, above.)