

## CURRICULUM VITAE

**Name:** Marylyn DeRiggi Ritchie, PhD, FACMI  
**Work Address:** Ritchie Lab  
University of Pennsylvania  
Richards Medical Research Building, A301  
3700 Hamilton Walk  
Philadelphia, PA 19104  
215-573-2438

**Home address:** 1030 Hatches Mill Drive,  
Media, PA 19063  
615-419-0689

**E-mail Address:** marylyn@pennmedicine.upenn.edu

**Website Address:** <http://ritchielab.org>, <http://visualization.ritchielab.org>, <http://marylynritchie.com>

**H-index:** 97 (Google Scholar; as of 11/27/2023)

### EDUCATION

1999, BS University of Pittsburgh at Johnstown (Biology)  
2002, MS Vanderbilt University (Applied Statistics)  
2004, PhD Vanderbilt University (Statistical Genetics)  
*Genetic Programming Optimized Neural Networks for Detecting Gene-Gene Interactions*

### PROFESSIONAL EMPLOYMENT

#### Academic Appointments

2004-2009 Assistant Professor  
Department of Molecular Physiology & Biophysics  
Vanderbilt University

2004-2011 Investigator  
Center for Human Genetics Research  
Vanderbilt University

2009-2011 Associate Professor with tenure  
Department of Molecular Physiology & Biophysics  
Vanderbilt University

2009-2011 Associate Professor, Secondary Appointment  
Department of Biomedical Informatics  
Vanderbilt University

2011- 2014 Associate Professor with tenure  
Department of Biochemistry and Molecular Biology  
Pennsylvania State University

## Curriculum Vitae: Marylyn DeRiggi Ritchie

- 2011-2016      Director, Center for Systems Genomics  
The Huck Institutes of the Life Sciences  
Pennsylvania State University
- 2014-2016      Professor with tenure  
Department of Biochemistry and Molecular Biology  
Pennsylvania State University
- 2015-2016      Paul Berg Professor  
Department of Biochemistry and Molecular Biology  
Pennsylvania State University
- 2015-2017      Director, Biomedical and Translational Informatics Institute  
Professor of Biomedical and Translational Informatics  
Geisinger Health System
- 2016-2017      Chief Research Informatics Officer  
Geisinger Health System
- 2016-2018      Fixed-term, Part-time Professor  
Department of Biochemistry and Molecular Biology  
Pennsylvania State University
- 2017-2018      Faculty Pending, Department of Genetics  
University of Pennsylvania, Perelman School of Medicine
- 2017-2022      Associate Director for Bioinformatics  
Institute for Biomedical Informatics  
University of Pennsylvania, Perelman School of Medicine
- 2017-2023      Associate Director, Center for Precision Medicine  
University of Pennsylvania, Perelman School of Medicine
- 2017-present    Director, Center for Translational Bioinformatics  
Institute for Biomedical Informatics  
University of Pennsylvania, Perelman School of Medicine
- 2018-present    Professor with tenure, Department of Genetics  
University of Pennsylvania, Perelman School of Medicine
- 2022-present    Director, Institute for Biomedical Informatics  
University of Pennsylvania, Perelman School of Medicine
- 2022-present    Vice President for Research Informatics  
University of Pennsylvania Health System
- 2022-present    Edward Rose, M.D. and Elizabeth Kirk Rose, M.D. Professor  
University of Pennsylvania, Perelman School of Medicine

## Curriculum Vitae: Marylyn DeRiggi Ritchie

2023- present     Director, Division of Informatics, Department of Biostatistics, Epidemiology, and Informatics. University of Pennsylvania, Perelman School of Medicine

### Other Professional Positions

2005-2010     Consultant, Boehringer-Ingelheim  
2018-2022     Scientific Advisory Board, CIPHEROME  
2019-2020     Scientific Advisory Board, Goldfinch Bio

### Honors and Awards

1999     Graduated Summa Cum Laude, University of Pittsburgh, Johnstown  
2000- 2002     NIH Breast Cancer Research Training Grant  
2001     Vanderbilt University, Charles R. Park Student Travel Award  
2002- 2003     NLM Bioinformatics Training Grant  
2002     Vanderbilt University Graduate School Travel Grant  
2003     Vanderbilt University Dissertation Enhancement Grant  
2003     Vanderbilt University Graduate School Travel Grant  
2003     Vanderbilt University, Charles R. Park Student Travel Award  
2004     Best Paper Award, Genetic and Evolutionary Computation Conference  
2006     *Genome Technology*, Rising Young Investigator Award  
2010     Sloan Research Fellow  
2011-2014     KAVLI Frontiers in Science fellow, National Academy of Science  
Jointly sponsored by the US National Academy of Sciences and The Kavli Foundation, the Kavli Frontiers of Science bring together some of the very best young scientists to discuss exciting advances and opportunities in their fields in a format that encourages informal collective, as well as one-on-one discussions among participants. It is an honor to be selected as a Kavli fellow, and Dr. Ritchie was selected four years in a row.  
2014     Member, Thomas Reuters, Most Highly Cited Researchers  
2015     Paul Berg Professor of Biochemistry and Molecular Biology, Penn State University  
2016     E. Allen Deaver, High Potential Leadership Fellow, Geisinger Health System  
2017     First Place, AMIA “Why Informatics” Video Contest  
2020     Group on Information Resources (GIR) Excellence Award, American Association of Medical Colleges (AAMC) – for our team’s PennChart Genomics Project  
2020     Elected as a fellow in the American College of Medical Informatics (ACMI)  
2021     Executive Leadership in Academic Medicine (ELAM) fellow  
2021     Elected to the National Academy of Medicine (NAM)  
2022     Edward Rose, M.D. and Elizabeth Kirk Rose, M.D. Professor, University of Pennsylvania, Perelman School of Medicine

### Membership in Professional Societies

American Association for the Advancement of Science (AAAS)  
American Society of Human Genetics (ASHG)

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International Society for Computational Biology (ISCB)  
American Medical Informatics Association (AMIA)  
American College of Medical Informatics (ACMI)  
National Academy of Medicine (NAM)

### Administrative and Service Contributions

#### Institutional Service

2003-2004	Center for Human Genetics Research Core Oversight Board Vanderbilt University Medical Center, Nashville, TN
2005	Organizing Committee—CHGR Annual Genetics Symposium Vanderbilt University Medical Center, Nashville, TN
2006	ACCRE Study Group, co-chair Vanderbilt University, Nashville, TN
2006	Panel Member—Women in Academe Series Vanderbilt University Medical Center, Nashville, TN
2008	Faculty Recruitment Committee Center for Human Genetics Research
2009	Faculty Recruitment Committee, chair Center for Human Genetics Research
2009	Personalized Medicine Task Force – Vision 2020 Vanderbilt University
2009	IGP Internal Review Administrative Subcommittee Vanderbilt University
2004-2001	Faculty Director, CHGR Computational Genomics Core Vanderbilt University Medical Center, Nashville, TN
2007-2011	ACCRE Faculty Advisory Board Vanderbilt University, Nashville, TN
2008-2011	Director, Program in Computational Genomics Vanderbilt University, Center for Human Genetics Research
2011	Biobehavioral Health Genetics Faculty Search Committee The Pennsylvania State University, University Park, PA
2011-2012	PSU Presidential Task Force The Pennsylvania State University, University Park, PA
2011-2013	BMB Graduate Student Recruitment Committee The Pennsylvania State University, University Park, PA

## Curriculum Vitae: Marylyn DeRiggi Ritchie

- 2012-2013 Institute of Cyberscience, Search Committee  
The Pennsylvania State University, University Park, PA
- 2012-2013 iBIOS Bioinformatics & Genomics Graduate Program Admissions Committee  
The Pennsylvania State University, University Park, PA
- 2012-2013 Research Data and Computing Committee  
The Pennsylvania State University, University Park, PA
- 2012-2014 IT Strategic Planning Committee  
The Pennsylvania State University, University Park, PA
- 2014-2015 Chair, BMB Promotion & Tenure Committee  
The Pennsylvania State University, University Park, PA
- 2011-2014 BMB Junior Faculty Mentoring Committee  
The Pennsylvania State University, University Park, PA
- 2011-2016 Director, Center for System Genomics  
The Pennsylvania State University, University Park, PA
- 2012-2014 BMB Promotion & Tenure Committee (2014 – Chair)  
The Pennsylvania State University, University Park, PA
- 2014 Research CI Governance Task Force  
The Pennsylvania State University, University Park, PA
- 2014 ICS Coordinating Committee for Advanced CI  
The Pennsylvania State University, University Park, PA
- 2014 Academic Integrity Committee – RA10  
The Pennsylvania State University, University Park, PA
- 2015-2017 Enterprise Data Strategy Steering Committee  
Geisinger Health System, Danville, PA
- 2016-2017 Research Space Committee, Chair  
Geisinger Health System Danville, PA
- 2016-2017 Chief Research Informatics Officer  
Geisinger Health System, Danville, PA
- 2018-2019 Faculty recruitment selection committee, Department of Genetics  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2018-2022 Senior IT Council (member)  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 2018-2019 Clinical and Medical Bioinformatics Working Group  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2019-2021 Clinical Research Informatics Oversight Committee  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2019-2022 Research Data Domain Committee, co-chair  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2019-present Clinical IS Genomics Oversight Committee  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2019-2021 Biomedical Informatics Graduate Group Planning Committee  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2019-2021 Epic Cosmos User Group member  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2020 DBEI Department Chair search Committee  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2020-present Committee on Appointments and Promotions  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2020-present Genomics and Computational Biology Graduate Group Committee on Equality, Diversity and Inclusion, co-chair  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2020-present Genomics and Computational Biology Graduate Group Executive Committee member  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2022-present Senior IT Council (co-chair)  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2022-2023 Pathology and Laboratory Medicine Department Chair search committee  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2022-present Genetics/IBI Faculty search committee  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2022-present Cardiology/Cardiovascular Institute Faculty search committee  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2022-present Computational and Data-Dependent Research committee  
University of Pennsylvania, Philadelphia, PA
- 2023-present Committee on AI Curriculum for Medical Education (chair)  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA

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### National / International Service

- 2002 Grant Reviewer, “Small Grants Program for Cancer Epidemiology.” PA-01-021, National Cancer Institute, National Institutes of Health
- 2004 Workshop Organizer, Biological Applications of Genetic and Evolutionary Computation
- 2005 Session Organizer, Computational Approaches for Pharmacogenomics, Pacific Symposium on Biocomputing
- 2005 Program Committee, Biological Applications of Genetic and Evolutionary Computation
- 2005 Workshop Organizer, Biological Applications of Genetic and Evolutionary Computation
- 2006 Grant Reviewer, “Toward Maximizing the Scientific Value of the Biologic Specimens from the Women’s Health Initiative.” RFP-NHLBI-WH-06-09, National Heart, Lung, and Blood Institute, National Institutes of Health
- 2006 Session Organizer, Computational Approaches for Pharmacogenomics, Pacific Symposium on Biocomputing
- 2006 Program Committee, Biological Applications of Genetic and Evolutionary Computation
- 2006 Workshop Organizer, Biological Applications of Genetic and Evolutionary Computation
- 2006 Program Committee, European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics
- 2006 Workshop Organizer, PGRN Data Analysis Workshop
- 2007 Program Committee, Genetic and Evolutionary Computation Conference
- 2007 Program Committee, European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics
- 2007 Grant Reviewer, “Facilitating Interdisciplinary Research via Methodological and Technological Innovation in the Behavioral and Social Sciences (R21).” RFA-RM-07-004, National Institutes of Health
- 2007 Grant Reviewer, “Small Grants Program in Cancer Epidemiology.” PAR-06-294, National Cancer Institute (June and November), National Institutes of Health
- 2008 Program Committee, Genetic and Evolutionary Computation Conference
- 2008 Program Committee, International Conference on Intelligent Systems in Molecular Biology
- 2008 Grant Reviewer, “PA Department of Health Final Performance Reviews.” Oak Ridge Associated Universities
- 2008 Grant Reviewer, “GWA Studies for the Genes, Environment, and Health Initiatives.” RFA-HG-07-012, National Human Genome Research Institute, National Institutes of Health

## Curriculum Vitae: Marylyn DeRiggi Ritchie

- 2008 Grant Reviewer, “Toward Maximizing the Scientific Value of the Biologic Specimens from the Women’s Health Initiative II.” BAA HLBI-WH-09-01, National Heart, Lung, and Blood Institute, National Institutes of Health
- 2008 Grant Reviewer, “Genomic Parsing of Bipolar Disorder and Schizophrenia: Collaborative R01’s (Teleconference)”. Special Emphasis Panel/Scientific Review Group 2008/08 ZMH1 ERB-S (08). National Institute of Mental Health, National Institutes of Health
- 2008 Grant Reviewer, Israel Science Foundation's FIRST (Focal Initiatives in Research in Science and Technology)
- 2008 Grant Reviewer, “Small Grants Program in Cancer Epidemiology.” PAR-06-294, National Cancer Institute (June), National Institutes of Health
- 2009 Grant Reviewer, “GWAS of Treatment Response in Randomized Clinical Trials – Study Investigators.” RFA-HG-08-004, National Human Genome Research Institute, National Institutes of Health
- 2009 Meeting Participant, “The Challenge of Mapping GWAS Signals.” Hosted by the Genes, Environment and Health Initiative (GEI), and National Cancer Institute. National Institutes of Health.
- 2009 Conference Chair, European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics
- 2010 Conference Chair, European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics
- 2010 Program Committee, Genetic and Evolutionary Computation Conference
- 2010 Program Committee, The 2010 International Conference on Intelligent Computing (ICIC 2010)
- 2010 Session Chair, Genetic and Evolutionary Computation Conference
- 2010 Program Committee, European Conference on Computational Biology
- 2010 Program Committee, Pattern Recognition in Bioinformatics
- 2010 Host, P-STAR Analysis Workshop, October 2010, Nashville, TN
- 2005-2010 Grant Reviewer, Alzheimer’s Association
- 2006-2010 Pharmacogenetics Research Network (PGRN) Analysis Working Group Co-Chair
- 2011 Workshop Chair, “Systems Pharmacogenomics: Birds of a Feather”, Pacific Symposium on Biocomputing 2011
- 2011 Conference Chair, European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics
- 2011 Program Committee, Asia-Pacific Translational Bioinformatics Conference
- 2011 External Examiner for Viva, University of Nottingham, Nottingham UK
- 2011 Program Committee, The 2011 International Conference on Intelligent Computing (ICIC 2011)



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- 2011 Grant Reviewer, “Computational Tool Development and Integrative Data Analysis for LINCS (U01)”, RFA- RM-10-005, Special Emphasis Panel, National Institutes of Health
- 2011 Grant Reviewer, Ad Hoc, Genomics, Computational Biology and Technology (GCAT), National Institutes of Health
- 2011 Bioinformatics Track Chair, Genetic and Evolutionary Computation Conference
- 2011 Program Committee, European Conference on Artificial Life 2011
- 2011 Program Committee, Pattern Recognition in Bioinformatics 2011
- 2011 Host, P-STAR Analysis Workshop, December 2011, Chicago, IL
- 2011 Session Chair, “Beyond GWAS: Integrating Transcriptome, Proteome, and Pathway Data in the Genetic Dissection of Complex Traits”, International Congress on Human Genetics, October 2011, Montreal, Canada
- 2012 Workshop Chair, “Systems Pharmacogenomics”, Pacific Symposium on Biocomputing
- 2012 Local Host, Genetic and Evolutionary Computation Conference, Philadelphia, PA
- 2012 Grant Reviewer, Genome Canada
- 2012 Program Committee, Asia-Pacific Translational Bioinformatics Conference
- 2012 External Examiner for PhD, University of Liege
- 2012 Host, P-STAR Analysis Workshop, December 2012, Austin TX
- 2012 Grant Reviewer, Special Emphasis Panel 2012/10 ZEY1 VSN, National Eye Institute
- 2012 Grant Reviewer, Special Emphasis Panel 2012/05 ZAI1 QV-I, National Institute of Allergy and Infectious Disease
- 2012 Grant Reviewer, Science Foundation Ireland
- 2012 Organizing Committee, KAVLI Frontiers in Science, American-Indonesian conference
- 2013 Organizing Committee, KAVLI Frontiers in Science, American-Indonesian conference
- 2013 Program Committee, Asia-Pacific Translational Bioinformatics Conference
- 2013 Guest Editor, PLOS Genetics
- 2013 Guest Editor, Frontiers in Genetics
- 2013 Program Committee, Translational Bioinformatics Conference
- 2013 Program Committee, The 2013 International Conference on Intelligent Computing
- 2013 Program Committee, Pattern Recognition in Bioinformatics 2013
- 2013 Host, P-STAR Analysis Workshop, December 2013, Nashville TN
- 2014 Organizing Committee, Pacific Symposium of Biocomputing
- 2014 Track Chair, Bioinformatics, ACM-BCB
- 2014 Program Committee, Translational Bioinformatics Conference
- 2014 Program Committee, ICCABS
- 2014 Program Committee, World Congress Psychiatric Genetics

## Curriculum Vitae: Marylyn DeRiggi Ritchie

- 2014 Program Committee, Asia-Pacific Translational Bioinformatics Conference
- 2014 Grant Reviewer, Medical Research Council (MRC), United Kingdom
- 2014 Organizing Committee, KAVLI Frontiers in Science, American-Indonesian conference
- 2015 Organizing Committee, Pacific Symposium on Biocomputing
- 2015 Program Committee, AMIA
- 2015 Program Committee, Translational Bioinformatics Conference
- 2016 Organizing Committee, Pacific Symposium on Biocomputing
- 2016 Program Committee, Translational Bioinformatics Conference
- 2017 Organizing Committee, Pacific Symposium on Biocomputing
- 2017 Vice Chair, AMIA Translational Bioinformatics Conference
- 2017 Co-Host, Translational Bioinformatics Conference
- 2017 Grant Reviewer, Canada Excellence Research Chair
- 2017 Grant Reviewer, Wellcome Trust, Sir Henry Dale Fellowship
- 2018 Organizing Committee, Pacific Symposium on Biocomputing
- 2007-2012 Grant Reviewer, Pennsylvania Performance Review, PA Department of Health
- 2007-2017 Member, Faculty of 1000 Biology
- 2008-2015 Member, Genetic Epidemiology Scientific Review Committee for the Department of Veterans Affairs
- 2009-2010 Executive Editor, Pharmacogenomics
- 2012-2018 Member, Genomics, Computational Biology and Technology (GCAT), National Institutes of Health
- 2015-2018 GWAS Catalog Scientific Advisory Board
- 2016-2018 Member, Parasite Award Committee
- 2007-2015 Managing Editor, BioData Mining
- 2008-present Member Editorial Board, Pharmacogenomics
- 2011-present Member Editorial Board, Pharmacogenetics & Genomics
- 2015-2022 Member, Standing Committee on Biological and Physical Sciences in Space (CBPSS), National Academy of Sciences
- 2015-present Editor-in-chief, BioData Mining
- 2017-2021 Grant Reviewer, Genome Canada
- 2017-present Institute for Computational Biology External Advisory Board, Case Western Reserve University
- 2017-2021 UCSF PREMIER (Precision Medicine in Rheumatology) External Advisory Committee
- 2017-present NIH Advisory panel, All of Us Cohort Program
- 2018-present NHGRI PhenX Steering Committee (Member)
- 2019-2020 Vice Chair, Translational Bioinformatics Track, AMIA Joint Summits
- 2019-present NHGRI ANVIL External Consultant Committee
- 2019-2022 NIA Dog Aging Project, Scientific Advisory Board
- 2019 Fusion Personalized Medicine Conference co-chair

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- 2019-2023 Genome Canada Research Oversight Committee, Turvey LSARP Project
- 2019-2023 Genome Canada Research Oversight Committee, Go PGx project
- 2019-2023 Vanderbilt DBMI T32, Scientific Advisory Board
- 2019-2022 NHGRI LIGHT Workshop Planning Committee
- 2019-2022 ANVIL Data Ingestion Working Group
- 2019-present iCOPE Advisory Board (Childhood Cancer project in Copenhagen, Denmark)
- 2020-present UK Biobank International Advisory Board (chair starting in 2022)
- 2020-present Annual Review of Biomedical Data Science Editorial Committee
- 2020-2022 H3ABioNet Scientific Advisory Board
- 2020 Grant Reviewer, COVID Special Emphasis Panel
- 2020 Grant Reviewer, Advancing Genomic Medicine, Special Emphasis Panel
- 2021 Grant Reviewer, NIH Director's Transformative Research Award (TRA)
- 2021-present Member, NHGRI Genomic Data Science Working Group (GDSWG) - working group of the National Advisory Council for Human Genome Research (NACHGR)
- 2021-present CalPenn Joint Steering Committee (chair starting in 2023)
- 2022-present ClinGen PGx Workgroup
- 2023-present ACMI 2024 symposium, program chair
- 2023-present NHLBI TopMed External Scientific Panel

## REVIEWER FOR JOURNALS

- 2005-Present Ad Hoc Reviewer, Pacific Symposium on Biocomputing
- 2005-Present Hoc Reviewer, Annals of Human Genetics
- 2005-Present Ad Hoc Reviewer, Current Bioinformatics
- 2005-Present Ad Hoc Reviewer, British Journal of Cancer
- 2006-Present Ad Hoc Reviewer, BMC Cancer
- 2006-Present Ad Hoc Reviewer, Epidemiology
- 2006-Present Ad Hoc Reviewer, Human Genomics
- 2006-Present Ad Hoc Reviewer, Clinical Pharmacology & Therapeutics
- 2006-Present Ad Hoc Reviewer, International Journal Artificial Intelligence in Medicine
- 2006-Present Ad Hoc Reviewer, Genetic Epidemiology
- 2006-Present Ad Hoc Reviewer, Psychiatry Research
- 2007-Present Ad Hoc Reviewer, BMC Medical Genomics
- 2007-Present Managing Editor, BMC BioData Mining
- 2007-Present Ad Hoc Reviewer, IBM Systems Journal
- 2007-Present Ad Hoc Reviewer, Clinical Cancer
- 2007-Present Ad Hoc Reviewer, Clinical Genetics
- 2007-Present Ad Hoc Reviewer, Cancer Epidemiology Biomarkers & Prevention
- 2007-Present Ad Hoc Reviewer, Cancer Informatics
- 2007-Present Ad Hoc Reviewer, American Journal of Human Genetics
- 2008-Present Ad Hoc Reviewer, Molecular Psychiatry
- 2008-Present Ad Hoc Reviewer, Neuropsychiatric Genetics
- 2008-Present Ad Hoc Reviewer, Neoplasia
- 2008-Present Ad Hoc Reviewer, Statistics in Medicine
- 2008-Present Ad Hoc Reviewer, Human Heredity

## Curriculum Vitae: Marylyn DeRiggi Ritchie

2009-Present Ad Hoc Reviewer, Biometrical Journal  
2009-Present Ad Hoc Reviewer, PLOS Genetics  
2009-Present Ad Hoc Reviewer, Nature Reviews Drug Discovery  
2009-Present Ad Hoc Reviewer, BMC Systems Biology  
2009-Present Ad Hoc Reviewer, Human Immunology  
2009-Present Ad Hoc Reviewer, Bioinformatics  
2009-Present Executive Editor, Pharmacogenomics  
2010-Present Ad Hoc Reviewer, European Journal of Operational Research  
2011-Present Ad Hoc Reviewer, Frontiers in Genetics  
2011-Present Ad Hoc Reviewer, Intelligent Systems in Molecular Biology  
2011-Present Ad Hoc Reviewer, In Silico Biology  
2011-Present Ad Hoc Reviewer, Source Code for Biology and Medicine  
2011-Present Ad Hoc Reviewer, OMICS Integrative Biology  
2011-Present Ad Hoc Reviewer, Pharmacogenomics  
2011-Present Ad Hoc Reviewer, PLOS One  
2011-Present Ad Hoc Reviewer, BioData Mining  
2012-Present Ad Hoc Reviewer, Journal of the American Medical Association (JAMA)  
2012-Present Ad Hoc Reviewer, Cellular and Molecular Life Sciences  
2012-Present Ad Hoc Reviewer, Annals of Neurology  
2012-Present Ad Hoc Reviewer, Pharmacogenetics and Genomics  
2012-Present Ad Hoc Reviewer, Human Molecular Genetics  
2013-Present Ad Hoc Reviewer, BMC Bioinformatics  
2013-Present Ad Hoc Reviewer, Nucleic Acids Research  
2013 Guest Editor, PLOS Genetics  
2013 Guest Editor, Frontiers in Genetics  
2013-Present Ad Hoc Reviewer, Biostatistics  
2013-Present Ad Hoc Reviewer, European Journal of Human Genetics  
2013-Present Ad Hoc Reviewer, IEEE Transactions in Evolutionary Computation  
2013-Present Ad Hoc Reviewer, Nature Reviews Genetics  
2013-Present Ad Hoc Reviewer, BMC Genetics  
2013-Present Ad Hoc Reviewer, Expert Reviews of Molecular Diagnostics  
2013-Present Ad Hoc Reviewer, Science Translational Medicine  
2014-Present Ad Hoc Reviewer, PLOS Biology  
2014-Present Ad Hoc Reviewer, PLOS Computational Biology  
2014-Present Ad Hoc Reviewer, Nature  
2014-Present Ad Hoc Reviewer, The Pharmacogenomics Journal  
2014-Present Ad Hoc Reviewer, Briefings in Bioinformatics  
2014-Present Ad Hoc Reviewer, Circulation Cardiovascular Genetics  
2014-Present Ad Hoc Reviewer, Proceedings of the National Academy of Science  
2014-Present Ad Hoc Reviewer, Human Genetics  
2015-Present Ad Hoc Reviewer, Science  
2015-Present Ad Hoc Reviewer, EvoBio  
2016-Present Ad Hoc Reviewer, Human Mutation  
2017-Present Ad Hoc Reviewer, Expert Reviews of Precision Medicine  
2018-Present Ad Hoc Reviewer, Nature Communications

## Curriculum Vitae: Marylyn DeRiggi Ritchie

2018-Present	Ad Hoc Reviewer, Nature Genetics
2019-present	Ad Hoc Reviewer, JAMA
2019-present	Ad Hoc Reviewer, Molecular Genetics and Genomics
2020-present	Ad Hoc Reviewer, Genome Medicine
2020-present	Ad Hoc Reviewer, Nature Metabolism
2020-present	Ad Hoc Reviewer, Sleep
2020-present	Ad Hoc Reviewer, Nature Medicine
2021-present	Ad Hoc Reviewer, iScience
2022-present	Ad Hoc Reviewer, Science Translational Medicine
2022-present	Ad Hoc Reviewer, Cell Genomics
2023-present	Ad Hoc Reviewer, Nature Protocols
2023-present	Ad Hoc Reviewer, Med by Cell Press

## Teaching activities

### Vanderbilt Contributions

2002	IGP Biostatistics Module, Lecturer Vanderbilt University
2004	Human Genetics—MPB 340, Lecturer Vanderbilt University
2004	IGP Biostatistics Module, Lecturer Vanderbilt University
2004	Health Systems Management Organization Course, Lecturer Vanderbilt University
2005	Human Genetics, HGEN 341, Lecturer Vanderbilt University
2005	Tutorials in Statistical and Population Genetics, HGEN 371, Co-Organizer Vanderbilt University
2006	Human Genetics, HGEN 341, Lecturer Vanderbilt University
2006	Tutorials in Statistical and Population Genetics, HGEN 371, Co-Organizer Vanderbilt University
2006	Cancer Biology Methodology Course, Lecturer Vanderbilt University
2007	Human Genetics, HGEN 341, Lecturer Vanderbilt University
2007	Tutorials in Statistical and Population Genetics, HGEN 371, Co-Organizer Vanderbilt University
2007	Cancer Biology Methodology Course, Lecturer Vanderbilt University
2008	Human Genetics, HGEN 341, Lecturer Vanderbilt University
2008	Organizer, Program in Computational Genomics Journal Club Vanderbilt University
2009	Human Genetics, HGEN 341, Lecturer Vanderbilt University
2009	Organizer, Program in Computational Genomics Journal Club Vanderbilt University
2009	Biomedical Informatics 310, Lecturer Vanderbilt University

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- 2009 IGP, Human Genetics, Lecturer  
Vanderbilt University
- 2010 Human Genetics, HGEN 341, Lecturer  
Vanderbilt University
- 2010 Biomedical Informatics 310, Lecturer  
Vanderbilt University
- 2011 Human Genetics, HGEN 341, Course Director  
Vanderbilt University

## The Pennsylvania State University Contributions

- 2012 Tutorials in Bioinformatics & Genomics, IBIOS 598B FA, Co-director  
The Pennsylvania State University, University Park, PA
- 2012 Genomics, IBIOS/BMMB 551 FA, Lecturer  
The Pennsylvania State University, University Park, PA
- 2013 Tutorials in Bioinformatics & Genomics, IBIOS 598B SP, Co-director  
The Pennsylvania State University, University Park, PA
- 2013 Human Genomics and Biomedical Informatics, BMB498D, Director  
The Pennsylvania State University, University Park, PA
- 2013 Tutorials in Bioinformatics & Genomics, IBIOS 598B FA, Co-director  
The Pennsylvania State University, University Park, PA
- 2013 Genomics, IBIOS/BMMB 551 FA, Lecturer  
The Pennsylvania State University, University Park, PA
- 2014 Critical Analysis in Bioinformatics and Genomics, IBIOS 541 SP, Co-director  
The Pennsylvania State University, University Park, PA
- 2014 Human Genomics and Biomedical Informatics, BMB498D SP, Director  
The Pennsylvania State University, University Park, PA
- 2014 Critical Analysis in Bioinformatics and Genomics, IBIOS 541 FA, Co-director  
The Pennsylvania State University, University Park, PA
- 2014 Genomics, IBIOS/BMMB 551 FA, Lecturer  
The Pennsylvania State University, University Park, PA
- 2015 Genomics, IBIOS/BMMB 551 FA, Lecturer  
The Pennsylvania State University, University Park, PA
- 2016 Genomics, IBIOS/BMMB 551 FA, Lecturer  
The Pennsylvania State University, University Park, PA

## University of Pennsylvania Contributions

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 2018 MS1 Genetics Course, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2019 BMIN504: Special Topics in Biomedical and Health Informatics, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2019 MS1 Genetics Course, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2019 GCB533: Statistics for Genomics and Biomedical Informatics, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2019 BMIN 505: Precision Medicine and Health Policy  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2020 BMIN504: Special Topics in Biomedical and Health Informatics, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2020 BMIN 505: Precision Medicine and Health Policy, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2020 GCB533: Statistics for Genomics and Biomedical Informatics, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2020 MS1 Genetics Course, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2021 BMIN504: Special Topics in Biomedical and Health Informatics, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2021 BMIN505: Precision Medicine and Health Policy, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2021 BMIN502: Database and Data Integration in Biomedical Research, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2021 GCB/CAMB 752: Seminar in Genomics, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2021 MS1 Genetics Course, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2021 GCB533: Statistics for Genomics and Biomedical Informatics, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2022 BMIN504: Special Topics in Biomedical and Health Informatics, Director  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2022 BMIN505: Precision Medicine and Health Policy, Lecturer

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- University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2022 BMIN502: Database and Data Integration in Biomedical Research, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2022 GCB/CAMB 752: Seminar in Genomics, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2022 MS4, Frontiers 519 Medical Informatics, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2022 MS1 Genetics Course, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2022 GCB533: Statistics for Genomics and Biomedical Informatics, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2023 BMIN504: Special Topics in Biomedical and Health Informatics, Director  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2023 BMIN502: Database and Data Integration in Biomedical Research, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2023 GCB/CAMB 752: Seminar in Genomics, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2023 MS1 Genetics Course, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA
- 2023 GCB533: Statistics for Genomics and Biomedical Informatics, Lecturer  
University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA

## External Contributions

- 2009 Course Co-Director, Genetic Analysis of Complex Disease  
Miami Institute of Human Genetics, University of Miami
- 2010 Course Co-Director, Genetic Analysis of Complex Disease  
Miami Institute of Human Genetics, University of Miami
- 2010 Lecturer, Vanderbilt-NARI-NIE Informatics Training Program (VNNIT)  
Workshop, Pune, India
- 2010 “A comparison of analytical methods for genetic association studies,” CDC  
Workshop, Atlanta, GA
- 2011 Course Co-Director, Genetic Analysis of Complex Disease  
Miami Institute of Human Genetics, University of Miami
- 2011 “A comparison of analytical methods for genetic association studies II”, CDC  
Workshop, Atlanta, GA
- 2011 “Next-generation Sequencing”, CDC Workshop, Atlanta, GA
- 2012 Course Co-Director, Genetic Analysis of Complex Disease  
Miami Institute of Human Genetics, University of Miami



## Curriculum Vitae: Marylyn DeRiggi Ritchie

2012	“Next-generation Sequencing”, CDC Workshop, Atlanta, GA
2013	“Next-generation Sequencing”, CDC Workshop, Atlanta, GA
2013	Course Co-Director, Genetic Analysis of Complex Disease Miami Institute of Human Genetics, University of Miami
2013	“Analysis Tools For Genetic Testing”, CDC Workshop, Atlanta, GA
2014	“Public Health Genomics”, CDC Workshop, Atlanta, GA
2014	“Gene-gene and Gene-environment interactions”, UAB's 4th Annual NIGMS- funded Short Course on Statistical Genetics & Genomics, Birmingham, AL
2014	“Intro to Bioinformatics”, CDC Workshop, Atlanta, GA
2014	“Precision Medicine: When Genomics Gets Personal”, CDC Workshop, Atlanta, GA
2015	“Next Generation Sequencing: What is it How is it Used and What Can We Learn”, CDC Workshop, Atlanta, GA
2021	“A tale of the 2020s, or a tale of the future?”, Precision Medicine Roundtable, Genetics in Medicine class, University of Deusto in Bilbao, Spain. Host: Urko Marigorta

## Advisory and Supervisory Responsibilities

### High School Students

2007	Xun Miao Martin Luther King High School, Nashville TN
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### Undergraduate Students

2005	Gordon Lemmon Vanderbilt Summer Science Academy
2006	Theresa Fanelli Vanderbilt Summer Science Academy
2012-2013	Christian Suri The Pennsylvania State University
2013-2014	Tomek Dobranski The Pennsylvania State University
2013-2015	Anastasia Lucas The Pennsylvania State University
2020	David Cornejo APSA Virtual Summer Research Program
2020	Mitsy Dominguez APSA Virtual Summer Research Program
2020-2021	Ly Nguyen APSA Virtual Summer Research Program
2020-2021	Abigail Bossa

Curriculum Vitae: Marylyn DeRiggi Ritchie

APSA Virtual Summer Research Program

- 2020-2021 Chelsea Okeh  
APSA Virtual Summer Research Program
- 2021-2022 Alexis Garofalo  
Penn SUIP Summer Research Program
- 2022 Mariah Antopia  
Penn SUIP Summer Research Program

Post-doctoral Fellows – Members of Lab

- 2009-2011 Sarah A. Pendergrass, PhD (now Rion K. Pendergrass)  
Vanderbilt University School of Medicine  
Currently, Scientific Manager in Human Genetics, Genentech
- 2009-2011 Rebecca Zuvich Essner, PhD  
Vanderbilt University School of Medicine  
Currently, Data Scientist, Advent Health
- 2013-2016 DoKyoon Kim, PhD  
The Pennsylvania State University  
Currently, Assistant Professor, University of Pennsylvania
- 2015-2017 Marta Byrska-Bishop, PhD  
Geisinger Health System  
Currently, Senior Bioinformatics Scientist, NY Genome Center
- 2016-2021 Jason Miller, PhD  
University of Pennsylvania  
Currently, Senior Scientist Statistical Genetics, Merck
- 2017-2022 Yogasudha Veturi, PhD  
University of Pennsylvania
- 2018-2022 Theodore Drivas, MD, PhD  
University of Pennsylvania
- 2020-2023 Milton Pividori, PhD  
University of Pennsylvania, co-mentor with Dr. Casey Greene
- 2023-present Zinhle Cindi, PhD  
University of Pennsylvania

Clinical Fellows – Members of Lab

- 2020-2022 Nosheen Reza, MD  
University of Pennsylvania, MTR program, co-mentor with Dr. Tom Cappola

## Curriculum Vitae: Marylyn DeRiggi Ritchie

### Graduate Students – Members of Lab

- 2004-2007 Alison A. Motsinger  
Vanderbilt University, Ph.D. Program in Human Genetics  
Currently Chief, Biostatistics & Computational Biology Branch and Principal Investigator, NIEHS
- 2005-2008 Todd L. Edwards  
Vanderbilt University, Ph.D. Program in Human Genetics  
Currently Associate Professor with tenure at Vanderbilt University (Department of Medicine, Center for Epidemiology)
- 2004-2009 William S. Bush  
Vanderbilt University, Ph.D. Program in Human Genetics  
Currently Tenure Track Associate Professor at Case-Western Reserve University (Department of Population and Quantitative Health Sciences)
- 2006-2010 Stephen D. Turner  
Vanderbilt University, Ph.D. Program in Human Genetics  
Currently senior informatics science & technology adviser at Signature Science, LLC.
- 2008-2012 Benjamin Grady  
Vanderbilt University, Ph.D. Program in Human Genetics
- 2009-2013 Emily R. Holzinger  
Vanderbilt University, Ph.D. Program in Human Genetics  
Currently Senior Scientist, Bristol Myers Squibb
- 2009-2013 Carrie C Buchanan Moore  
Vanderbilt University, Ph.D. Program in Human Genetics  
Currently Surgical Resident, Duke University School of Medicine
- 2011-2013 Neerja Katiyar  
Pennsylvania State University, Ph.D. Program in Bioinformatics & Genomics
- 2011-2015 Molly A Hall  
Pennsylvania State University, Ph.D. Program in BMMB  
Currently Tenure-track Asst. Prof at Penn State University
- 2012-2016 Ruowang Li  
Pennsylvania State University, Ph.D. Program in Bioinformatics & Genomics  
Currently Assistant Professor, Cedars-Sinai
- 2013-2018 Anna Okula Basile  
Pennsylvania State University, Ph.D. Program in BMMB  
Currently Bioinformatics Scientist, NY Genome Center

## Curriculum Vitae: Marylyn DeRiggi Ritchie

- 2014-2018 Anurag Verma  
Pennsylvania State University, Ph.D. Program in Bioinformatics & Genomics  
Currently Instructor, University of Pennsylvania, Perelman School of Medicine
- 2014-2018 Shefali Setia Verma  
Pennsylvania State University, Ph.D. Program in Bioinformatics & Genomics  
Currently Instructor, University of Pennsylvania, Perelman School of Medicine
- 2016-2020 Binglan Li  
University of Pennsylvania, Genomics and Computational Biology Grad Group  
Currently Postdoc, Stanford University
- 2016-2020 Xinyuan (Blair) Zhang  
University of Pennsylvania, Genomics and Computational Biology Grad Group  
Currently: Senior Statistical Geneticist at Regeneron Genetics Center
- 2018-2021 Joseph Park, MD-PhD student, Genomics and Computational Biology Grad Group, University of Pennsylvania, co-mentor with Dr. Dan Rader  
Currently: Resident, Weill Cornell School of Medicine
- 2018-2023 William Bone, Genomics and Computational Biology Grad Group, University of Pennsylvania, co-mentor with Dr. Ben Voight  
Currently: Scientist, Recursion
- 2018-2023 Pankhuri Singhal, Genetics Student in the Cellular and Molecular Biology program, University of Pennsylvania
- 2020-present Daniel Hui, Genomics and Computational Biology Grad Group, University of Pennsylvania, co-mentor with Dr. Sarah Tishkoff
- 2020-present Brenda Zhao, Genomics and Computational Biology Grad Group, University of Pennsylvania, co-mentor with Dr. Dokyoon Kim
- 2020-2023 John Crawford, Genomics and Computational Biology Grad Group, University of Pennsylvania, co-mentor with Dr. Casey Greene
- 2021-present Karl Keat, Genomics and Computational Biology Grad Group, University of Pennsylvania, co-mentor with Dr. Dokyoon Kim
- 2021-present Van Truong, Genomics and Computational Biology Grad Group, University of Pennsylvania, co-mentor with Dr. John Wherry
- 2022-present Anni Moore, Genomics and Computational Biology Grad Group, University of Pennsylvania
- 2022-present Chris Jones, Genomics and Computational Biology Grad Group, University of Pennsylvania, co-mentor with Dr. Sarah Tishkoff

## Curriculum Vitae: Marylyn DeRiggi Ritchie

- 2022-present David Zhang, MD-PhD student, Genomics and Computational Biology Grad Group, University of Pennsylvania, co-mentor with Dr. Dan Rader
- 2022-present Rachit Kumar, MD-PhD student, Genomics and Computational Biology Grad Group, University of Pennsylvania
- 2023-present Rasika Venkatesh, PhD student, Genomics and Computational Biology Grad Group, University of Pennsylvania, co-mentor with Dr. Yoseph Barash

## Thesis Committees

- 2005-2006 Zheng (Roger) Liu  
Microbiology & Immunology  
Vanderbilt University School of Medicine
- 2005-2006 Tricia Thornton-Wells  
Neuroscience Program  
Vanderbilt University School of Medicine
- 2005-2007 Xueying (Sharon) Liang  
Human Genetics Ph.D. Program  
Vanderbilt University School of Medicine
- 2006-2008 Digna Velez  
Human Genetics Ph.D. Program  
Vanderbilt University School of Medicine
- 2007-2009 Daniel Kinnamon  
Statistical Genetics  
University of Miami Miller School of Medicine
- 2008-2009 Rebecca Zuvich  
Human Genetics PhD Program  
Vanderbilt University School of Medicine
- 2007-2010 Britney Grayson  
Microbiology & Immunology  
Vanderbilt University School of Medicine
- 2008-2010 Logan Dumitriscu  
Human Genetics PhD Program  
Vanderbilt University School of Medicine
- 2010-2012 Janina Jeff  
Human Genetics PhD Program  
Vanderbilt University School of Medicine
- 2013-2014 Matt Oetgens  
Human Genetics PhD Program  
Vanderbilt University School of Medicine

## Curriculum Vitae: Marylyn DeRiggi Ritchie

- 2013-2016    Jacob Hall  
Human Genetics PhD Program  
Vanderbilt University School of Medicine
- 2013-2017    Claire Reynolds  
Biochemistry, Microbiology and Molecular Biology PhD Program  
The Pennsylvania State University
- 2013-2015    Marta Byrska-Bishop  
Bioinformatics and Genomics PhD Program  
The Pennsylvania State University
- 2013-2016    Rohit Reja  
Bioinformatics and Genomics PhD Program  
The Pennsylvania State University
- 2018-2022    Laura Ritenour  
Cell and Molecular Biology (CAMB) PhD Program  
University of Pennsylvania, Perelman School of Medicine
- 2018-2021    David Lee  
Genomics and Computational Biology (GCB) PhD Program  
University of Pennsylvania, Perelman School of Medicine
- 2019-2021    Jennifer Shah  
Cell and Molecular Biology (CAMB) PhD Program  
University of Pennsylvania, Perelman School of Medicine
- 2019-2021    Victoria Arthur  
Epidemiology PhD Program  
University of Pennsylvania, Perelman School of Medicine
- 2020-2022    Benjamin Heil  
Genomics and Computational Biology (GCB) PhD Program  
University of Pennsylvania, Perelman School of Medicine
- 2020-2022    Alexa Woodward  
Epidemiology PhD program  
University of Pennsylvania, Perelman School of Medicine
- 2020-2023    John Gregg  
Genomics and Computational Biology (GCB) PhD Program  
University of Pennsylvania, Perelman School of Medicine
- 2021-present    Jenea Adams  
Genomics and Computational Biology (GCB) PhD Program  
University of Pennsylvania, Perelman School of Medicine

## Curriculum Vitae: Marylyn DeRiggi Ritchie

- 2021-present Kaylyn Clark  
Genomics and Computational Biology (GCB) PhD Program  
University of Pennsylvania, Perelman School of Medicine
- 2021-present Jacob Leiby  
Genomics and Computational Biology (GCB) PhD Program  
University of Pennsylvania, Perelman School of Medicine
- 2021-present Vivek Sriram  
Genomics and Computational Biology (GCB) PhD Program  
University of Pennsylvania, Perelman School of Medicine
- 2022-present Erica Suh  
Genomics and Computational Biology (GCB) PhD Program  
University of Pennsylvania, Perelman School of Medicine
- 2022-present Stacy Guzman  
Biochemistry and Molecular Biology (BMB) PhD program  
University of Pennsylvania, Perelman School of Medicine

## MAJOR RESEARCH INTERESTS

Computational Genomics	Genetic Epidemiology
Translational Bioinformatics	Statistical Genetics
Epistasis	Systems Genomics
Pharmacogenomics	Computational Biology
Big Data	Biomedical Informatics
Evolutionary Computation	Cardiovascular Disease

## SOFTWARE AND PATENTS

- 2001 [Multifactor Dimensionality Reduction \(MDR\)](#)
- 2003 [MDR-PDT](#)
- 2002 U.S. Provisional Patent: “Method and Apparatus for Multifactor Dimensionality Reduction”
- 2006 [genomeSIMLA](#)
- 2009 [LD-Plus](#)
- 2009 [LD-Spline](#)
- 2010 [Synthesis-View](#)
- 2012 [ATHENA](#)
- 2012 [Biofilter 2.0](#)
- 2012 [BioBin](#)
- 2012 [PheWAS-view](#)
- 2013 [Phenogram](#)
- 2016 iPhenogram

## PODCASTS

The Biomedical Informatics Roundtable podcast, cohost

<http://bmipodcast.org/>

The CALM (Combining Academic and Life with Marylyn) podcast, host

<https://marylynritchie.com/podcast>

## RESEARCH FUNDING

### Active Funding

5R01 AI077505 (**MPI, Haas and Ritchie**) 04/01/2021-03/31/2026 1.2 calendar months  
NIH/NIAID – Subcontract from Vanderbilt Total Award Amount (including Indirect Costs): \$1,804,980

Pharmacogenomics of HIV Therapy

The goal of this project is to identify genetic variation associated with adverse reactions to HIV therapy, including PheWAS, epistasis, and gene-environment interaction analyses.

R01HL141232-01A1 (**MPI, Cappola and Musurunu**) 07/01/2019-06/30/2023 0.24 calendar months  
NIH Total Award Amount (including Indirect Costs): \$3,164,978

MTSS1 in Myocardial Disease

The goal of this project is to explore the relationship of MTSS1 to different types of heart failure, to establish that reducing MTSS1 activity is protective against heart failure in mouse models and human heart muscle cells, and to test a therapeutic strategy to reduce MTSS1 in the heart.

Team Science Grant (**PI, Nathanson**) 07/01/2019-6/30/2023 0.12 calendar months  
Gray Foundation Total Award Amount (including Indirect Costs): \$3,000,000

Determinants of immune activity and molecular features in BRCA 1 / 2 mutation carriers

We will build a biorepository of BRCA1/2 mutation-associated tumors, study the immune health of unaffected mutation carriers and correlate molecular features and immunogenicity in the tumors.

State of Pennsylvania Department of Health Nonformula Tobacco Settlement Act Grant:

Berrettini (PI) **Ritchie (CO-PI)** 6/1/2019 – 5/30/2023 0.12 calendar months  
Total Award Amount (including Indirect Costs): \$3,952,162

Pharmacogenetics of Opioid Use Disorder

The goal is to conduct genome-wide association studies of the efficacy of buprenorphine and methadone treatment for opioid use disorder.

1R01GM138597-01 (**PI, Kim**) 08/01/2020-07/31/2024 0.24 calendar months  
NIH/NIGMS Total Award Amount (including Indirect Costs): \$1,915,421

Unravelling genetic basis of comorbidity using EHR-linked biobank data

In this proposal, we will construct a disease comorbidity map of 2.1 million patients using longitudinal EHRs in Penn Medicine (Aim 1), construct a disease-gene map derived from phenome-wide association study using Penn Medicine Biobank Participants (Aim 2), and develop a novel scoring system using graph-based machine learning and predict comorbidity risk scores (CRS) for a given disease (Aim 3).

1U24HG010862-01A1 (**MPI, Klein and Ritchie**) 08/07/2020-05/31/2023 1.44 calendar months



Curriculum Vitae: Marylyn DeRiggi Ritchie

NHGRI

Total Award Amount (including Indirect Costs): \$560,000

Pharmacogenomics Clinical Annotation Tool (PharmCAT)

The goal of this project is to build an annotation tool for all pharmacogenomic variants with clinical guidelines and to create a report with the clinical recommendations based on those variants.

R01 (Subcontract with Mt. Sinai)

09/01/20-08/31/23

0.12 calendar months

NIH

Total Award Amount (including Indirect Costs): \$292,380

Elucidating hereditary transthyretin-mediated heart failure risk using machine learning, polygenic risk and recall by genotype approaches in African ancestry individuals

The proposed work will allow us to determine whether an integrated, data-driven approach can improve identification of V122I carriers as well as lead to improved insights about the interplay between polygenic risk scores and V122I.

3R01RY023557-06 (PI, O'Brien)

09/01/2020-08/31/2025

1.2 calendar months

NIH/NEI

Total Award Amount (including Indirect Costs): \$6,645,134

Primary Open Angle African-American Glaucoma Genetics Study Renewal

This proposal will identify and investigate genetic variants of biologic importance to this disease using genotypic and phenotypic data from the Primary Open-Angle African American Glaucoma Genetics study cohort. Our findings will contribute to the development of more targeted screening and precise therapeutic interventions for this blinding disease.

1 R01 AG066833-01A1 (MPI, Moore, Ritchie, Li)

9/30/2021-08/31/2026

1.86 calendar months

NIH/NIA

Total Award Amount (including Indirect Costs): \$8,046,920

Artificial Intelligence Strategies for Alzheimer's Disease Research

The goal of this project is to develop artificial intelligence (AI) approaches for extracting unforeseen patterns from clinical, genetic, genomic, and imaging data that could lead to ideas for new drug development. Our proposed AI methods and software will be open-source, user-friendly, and freely available for all to use.

1 P30 1P30AG073105-01 (Ritchie)

9/30/2021-08/31/2026

1.2 calendar months

NIH/NIA

Total Award Amount (including Indirect Costs): \$817,513

Networking and Mentoring Core of the Penn Artificial Intelligence and Technology (PennAITech) Collaboratory

Successful aging in the home can greatly improve quality of life, improve health outcomes, and reduce burden on the healthcare system. The goal of the overall project is to establish a national collaboratory for the development, evaluation, and implementation of artificial intelligence software and new technologies to facilitate health aging in the home. The Networking and Mentoring Core (Core E) will organize networking, mentoring, and dissemination opportunities for the awardees of the pilot programs.

1 R01HG010067 (Ritchie, PI subcontract)

06/12/22 – 04/30/23

0.6 calendar months

NIH/NHGRI

Total Award Amount (including Indirect Costs): \$1,396,502

Network-based algorithms for target identification and drug repositioning from genetic associations

The major goal of this application is to develop and evaluate algorithms that use tissue-specific functional relationship networks to identify new gene targets and to suggest opportunities for drug repositioning.

2-UL1-TR-001878-06 (Ritchie, PI Informatics core)

06/30/2021-05/31/2026

1.2 calendar months

NIH/NCATS

Total Award Amount (including Indirect Costs): \$12,720,728

Institutional Clinical and Translational Sciences Award

To provide translational informatics technologies and a knowledge base for more effectively conducting clinical and translational science.

Curriculum Vitae: Marylyn DeRiggi Ritchie

U01-HL160277 (**Chirinos**) 9/10/2021 - 7/31/2026 0.18 calendar months  
NIH/NHLBI Total Award Amount (including Indirect Costs): \$1,354,700  
HeartShare: Next-Generation Phenomics to Define Heart Failure Subtypes and Treatment Targets – Clinical Centers

The goal of the current proposal is to establish a large cohort of deeply phenotyped patients with HF to help with better understanding differential mechanisms of adverse outcomes in patients with HFpEF and identifying subgroups of patients that are likely to benefit from targeted therapy.

R01 HG012670-01 (**Ritchie, Nathanson, Schnoll, MPIs**) 07/01/2022- 06/30/2027 1.8 calendar months  
NIH/NHGRI Total Award Amount (including Indirect Costs): \$4,379,282  
Using Behavioral Economics and Implementation Science to Advance the Use of Genomic Medicine Utilizing an EHR Infrastructure across a Diverse Health System

We propose a highly innovative study using implementation science to study nudges in the electronic health record (EHR) to influence both clinicians and patients to increase the use of genetic testing in clinical care, building upon the infrastructure that we have already built to deliver genomic medicine in the EHR

Completed Funding

2004-2005	Development award supported by CFAR - P30 AI54999 (PI) Genetic Basis of NNRTI Toxicity in HIV Patients
2004-2005	Development award supported by CFAR - P30 AI54999 (Co-PI) A Pilot Study of Mitochondrial Genetics and Peripheral Neuropathy during Antiretroviral Therapy
2004-2008	NIH R01 AG020135 (PI of subcontract) Revealing Epistasis in Alzheimer Disease
2005-2007	Development award supported by SPORE - P50 CA098131 (PI) Approaches to Genome-Wide Association in Sporadic Breast Cancer
2006-2009	AVCF- Vanderbilt (Co-investigator) DNA Capture Project – Dan Roden 9/28/2007-7/31/2011
2006-2009	NIH R21 HL0877226 (Co-investigator) Iron as a Nutritional Modifier of Toxic Neuropathy in HIV/AIDS – Asha Kallianpur 9/27/06-7/31/09
2007-2009	NIH R01 CA122756 (Co-investigator) Cell Cycle/Apoptosis Gene Variants and Breast Cancer – Jiyang Cai 12/1/2007-11/30/2011
2007-2009	NIH/NIA R01 AG027944 (Co-investigator) Genomic Convergence in Alzheimer Disease – Pericak-Vance, Univ. of Miami 12/01/2007-11/30/2012

Curriculum Vitae: Marylyn DeRiggi Ritchie

2008-2009 NCCAM R01 AT004660 (Co-investigator)  
Dietary Calcium and Magnesium, Genetics and Colorectal Adenoma – Qi Dai  
06/01/2008-05/31/2012

2006-2009 NIH R21 NS059330 (Co-investigator)  
Mitochondrial Genomics and Peripheral Neuropathy during HIV Therapy – Todd  
Hulgan  
3/15/2007-6/30/2010

2004-2010 NIH U01 HL065962 (PI of core)  
Pharmacogenomics of Arrhythmia Therapy – Dan Roden  
9/01/2005-8/31/2010

2007-2011 NIH U01 HG004603-01 (Co-investigator)  
Vanderbilt Genome-Electronic Records Project – Dan Roden  
9/28/2007-7/31/2011

2007-2011 NIH U01 HG004608 (PI of subcontract)  
Genome-Wide Study of Cataract and Low HDL in the Personalized Medicine  
Research Project – Catherine McCarty  
9/30/2007-9/29/2011

2009-2013 NIH/NLM 1R01LM009989-01A1 (Malin)  
Technologies to Enable Privacy in Biomedical Databanks  
07/01/2009-06/30/2013

2009-2011 NIH/NIGMS 1RC2GM092618-01 (Masys)  
VESPA: Vanderbilt Electronic Systems for Pharmacogenomic Assessment  
09/30/2009-09/29/2011

2010-2015 NIH U01 HL065962 (PI of core)  
Pharmacogenomics of Arrhythmia Therapy – Dan Roden  
9/01/2010-8/31/2015

2009-2013 NIH/NLM 1R01 LM010040-01(PI)  
Analysis Tool for Heritable and Environmental Network Associations  
07/01/2009-06/30/2013

2008-2013 NIH/NIAID 5R01 AI077505-03 (Haas)  
Pharmacogenomics of HIV Therapy  
07/08/2008-06/30/2013

2009-2013 NIH/NHGRI 5U01 HG004798-03  
Epidemiologic Architecture for Genes Linked to Environment (Crawford)  
07/17/2008-12/31/2013

2011-2015 NIH/NHGRI 5U01 HG006385 (Haines, Ritchie PI subcontract)  
eMERGE II Coordinating Center  
08/15/2011-07/31/2015

2013-2014 Geisinger contract (Ritchie PI)  
Geisinger Clinic Genetic Studies: Mining Electronic Health Records for Genetic  
Associations  
8/01/2013-7/31/2014

## Curriculum Vitae: Marylyn DeRiggi Ritchie

2010-2016	5U01 HL065962 (Roden, Ritchie PI U19-subcontract) Pharmacogenomics of Arrhythmia Therapy: P-STAR Network Resource 09/01/2010-08/31/2016
2011-2016	5U01 HG006389 (McCarty, Ritchie PI subcontract) IRIS: Incorporating Research into Sight: eMERGE II 08/15/2011-07/31/2016
2011-2016	3 UL1 RR033184-01 (Sinoway) CTSA (Clinical and Translational Science Award) 3/1/2011-2/29/2016
2015-2016	R01GM111913 (Mirshahi and Robishaw) An integrated approach to study GPCR variants associated with complex diseases. 06/01/2015-8/30/2016
2016-2017	1OT2OD024609-01 (Ledbetter and Ritchie) Precision Medicine at Geisinger 09/27/2016 – 05/31/2017
2015-2017	1 U01 HG008679-01 (Williams and Ritchie) EMR-Linked Biobank for Translational Genomics (part of eMERGE-III network) 09/01/2015-12/18/2017
2015-2017	SAP 4100070267 (Ritchie) (Pennsylvania Department of Health) Integrating Big Data for Biomedical Discovery: Methods, Tools, and Applications 6/1/2015-12/18/2017
2013-2017	2 P01 ES011269-11 (Van de Water, Ritchie sub) EPA: 83543201 (Van de Water, Ritchie sub) UC. Davis Center for Children's Environmental Health and Disease Prevention (CCEH) 06/01/2013 – 12/18/2017
2018-2019	P50GM115318-04S1 (Krauss, Ritchie PI Informatics Core) Pharmacogenomics of Statin Therapy (Informatics Core) – administrative supplement \$245,954 09/01/2018-08/31/2019
2015-2021	P50GM115318-01 (Krauss, Ritchie PI Informatics Core) Pharmacogenomics of Statin Therapy (Informatics Core) \$150,000 07/01/2015-08/30/2021
2015-2021	5R01 AI077505 (MPI, Haas and Ritchie) Pharmacogenomics of HIV Therapy \$243,000 07/01/2015-12/31/2021
2016-2021	R01AI116794-01A1 (Moore) Biomedical Computing and Informatics Strategies for Infectious Disease Research \$343,833 04/01/16 – 03/31/21

## BIBLIOGRAPHY

### Peer-Reviewed Research Papers

1. **Ritchie MD**, Hahn LW, Roodi N, Bailey LR, Dupont WD, Plummer WD, Parl FF, Moore JH. Multifactor dimensionality reduction reveals high-order interactions among estrogen metabolism

Curriculum Vitae: Marylyn DeRiggi Ritchie

- genes in sporadic Breast Cancer. *American Journal of Human Genetics*, 69:138-147 (2001). PMID: 11404819, PMCID: PMC1226028
2. Moore JH, Hahn LW, **Ritchie MD**, Thornton TA, White BC. Application of genetic algorithms to the discovery of complex genetic models for simulation studies in human genetics. In: Langdon WB, Cantu-Paz E, Mathias K, Roy R, Davis D, Poli R, Balakrishnan K, Honavar V, Rudolph G, Wegener J, Bull L, Potter MA, Schultz AC, Miller JF, Burke E, and Jonoska N, eds. *Proceedings of the Genetic and Evolutionary Computation Conference, Morgan Kaufmann Publishers*, San Francisco, 1150-55 (2002). PMID: 23413413, PMCID: PMC3569849
  3. Donaldson JC, Dise RS, **Ritchie MD**, Hanks SK. Nephrocystin conserved domains involved in targeting to epithelial cell-cell junctions, interaction with filamins, and establishing cell polarity. *Journal of Biological Chemistry*, 277, 29028-29035 (2002). PMID: 12006559
  4. Hahn LW, **Ritchie MD**, Moore JH. Multifactor dimensionality reduction software for detecting gene-gene and gene-environment interactions. *Bioinformatics*, 19, 376-382 (2003). PMID: 12584123
  5. **Ritchie MD**, Hahn LW, Moore JH. Power of Multifactor Dimensionality Reduction for detecting gene-gene and gene-environment interactions in the presence of genotyping error, missing data, phenocopy, and genetic heterogeneity. *Genetic Epidemiology*, 24, 150-157 (2003). PMID: 12548676
  6. **Ritchie MD**, White B, Parker JS, Hahn LW, and Moore JH. Optimization of neural network architecture improves the power to identify gene-gene interaction in common diseases. *BMC Bioinformatics*, 4:28 (2003). PMID: 12846935, PMCID: PMC183838
  7. Moore JH, Thornton TA, **Ritchie MD**. Basic statistics. *Curr Protoc Hum Genet*. 2003 Aug; Appendix 3: Appendix 3M. doi: 10.1002/0471142905.hga03ms37. PMID: 18428338
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389. Wen J, Zhao B, Yang Z, Erus G, Skampardon I, Mamourian E, Cui Y, Hwang G, Bao J, Boquet-Pujadas A, Zhou Z, Veturi Y, Ritchie MD, Shou H, Thompson PM, Shen L, Toga AW, Davatzikos C. The Genetic Architecture of Multimodal Human Brain Age. *bioRxiv.* 2023 Sep 30:2023.04.13.536818. doi: 10.1101/2023.04.13.536818. Preprint. PMID: 37333190. PMCID: PMC10274645
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391. Tong B, Risacher SL, Bao J, Feng Y, Wang X, Ritchie MD, Moore JH, Urbanowicz R, Saykin AJ, Shen L. Comparing Amyloid Imaging Normalization Strategies for Alzheimer's Disease Classification using an Automated Machine Learning Pipeline. *AMIA Jt Summits Transl Sci Proc.* 2023 Jun 16;2023:525-533. eCollection 2023. PMID: 37350880. PMCID: PMC10283108
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## Curriculum Vitae: Marylyn DeRiggi Ritchie

- Giles JR, Skelly AN, Felley LE, McLaughlin M, Weaver J; Penn Medicine BioBank; Kuthuru O, Dougherty J, Adamski S, Long S, Kee M, Clendenin C, da Silva Antunes R, Grifoni A, Weiskopf D, Sette A, Huang AC, Rader DJ, Hensley SE, Bates P, Greenplate AR, Wherry EJ. Prior vaccination promotes early activation of memory T cells and enhances immune responses during SARS-CoV-2 breakthrough infection. *Nat Immunol.* 2023 Oct;24(10):1711-1724. doi: 10.1038/s41590-023-01613-y. Epub 2023 Sep 21. PMID: 37735592
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## Peer-Reviewed Review Papers

1. Moore JH, **Ritchie MD**. STUDENTJAMA. The challenges of whole-genome approaches to common diseases. *JAMA*, 291:1642-1643 (2004). PMID: 15069055
2. **Ritchie MD**. Trends in genomic variation: a view of some of the latest technologies. *Drug Discovery Today*, 10(21):1417-1418 (2005). PMID: 16243260
3. **Ritchie MD**. Bioinformatics approaches for detecting gene-gene and gene-environment interactions in studies of human disease: a neurological focus. *Neurosurgical Focus*, 19(4):E2 (2005). PMID: 16241104
4. **Ritchie MD**, Motsinger AA. Multifactor Dimensionality Reduction for detecting gene-gene and gene-environment interactions in pharmacogenomics studies. *Pharmacogenomics*, 6(8):823-34 (2005). PMID: 16296945

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5. McKinney BA, **Ritchie MD**, Moore JH. Machine learning for detecting gene-gene interactions. *Applied Bioinformatics*, 5:77-88 (2006). PMID: 16722772, PMCID: PMC3244050
6. Motsinger A, Haas D, Hulgán T, **Ritchie M**. Human genomic association studies: a primer for infectious disease specialists. *Journal of Infectious Disease*, 195:1737-44 (2007). PMID: 17492588
7. Crawford DC, **Ritchie MD**, Rieder MJ. Identifying the genotype behind the phenotype: a role model found in VKORC1 and its association with warfarin dosing. *Pharmacogenomics*, 8:487-96 (2007). PMID: 17465713, PMCID: PMC3112050
8. **Ritchie MD**, Edwards TL, Fanelli TJ, Motsinger AA. Genetic heterogeneity is not as threatening as you might think. *Genetic Epidemiology*, 31:797-800 (2007). PMID: 17654613
9. Motsinger AA, **Ritchie MD**, Reif DM. Novel methods for detecting epistasis in pharmacogenomics studies. *Pharmacogenomics*, 8:1229-1241 (2007). PMID: 17924838
10. Motsinger AA, **Ritchie MD**. Neural networks for genetic epidemiology: past, present, and future. *BMC BioData Mining*, 1:3 (2008). doi: 10.1186/1756-0381-1-3. PMID: 18822147, PMCID: PMC2553772
11. Vineis P, Brennan P, Canzian F, Ioannidis JPA, Matullo G, **Ritchie M**, Stromberg U, Taioli E, Thompson J. Expectations and challenges stemming from genome-wide association studies. *Mutagenesis*, 23(6):439-44 (2008). doi: 10.1093/mutage/gen042. Epub 2008 Sep 2. PMID: 18765424
12. Srinivasan BS, Chen J, Cheng C, Conti D, Duan S, Fridley BL, Gu X, Haines JL, Jorgenson E, Kraja A, Lasky-Su J, Li L, Rodin A, Wang D, Province M, and **Ritchie MD**. Methods for analysis in pharmacogenomics: Lessons from the Pharmacogenetics Research Network (PGRN) Analysis Group. *Pharmacogenomics*, 10:243-51 (2009). doi: 10.2217/14622416.10.2.243. PMID: 19207025, PMCID: PMC2737060
13. **Ritchie MD**, Bush WS. Genome simulation approaches for synthesizing in silico datasets for human genomics. *Adv Genet*, 72: 1-24 (2010). doi: 10.1016/B978-0-12-380862-2.00001-1. PMID: 21029846
14. Grady BJ and **Ritchie MD**. Statistical optimization of pharmacogenomics association studies: Key Considerations from Study Design to Analysis. *CPPM*, 9:1; 41-66. 2011 PMID: 21887206, PMCID: PMC3163263
15. Holzinger ER, **Ritchie MD**. Integrating heterogeneous high-throughput data for meta-dimensional pharmacogenomics and disease-related studies. *Pharmacogenomics*. 2012 Jan;13(2):213-22. doi: 10.2217/pgs.11.145. PMID: 22256870, PMCID: PMC3350322
16. **Ritchie MD**. The success of pharmacogenomics in moving genetic association studies from bench to bedside: study design and implementation of precision medicine in the post-GWAS era. *Hum Genet*. 2012 Oct;131(10):1615-26. doi: 10.1007/s00439-012-1221-z. Epub 2012 Aug 25. PMID: 22923055, PMCID: PMC3432217
17. Chhibber A, Kroetz DL, Tantisira KG, McGeachie M, Cheng C, Plenge R, Stahl E, Sadee W, **Ritchie MD**, Pendergrass SA. Genomic architecture of pharmacological efficacy and adverse events. *Pharmacogenomics*. 2014 Dec;15(16):2025-48. doi: 10.2217/pgs.14.144. PMID: 25521360, PMCID: PMC4308414.
18. **Ritchie MD**, Holzinger ER, Li R, Pendergrass SA, Kim D. Methods of integrating data to uncover genotype-phenotype interactions. *Nat Rev Genet*. 2015 Feb;16(2):85-97. doi: 10.1038/nrg3868. Epub 2015 Jan 13. Review. PMID: 25582081
19. Klein TE, **Ritchie MD**. PharmCAT: A Pharmacogenomics Clinical Annotation Tool. *Clin Pharmacol Ther*. 2017 Dec 1. PMID: 29194583
20. Verma A, **Ritchie MD**. Current Scope and Challenges in Phenome-Wide Association Studies. *Current Epidemiology Reports*. December 2017, Volume 4, Issue 4, pp 321-329. PMID:29545989; PMCID:PMC5846687

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21. Verma SS, **Ritchie MD**. Another Round of "Clue" to Uncover the Mystery of Complex Traits. *Genes* (Basel). 2018 Jan 25;9(2). pii: E61. [PMID: 29370075](#)
22. Basile AO, **Ritchie MD**. Informatics and machine learning to define the phenotype. *Expert Rev Mol Diagn*. 2018 Mar;18(3):219-226. doi: 10.1080/14737159.2018.1439380. Epub 2018 Feb 16. [PMID:29431517](#)
23. **Ritchie MD**, Van Steen K. The search for gene-gene interactions in genome-wide association studies: challenges in abundance of methods, practical considerations, and biological interpretation. *Ann Transl Med*. 2018 Apr;6(8):157. doi: 10.21037/atm.2018.04.05. [PMID:29862246](#). [PMCID: PMC5952010](#)
24. **Ritchie MD**, Large-Scale Analysis of Genetic and Clinical Patient Data. *Annual Rev Biomedical Data Science*. 2018. Vol. 1:263-274.
25. Li R, Chen Y, **Ritchie MD**, Moore JH. Electronic health records and polygenic risk scores for predicting disease risk. *Nat Rev Genet*. 2020 Mar 31. doi: 10.1038/s41576-020-0224-1. [PMID: 32235907](#).

## Non-Peer Reviewed Papers/Chapters/Books

1. Moore JH, Thornton TA, **Ritchie MD**. Basic statistics. In: Dracopoli NC, Haines JL, Korf BR, Moir DT, Morton CC, Seidman CE, Seidman JG, Smith DR. (eds). *Current Protocols in Human Genetics*. Wiley-Liss, Inc., New York, A.3M.1-A.3M.10 (2003).
2. **Ritchie MD**, White BC, Parker JS, Hahn LW, Moore JH. Optimization of neural networks using genetic programming improves detection and modeling of gene-gene interactions in studies of human diseases. *Genetic and Evolutionary Computation Conference Proceedings* (2003). [PMID: 12846935](#), [PMCID: PMC183838](#)
3. **Ritchie MD**, Moore JH. Biological applications of genetic and evolutionary computation. *Genetic and Evolutionary Computation Conference Workshop Proceedings* (2004).
4. **Ritchie MD**. Model Validation in Biological Applications of Genetic and Evolutionary Computation. *Genetic and Evolutionary Computation Conference Workshop Proceedings* (2004).
5. **Ritchie MD**. A review of computational approaches for detecting interactions. Educational Program. *American Association of Cancer Research* (2005).
6. Wilke RA, Carrillo MW, **Ritchie MD**. Pacific symposium on biocomputing - computational approaches for pharmacogenomics. *Pharmacogenomics*, 6(2):111-3 (2005). [PMID: 15882130](#)
7. **Ritchie MD**, Carillo MW, Wilke RA. Computational approaches for pharmacogenomics. *Pacific Symposium on Biocomputing Proceedings*. 2005:245-7. [PMID: 15759630](#)
8. Carillo MW, Wilke RA, **Ritchie MD**. Computational approaches for pharmacogenomics. *Pacific Symposium on Biocomputing Proceedings*, 11:544-546 (2006). [PMID: 15759630](#)
9. Williams SM, Canter JA, Crawford DC, Moore JH, **Ritchie MD**, Haines JL. Problems with genome-wide association studies. *Science*. 2007 Jun 29;316(5833):1840-2. [PMID: 17605173](#)
10. Aguilar-Ruiz J, Moore JH, **Ritchie MD**. Filling the gap between Biology and Computer Science. *BioData Mining*, 1:1 (2008). doi: 10.1186/1756-0381-1-1. [PMID: 18822148](#), [PMCID: PMC2547862](#)
11. Haines JL, Crawford DC, **Ritchie MD**. A Primer in Statistical Methods in Genetics. In: Roden DM (ed), *Cardiovascular Genetics and Genomics*, Blackwell publishing (2009).
12. Pizzuti C, **Ritchie MD**, Giacobini M (eds). *Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics: 7<sup>th</sup> European Conference, Proceedings EvoBIO 2009*. Springer publishing (2009).

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13. Moore JH, Clegg J, Marchiori E, **Ritchie MD**, and Smith S. Artificial Evolution Methods in the Biological and Biomedical Sciences. *JAEA*. 2009.
14. Pizzuti C, **Ritchie MD**, Giacobini M (eds). *Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics: 8<sup>th</sup> European Conference, Proceedings EvoBIO 2010*. Springer publishing (2010).
15. **Ritchie MD**, Bush WS. Genome Simulation: Approaches for Synthesizing *In Silico* Datasets for Human Genomics. In: *Advances in Genetics, Vol. 72*, Elsevier Inc (2010). doi: 10.1016/B978-0-12-380862-2.00001-1. [PMID: 21029846](#)
16. Moore JH, **Ritchie MD**. The central role of biological data mining in connecting diverse disciplines. *BioData Mining* 2013, 6:14. doi: 10.1186/1756-0381-6-14. [PMID: 23937773](#), [PMCID: PMC3765075](#)
17. **Ritchie MD**, Reducing Dimensionality in the Search for Gene-Gene Interactions. In: *Between the Lines of Genetic Code*. Elsevier Inc (2014).
18. **Ritchie MD**. Finding the Epistasis Needles in the Genome-Wide Haystack. In: *Epistasis: Methods and Protocols, Methods Mol Biol*. 2015;1253:19-33. doi: 10.1007/978-1-4939-2155-3\_2. [PMID: 25403525](#)
19. **Ritchie MD**, Study design and analysis approaches in pharmacogenomics research. In: *Pharmacogenomics: Applications to Patient Care*, Third Edition. ACCP (2015).
20. **Ritchie MD**, Moore JH, Kim JH. Translational Bioinformatics: Biobanks in the Precision Medicine Era. *Pac Symp Biocomput*. 2020;25:743-747. [PMID: 31797645](#)
21. Moore JH, Barnett I, Boland MR, Chen Y, Demiris G, Gonzalez-Hernandez G, Herman DS, Himes BE, Hubbard RA, Kim D, Morris JS, Mowery DL, **Ritchie MD**, Shen L, Urbanowicz R, Holmes JH. Ideas for how informaticians can get involved with COVID-19 research. Version 2. *BioData Min*. 2020 May 12;13:3. doi: 10.1186/s13040-020-00213-y. eCollection 2020. [PMID: 32419848](#); [PMCID: PMC7216865](#)
22. Scott WS, **Ritchie MD** (eds.) *Genetic Analysis of Complex Disease*, 3<sup>rd</sup> edition. Wiley, in press 2021. <https://www.wiley.com/en-us/Genetic+Analysis+of+Complex+Disease%2C+3rd+Edition-p-9781118123911> ISBN: 978-1-118-12391-1

## ABSTRACT CONTRIBUTED PRESENTATIONS

2003 “Optimization of Neural Networks using Genetic Programming to Improve Detection and Modeling of Gene-Gene Interactions in Studies of Human Diseases,” Biological Applications in Genetic and Evolutionary Computation, Chicago, IL (Host: Wolfgang Banzhaf, peer-reviewed)

2003 “Optimization of Neural Networks using Genetic Programming to Improve Detection and Modeling of Gene-Gene Interactions in Studies of Human Diseases,” Genetic and Evolutionary Computation Conference, Chicago, IL (Host: James Foster)

2004 “How Can We Detect Gene-Gene Interactions in Pharmacogenomic Studies?” Pharmacogenetics Research Network - Statistics Workshop, Los Angeles, CA (Host: Mike Province)

2004 “Model Validation Strategies in Biological Applications of Genetic and Evolutionary Computation,” Biological Applications of Genetic and Evolutionary Computation Workshop, Seattle, WA (Host: Jason Moore, peer-reviewed)

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2004 “GPNN as a Bioinformatics Tool for Human Genetics,” Genetic and Evolutionary Computation Conference, Seattle, WA (Host: James Foster, peer reviewed)

2004 “MDR Reveals Gene-Gene Interactions Associated with Multiple Sclerosis,” American Society of Human Genetics, Toronto, Canada, peer-reviewed

2004 “Gene-Gene Interaction Associated with Response to Treatment of Unipolar Major Depression Disorder,” Cold Spring Harbor Laboratory: Pharmacogenomics, Cold Spring Harbor, NY, Peer-reviewed

2005 “Computational Approaches for Pharmacogenomics,” Session Introduction at the Pacific Symposium on Biocomputing, The Big Island, HI (Host: Russ Altman, peer-reviewed)

2005 “Computational Approaches for Pharmacogenomics,” Leader of Discussion Session at the Pacific Symposium on Biocomputing, The Big Island, HI (Host: Russ Altman)

2005 “Can Neural Network Constraints in GP Provide Power to Detect Genes Associated with Human Disease?” European Workshop on Evolutionary Computation and Bioinformatics, Lausanne, Switzerland (Host: Elena Marchiori, peer-reviewed)

2005 “Multifactor Dimensionality Reduction and the Power to Detect Pharmacogenomic Effects in Treatment of Tenureitis,” Pharmacogenetics Research Network Statistics Workshop, Chicago, IL (Host: Nancy Cox and Mike Province, peer-reviewed)

2005 “Challenges and Strategies for Whole Genome Association Studies,” American Society of Human Genetics, Salt Lake City, UT (Host: David Cox, peer-reviewed) *Given by Dr. Jonathan Haines due to maternity leave*

2006 “Tutorial on Computational Approaches for Pharmacogenomics,” Pacific Symposium on Biocomputing, Maui, Hawaii (Host: Larry Hunter, peer-reviewed) *Given by Alison A. Motsinger due to maternity leave*

2006 “GenomeSim: Data Simulation Software for Whole-Genome Association Studies,” Pacific Symposium on Biocomputing, Maui, HI (Host: Russ Altman, peer-reviewed) *Given by Alison A. Motsinger due to maternity leave*

2006 “Grammatical Evolution Neural Networks: A Powerful Gene-Gene Interaction Detection Method,” Genetic Analysis Workshop Special Session, St. Petersburg, FL (Host: Jean MacCleur, peer-reviewed)

2006 “The Potential of a Sequential Replication Approach for Whole Genome Association Studies,” International Genetic Epidemiology Society, Tampa, FL (Host: Jeanne Cashman, peer-reviewed)

2006 “PLATO: A Platform for the Analysis, Translation, and Organization of Large Scale Data,” Pharmacogenetics Research Network Analysis Workshop, Nashville, TN (Host: Mike Province, peer-reviewed)

2008 “Thinking about Epistasis in Whole Genome Association Studies,” Pharmacogenetics Research Network Analysis Workshop, Memphis, TN (Host: Mary Relling, peer-reviewed)

2009 “Genome-wide association study identifies novel genomic regions associated with drug-induced Long QT Syndrome,” CSHL-Wellcome Trust Pharmacogenomics Meeting, Hinxton, UK. (Host: Steve Leeder, peer-reviewed)

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- 2009 “Genome-wide association study identifies novel genomic regions associated with drug-induced Long QT Syndrome,” American Society for Human Genetics, Honolulu, HI. (peer-reviewed)
- 2010 “Using Biological Knowledge to Guide the Search for Epistasis in Genome-Wide Association Studies”, American Society of Human Genetics, Washington DC. peer-reviewed
- 2010 “Chromosome 4q25 variants are genetic modifiers of rare ion channel mutations associated with familial atrial fibrillation”, American Society of Human Genetics, Washington DC. peer-reviewed
- 2010 “Rare and Common Variants for Atrial Fibrillation”, PGRN Statistical Analysis Workshop, Nashville, TN. peer-reviewed
- 2011 “Meta-dimensional analysis of phenotypes”, International Congress on Human Genetics, Montreal, Canada, peer-reviewed
- 2012 “Meta-dimensional Analysis Of Complex Biological Traits Using ATHENA”, Genetic Programming Theory in Practice, Ann Arbor, MI. peer-reviewed
- 2013 “Using Biological Knowledge in Modern Genomic Analysis of Complex Traits”, Epistasis Discovery in Genetic Epidemiology (EDGE) 2013 Workshop, Key West, FL
- 2013 “Next generation analysis of human genome sequence”, Pharmacogenomics Research Network Scientific Meeting, Chicago IL. peer-reviewed
- 2014 “Rare Variants in the Pharmacogenomics Studies “, American Society of Clinical Pharmacology and Therapeutics (ASCPT), Atlanta, GA
- 2015 “Binning Somatic Mutations based on Biological Knowledge for Predicting Survival: an Application in Renal Cell Carcinoma”, Pacific Symposium on Biocomputing (PSB), Big Island, Hawaii
- 2016 “The Public Sharing of Genomic Data from the DiscovEHR Collaboration”, American Society of Human Genetics, Vancouver, Canada

**INVITED PRESENTATIONS**

- 2001 “Approaches to Detecting Epistasis in Sporadic Breast Cancer,” The Second Annual Genetics Symposium, Meharry Medical College, Nashville, TN (Host: Ellen Wright Clayton)
- 2001 “An Introduction to Neural Network Models for Statistical Data Analysis,” Quantitative Brown Bag Seminar Series, Vanderbilt University, Nashville, TN (Host: Niels Waller)
- 2001 “Quantitative Resources on the WWW,” Quantitative Brown Bag Seminar Series, Vanderbilt University, Nashville, TN (Host: Niels Waller)
- 2001 “Gene-Gene Interactions in Common, Complex Diseases,” Molecular Physiology and Biophysics Seminar Series, Vanderbilt University, Nashville, TN (Host: Alan Cherrington)



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- 2002 “Genetic Programming Optimization of Neural Network Architecture for the Detection of Gene-Gene Interactions,” Biomathematics Seminar Series, Vanderbilt University, Nashville, TN (Host: Peter Hinow)
- 2002 “Neural Networks for Detecting Gene-Gene Interactions,” Molecular Physiology and Biophysics Seminar Series, Vanderbilt University, Nashville, TN (Host: Alan Cherrington)
- 2003 “Data Reduction and Pattern Recognition Approaches for Complex Genetic Analysis,” Statistical Genetics Seminar Series, Rockefeller University, New York, NY (Host: Jurg Ott, invited)
- 2003 “Data Reduction and Pattern Recognition Approaches for Complex Genetic Analysis,” Clinical Epidemiology and Biostatistics Faculty Candidate Seminar, University of Pennsylvania, Philadelphia, PA (Host: Tim Rebbeck, invited)
- 2003 “Data Reduction and Pattern Recognition Approaches for Complex Genetic Analysis,” Bioinformatics Faculty Candidate Seminar, Medical University of South Carolina, Charleston, SC (Host: Eberhard Voit, invited)
- 2003 “Data Reduction and Pattern Recognition Approaches for Complex Genetic Analysis,” Human Genetics Faculty Candidate Seminar Series, Wake Forest University, Winston-Salem, NC (Host: Stephen Rich, invited)
- 2003 “Computational Approaches for Detecting Gene-Gene Interactions,” Intelligent Systems for Molecular Biology Conference, Brisbane, Australia (Host: Mark Ragan, invited)
- 2003 “Optimization of Neural Networks using Genetic Programming to Improve Detection and Modeling of Gene-Gene Interactions in Studies of Human Diseases,” National Library of Medicine Training Directors’ Conference, Bethesda, MD (Host: Carol Bean, invited)
- 2003 “Neural Networks for Detecting Gene-Gene Interactions,” Epidemiology Faculty Candidate Seminar Series, Wake Forest University, Winston-Salem, NC (Host: Lynne Wagenknecht, invited)
- 2003 “Data Mining and Pattern Recognition Approaches for Detecting Gene-Gene Interactions,” Statistical Genetics Interview Seminar, Bristol-Myers Squibb, Hopewell, NJ (Host: Kim Zerba, invited)
- 2003 “Computational Approaches for Detecting Gene-Gene Interactions,” Molecular Physiology & Biophysics Faculty Candidate Seminar Series, Vanderbilt University, Nashville, TN (Host: Alan Cherrington, Jonathan Haines)
- 2003 “Neural Networks for Detecting Gene-Gene Interactions,” Department of Human Genetics, University of Pittsburgh, Pittsburgh, PA (Host: Bob Ferrell, invited)
- 2004 “Analysis of Genome-Wide Epistasis via Dimensionality Reduction Procedures,” International Biometric Society, Eastern North American Region 2004, Pittsburgh, PA (Host: David Allison, invited)
- 2004 “How to Look for Gene-Gene Interactions using Multifactor Dimensionality Reduction,” Vanderbilt University GCRC Skills Workshop, Nashville, TN (Host: Dan Byrne)
- 2004 “Genome-Wide Association Studies: Challenges, Strategies, and MDR,” Vanderbilt University Genetic Interest Group Seminar Series, Nashville, TN (Host: Kelly McDermott)

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2004 “Neural Networks Approaches for Genetic Studies,” Marshfield Clinic Research Foundation Scientific Seminar Series, Marshfield, WI (Host: Russell Wilke, invited)

2004 “Dissecting the Genetics of Complex Disease,” National Society of Genetic Counselors, Washington, DC, invited

2005 “Parallel Multifactor Dimensionality Reduction: Applications in Rheumatoid Arthritis,” Invited Presentation, Universitat Politecnica, Barcelona, Spain (Host: Sara Marsal, invited)

2005 “Computational Approaches to Detecting Interactions,” Educational Session on Gene-Gene Interactions in Cancer Etiology at the AACR, Anaheim, CA (Host: Jason Moore, invited)

2005 “Multifactor Dimensionality Reduction for Detecting Epistasis,” Joint Conference of the Classification Society of North America and the Interface Foundation of North America, St. Louis, MO (Host: Rob Culverhouse, invited)

2005 “Multifactor Dimensionality Reduction for the Analysis of Pharmacogenomics Data,” Beyond Genome 2005: Genomic Variation, San Francisco, CA (Host: Catherine Liscandra, peer-reviewed)

2005 “Detecting Gene-Gene Interactions Using Multifactor Dimensionality Reduction,” Joint Statistical Meetings, Minneapolis, MN (Host: Cheng Cheng, invited)

2005 “Multifactor Dimensionality Reduction for the Analysis of Epistasis in Studies of Human Disease and Pharmacogenomics,” Boehringer-Ingelheim Invited Special Seminar, Danbury, CT (Host: Supriya Jayadev, invited)

2005 “Data Mining Approaches in Biological Sciences,” Fields Institute on Data Mining, Toronto, Canada (Host: Helmut Kroger, invited)

*Given by Will Bush due to maternity leave*

2006 “The Complexities of Data Analysis in Human Genetics,” Complex Data Conference, Vanderbilt University Kennedy Center, Nashville, TN (Host: Jennifer Blackford, invited)

2006 “Multifactor Dimensionality Reduction for Detecting Gene-Gene and Gene-Environment Interactions,” Vanderbilt University Center for AIDS Research, Nashville, TN (Host: Todd Hulgan, invited)

2006 “Challenges and Strategies for Whole-Genome Association Studies,” Boehringer Ingelheim Invited Speaker, Danbury, CT (Host: Jing Yuan, invited)

2007 “Computational Genetics Approaches in Cancer Epidemiology,” University of Miami Bio-behavioral Oncology and Cancer Control Program Meeting, Miami, FL (Host: Jennifer Hu, invited)

2007 “The MDR Approach,” ECNIS WP 7-8 Workshop, “AFTER GWAS: an Exercise in Problem Solving,” Venice, Italy (Host: Paolo Vineis, invited)

2007 “Computational Genomics in the Whole Genome Era,” University of Virginia, Charlottesville, NC (Host: Stephen Rich, invited)

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2008 “Computational Genomics in the Whole Genome Era,” Washington University in St. Louis, St. Louis, MO (Host: Mike Province, invited)

2008 “A Bio-filter for Systems Biology,” NEWGENERIS Workshop, Athens, Greece (Host: S.A. Kyrtopoulos, invited)

2008 “Epistasis Modeling,” Keystone Symposium on Towards Identifying the Pathophysiology of Autistic Syndromes, Santa Fe, NM (Host: Joseph Piven and Pat Levitt, invited)

2008 “Epistasis, Stratification, and Confounding: Lessons from Genomic Analyses,” ASCPT, Orlando, FL (Host: Issam Zineh, invited)

2008 “Computational Genomics in the GWAS Era,” NIEHS, Raleigh-Durham, NC (Host: Gregg Dinse, invited)

2009 Invited Seminar, University of Alabama Department of Genetics, Birmingham, AL (Host: Hemant Tiwari, invited)

2009 “Computational Strategies for Genome-Wide Association Studies,” Korea Pharmacogenetics Research Network Annual Symposium, Seoul, Korea (Host: Ju Han Kim, invited)

2009 “Individual Opt-Out: Efficacy, Challenges, and Concerns,” American Society for Human Genetics, Honolulu, HI. (Host: Laura Rodriguez, invited)

2009 “Genome Wide Association Studies,” Annual Education Conference of the National Society of Genetic Counselors, Atlanta, GA.

2010 “Summary of the state-of-the-art for gene-gene interaction analysis,” CDGCA, Belgium, Host: Kristel Van Steen, invited

2010 “Beyond GWAS: Integrating Transcriptome, Proteome, and Pathway Data in the Genetic Dissection of Complex Traits”, Huck Institutes of Life Sciences, Pennsylvania State University, State College, PA

2011 “Pharmacogenetics using the electronic medical record and a large institutional biobank”, Dartmouth Medical School, Lebanon, NH

2011 “Bringing Biology Back to Human Genomics”, University of Nottingham, Nottingham, UK

2011 “Surfing the Tsunami of Human Genetic Data”, University of Idaho, Moscow, ID

2011 “Phenotype-Genotype Associations in DNA Biobanks Linked to Electronic Medical Records”, Asia-Pacific Translational Bioinformatics Conference, Seoul, Korea

2011 “Using Biological Knowledge in Modern Genomic Analysis of Complex Traits”, University of California at Davis (Host: Isaac Pessah)

2011 “Using biological knowledge to inform complex genetics analysis”, NIEHS meeting Bioinformatics and Computational Approaches to Integrate Genes and Environment in Autism Research, Durham, NC

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- 2011 “Beyond GWAS: Integrating Transcriptome, Proteome, and Pathway Data in the Genetic Dissection of Complex Traits”, Flash Poster Talk, Kavli Frontiers in Science, National Academy of Science, Irvine, CA
- 2011 “Genomics and Pharmacogenomics using the electronic medical record and a large institutional biobank”, Geisinger Clinic, Weis Center for Research, Danville, PA (Host: David Carey)
- 2012 “Meta-Dimensional Analysis of Phenotypes to Dissect the Architecture of Complex Traits”, Keystone Symposium, Complex Traits: Genomics and Computational Approaches, Breckenridge, CO
- 2012 “Mining electronic health records for genomic research – experiences of the eMERGE network”. Inaugural Symposium of Penn State Hershey Institute for Personalized Medicine, Hershey, PA
- 2012 “Searching for the missing heritability in gene-gene and gene-environment interactions”, University of Georgia Symposium, Methodological and Statistical Issues in Gene-Environment and Gene-Gene Interaction Research, Atlanta, GA
- 2012 “The phenome and pleiotropy: Dissecting the architecture of complex traits”, AACR-MEG Special Conference on Post-GWAS Horizons in Molecular Epidemiology: Digging Deeper into the Environment, Hollywood, FL
- 2012 “Meta-Dimensional Analysis for Dissecting the Architecture of Complex Traits”, University of Liege, Liege, Belgium
- 2013 “Overview of pharmacogenomics, gene-gene interactions, system genomics”, Eastern North America Region International Biometric Society 2013, Orlando, FL
- 2013 “Analytic approaches for complex trait analysis”, American Association of Cancer Research Educational Session, Washington DC
- 2013 “The Next Frontier in Genomics: Data Analysis Strategies”, Ohio State University Comprehensive Cancer Center Annual Scientific Meeting, Columbus OH
- 2013 “Complex genetic analysis: Searching for the missing heritability”, Ohio State University, Columbus OH
- 2013 “Analysis technologies to go beyond a single gene: the quest for understanding genetic architecture”, University of Maryland, Baltimore MD
- 2013 “Bioinformatics tools for incorporating biological knowledge into genetic analysis”, Advances in Statistical Methods for Cancer Genetic Epidemiology. Memorial Sloan-Kettering, New York, NY. Host: Sanjay Shete.
- 2013 “Bringing Biology back to Genomics”. University of Pittsburgh, Pittsburgh, PA. Host: Robert Ferrell.
- 2013 “The quest for understanding genetic architecture”, University of Chicago, Chicago IL. Host: Barbara Stranger.
- 2014 “Challenges in Modeling Interactions”, EDGE: Epistasis Discovery in Genetic Epidemiology, Key West, Florida, Host: Jason Moore.

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- 2014 “Top Ten Challenges in Data Simulations”, Genetic Simulation Tools Post-GWAS, National Cancer Institute Workshop, Host: Elizabeth Gillanders and Leah Mechanic
- 2014 “Making sense of genome-phenome relationships“, The Biology of Genomes, Cold Spring Harbor, NY, Host: Carlos Bustamante
- 2014 “Mining the EMR for genome-phenome associations“, Big Data in Biomedicine, Stanford University, Host: Russ Altman
- 2014 “Data fusion in the omic universe”, Mid-Atlantic Genetic Epidemiology & Statistics (MAGES), Children’s Hospital of Philadelphia-U Penn, Host: Marcella Devoto
- 2014 “Big Data”, KAVLI Frontiers in Science, Medan Indonesia, Host: Edward Patte
- 2014 “Exploring the Genetic Architecture of Complex Traits“, UC Davis, Host: Irva Hertz-Piccoto
- 2014 “Exploring Genome-Phenome Relationships in an Electronic Health Record“, CTSI Lecture, Penn State Medical Center, Hershey, PA, Host: Larry Sinoway
- 2014 “Mining electronic health records and genomics”, KOSMI, Pusan S. Korea, Host: Ju Han Kim
- 2015 “Significance of Gene-Gene Interactions/Epistasis”, Pacific Symposium on Biocomputing (PSB), Big Island, Hawaii, Host: Sarah Pendergrass
- 2015 “Exploration of the EHR Universe: Big Data for Predictive Genomics”, Indo-US Bilateral Conferences-cum-Workshop: Big Data Analysis and Translation in Disease Biology (Big Data and Disease)-2015, New Delhi, India, Host: Indira Ghosh
- 2015 “Genomics and the Electronic Health Record - a dynamic duo made for Precision Medicine”, Biomedical Informatics Annual Retreat keynote, Ohio State University, Columbus, Ohio, Host: Phillip Payne
- 2015 “Genomics and the Electronic Health Record - a dynamic duo made for Precision Medicine”, Institute for Computational Biology Symposium, Case-Western Reserve University, Host: Dana Crawford
- 2015 “A game of Clue – which ‘omics are guilty?” IGES-ASHG Joint Symposium, Baltimore, Maryland
- 2015 “Electronic health records and genomics: A dynamic duo for precision medicine”, Presidential Symposium, American Society of Human Genetics, Baltimore, Maryland, Host: Neil Risch
- 2015 “Using genomics and electronic health records for precision medicine - thinking about the future”, Pharmacogenomics Research Network: Research in Progress seminar series, Webinar, Host: Kathy Giacomini
- 2015 “Exploring the Use of Electronic Health Records and Genomics for Precision Medicine”, Biotech Symposia, Simons Foundation and the New York Bioinformatics Group, New York, New York, Host: Doron Betel

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2015 “Electronic health records and genomics – a dynamic duo for precision medicine”, Integrative Biostatistics Research for Imaging, Genomics, & High-throughput Technologies in Precision Medicine (iBRIGHT), Houston, Texas, Host: Pei Weng

2015 “Electronic health records and genomics – a dynamic duo for precision medicine”, Translational Bioinformatics Conference (TBC), Tokyo, Japan, Host: Tomohiro Sawa

2016 “Integrating Genomics into the Electronic Health Record for Precision Medicine”, HCSRN Precision Oncology Symposium, Atlanta, Georgia, Host: Larry Kushi

2016 “Precision Medicine – The Beginning of a Long Voyage”, Keynote at Annual Retreat, Institute for Biomedical Informatics (IBI) and the Graduate Group in Genomics and Computational Biology (GCB), University of Pennsylvania, Philadelphia, Pennsylvania, Hosts: Li-San Wang and Ben Voight

2016 “Methods for Integrating Data to Uncover Genotype-phenotype Interactions”, American Society for Bone and Mineral Research (ASBMR), Atlanta, Georgia, Host: Fernando Rivadeneira

2016 “DNAnexus: The Geisinger Experience”, DNAnexus Connect, San Francisco, California, Host: Angela Anderson

2016 “Genomics and Precision Medicine: approaches and challenges”, University of Pennsylvania, Philadelphia, Pennsylvania, Host: Dan Rader

2017 “Applications in Multi-omics data integration”, No Boundary Thinking Workshop, Pacific Symposium on Biocomputing, Big Island, Hawaii, Host: Jason Moore

2017 “Phenotypes: The next frontier for precision medicine” Precision Medicine Fusion Conference, Cancun, Mexico (my talk by video broadcast), Host: Michael Snyder

2017 “PharmCAT: Pharmacogenomics Clinical Annotation Tool”, Precision Medicine Fusion Conference, Cancun, Mexico (my talk by video broadcast), Host: Michael Snyder

2017 “PharmCAT: A Tool for Pharmacogenomics Implementation”, Clinical Pharmacogenetics Implementation Consortium Meeting, Washington DC, Host: Mary Relling

2017 “PharmCAT: A Tool for Pharmacogenomics Implementation”, NHGRI Genomic Medicine X: Pharmacogenomics, Silver Spring, Maryland, Host: Teri Manolio

2017 “Machine Learning Strategies in the Genome and the Phenome – Toward a Better Understanding of Complex Traits”, Department of Biomedical Informatics, Harvard Medical School, Boston, Massachusetts, Host: Isaac Kohane

2017 “Multi-omics data integration”, European Society of Human Genetics annual meeting, Copenhagen, Denmark

2017 “Meta-dimensional methods for ‘omics data integration”, Retreat talk, Department of Genetics, University of Pennsylvania

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2017 “Precision Medicine: Study Designs, Tools, and Applications”, Tutorial, Translational Bioinformatics Conference, Long Beach, CA, Host: Dokyoon Kim

2017 “What does the future hold in precision medicine?”, Illumina workshop, American Society of Human Genetics annual meeting, Orlando, FL. Host: Jay Kaufman

2017 “Machine learning strategies in the Genome and the Phenome”, University of Virginia seminar, Host: Charles Farber

2017 “It’s All in the Genes: The Science Behind Customizing Patient Care”, ASHP midyear clinical meeting and exposition, Orlando, FL. Host: Cynthia Von Heerigan

2018 “Machine Learning in the Genome and Phenome to Understand Complex Traits: Discovery Science for Precision Medicine”, University of California, San Francisco, PREMIER Symposium. Host: Lindsey Criswell

2018 “PheWAS in Populations: Exploring the relationship between the genome and the phenome”, Lorne Genome Conference 2018, Lorne Australia. Host: Traude Beilharz

2018 “Exploring the relationship between the genome and the phenome”, Melbourne Integrative Genomics (MIG) at The University of Melbourne. Host: Andrew Siebel

2018 “PheWAS in Populations: Exploring the relationship between the genome and the phenome”, Institute for Computational Biomedicine (ICB) seminar, Weill Cornell. Hosts: Drs. Doron Betel and Olivier Elemento

2018 “Experiences from Electronic Health Records (EHRs) and what we can expect in the future”, Informing Environmental Health Decisions Through Data Integration Workshop, National Academy of Science, Washington DC, Host: Ben Wender

2018 “Exploring the Genome and the Phenome – Toward a Better Understanding of Complex Traits”, Academic Health Center, University of Minnesota, Duluth campus. Host: Catherine McCarty

2018 “Exploring the Genome and the Phenome – Toward a Better Understanding of Complex Traits”, 3rd Midwest Bioinformatics Conference, University of Missouri, Columbia, MO. Host: Mark Hoffman.

2018 “Exploring the Genome and the Phenome with Machine Learning”, Copenhagen Novo Nordisk Foundation (NNF) symposium. Copenhagen, Denmark. Host: Ramneek Gupta

2018 “Using your spidey sense to guide research using machine learning in electronic health records”, Denmark Technical University, Big Data Workshop, Copenhagen, Denmark, Host: Ramneek Gupta

2018 “Pharmacogenomics: Personalizing Medicine since 2005” Keynote at Penn 2nd annual precision medicine symposium, Philadelphia PA, Host: David Roth

2018 “Gene-Environment interaction = the missing piece of precision medicine?”, Total Exposure Health 2018 Conference, Bethesda, MD, Host Justin Teegarden

2018 “Machine Learning Strategies in the Genome and the Phenome – Toward a Better Understanding of Complex Traits”, NY Genome Center, New York, NY, Host: Nicolas Robine

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2018 “Exploring the World of Phenomics”, IGES Educational Symposium, San Diego, CA, Host: Stephanie A. Santorico

2018 “Meta-dimensional analysis of multi-omics data”, CHOP/UPENN Mid Atlantics Bioinformatics conference, Philadelphia, PA, Host: Kai Wang

2018 “Exploring the world of phenomics in electronic health records”, CIFAR Genetic Networks symposium, Toronto, Canada, Host: Charlie Boone

2019 “Training the next generation of biomedical scientists for success in today’s world” Pacific Symposium on Biocomputing, Big Island, HI, Host: Teri Klein

2019 “Machine Learning Strategies in the Genome and the Phenome – Toward a Better Understanding of Complex Traits”, Vanderbilt University, Nashville, TN, Host: Nancy Cox

2019 “Exploring meta-dimensional models of multi-omics data using machine learning” NMBIST, Sante Fe, NM, Host: Lisana Chavez

2019 “Phenomics in Electronic Health Records”, CHOP Scientific Symposium, Philadelphia, PA, Host: Yi Xing.

2019 “When Precision Medicine Get Personal”, Fusion Personalized Medicine Conference, Puerto Vallarta, Mexico, Host: David Roth

2019 “Machine Learning to Identify Phenotypes from Electronic Health Records”, Fusion Personalized Medicine Conference, Puerto Vallarta, Mexico, Host: David Roth

2019 “Embracing the Complexity of Complex Traits”, Workshop on Statistical Challenges in Medical Data Science, Ascona, Switzerland, Host: Niko Beerenwinkel

2019 “Phenotype opportunities from electronic health records”, International Society of Pharmacoepidemiology (ISPE), Philadelphia, PA, Host: Leah Sansbury

2019 “EHR phenomics for precision medicine”, University of Pennsylvania Department of Genetics retreat, Bear Creek, PA, Host: Dan Rader

2019 “Leveraging Translational Research for the Advancement of Drug Discovery and Understanding of Complex Disease”, DNAnexus Connect, Boston, MA, Host: Brady Davis

2019 “The power of the EHR for genome-phenome exploration”, VA Million Veterans Program Research meeting, Philadelphia, PA, Host: Kyong-Mi Kim

2019 “The power of the EHR for genome-phenome exploration”, First Penn Conference on Big Data in Population Health Sciences, Philadelphia, PA, Host: Jason Moore

2019 “Exploring genomics and phenomics with machine learning toward an improved understanding of complex traits”, EMBO|EMBL Symposium “Systems Genetics: From genotypes to complex traits”, Heidelberg, Germany, Host: Tuuli Lappalainen, PhD



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- 2019 “Translational bioinformatics using the electronic health record: harnessing the power of clinical data”, Institute for Translational Medicine and Therapeutics Symposium, Philadelphia, PA, Host: Garret Fitzgerald
- 2019 “Exploring the phenome and the relationship with the genome using EHR-linked biobanks”, American Society of Human Genetics, Houston, TX, Host: ASHG Program Committee
- 2019 “Implementing genomics into clinical care – a vision for the future of medicine”, Thomas Jefferson Departmental seminar, Clinical Pharmacology, Philadelphia, PA, Host: Scott Waldman
- 2019 “Pharmacogenomics for precision medicine”, American Society of Health System Pharmacists (ASHP), Las Vegas, NV, Host: ASHP program committee
- 2020 “Why use biobanks for precision medicine”, Pacific Symposium on Biocomputing, Big Island, Hawaii, Host: Ju Han Kim
- 2020 “Making Precision Medicine Mainstream with Health Data: Challenges to Acceleration: Informatics and Analytics”, Precision Medicine World Conference, San Jose, CA, Host: Tal Behar
- 2020 “The power of electronic health records for precision medicine research”, Calico Life Sciences invited seminar, San Francisco, CA, Host: David Botstein
- 2020 “Machine learning for identifying phenotypes in electronic health records”, International Molecular Medicine Tri-Conference, San Francisco, CA, Host: Emily Le.
- 2020 “Translational bioinformatics using the electronic health record: harnessing the power of clinical data”, Northwestern University, Feinberg School of Medicine, Distinguished Lectures in Life Sciences, Chicago, IL, Host: Justin Starren
- 2020 “The power of medical biobanks for precision medicine”, Columbia University Precision Medicine Initiative Conference, Virtual Conference, Host: Tom Maniatis
- 2020 “COMPACTS: COVID Observational and Multiomic Penn and Community Together Study”, Cancer Center COVID-19 Retreat, University of Pennsylvania, Abramson Cancer Center, Virtual Conference, Host: Angela DiMichele
- 2020 “The Future is Now: how technology and AI have advanced genomics and medicine”, UCSF AI4All Camp ,Closing Keynote, Virtual Program, Host: Mirina Sirota and Tomiko Oskotsky
- 2020 “Electronic Health Records – Fueling Precision Medicine”, 9<sup>th</sup> Annual Big Data in Biomedicine Symposium, Georgetown University, Virtual Conference, Host: Subha Madhavan
- 2020 “Electronic Health Records – Fueling Precision Medicine”, Margaret Prine Joy Lecture in Reproductive Sciences, Magee Women’s Research Institute Retreat, Virtual Conference, Host: Judith Yanowitz
- 2020 “Medical Biobanks for Precision Medicine Research”, Cancer Outcomes Seminar at the University of Alabama at Birmingham, Virtual seminar, Host: Smita Bhatia

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2020 “Predictive Analytics: An Introduction to Machine Learning”, Precision Medicine Leaders’ Summit, Virtual Conference, Host: The Journal of Precision Medicine

2021 “Electronic Health Records – Fueling Precision Medicine Research and Learning Healthcare Systems”, The Adler Lecture at Scheie Eye Institute’s Grand Rounds, Department of Ophthalmology, University of Pennsylvania, Virtual lecture, Host: Dr. Joan O’Brien.

2021 “Making use of our genome for life: strategic opportunities and challenges”, NHGRI Genomic Medicine XIII: Developing a Clinical Genomic Informatics Research Agenda, Virtual meeting, Host: Ken Wiley and Marc Williams

2021 “Polygenic Risk Scores: For some or for all?”, Importance and Challenges of Increasing Ethnic Diversity in Human Genomics Research Symposium, Virtual symposium by the Center for Global Genomics and Health Equity and the Department of Genetics at the University of Pennsylvania, Host: Sarah Tishkoff and Dan Rader

2021 “Deep representation learning of electronic health records to unlock patient stratification at scale”, DBMI Journal Club at Harvard University, Virtual journal club, Host: Isaac Kohane

2021 “Leveraging Electronic Health Records for Precision Health”, Department of Medicine Grand Rounds, University of Pennsylvania Perelman School of Medicine, Host: Michael Parmacek

2021 “Leveraging Electronic Health Records for Precision Health”, IEEE EMBS conference on Biomedical and Health Informatics (BHI2021) keynote speaker, Virtual conference, Host: May Wang

2021 “PharmCAT: Current Status and Strategies for the Future”, Pharmacogenomics Research Network, Research in Progress Series, co-presenter with Dr. Michelle Whirl-Carrillo, Host: Jun Yang

2021 “Use of EHR for Understanding disease”, BEYOND THE SYMPTOM: THE BIOLOGY OF FATIGUE A Joint NIH Blueprint/Sleep Research Society Workshop, Virtual Workshop, Host: Vicky H Whittemore

2021 “The power of medical biobanks for precision medicine”, Genetics and Pharmacogenomics (GpGx) seminar series at Merck & Co., Inc., Virtual seminar, Host: Myung K. Shin

2021 “The power of medical biobanks for precision medicine”, Precision Medicine Resource at the Irving Institute for Clinical and Translational Research, Columbia University, virtual seminar, Host: Dr. Krzysztof Kiryluk, Dr. Ronald Wapner, and Dr. Wendy Chung

2021 “AI for Precision Medicine”, Workshop on Trustworthy AI in Medicine, University of Pennsylvania, Perelman School of Medicine and School of Engineering, Host: Qi Long

2022 “Leveraging Electronic Health Records for Precision Health”, Grand Rounds, Division of Cardiology, University of Pennsylvania, Perelman School of Medicine, Host: Thomas Cappola

2022 “Surviving Season 8 of the Pandemic”, Wellness Seminar Series, Department of Radiology, University of Pennsylvania, Perelman School of Medicine, Host: Despina Kontos

2022 “Future Directions of the NHGRI Analysis, Visualization, and Informatics Lab-space (AnVIL)”, NHGRI Council Meeting, Virtual, Host: Eric Green

2022 “PharmCAT: Pharmacogenomics Clinical Annotation Tool”, CDC NGS Workgroup, Virtual

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2022 “Next generation work life balance amid the COVID-19 pandemic”, American Society of Human Genetics (ASHG) webinar, Virtual, Host: Career Development Committee of ASHG – Lucia Hindorff

2022 “Precision Medicine Research in Electronic Health Records”, Clinical and Translational Research Certificate of Added Qualification (CTR-CAQ) graduate program seminar, Baylor College of Medicine, Virtual, Host: Sundararajah ‘Thev’ Thevananther and Carolyn Smith

2022 “The Power of the Electronic Health Record for Precision Medicine”, Penn Cardiovascular Institute (CVI) seminar series, University of Pennsylvania, Philadelphia, PA, Host: Rajan Jain

2022 “Taking a Big Data View of Aging”, NIA Workshop on Genetic Variation and Aging, Seattle, WA, Host: Daniel Promislow and Pankaj Kapahi

2022 “From Genomics to Genomic Medicine: Embracing the complexity”, NHGRI Center for Precision Health Research seminar, virtual, Host: Josh Denny

2022 “Exploring genetics and electronic health record data to identify sex differences in disease”, Penn FOCUS Fall Leadership Mentoring Conference, Successful Strategies for Women in Academic Medicine, virtual, Host: Mira Mamtani

2022 “Medical Biobanks: A Powerful Resource for Precision Medicine”, Penn-Stanford CVI Symposium, Philadelphia, PA, Host: Dr. Daniel Kelly

2022 “Using the electronic health record to advance translational research”, P30 symposium on High Dimensional Analytics in Digestive and Liver Disease: From Single Cell to the Whole Human, Philadelphia, PA, Host: Dr. Gary Wu

2022 “Beyond GWAS: innovative ways to use genomics for complex disease research”, MPaCT T2D Symposium: Genome Sequencing and Precision Medicine for Type 2 Diabetes, Centre of Genomic Regulation, Barcelona, Spain, Host: Carme Sanahuja

2022 “Precision medicine research dimensions made accessible by electronic health records”, IEEE BIBM, Las Vegas, NV, Host: Qi Long

2023 “Mind the Gaps: How to Fill the Holes in EHR Data”. American College of Medical Informatics (ACMI) Annual Symposium, San Juan, Puerto Rico, Host: Kevin Johnson

2023 “Statistical Approaches for Integrating Environmental Data and Omics Data in Cancer Epidemiology Studies”, panelist, virtual workshop sponsored by NIEHS, Host: Kimberly McCallister

2023 “From Genomics to Genomic Medicine: Embracing the complexity.” Seminar, Department of Biostatistics, Epidemiology, and Informatics, University of Pennsylvania, Perelman School of Medicine. Host: Jeff Morris.

2023 “Using Large Biobanks, Medical Records, and Genetic Data for Disease Understanding”. Keynote at the 14th Biennial International Podocyte Conference, Philadelphia, PA. Host: Katalin Suzstak

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2023 “Pharmacogenomics: Improving Quality and Safety of Healthcare”. ASHP Summer Meeting, Baltimore, MD. Host: Cynthia Von Heeringen

2023 “ Integrated risk scores for precision medicine”, Pharmacogenomics Research Network (PGRN) Annual Meeting, Memphis, TN. Host: Marisa Medina

2023 “From Genomics to Genomic Medicine: Embracing the complexity,” Multi-omics in Precision Medicine Conference, Philadelphia, PA. Host: GenomeWeb

2023 “The Collection, Management and Integration of Big Genomic Data Using the Penn Medicine Biobank,” Festival of Genomics, Boston, MA. Host: Diana Georgi

2023 “AI and Direct to Consumer Genetic Testing: the Good, the Bad, and the Ugly,” ASHP Midyear Meeting, Anaheim, CA. Host: Cynthia Von Heeringen

2023 “Pharmacogenetics and the UK Biobank,” American Society for Human Genetics, Washintgon DC. Host: Jenny Mills