

Curriculum Vitae

Veronica J. Vieland, Ph.D.
Executive Director, Mathematical Medicine LLC
Professor Emerita, Departments of Pediatrics & Statistics
The Ohio State University

Contact Information

Mathematical Medicine LLC
 3800 N Lake Shore Dr #2E
 Chicago IL 60613
 Veronica.Vieland@MathMed.org

Areas of Research Interest

Statistical genetics
 Genetic architecture of psychiatric and other complex human disorders
 Genetic modifiers of Mendelian disorders
 Genetic and genomic data repositories
 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 | Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2006-07 | Director, Center for Quantitative and Computational Biology | Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2007-2022 | Battelle Chair in Quantitative and Computational Biology | Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2007-2022 | Director, Battelle Center for Mathematical Medicine | Abigail Wexner Research Institute at Nationwide Children's Hospital |

| | | |
|-----------|---|--|
| | (formerly known as Center for Quantitative and Computational Biology) | |
| 2006-2022 | Professor (Primary) | Department of Pediatrics College of Medicine The Ohio State University |
| 2007-2022 | Professor (Secondary) | Department of Statistics The Ohio State University |
| 2007-2020 | Professor (Adjunct) | Department of Biomedical Informatics The Ohio State University |
| 2007-2010 | Professor (Adjunct) | Department of Genetics Rutgers University |
| 2011-2022 | Vice-President for Computational Research | Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2022- | Founder and Executive Director | Mathematical Medicine LLC |

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, 1990-2015

International Genetic Epidemiology Society, founding member, 1991-2017

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

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

Member, Genetics Society of America, 2012-2014

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 Abigail Wexner Research Institute, 2006-2007.

Primary Mentor for Sang-Cheol Seok, Ph.D., Postdoctoral Research Fellow
 Battelle Center for Mathematical Medicine, Abigail Wexner 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, Abigail Wexner 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, Abigail Wexner Research Institute at
 Nationwide Children's Hospital 2012-2015

Primary Mentor for Joseph McEwen, Ph.D., Postdoctoral Research Fellow
 Battelle Center for Mathematical Medicine, Abigail Wexner Research Institute at Nationwide Children's Hospital.
 2017

Research Supervisor for Daniel Nolan, M.D., Ph.D., Fellow, Medical Genetics and Genomics, Nationwide Children's
 Hospital 2020-2022

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, Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2011-2014 | Chair, Research Information Technology Advisory Council, Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2010-2022 | Member, Research Conflict of Interest Committee, Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2011-2012 | Member, Research Strategic Planning Committee, The Ohio State University |
| 2011-2018 | Member, Enterprise Data Strategy Committee, Nationwide Children's Hospital |
| 2012 | Chair, The Chief Research Information Officer Search Committee, Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2013-2014 | Member, The Chief Research Information Officer Search Committee, Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2013-2014 | Chair, Research Computing Executive Committee, Abigail Wexner 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 |

| | |
|-----------|---|
| 2014-2022 | Member, Internal Advisory Board for the Center for Genomic Medicine & Pharmacogenomics, The Ohio State University College of Medicine |
| 2016 | Member, Research Retreat Planning Committee, Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2016-2017 | Member, Biostatistical Core Director Search Committee, Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2016-2017 | Member, Biobehavioral Health Faculty Search Committee, Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2017-2022 | Member, Bremer Lecture Selection Committee, Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2017-2022 | Member, Promotion and Tenure Committee, Department of Pediatrics, The Ohio State College of Medicine |
| 2019-2020 | Member, Center for Childhood Cancer and Blood Diseases Faculty Search Committee, Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2019-2020 | Member and Affirmative Action Advocate, Center for Innovation in Pediatric Practice Faculty Search Committee, Abigail Wexner Research Institute at Nationwide Children's Hospital |
| 2020 | Member, Review Committee, Additional Ventures Fund Grant Proposals, Abigail Wexner Research Institute at Nationwide Children's Hospital |

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)
- 2010-2013 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.
- 2015 - 2022 Director, Institutional High Performance Computing facility, Nationwide Children’s Hospital
- 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.)
- 2018 - 2020 Member, Ohio Supercomputing Center/OARnet Advisory Board
- 2019 - 2022 Advisory Board Member, The Ohio State University Research Cyberinfrastructure and Advanced Computing Advisory Council

Research Grants

| <u>Title & 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 | 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 | Co-I | 2005-2010 |

| | | |
|--|---------------|-----------|
| In Extended Pedigrees NIMH RO1 MH076028 (Joseph Piven, PI) | | |
| 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 (LM Brzutowicz, J Tischfield, PI) | PI (CAPS) | 2012-2025 |
| 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, Robert Weiss PIs) | Co-I | 2014-2021 |
| 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 |
| The Nature and Uses of Evidence in Science Columbia University Center for Science and Society | Co-PI | 2019 |

| | | |
|--|------|-------------|
| PediAtric ReseArch of Drugs, Immunoparalysis and Genetics during MODS NIH R01 HD 095976 (Mark Hall, PI) | Co-I | 2019 – 2024 |
| Genetic Modifiers of Duchenne Muscular Dystrophy NIH R01 NS 085238 (MPIs K Flanigan, R Weiss, VJ Vieland) | MPI | 2022-2027 |

Patents

Modulators of Disease Severity in Muscular Dystrophy. Flanigan K, Weiss RB, **Vieland VJ**. *Submitted September 22, 2017.*

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: An 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 Epidemiol* 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 (Neuropsychiatr 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 Epidemiol (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 Epidemiol (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, Haghghi 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 (Neuropsychiatr 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 Epidemiol* 17 (Suppl 1):S749-S754, 1999.
27. Collaborative Linkage Study of Autism (CLSA). An autosomal genomic screen for autism. *Am J Med Genet (Neuropsychiatr 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 Epidemiol (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 (Neuropsychiatr 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 (Neuropsychiatr 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 (Neuropsychiatr 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 (Neuropsychiatr 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 Genet, Neuropsychiatr 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 Epidemiol* 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 (Neuropsychiatr 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 Epidemiol 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, **Vieland VJ**, 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 7th 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, **Vieland VJ**. 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 Epidemiol*, 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 Epidemiol*, 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, Kalemba 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, Riquad 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 IP₄ 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, Thiruvahindrapuram 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* 84(5):853-865, 2017.
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.
128. **Vieland VJ**, Chang H. No Evidence Amalgamation without Evidence Measurement. *Synthese* 196:3139-3161, 2019. DOI: 10.1007/s11229-017-1666-7, 2018.
129. Manley W, Moreau MP, Azaro M, Siecinski SK, Davis G, Buyske S, **Vieland V**, Bassett AS, Brzustowicz L. Validation of a microRNA target site polymorphism in *H3F3B* that is potentially associated with a broad schizophrenia phenotype. *PLoS One*, 13(3):e0194233, 2018.
130. Woodbury-Smith M, Paterson A, O'Connor, Zarrei M, Yuen RKC, Howe JL, Thompson A, Parlier M, Fernandez B, Piven J, Scherer SW, **Vieland VJ**, Szatmari P. A genome-wide linkage study of autism spectrum disorder and the broad autism phenotype in extended pedigrees. *J Neurodev Disord* 10(1):20, 2018.
131. Weiss RB, **Vieland VJ**, Dunn DM, Kaminoh Y, Flanigan KM. United Dystrophinopathy Project. Long-range genomic regulators of *THBS1* and *LTBP4* modify disease severity in Duchenne muscular dystrophy. *Ann Neurol* 84(2):234-245, 2018.
132. Woodbury-Smith M, Zarrei M, Wei J, Thiruvahindrapuram B, O'Connor I, Paterson A, Yuen R, Dastan J, Stavropoulos J, Howe J, Parlier M, Fernandez B, Piven J, Anagnostou E, Scherer S, **Vieland V**, Szatmari P. Segregating patterns of copy number variations in extended autism spectrum disorders (ASD) pedigrees. *Am J Med Genet (Neuropsychiatr Genet)* 183(5):268-276, 2020.
133. **Vieland VJ**, Seok SC, Stewart WCL. A new linear regression-like residual for survival analysis, with application to genome wide association studies of time-to-event data. *PLoS One*, 15(5):e0232300, 2020.

134. **Vieland VJ**, Seok SC. The PPLD has advantages over conventional regression methods in application to moderately sized genome-wide association studies. *PLoS One*, Sep 22;16(9):e0257164, 2021.
135. **Vieland VJ**, Seok SC. Absolutely 0 Evidence. *Phil of Science*, 90:1173-1182, 2023.
136. Flanigan KM, Waldrop MA, Martin PT, Alles R, Dunn DM, Alfano LN, Simmons TR, Moore-Clingenpeel M, Burian J, Seok S-C, Weiss RB, **Vieland VJ**. A genome-wide association analysis of loss of ambulation in dystrophinopathy patients suggests multiple candidate modifiers of disease severity. *Eur J Human Genet*, 31(6):663-673, 2023.
137. Paterson AD, Seok S-C, **Vieland VJ**. The effect of ascertainment on penetrance estimates for rare variants: implications for establishing pathogenicity and for genetic counseling. *PloS ONE*, <https://doi.org/10.1371/journal.pone.0290336>, 2023.

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 für Frauen* (Walmart 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 (Neuropsychiatr Genet)* 88(3):229-232, 1999.
12. 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 Epidem* 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 2nd Edition, P. Armitage, T. Colton, Eds. Wiley: Chichester, 2005.
17. Bailey-Wilson JE, Almasy L, de Andrade M, Bailey J, Bickebölller 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, Bickebölller 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, Tritchler D, **Vieland VJ**, Wijsman 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.
22. **Vieland VJ**. Foreword to Heterogeneity in Statistical Genetics: How to Assess, Address, and Account for Mixtures in Association Studies by Derek Gordon. Springer Nature: New York, 2020.

Papers on arXiv, bioRxiv, MedRxiv (list overlaps with Peer-reviewed Publications, above)

1. **Vieland VJ**. An evidential interpretation of the 1st and 2nd 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.
8. **Vieland VJ**. Absolutely 0 Evidence. arXiv:1805.11516, 2018.
9. **Vieland VJ**, Seok S-C. The PPLD has advantages over conventional regression methods in application to moderately sized genome-wide association studies. bioRxiv 2021.10.1101/2021.05.03.442456

10. Flanigan KM, Waldrop MA, Martin PT, Alles R, Dunn DM, Alfano LN, Simmons TR, Moore-Clingenpeel M, Burian J, Seok S-C, **Vieland VJ**, Weiss RB. Candidate gene modifiers of dystrophinopathy identified by the uniform application of genome-wide datasets to novel GWAS-identified loci. medRxiv 2021.11.03.21265899; doi: <https://doi.org/10.1101/2021.11.03.21265899>
11. Flanigan KM, Waldrop MA, Martin PT, Alles R, Dunn DM, Alfano LN, Simmons TR, Moore-Clingenpeel M, Burian J, Seok S-C, Weiss RB, **Vieland VJ**. A genome-wide association analysis of loss of ambulation in dystrophinopathy patients suggests multiple candidate modifiers of disease severity. medRxiv 2021.11.03.21265887; doi: <https://doi.org/10.1101/2021.11.03.21265887>
12. **Vieland VJ**, Seok S-C. Absolutely zero evidence. PhilSci Archive 2021 <http://philsci-archive.pitt.edu/21119/>
13. Paterson AD, Seok S-C, **Vieland VJ**. The effect of ascertainment on penetrance estimates for rare variants: implications for establishing pathogenicity and for genetic counseling. bioRxiv 2023 <https://doi.org/10.1101/2023.02.17.528910>

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 (Neuropsychiatr 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 13th 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 54th 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 54th 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 54th 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 54th 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 55th 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 55th 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 55th 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 Epidemiol* 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 Epidemiol* 29:252-253 #65, 2005.
53. Logue MW, Li Y, Vieland VJ. The importance of "uninformative" models in Bayesian linkage analysis. *Genet Epidemiol* 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 56th 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 56th annual meeting, American Society of Human Genetics 1496/A, 2006.
56. Huang Y, Segre A, O'Connell J, Wang H, Vieland VJ. KELVIN: a 2nd generation distributed multiprocessor linkage and linkage disequilibrium analysis program. ASHG 56th 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 56th 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 56th 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 56th 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. 29th 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. 15th 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 57th 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 57th 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. 7th 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 2nd generation software package for computation of the PPL framework, ASHG 58th 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 58th 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 58th annual meeting, American Society of Human Genetics, poster #2346/w, 2008.
68. Nouanesengsy B, Seok SC, Vieland VJ. Visualization of multidimensional genetic likelihoods. ASHG 58th 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 58th 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 58th 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 58th 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 58th 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 58th 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 58th 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 58th 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 60th 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 60th 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 60th 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 60th 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 60th 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 60th annual meeting, American Society of Human Genetics, #2979/f, 2010.
83. Walters KA, Vieland VJ. Handling hierarchical phenotypes in the PPL framework. ASHG 60th annual meeting, American Society of Human Genetics, #2984/f, 2010.
84. Huang Y, Seok SC, Valentine-Cooper W, Burian J, Mangin L, Nouanesengsy B, Modi A, Vieland VJ. KELVIN 2.1: A tool for modeling genetic architecture for complex disorders. ASHG 60th annual meeting, American Society of Human Genetics, #3013/f, 2010.
85. Nouanesengsy B, Seok SC, Vieland VJ. Visualizing multidimensional support intervals for genetic models. ASHG 60th 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 61st annual meeting, American Society of Human Genetics, Poster 694W, 2011.
88. Seok SC, Nouanesengsy B, Vieland VJ. KELVIZ: A Graphing and Annotating Tool for Statistical Evidence in Human Genetics. ASHG 61st 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 61st 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 61st 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 (HGM2013/21st 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. Trittmann JK, Gastier-Foster JM, Vieland VJ, Klebanoff MA, Chicoine LG, Nelin LD. Bronchopulmonary dysplasia-associated pulmonary hypertension and mutations in the *DDAHI* 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.
97. Brzustowicz L, Vieland V, Ambite JL, Lehner T, Tischfield J. NRGR: NIMH Repository and Genomics Resource: New Collections, Services and Access Tools to Search Data and Biosamples. European Neuropsychopharm, Oct 1, 2017.
98. Ruocco B, Mayani R, Sharma S, Wilson S, Vahi K, Voinea S, Davis G, Valentine-Cooper W, Mathew J, Arens Y, Deelman E, Azaro M, Vieland V, Ambite JL, Brzustowicz L. Enhancing Access to Data at the National Institute of Health Repository and Genomics Resource. XXVIIth World Congress of Psychiatric Genetics, October 26-31, 2019, Los Angeles, CA. European Neuropsychopharm 29(5) Suppl: S173-S174, 2019.
99. Nolan DK, Valentine-Cooper W, Burian J, Vieland VJ. Major Depressive Disorder with Chronic Pain: a Genome Wide Linkage and Association Study. Poster, Am Soc Hum Genet, 2022.

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, <https://www.pnas.org/post/podcast/overdependence-p-values>, 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 Abigail Wexner 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. Measuring statistical evidence in the age of a million SNPs. Second Annual Canadian Genetic Epidemiology & Statistical Genetics Meeting, Toronto CA, April 2007.

48. 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.
49. 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.
50. 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.
51. 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.
52. What does it mean to measure statistical evidence? Invited presentation, Columbia University, New York, New York, February 2009.
53. Disease mapping via the coalescent. Hoffman L (presenting author), Kubatko L, Vieland VJ, Huang Y. Joint Statistical Meeting, Washington DC, August 2009.
54. 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.
55. 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.
56. 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.
57. Measurement of evidence and evidence of measurement. Invited presentation, Offord Centre, McMaster University, Hamilton Ontario, December 2010.
58. Association statistics in the PPL framework. Invited Rounds, Population Genomics Program, McMaster University, Hamilton Ontario, December 2010.
59. The importance of being accurate: Measurement in psychiatric genetic research, Child Psychiatry Grand Rounds, Columbia University, New York, NY, November 2011.
60. Searching for a good measure of evidence: A work in progress, Genetic Epidemiology Seminar, Columbia University, New York, NY, November 2011.
61. Calibration of statistical evidence using principles of thermodynamics. Invited presentation, University of Toronto, Toronto, Ontario, April 2012.
62. Calibration of statistical evidence using principles of thermodynamics. Invited presentation, Johns Hopkins University, Baltimore, MD, May 2012.
63. Measurement of evidence: What's the problem? Workshop on Measure Theoretic Issues in Biology, Columbus, OH, June 2012.
64. Measurement of evidence on an absolute scale using thermodynamic principles. Workshop on Measure Theoretic Issues in Biology, Columbus, OH, June 2012.
65. 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.

66. Is the universe made of information? Plenary Speaker, MidSouth Computational Biology and Bioinformatics Society (MCBIOS) X Conference, Columbia, MO, April 2013.
67. Is the universe made of information? Invited presentation, Mathematical Biosciences Institute, The Ohio State University, Columbus, OH, April 2013.
68. Genomic Medicine: The view from genetics. Invited talk, “Road to Collaboration: NCH and OSU Human Genetics Community”, Columbus, OH, May 2014.
69. 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.
70. 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.
71. An information-dynamic framework for measuring statistical evidence. Plenary speaker, The Second Annual Zing Conference on Mathematical and Computational Medicine, Cancun, Mexico, December, 2014.
72. Towards a new information-dynamic framework for measuring evidence in biology. American Association for the Advancement of Science, San Jose, CA, February 14, 2015.
73. Measuring statistical evidence in biological research. Invited talk, Department of Biological Sciences, Columbia University, New York, NY, March 2015.
74. Guest speaker, Columbia University Biological Sciences SCNC W3920 (Ignorance, S Firestein Instructor), New York, NY, March 11, 2015.
75. Is rigorous measurement of statistical evidence possible? Invited speaker, Society for Philosophy of Science in Practice, Aarhus, Denmark, June 24, 2015.
76. Measurement of evidence in theory and in practice. Invited speaker, Making of Measurement, Cambridge, UK, July 23, 2015.
77. Reproducibility, Replication and Scientific Evidence. Invited speaker, Sickkids Centre for Brain and Mental Health and Child Health, Toronto, CAN, December 9, 2015.
78. Measurement of Statistical Evidence in Scientific Applications. Invited speaker, Department of Statistical Sciences, University of Toronto, Toronto, CAN, December 10, 2015.
79. 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.
80. Replication, Evidence, and Statistical Practice. Platform presentation, Society for Philosophy of Science in Practice (SPSP) Biennial Conference, Glassboro NJ, June 17-19, 2016.
81. Measurement of Statistical Evidence: Picking up Where Hacking (et al.) Left Off. Platform presentation, Philosophy of Science Biennial meeting, Atlanta, GA, November 2016.
82. 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.)
83. 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.

84. 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.)
85. Some Topics in Statistical Measurement. Invited lecture at Workshop: “How do we decide what to measure?” Centre for Biodiversity Dynamics, Norwegian University of Science and Technology, Trondheim, Norway, June 6-10, 2017. (See also Other Professional Activities, above.)
86. Measurement of Statistical Evidence on an Absolute Scale Following Thermodynamic Principles: Measurement Scales and Minimal Evidence. Invited participant in Symposium, “The Concept of Statistical Evidence,” Statistical Society of Canada annual meeting, Montreal CA, June 4-June 6, 2018
87. Who Knows Which Way the Evidence is Going? Platform presentation, Society for Philosophy of Science in Practice (SPSP) Biennial Conference, Ghent, Belgium, June 29-July 2, 2018
88. Linkage Analysis of Complex Traits: Failed paradigm or powerful tool? Invited presentation. Mathematical Bioscience Institute, The Ohio State University, Columbus, Ohio, September 17-19, 2018.
89. Evidentialist Statistics for Scientific Applications: Thinking in terms of likelihood ratios rather than p-values. Invited speaker. The Fifth International Conference on Mathematical and Computational Medicine, Telluride CO, June 7-11, 2021.
90. Absolutely Zero Evidence. Platform presentation, Philosophy of Science Association (PSA) 28th Biennial Meeting, Pittsburgh PA, Nov 10-13, 2022.