

CURRICULUM VITAE

Name: Marylyn DeRiggi Ritchie, PhD
Work Address: Ritchie Lab
University of Pennsylvania
Anatomy/Chemistry Building, 214/215
3620 Hamilton Walk
Philadelphia, PA 19104
215-573-2438

E-mail Address: marylyn@upenn.edu
Website Address: <http://ritchielab.org> and <http://visualization.ritchielab.psu.edu>
H-index : 70 (Google Scholar)

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
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

Curriculum Vitae: Marylyn DeRiggi Ritchie

Department of Biochemistry and Molecular Biology

Pennsylvania State University

2015-2017 Director, Biomedical and Translational Informatics Institute

Professor

Geisinger Health System

2016-2017 Chief Research Informatics Officer

Geisinger Health System

2016-present Fixed-term, Part-time Professor

Department of Biochemistry and Molecular Biology

Pennsylvania State University

2017-present Faculty Pending,

Department of Genetics

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

2017-present Associate Director for Bioinformatics

Institute for Biomedical Informatics

University of Pennsylvania, Perelman School of Medicine

2017-present Associate Director, Center for Precision Medicine

University of Pennsylvania, Perelman School of Medicine

Other Professional Positions

2005-2010 Consultant, Boehringer-Ingelheim

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

Membership in Professional Societies

American Statistical Association (ASA)
- Middle TN Chapter Representative (2004-2006)
American Society of Human Genetics (ASHG)
International Genetic Epidemiology Society (IGES)
- Member of Education Committee (2009-2013)
International Society for Computational Biology (ISCB)
American Medical Informatics Association (AMIA)
European Society of Human Genetics (ESHG)

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

Curriculum Vitae: Marylyn DeRiggi Ritchie

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

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

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
- 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

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 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)
- 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

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 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
- 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 (ICIC 2013)
- 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
- 2014 Program Committee, Asia-Pacific Translational Bioinformatics Conference
- 2014 Grant Reviewer, Medical Research Council (MRC), United Kingdom

- 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

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 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
- 2007-present Managing Editor, BMC BioData Mining
- 2008-present Member Editorial Board, Pharmacogenomics
- 2009-present Executive Editor, Pharmacogenomics
- 2010-present Grant Reviewer, European Research Council
- 2011-present Member Editorial Board, Pharmacogenetics & Genomics
- 2012-present Member, Genomics, Computational Biology and Technology (GCAT), National Institutes of Health
- 2015-present Member, Standing Committee on Biological and Physical Sciences in Space (CBPSS), National Academy of Sciences
- 2015-present GWAS Catalog Scientific Advisory Board
- 2016-2018 Member, Parasite Award Committee
- 2017-present Grant Reviewer, Genome Canada
- 2017-present Institute for Computational Biology External Advisory Board, Case Western Reserve University
- 2017-present UCSF PREMIER (Precision Medicine in Rheumatology) External Advisory Committee
- 2017-present NIH Advisory panel, All of Us Cohort Program

REVIEWER FOR JOURNALS

American Journal of Human Genetics, Annals of Human Genetics, Annals of Neurology, BioData Mining, Bioinformatics, Biometrical Journal, Biostatistics, BMC Bioinformatics, BMC Cancer, BMC Genetics, BMC Medical Genomics, BMC Systems Biology, Briefings in Bioinformatics, British Journal of Cancer, Cancer Epidemiology Biomarkers & Prevention, Cancer Informatics, Cellular and Molecular Life Sciences, Circulation Cardiovascular Genetics, Clinical Cancer, Clinical Genetics, Clinical Pharmacology & Therapeutics, Computer Methods and Programs in Biomedicine, Current Bioinformatics, Epidemiology, Expert Reviews of Molecular Diagnostics, Expert Reviews of Precision Medicine, European Journal of Human Genetics, European Journal of Operational Research, EvoBio, Frontiers in Genetics, Genetic Epidemiology, Human Genetics, Human Genomics, Human Heredity, Human Immunology, Human Molecular Genetics, Human Mutation, IBM Systems Journal, IEEE Transactions in Evolutionary Computation, In Silico Biology, Intelligent Systems in Molecular Biology, International Journal Artificial Intelligence in Medicine, Journal of the American Medical

Curriculum Vitae: Marylyn DeRiggi Ritchie

Association (JAMA), Molecular Psychiatry, Nature, Nature Reviews Drug Discovery, Nature Reviews Genetics, Neoplasia, Neuropsychiatric Genetics, Nucleic Acids Research, OMICS Integrative Biology, Pacific Symposium on Biocomputing, Pharmacogenetics and Genomics, Pharmacogenomics, PLOS Biology, PLOS Computational Biology, PLOS Genetics, PLOS One, PNAS: Proceedings of the National Academy of Science, Psychiatry Research, The Pharmacogenomics Journal, Science, Science Translational Medicine, Source Code for Biology and Medicine, Statistics in Medicine

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
2009 IGP, Human Genetics, Lecturer
Vanderbilt University
2010 Human Genetics, HGEN 341, Lecturer
Vanderbilt University

Curriculum Vitae: Marylyn DeRiggi Ritchie

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

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

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 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
- 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

Advisory and Supervisory Responsibilities

High School Students

- 2007 Xun Miao
Martin Luther King High School

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

Post-doctoral Fellows – Members of Lab

- 2009-2011 Sarah A. Pendergrass, PhD
Vanderbilt University School of Medicine

Curriculum Vitae: Marylyn DeRiggi Ritchie

2009-2011 Rebecca Zuvich, PhD
Vanderbilt University School of Medicine
2013-2016 DoKyoon Kim, PhD
The Pennsylvania State University

2015-2017 Marta Byrska-Bishop
Geisinger Health System

2016-present Jason Miller
University of Pennsylvania

2017-present Yogasudha Veturi
University of Pennsylvania

Graduate Students – Members of Lab

2004-2007 Alison A. Motsinger
Vanderbilt University, Ph.D. Program in Human Genetics
Currently Tenured Assoc. Prof. at North Carolina State University (Department of
Statistics)

2005-2008 Todd L. Edwards
Vanderbilt University, Ph.D. Program in Human Genetics
Currently Tenure Track Asst. Prof. 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 Asst. Prof. at Case-Western Reserve University
(Department of Biostatistics and Epidemiology)

2006-2010 Stephen Turner
Vanderbilt University, Ph.D. Program in Human Genetics
Currently Director Bioinformatics Core, University of Virginia

2008-2012 Benjamin Grady
Vanderbilt University, Ph.D. Program in Human Genetics

2009-2013 Emily Holzinger
Vanderbilt University, Ph.D. Program in Human Genetics
Currently Post-doctoral fellow, National Human Genome Research
Institute

2009-2013 Carrie Buchanan
Vanderbilt University, Ph.D. Program in Human Genetics
Currently 4th year Medical Student, MD/PhD program, Vanderbilt University

2011-2013 Neerja Katiyar
Pennsylvania State University, Ph.D. Program in Bioinformatics & Genomics

2011-2015 Molly Hall
Pennsylvania State University, Ph.D. Program in BMMB
Currently Post-doctoral fellow, University of Pennsylvania

2012-2016 Ruowang Li
Pennsylvania State University, Ph.D. Program in Bioinformatics & Genomics

Curriculum Vitae: Marylyn DeRiggi Ritchie

2013-2018 Anna Okula Basile
Pennsylvania State University, Ph.D. Program in BMMB

2014-2018 Anurag Verma
Pennsylvania State University, Ph.D. Program in Bioinformatics & Genomics

2014-2018 Shefali Setia Verma
Pennsylvania State University, Ph.D. Program in Bioinformatics & Genomics

2016-present Binglan Li
University of Pennsylvania, Graduate Group in Genomics and Computational Biology

2016-present Xinyuan (Blair) Zhang
University of Pennsylvania , Graduate Group in Genomics and Computational Biology

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

2013-2016 Jacob Hall
Human Genetics PhD Program
Vanderbilt University School of Medicine

2013-2017 Claire Reynolds

Curriculum Vitae: Marylyn DeRiggi Ritchie

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

MAJOR RESEARCH INTERESTS

Computational Genomics	Genetic Epidemiology
Bioinformatics	Statistical Genetics
Epistasis	Systems Genomics
Pharmacogenomics	Computational Biology
Big Data	Translational 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

RESEARCH FUNDING

Active Funding

5R01 AI077505 (Haas and Ritchie) 07/01/2015-6/30/2020 2.4 calendar months
NIH/NIAID \$126,540
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.

P50GM115318-01 (Krauss, Ritchie PI Informatics Core) 07/01/2015-06/30/2020 1.8 calendar months
NIH \$150,000
Pharmacogenomics of Statin Therapy (Informatics Core)

The goal of this proposal is to provide an informatics core to the POST PGRN center.

R01AI116794-01A1 (Moore) 04/01/16 – 03/31/21 1.2 calendar months
NIH \$343,833
Biomedical Computing and Informatics Strategies for Infectious Disease Research

The goal of this project is to look for interactions between rare and common genetic variants associated with HIV drug response traits.

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

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 2007-2009 NIH/NIA R01 AG027944 (Co-investigator)
Genomic Convergence in Alzheimer Disease – Pericak-Vance, Univ. of Miami
12/01/2007-11/30/2012
- 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)

Curriculum Vitae: Marylyn DeRiggi Ritchie

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
- 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

BIBLIOGRAPHY

Peer-Reviewed Research Papers

Curriculum Vitae: Marylyn DeRiggi Ritchie

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 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](#)
8. Moore JH, Hahn LW, Ritchie MD, Thornton TA, White BC. Routine Discovery of Complex Genetic Models using Genetic Algorithms. *Appl Soft Comput*. 2004 Feb 1;4(1):79–86. [PMID: 20948983](#), [PMCID: PMC2952957](#)
9. Cho YM, **Ritchie MD**, Moore JH, Moon MK, Lee YY, Yoon KH, Sung YA, Lang HC, Park JY, Lee KU, Shin HD, Kim SY, Lee HK, Park KS. Multifactor Dimensionality Reduction reveals a two-locus interaction associated with Type 2 Diabetes Mellitus. *Diabetologia*, 47:549-554 (2004). [PMID: 14730379](#)
10. Tsai CT, Lai LP, Chiang FT, Fallin D, Hwang JJ, **Ritchie MD**, Moore JH, Hsu KL, Tseng CD, Liao CS, Lin JL, Tseng YZ. Renin-angiotensin system gene polymorphisms and Atrial Fibrillation. *Circulation*, 109:1640-1646 (2004). [PMID: 15023884](#)
11. Williams SM, **Ritchie MD**, Phillips JA, Wong LJ, Felder RA, Jose PA, Moore JH. Multilocus analysis of hypertension: a hierarchical approach. *Human Heredity*, 57:28-38 (2004). [PMID: 15133310](#)
12. Coffey CS, Hebert PR, **Ritchie MD**, Krumholz HM, Morgan TM, Gaziano JM, Ridker PM, Moore JH. An application of conditional logistic regression and Multifactor Dimensionality Reduction for detecting gene-gene interactions on risk of Myocardial Infarction: the importance of model validation. *BMC Bioinformatics*, 5:49 (2004). [PMID: 15119966](#), [PMCID: PMC419697](#)
13. **Ritchie MD**, Coffey CS, Moore JH. Genetic programming neural networks: a bioinformatics tool for human genetics. *Lecture Notes in Computer Science*, 3102: 438-448 (2004). [PMID: 20948988](#), [PMCID: PMC2952963](#)
14. Shin N, Dise RS, Schneider-Mergener J, **Ritchie MD**, Kilkenny DM, Hanks SK. Subsets of the major tyrosine phosphorylation sites in Crk-associated substrate (CAS) are sufficient to promote cell migration. *Journal of Biological Chemistry*, 279(37): 38331-38337 (2004). [PMID: 15247284](#)

Curriculum Vitae: Marylyn DeRiggi Ritchie

15. Vanhose AM, **Ritchie MD**, Winder DG. Regulation of cAMP levels in area CA1 of hippocampus by Gi/o-coupled receptors is stimulus dependent in mice. *Neuroscience Letters*, 370(1):80-3 (2004). [PMID: 15489022](#)
16. Soares ML, Coelho T, Sousa A, **Ritchie MD**, Williams SM, Batalov S, Conceição I, de Lurdes M, Luís S, Saraiva MJ, Buxbaum JN. Susceptibility and modifier genes in familial amyloid polyneuropathy type I. *Human Molecular Genetics*, 14:543-53 (2005). [PMid: 15649951](#)
17. Bush WS, Motsinger AA, Dudek, SM, **Ritchie MD**. Can neural network constraints in GP provide power to detect genes associated with human disease? *Lecture Notes in Computer Science*, 3449:44-53 (2005). [PMid: 20419044](#), [PMCID: PMC2858417](#)
18. Hulgán T, Haas DW, Haines JL, **Ritchie MD**, Robbins GK, Shafer RW, Clifford DB, Kallianpur A, Summar M, Canter JA. Mitochondrial haplogroups and peripheral neuropathy during antiretroviral therapy: an adult AIDS clinical trials group study. *AIDS*, 19(13):1341-1349 (2005). [PMID: 16103764](#)
19. Ma DQ, Whitehead PL, Menold MM, Martin ER, Ashley-Koch AE, Mei H, **Ritchie MD**, DeLong GR, Abramson RK, Wright HH, Cuccaro ML, Hussman JP, Gilbert JR, Pericak-Vance MA. Identification of significant association and gene-gene interaction on GABA receptor subunit genes in Autism. *American Journal of Human Genetics*, 77(3):377-88 (2005). [PMID: 16080114](#), [PMCID: PMC1226204](#)
20. Martin ER, **Ritchie MD**, Kang S, Hahn L, Moore JH. A novel method to identify potential interactions in nuclear families: The MDR-PDT. *Genetic Epidemiology*, 30:111-23 (2006). [PMID: 16374833](#)
21. Takahashi H, Wilkinson GR, PhD, Nutescu EA, Morita T, **Ritchie MD**, Scordo MG, Pengo V, Barban M, Padriani R, Ieiri I, Otsubo K, Kashima T, Kimura S, Kijima S, Echizen H. Different contributions of polymorphisms in *VKORC1* and *CYP2C9* to intra- and inter-population differences in maintenance dose of warfarin in Japanese, Caucasians and African Americans. *Pharmacogenetics and Genomics*, 16:101-110 (2006). [PMID: 16424822](#)
22. Ashley-Koch A, Mei H, Jaworski J, Ma D, **Ritchie MD**, Menold M, Abramson R, Wright H, Cuccaro M, Gilbert J, Martin E, Pericak-Vance M. An analysis paradigm for investigating multi-locus effects in complex disease: examination of three GABA receptor subunit genes on 15q11-q13 as risk factors for Autistic disorder. *Annals of Human Genetics*, 70:281-92 (2006). [PMID: 16674551](#)
23. Motsinger AA, Lee SL, Mellick G, **Ritchie MD**. GPNN: power studies and applications of a neural network method for detecting gene-gene interactions in studies of human disease. *BMC Bioinformatics*, 7:39 (2006). [PMID: 16436204](#), [PMCID: PMC1388239](#)
24. Motsinger AA, Donahue BS, Brown NJ, Roden DM, **Ritchie MD**. Risk factor interactions and genetic effects associated with post-operative Atrial Fibrillation. *Pacific Symposium on Biocomputing Proceedings*, 11:584-595 (2006). [PMID: 17094271](#)
25. Dudek SM, Motsinger AA, Velez DR, Williams SM, **Ritchie MD**. Data simulation software for whole-genome association studies and other studies in human genetics. *Pacific Symposium on Biocomputing Proceedings*, 11:499-510 (2006). [PMID: 17094264](#)
26. Sanda H, Yatabe J, Midorikawa S, Hashimoto S, Watanabe T, Moore JH, **Ritchie MD**, Williams SM, PExzullo JC, Eisner GM, Jose PA, Felder RA. Salt sensitivity and G-protein-coupled receptor kinase type 4 polymorphisms. Single-nucleotide polymorphisms for diagnosis of salt-sensitive hypertension. *Clinical Chemistry*, 52:352-360 (2006). [PMID: 16439609](#)
27. Motsinger AA, **Ritchie MD**. Multifactor Dimensionality Reduction: an analysis strategy for modeling and detecting gene-gene interactions in human genetics and pharmacogenomics studies. *Human Genomics*, 2:318-328. (2006). [PMID: 16595076](#), [PMCID: PMC3500181](#)
28. Brassat D, Motsinger AA, Walker K, Steiner LL, Erlich HA, Barcellos L, Pericak-Vance MA, Hauser SL, Haines JL, Oksenberg JR, **Ritchie MD**. Multifactor dimensionality reduction reveals

Curriculum Vitae: Marylyn DeRiggi Ritchie

- gene-gene interactions associated with Multiple Sclerosis in African Americans. *Genes and Immunity*, 7:310-315 (2006). PMID: 16625214, PMCID: PMC4339061
29. Motsinger AA, Dudek SM, Hahn LW, **Ritchie MD**. Comparison of neural network optimization approaches for studies of human genetics. *Lecture Notes in Computer Science*, 3907:103-114 (2006). PMID: 20191104, PMCID: PMC2828685
 30. Motsinger AA, **Ritchie MD**, Dobrin SE. Clinical applications of whole-genome association studies (WGAS): future applications at the bedside. *Expert Reviews in Molecular Diagnostics*, 6:551-65 (2006). PMID: 16824029
 31. Motsinger AA, Hahn LW, Dudek SM, Ryckman KK, **Ritchie MD**. Alternative cross-over strategies and selection techniques for grammatical evolution optimized neural networks. *Proceedings of Genetic and Evolutionary Computation Conference*, Association for Machine Learning Press, New York, 947-949 (2006). PMID: 20634918, PMCID: PM2903763
 32. Kallianpur AR, Hulgan T, Canter JA, **Ritchie MD**, Haines JL, Robbins GK, Shafer RW, Clifford DB, Haas DW. Hemochromatosis (HFE) gene mutations and peripheral neuropathy during antiretroviral therapy: an AIDS clinical trials group study. *AIDS*, 20:1503-1513 (2006). PMID: 16847405
 33. Motsinger AA, **Ritchie MD**. The effect of reduction in cross-validation intervals on the performance of multifactor dimensionality reduction. *Genetic Epidemiology*, 30: 546-555 (2006). PMID: 16800004
 34. Haas DW, Geraghty DE, Andersen J, Mar J, Motsinger AA, D'Aquila RT, Unutmaz D, Benson CA, **Ritchie MD**, Landay A. Immunogenetics of CD4 lymphocyte recovery during antiretroviral therapy: an AIDS clinical trials group study. *Journal of Infectious Disease*, 198:1098-1107 (2006). PMID: 16991084
 35. Motsinger AA, **Ritchie MD**, Shafer RW, Robbins GK, Morse GD, Labbé L, Wilkinson GR, Clifford DB, D'Aquila RT, Johnson VA, De Gruttola V, Pollard RB, Merigan TC, Hirsch MS, Donahue JP, Kim RB, Haas DW. Multilocus gene-gene interactions and response to efavirenz-containing regimens: an adult AIDS clinical trials group study. *Pharmacogenetics and Genomics*, 16:837-845 (2006). PMID: 17047492
 36. **Ritchie MD**, Haas DW, Motsinger AA, Donahue JP, Erdem H, Raffanti S, Rebiero P, George AL, Kim RB, Haines JL, Sterling TR. Drug transporter and metabolizing enzyme gene variants and non-nucleoside reverse transcriptase inhibitor hepatotoxicity. *Clinical Infectious Diseases*, 43:779-82 (2006). PMID: 16912956
 37. Bush WS, Dudek SM, **Ritchie MD**. Parallel Multifactor Dimensionality Reduction: a tool for the large scale analysis of gene-gene interactions. *Bioinformatics*, 22:2173-4 (2006). PMID: 16809395, PMCID: PMC4939609
 38. Crooke PS, **Ritchie MD**, Hachey DL, Dawling S, Roodi N, Parl FF. Estrogens, enzyme variants, and Breast Cancer. A risk model. *Cancer, Epidemiology, Biomarkers, and Prevention*, 15:1620-9 (2006). PMID: 16985022
 39. Tsai CT, Hwang JJ, **Ritchie MD**, Moore JH, Fallin D, Chiang FT, Lai LP, Hwang JJ, Hsu KL, Tseng CD, Liao CS, Lin JL, Tseng YZ. Renin-angiotensin system gene polymorphisms and Coronary Artery disease in a large angiographic cohort: detection of high-order gene-gene interaction. *Atherosclerosis*, 195(1):172-80 (2007). PMID: 17118372
 40. Motsinger AA, Reif DM, Dudek SM, **Ritchie MD**. Understanding the Evolutionary Process of Grammatical Evolution Neural Networks for Feature Selection in Genetic Epidemiology. *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*, 1-8 (2006). PMID: 20634919, PMCID: PMC2903766
 41. Motsinger AA, Brassat D, Caillier SC, Erlich HA, Walker K, Steiner LL, Barcellos L, Pericak-Vance MA, Schmidt S, Gregory S, Hauser SL, Haines JL, Oksenberg JR, **Ritchie MD**. Complex

Curriculum Vitae: Marylyn DeRiggi Ritchie

- gene-gene interactions in Multiple Sclerosis: a multi-factorial approach reveals associations with inflammatory genes. *Neurogenetics*, 8:11-20 (2007). PMID: 17024427
42. Nordgard SH, **Ritchie MD**, Motsinger AA, Lemmon G, Fjelstad S, Alnæs GIG, Jensrud SD, Berg M, Geisler S, Moore JH, Lønning PE, Børresen-Dale AL, Kristensen VN. ABCB1 and GST polymorphisms associated with TP53 status in breast cancer. *Pharmacogenetics and Genomics*, 17:127-36 (2007). PMID: 17301692, PMCID: PMC2954594
 43. Canter JA, Summar ML, Smith HB, **Ritchie MD**, Motsinger AA, Christian K, Drinkwater D, Dyer KL, Kavanaugh A, Barr FE. Genetic variation in the mitochondrial enzyme carbamyl-phosphate synthetase I predisposes children to increased pulmonary artery pressure following surgical repair of congenital heart defects: a validated genetic association study. *Mitochondrion*, 7:204-210 (2007). PMID: 17188582, PMCID: PMC1929167
 44. Velez DR, White BC, Motsinger AA, Bush WS, **Ritchie MD**, Williams SM, Moore JH. A balanced accuracy metric for epistasis modeling in imbalanced datasets using Multifactor Dimensionality Reduction. *Genetic Epidemiology*, 31:306-315 (2007). PMID: 17323372
 45. Motsinger AA, Reif DM, Fanelli TJ, Davis AC, **Ritchie MD**. Linkage disequilibrium in genetic association studies improves the performance of grammatical evolution neural networks. *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*, 1-8 (2007). PMID: 21572972, PMCID: PMC3092290, MIHMS 160137
 46. Bush WS, Thornton-Wells TA, **Ritchie MD**. Association rule discovery has the ability to model complex genetic effects. *Proceedings of the 2007 IEEE Symposium on Computational Intelligence and Data Mining*, 624-629 (2007). PMID: 20953276, PMCID: PMC2954594
 47. **Ritchie MD**, Motsinger AA, Bush WS, Coffey CS, Moore JH. Genetic programming neural networks: a powerful bioinformatics tool for human genetics. *Applied Soft Computing*, 7:471-479 (2007). PMID: 20948988, PMCID: PMC2952963
 48. Ashley-Koch AE, Jaworski J, Ma D, Mei H, **Ritchie MD**, Skaar DA, DeLong GR, Abramson RK, Wright HH, Cuccaro ML, Gilbert JR, Martin ER, Pericak-Vance MA. Investigation of potential gene-gene interactions between APOE and RELN contributing to Autism risk. *Psychiatric Genetics*, 17:221-226 (2007). PMID: 17621165, PMCID: PMC2749242
 49. Darbar D, Motsinger AA, **Ritchie MD**, Gainer JV, Roden DM. Polymorphism modulates symptomatic response to antiarrhythmic drug therapy in patients with lone Atrial Fibrillation. *Heart Rhythm*, 4:743-749 (2007). PMID: 17556195, PMCID: PMC1948880
 50. **Ritchie MD**, Bartlett J, Bush WS, Edwards TL, Motsinger AA, Torstenson ES. Exploring epistasis in candidate genes for Rheumatoid Arthritis. *BMC Proceedings*, 1 Suppl 1:S70 (2007). PMID: 18466572, PMCID: PMC2367541
 51. Bartlett CW, Vieland VJ, Bartlett J, Bell JT, Bhattacharjee S, Clerget-Darpoux F, Bush WS, Edwards TL, Gao G, Halder I, Huang Y, Kotti S, Larkin EK, Li H, Motsinger AA, Mukhopadhyay N, Namkung J, Park T, **Ritchie MD**, Stein CM, Zhou JY. Discussing gene-gene interaction: warning--translating equations to English may result in jabberwocky. *Genetic Epidemiology*, 31 Suppl 1:S61-7 (2007). PMID: 18046759, PMCID: PMC2749242
 52. Pretorius MM, Gainer JV, Van Guilder GP, Coelho EB, Luther JM, Fong P, Rosenbaum DD, Malave HA, Yu C, **Ritchie MD**, Vaughan DE, Brown NJ. The Bradykinin type 2 receptor BE1 polymorphism and ethnicity influence systolic blood pressure and vascular resistance. *Clinical Pharmacology and Therapeutics*, 83(1):122-9 (2008). PMID: 17522594, PMCID: PMC1948880
 53. Canter JA, Haas DW, Kallianpur AR, **Ritchie MD**, Robbins GK, Shafer RW, Murdock DG, Hulgán T. The mitochondrial pharmacogenomics of haplogroup T: MTND2(*)LHON4917G and antiretroviral therapy-associated peripheral neuropathy. *Pharmacogenomics Journal*, 8(1):71-7 (2008). PMID: 17684475
 54. Schwartz UI, **Ritchie MD**, Bradford Y, Dudek S, Frye-Anderson A, Kim RB, Roden DM, Stein CM. Genetic determinants of response to warfarin during initial anticoagulation. *NEJM*,

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 358(10):999-1008 (2008). doi: 10.1056/NEJMoa0708078. PMID: 18322281, PMCID: PMC3894627
55. Edwards TL, Bush WS, Turner SD, Dudek SM, Torstenson ES, Schmidt M, Martin E, **Ritchie MD**. Generating linkage disequilibrium patterns in data simulations using genomeSIMLA. *Lecture Notes in Computer Science*, 4973: 24-35 (2008). PMID: 19779634, PMCID: PMC749242
 56. Darbar D, Kimbrough J, Jawaid A, McCray R, **Ritchie MD**, Roden DM. Persistent atrial fibrillation is associated with reduced risk of torsades de pointes in patients with drug-induced long QT syndrome. *J Am Coll Cardiol*, 51(8):836-42 (2008). PMID: 18294569, PMCID: PMC2271078
 57. Motsinger-Reif AA, Dudek SM, Hahn LW, **Ritchie MD**. Comparison of approaches for machine learning optimization of neural networks for detecting gene-gene interactions in genetic epidemiology. *Genetic Epidemiology*, 32(4):325-40 (2008). doi: 10.1002/gepi.20307. PMID: 18265411
 58. Motsinger-Reif AA, Reif DM, Fanelli TJ, **Ritchie MD**. A comparison of analytical methods for genetic association studies. *Genetic Epidemiology*, 32(8):767-78 (2008). PMID: 18561203, PMCID: PMC2459220
 59. Bush WS, Edwards TL, Dudek SM, McKinney BA, **Ritchie MD**. Alternative contingency table measures improves the power and detection of Multifactor Dimensionality Reduction. *BMC Bioinformatics*, 9:238 (2008). PMID: 18485205, PMCID: PMC2412877
 60. Cooper GM, Johnson JA, Langaee TY, Feng H, Stanaway IB, Schwartz U, **Ritchie MD**, Stein CM, Roden DM, Smith JD, Veenstra DL, Rettie AE, Rieder MJ. A Genome-Wide Scan for Common Genetic Variants with a Large Influence on Warfarin Maintenance Dose. *Blood*, 112:1022-7 (2008). PMID: 18535201, PMCID: PMC2515139
 61. Edwards TL, Lewis KG, Velez DR, Dudek SM, **Ritchie MD**. Exploring the Performance of Multifactor Dimensionality Reduction in Large Scale SNP Studies and in the Presence of Genetic Heterogeneity among Epistatic Disease Models. *Human Heredity*, 67(3):183-92 (2008). PMID: 19077437, PMCID: PMC3078287
 62. Motsinger-Reif AA, Fanelli TJ, Davis AC, **Ritchie MD**. Power of grammatical evolution neural networks to detect gene-gene interactions in the presence of error. *BMC Research Notes*, 1:65 (2008). PMID: 18710518, PMCID: PMC2531119
 63. Edwards TL, Wang X, Chen Q, Wormly B, Riley B, O'Neill FA, Walsh D, **Ritchie MD**, Kendler KS, Chen X. Interaction between interleukin 3 and dystrobrevin-binding protein 1 in schizophrenia. *Schizophrenia Research*, 106(2-3); 208-17 (2008). PMID: 18804346, PMCID: PMC2746913
 64. Li C, Schwartz UI, **Ritchie MD**, Roden DM, Stein CM, Kurnik D. Relative contribution of *CYP2C9* and *VKORC1* genotypes and early INR response to the prediction of warfarin sensitivity during initiation of therapy. *Blood*, 113(17):3925-30 (2009). doi: 10.1182/blood-2008-09-176859. PMID: 19074728, PMCID: PMC2673121
 65. Edwards TL, Pericak-Vance M, Gilbert JR, Haines JL, Martin ER, **Ritchie MD**. An association analysis of Alzheimer disease candidate genes detects an ancestral risk haplotype clade in ACE and putative multilocus association between ACE, A2M, and LRRTM3. *American Journal of Medical Genetics Part B, Neuropsychiatric Genetics*, 67(3):183-92 (2009). doi: 10.1002/ajmg.b.30899. PMID: 19105203, PMCID: PMC2821734
 66. Hardison NE, Fanelli TJ, Dudek SM, Reif DM, **Ritchie MD**, Motsinger AA. A balanced accuracy fitness function leads to robust analysis using grammatical evolution neural networks in the case of class imbalance. *GECCO*, 353-4 (2008). PMID: 21197143, PMCID: PMC3011228

Curriculum Vitae: Marylyn DeRiggi Ritchie

67. Bush WS, Dudek SM, **Ritchie MD**. Biofilter: a knowledge-integration system for the multi-locus analysis of genome-wide association studies. *Pacific Symposium on Biocomputing*, 368-79 (2009). PMID: [19209715](#), PMCID: [PMC2859610](#)
68. Body SC, Collard CD, Shernan SK, Fox AA, Liu KY, **Ritchie MD**, Perry TE, Muehlschlegel JD, Aranki S, Donahue BS, Pretorius M, Estrada J, Ellinor PT, Newton-Cheh C, Seidman CE, Seidman, Hermann DS, Lichtner P, Meitinger T, Pfeufer A, Käab S, Brown NJ, Roden DM, Darbar D. Variation in the 4q25 Chromosomal Locus Predicts Atrial Fibrillation after Coronary Artery Bypass Graft Surgery. *Circulation Cardiovascular Genetics*, 2(5):499-506 (2009). doi: 10.1161/CIRCGENETICS.109.849075. PMID: [20031626](#), PMCID: [PMC2801871](#)
69. **International Warfarin Pharmacogenetics Consortium**, Klein TE, Altman RB, Eriksson N, Gage BF, Kimmel SE, Lee MT, Limdi NA, Page D, Roden DM, Wagner MJ, Caldwell MD, Johnson JA. Estimation of the warfarin dose with clinical and pharmacogenetic data. *NEJM*, 360(8):753-64 (2009). PMID: [19228618](#), PMCID: [PMC2722908](#)
70. Bush WS, Crawford DC, Alexander C, George A, Roden DM, **Ritchie MD**. Genetic variation in the rhythmome: ethnic variation and haplotype structure in candidate genes for arrhythmias. *Pharmacogenomics*, 10(6):1043-53 (2009). doi: 10.2217/pgs.09.67. PMID: [19530973](#), PMCID: [PMC2746955](#)
71. Turner SD, **Ritchie MD**, Bush WS. Conquering the Needle-in-a-Haystack: How Correlated Input Variables Beneficially Alter the Fitness Landscape for Neural Networks. *Lect Notes Comput Sci*, 5483:80-91 (2009). PMID: [19578549](#), PMCID: [PMC2704607](#)
72. Turner SD, Crawford DC, **Ritchie MD**. Methods for optimizing statistical analyses in pharmacogenomics research. *Expert Rev. Clin. Pharmacol.* 2(5), 559-570 (2009). PMID: [20221410](#), PMCID: [PMC2835152](#)
73. **Ritchie MD**. Using Prior Knowledge for Genome-Wide Association Studies in Multiple Sclerosis: a model for identifying pathways important for common, complex disease. *Genome Medicine*, 1(6):65 (2009). doi: 10.1186/gm65. PMID: [19566917](#), PMCID: [PMC2703874](#)
74. Edwards TL, Torstenson ES, Martin EM, **Ritchie MD**. A cross-validation procedure for general pedigrees and matched odds ratio fitness metric implemented for the multifactor dimensionality reduction pedigree disequilibrium test MDR-PDT and cross-validation: power studies. *Genetic Epidemiology*, 34(2):194-9 (2010). doi: 10.1002/gepi.20447. PMID: [19697353](#), PMCID: [PMC2811750](#)
75. Canter JA, Robbins GK, Selph D, Clifford DB, Kallianpur AR, Shafer R, Levy S, Murdock DG, **Ritchie MD**, Haas DW, Hulgian T, for the AIDS Clinical Trials Group Study 384 and New York Concept Sheet 273 Teams. African Mitochondrial DNA Subhaplogroups and Peripheral Neuropathy during Antiretroviral Therapy. *The Journal of Infectious Diseases*, 201(11):1703-7 (2010). doi: 10.1086/652419. PMID: [20402593](#), PMCID: [PMC2862090](#)
76. Bush WS, Chen G, Torstenson ES, **Ritchie MD**. LD-Spline: Mapping SNPs on genotyping platforms to genomic regions using patterns of linkage disequilibrium. *BMC BioData Mining*, 2(1):7 (2009). doi: 10.1186/1756-0381-2-7. PMID: [19954552](#), PMCID: [PMC2795743](#)
77. Grady BJ, Torstenson ES, Dudek SM, Giles J, Sexton D, **Ritchie MD**. Finding unique filter sets in PLATO: a precursor to efficient interaction analysis in GWAS data. *Pacific Symposium on Biocomputing*, 315-26 (2010). PMID: [19908384](#), PMCID: [PMC2903053](#)
78. Bush WS, Dudek SM, Torstenson ES, **Ritchie MD**. Visualizing SNP statistics in the context of linkage disequilibrium using LD-Plus. *Bioinformatics*, 26(4):578-9 (2010). doi: 10.1093/bioinformatics/btp678. PMID: [20130027](#), PMCID: [PMC2820673](#)
79. Edwards TL, Turner SD, Torstenson ES, Dudek SM, Martin EM, **Ritchie MD**. A general framework for formal tests of interaction after exhaustive search methods with applications to MDR and MDR-PDT. *PLOS ONE*, 5(2):e9363 (2010). doi: 10.1371/journal.pone.0009363. PMID: [20186329](#), PMCID: [PMC2826406](#)

Curriculum Vitae: Marylyn DeRiggi Ritchie

80. Limdi NA, Wadelius M, Cavallari L, Eriksson N, Crawford DC, Lee MT, Chen CH, Motsinger-Reif A, Sagreiya H, Liu N, Wu AH, Gage BF, Jorgensen A, Pirmohamed M, Shin JG, Suarez-Kurtz G, Kimmel SE, Johnson JA, Klein TE, Wagner MJ; **International Warfarin Pharmacogenetics Consortium**. Warfarin pharmacogenetics: a single VKORC1 polymorphism is predictive of dose across 3 racial groups. *Blood*. 115(18):3827-34 (2010). doi: 10.1182/blood-2009-12-255992. PMID: 20203262, PMCID: PMC2865873
81. Turner SD, Dudek SM, **Ritchie MD**. Grammatical Evolution of Neural Networks for Discovering Epistasis among Quantitative Trait Loci. *Lect Notes Comput Sci*. 6023:86-97. (2010). PMID: 20526438, PMCID: PMC2880550
82. Denny JC, **Ritchie MD**, Basford M, Pulley J, Bastarache L, Brown-Gentry K, Wang D, Masys DR, Roden DM, Crawford DC. PheWAS: Demonstrating the feasibility of a phenome-wide scan to discover gene-disease associations. *Bioinformatics*, 26(9):1205-10 (2010). doi: 10.1093/bioinformatics/btq126. PMID: 20335276, PMCID: PMC2859132
83. Zabaleta J, Piazuolo MB, Camargo MC, Correa P, Ochoa A, Sierra R, **Ritchie MD**, Turner S, Fonham E, Delgado AG, Schneider B. Association of haplotypes of inflammation-related genes with gastric preneoplastic lesions in African Americans and Caucasians. *International Journal of Cancer*, 128(3):668-75 (2011). doi: 10.1002/ijc.25385. PMID: 20473875, PMCID: PMC2964400
84. Cattaert T, Urrea V, Naj AC, De Lobel L, De Wit V, Fu M, John JM, Shen H, Calle LM, **Ritchie MD**, Edwards T, Van Steen K. FAM-MDR: a flexible family-based multifactor dimensionality reduction technique to detect epistasis using related individuals. *PlosONE*, 5(4):e10304 (2010). PMID: 20421984, PMCID: PMC2858665
85. Ribaud HJ, Liu H, Schwab M, Schaeffeler E, Eichelbaum M, Motsinger-Reif AA, **Ritchie MD**, Zanger UM, Acosta EP, Morse GD, Gulick RM, Robbins GK, Clifford D, Haas DW. Impact of CYP2B6, ABCB1 and CYP3A5 Polymorphisms on Efavirenz Pharmacokinetics and Treatment Response: An AIDS Clinical Trials Group Study. *Journal of Infectious Disease*, 202(5):717-22 (2010). doi: 10.1086/655470. PMID: 20662624, PMCID: PMC2919241
86. Wilke RA, Berg RL, Linneman JG, Peissig P, Starren J, **Ritchie MD**, McCarty CA. Quantification of the clinical modifiers impacting high-density lipoprotein cholesterol in the community: personalized medicine research project. *Prev Cardiol*, Spring; 13(2):63-8 (2010). doi: 10.1111/j.1751-7141.2009.00055.x. PMID: 20377807, PMCID: PMC 2862090
87. Holzinger ER, Buchanan CC, Dudek SC, Torstenson EC, Turner SD, **Ritchie MD**. Initialization Parameter Sweep in ATHENA: Optimizing Neural Networks for Detecting Gene-Gene Interactions in the Presence of Small Main Effects. *GECCO 2010*, 12: 203-210 (2010). PMID: 21152364, PMCID: PMC 2997651
88. Dumitrescu L, **Ritchie MD**, Brown-Gentry K, Pulley JJ, Basford M, Denny J, Oksenberg JR, Roden DM, Haines JL, Crawford DC. Assessing the accuracy of observer-reported ancestry in a biorepository linked to electronic medical records. *Genetics in Medicine*, 12(10):648-50. (2010) doi: 10.1097/GIM.0b013e3181efe2df. PMID: 20733501, PMCID: PMC2952033
89. **Ritchie MD**, Denny JC, Crawford DC, Havens A, Weiner J, Pulley JM, Basford M, Balsler JR, Masys DR, Haines JL, Roden DM. Robust replication of genotype-phenotype associations across multiple diseases in an electronic medical record. *American Journal of Human Genetics*, 86(4):560-72 (2010). doi: 10.1016/j.ajhg.2010.03.003. PMID: 20362271, PMCID: PMC2850440
90. Turner SD, Dudek SM, **Ritchie MD**. ATHENA: A Knowledge-Based Hybrid Backpropagation-Grammatical Evolution Neural Network Algorithm for Discovering Epistasis among Quantitative Trait Loci. *BMC BioData Mining*, 3(1):5 (2010). doi: 10.1186/1756-0381-3-5. PMID: 20875103, PMCID: PMC 2955681
91. Pendergrass SA, Dudek SM, Crawford DC, **Ritchie MD**. Synthesis-View: visualization and interpretation of SNP association results for multi-cohort, multi-phenotype data and meta-

Curriculum Vitae: Marylyn DeRiggi Ritchie

- analysis. *BMC BioData Mining*, 3(1): 10 (2010). doi: 10.1186/1756-0381-3-10. PMID: 21162740 , PMCID: PMC 3012023
92. Hulgán T, Haubrich R, Riddler SA, Tebas P, **Ritchie MD**, McComsey GA, Haas DW, Canter JA. European Mitochondrial DNA Haplogroups and Metabolic Changes during Antiretroviral Therapy in AIDS Clinical Trials Group Study A5142. *AIDS*, (1):37-47. (2011) doi: 10.1097/QAD.0b013e32833f9d02. PMID: 20871389 PMCID: PMC2995830
93. McCarty CA, Chisholm RL, Chute C, Kullo I, Jarvik G, Larson EB, Li R, Masys DR, **Ritchie MD**, Roden DM, Struwing J, Wolf WA; the eMERGE Team. (2011) The eMERGE Network: A consortium of biorepositories linked to electronic medical records data for conducting genomic studies. *BMC Genomics*, 4(1):13. doi: 10.1186/1755-8794-4-13. PMID: 21269473, PMCID: PMC3038887
94. Denny JC, **Ritchie MD**, Crawford DC, Schildcrout JS, Ramirez AH, Pulley JM, Basford MA, Masys DR, Haines JL, Roden DM. (2011) Identification of genomic predictors of atrioventricular conduction: Using electronic medical records as a tool for genome science. *Circulation*, 122: 2016-2021. doi: 10.1161/CIRCULATIONAHA.110.948828. PMID: 21041692, PMCID: PMC2991609
95. Turner SD, Dudek SM, **Ritchie MD**. Incorporating Domain Knowledge into Evolutionary Computing for Discovering Gene-Gene Interaction. *11th Int'l Conference on Parallel Problem Solving From Nature (PPSN), Lecture Notes in Computer Science*. 6238:394-403. (2011) PMID: 20938492, PMCID: PMC2951735
96. Grady BJ, Torstenson ES, McLaren PJ, de Bakker P, Haas DW, Robbins GK, Gulick RM, Haubrich R, Ribaudó H, **Ritchie MD**. Use of biological knowledge to inform the analysis of gene-gene interactions involved in modulating virologic failure with efavirenz-containing treatment regimens in art-naïve actg clinical trials participants. *Pacific Symposium on Biocomputing*, 253-64. (2011) PMID: 21121053, PMCID: PMC 3094912
97. Pendergrass S, Dudek SM, Roden DM, Crawford DC, **Ritchie MD**. Visual integration of results from a large DNA Biobank (BioVU) using Synthesis-View. *Pacific Symposium on Biocomputing*, 265-275 (2011). PMID: 21121054, PMCID: PMC 3065108
98. **Ritchie MD**. Using Biological Knowledge to Uncover the Mystery in the Search for Epistasis in Genome-Wide Association Studies. *Ann. of Human Genetics*, 75(1): 172-82. (2011). PMID: 21158748, PMCID: PMC3092784
99. Bush WS, McCauley JL, DeJager PL, Dudek SM, Hafler DA, Gibson RA, Matthews PM, Kappos L, Naegelin Y, Polman CH, Hauser SL, Oksenberg J, Haines JL, **Ritchie MD**. A knowledge-driven interaction analysis reveals novel mechanism of MS susceptibility. *Genes & Immunity*, 2011 Feb 24 (Epub ahead of print). PMID: 21346779, PMCID: PMC 3136581
100. Turner SD, Armstrong L, Bradford Y, Carlson C, Crawford DC, Crenshaw AT, de Andrade M, Doheny K, Haines JL, Hayes G, Jarvik G, Jiang L, Ling H, Kullo I, Li R, Manolio TA, Matsumoto M, McCarty CA, McDavid A, Mirel D, Paschall J, Pugh E, Rasmussen LV, Wilke RA, Zuvich RL, **Ritchie MD**. Quality Control procedures for Genome-Wide Association Studies. *Current Protocols in Human Genetics*, Chapter 1: Unit1.19. (2011) PMID: 21234875, PMCID: PMC 3066182
101. Cattaert T, Calle ML, Dudek SM, Mahachie John JM, Van Lishout F, Urrea V, **Ritchie MD**, Van Steen K. Model-Based Multifactor Dimensionality Reduction for detecting epistasis in case-control data in the presence of noise. *Ann Hum Genet*, 75(1): 78-89 (2011). PMID: 21158747, PMCID: PMC 3059142
102. Lehr T, Yuan J, Zeumer D, Jayadev S, **Ritchie MD**. Rule based classifier for the analysis of gene-gene and gene-environment interactions in genetic association studies. *BMC Biodata Mining*, 4(1): 4 (2011). PMID: 21362183, PMCID: PMC 3060133

Curriculum Vitae: Marylyn DeRiggi Ritchie

103. Yaspan BL, Bush WS, Torstenson ES, Ma D, Pericak-Vance MA, **Ritchie MD**, Sutcliffe JS, Haines JL. Genetic analysis of biological pathway data through genomic randomization. *Human Genetics*, 2011 Jan 30 (Epub ahead of print). [PMID: 21279722](#), [PMCID: PMC3107984](#)
104. Pendergrass SA, Brown-Gentry K, Dudek SM, Torstenson ES, Ambite JL, Avery CL, Buyske S, Cai C, Fesinmeyer MD, Haiman C, Heiss G, Hindorff LA, Hsu C-N, Jackson RD, Kooperberg C, Le Marchand L, Lin Y, Matisse TC, Moreland L, Monroe K, Reiner AP, Wallace R, Wilkens LR, Crawford DC, **Ritchie MD**. The Use of Phenotype-Wide association study (PheWAS) for exploration of novel genotype-phenotype relationships and pleiotropy discovery. *Genetic Epidemiology*, 35: 410-22 (2011) [PMID: 21594894](#), [PMCID: PMC3116446](#)
105. Holzinger ER, Dudek SM, Torstenson EC, **Ritchie MD**. ATHENA Optimization: The Effect of Initial Parameter Settings Across Different Genetic Models. *Lect Notes Comput Sci*. 2011 Jan 1;6623(2011):48-58. [PMID: 21966082](#), [PMCID: PMC 3182152](#)
106. Matisse T, Ambite JL, Buyske, Cole S, Crawford DC, Haiman C, Heiss G, Kooperberg C, Le Marchand L, Manolio T, North K, Peters R, **Ritchie MD**, Hindorff L, Haines JL, for PAGE. The next PAGE in understanding complex traits: study design for analysis of Population Architecture using Genetics and Epidemiology. *American Journal of Epidemiology*, 2011 Oct 1;174(7):849-59. [PMID: 21836165](#), [PMCID: PMC3176830](#)
107. Grady BJ, Torstenson ES, **Ritchie MD**. The effects of linkage disequilibrium in large scale SNP datasets for MDR. *Biodata Mining*, 2011 May 5; 4(1):11. [PMID: 21545716](#), [PMCID: PMC 3108918](#)
108. Hsu Ch-N, Kuo Ch-J, Cai C, Pendergrass SA, **Ritchie MD**, Ambite JL. Learning Phenotype Mapping for Integrating Large Genetic Data. *Proceedings of BioNLP 2011 Workshop*, June 2011, 19-27.
109. Turner SD, Berg RL, Linneman JG, Peissig PL, Crawford DC, Denny JC, Roden DM, McCarty CA, **Ritchie MD**, Wilke RA. Knowledge-Driven Multi-Locus Analysis Reveals Gene-Gene Interactions Influencing HDL Cholesterol Level in Two Independent EMR-Linked Biobanks. *PLoS One*. 2011 May 11;6(5):e19586. doi: 10.1371/journal.pone.0019586. [PMID: 21589926](#), [PMCID: PMC 3092760](#)
110. Kullo IJ, Ding K, Shameer K, McCarty CA, Jarvik GP, Denny JC, **Ritchie MD**, Zi Y, Crosslin DR, Chisholm RL, Manolio TA, Chute CG. Complement Receptor 1 Gene Variants are Associated with Erythrocyte Sedimentation Rate. *AJHG*, 2011 Jul 15;89(1):131-8. [PMID: 21700265](#), [PMCID: PMC 3135803](#)
111. Xu H, Jiang M, Oetjens M, Bowton EA, Ramirez AH, Jeff JM, Basford MA, Pulley JM, Cowan JD, Wang X, **Ritchie MD**, Masys DR, Roden DM, Crawford DC, Denny JC. Facilitating pharmacogenetic studies using electronic health records and natural-language processing: a case study of warfarin. *J Am Med Inform Assoc*. 2011 Jul 1;18(4):387-91. [PMID: 21672908](#), [PMCID: PMC 3128409](#)
112. Avery CL, He Q, North KE, Ambite JL, Boerwinkle E, Fornage M, Hindorff LA, Kooperbert C, Meigs JB, Pankow JS, Pendergrass SA, Psaty BM, **Ritchie MD**, Rotter ji, Taylor KD, Wilkens LR, Heiss G, Lin DY. A Phenomics-Based Strategy Identifies Loci on *APOC1*, *BRAP*, and *PLCG1* Associated with Metabolic Syndrome Phenotype Domains. October 2011 *PLOS Genetics*. [PMID: 2202282](#), [PMCID: PMC 3192835](#)
113. Delaney JT, Ramirez AH, Bowton E, Pulley JM, Basford MA, Schildcrout JS, Shi Y, Oetjens M, Cleator JH, Jahangir E, **Ritchie MD**, Masys DR, Crawford DC, Roden DM, Denny JC. Predicting clopidogrel response using DNA samples linked to an electronic health record. *CPT*, 2012 Feb;91(2):257-63. [PMID: 22190063](#), [PMCID: PMC 3621954](#)
114. Mechanic LE, Cheng HS, Amos CI, Chatterjee N, Cox NJ, Divi RL, Fan R, Harris EL, Jacobs K, Kraft P, Leal SM, McAllister K, Moore JH, Paltoo DN, Province MA, Ramos EM, **Ritchie MD**,

Curriculum Vitae: Marylyn DeRiggi Ritchie

- roeder K, Schaid DJ, Stephens M, Thomas DC, Weinberg CR, Witte JS, Zhang S, Zöllner S, Feuer EJ, Gillanders EM. Next Generation Analytic Tools for Large Scale Genetic Epidemiology Studies of Complex Diseases. *Genetic Epidemiology*, 2011 Dec 6. doi: 10.1002/gepi.20652. [Epub ahead of print]. PMID: 22147673, PMCID: PMC 3368075
115. Crosslin DR, McDavid A, Weston N, Nelson SC, Zheng X, Hart E, deAndrade M, Kullo IJ, McCarty CA, Doheny KF, Pugh E, Kho A, Hays MG, Pretel S, Saip A, **Ritchie MD**, Crawford DC, Crane PK, Newton K, Li R, Mirel D, Crenshaw A, Larson EB, Carlson C, Jarvik GP, eMERGE . Genetic variants associated with the white blood cell count in 13,923 subjects in the eMERGE Network. *Human Genetics*. October 2011 PMID: 22037903 PMCID: PMC 22037903
116. Haas DW, Kuritzkes D, **Ritchie MD**, Smur S, Gage BF, Maartens G, Masys D, Fellay J, Phillips E, Ribaud HJ, Freedberg KA, Petropoulos C, Manolio TA, Gulick RM, Haubrich R, Kim P, Dehlinger M, Abebe R, Telenti A. Pharmacogenomics of HIV Therapy: Summary of a Workshop Sponsored by the National Institute of Allergy and Infectious Diseases. *HIV Clinical Trials*. Sept/Oct 2011 12; 12(5): 277-85 PMID: 22180526, PMCID: PMC3322423
117. Denny JC, Crawford DC, **Ritchie MD**, Bielinski SJ, Basford MA, Bradford Y, Chai HS, Bastarache L, Zuvich R, Peissig P, Carrell D, Ramirez AH, Pathak J, Wilke RA, Rasmussen L, Wang X, Pacheco JA, Kho AN, Hayes MG, Weston N, Matsumoto M, Kopp PA, Newton KM, Jarvik GP, Li R, Manolio TA, Kullo IJ, Chute CG, Chisholm RL, Larson EB, McCarty CA, Masys DR, Roden DM, de Andre M. Variants Near FOXE1 Are Associated with Hypothyroidism and Other Thyroid Conditions: Using Electronic Medical Records for Genome- and Phenome-wide Studies. *The American Journal of Human Genetics* 89, 529-542, October 7, 2011. PMID: 21981779, PMCID: PMC3192835
118. Kääb S, Crawford DC, Sinner MF, Behr ER, Schulze-Bahr E, Guicheney P, Bishopric NH, Myerburg RJ, Schott JJ, Pfeufer A, Beckmann BM, Martens E, Zhang T, Stallmeyer B, Sumhagen S, Denjoy I, Bardai A, Van Gelder IC, Jamshidi Y, Dalageorgou C, Marshal V, Jeffery S, Shakir S, Camm AJ, Steinbeck G, Perz S, Lichtner P, Meitinger T, Peters A, Wichmann HE, Ingram C, Bradford Y, Carter S, Norris K, **Ritchie MD**, George AL, Roden DM. A Large Candidate Gene Survey Identifies the *KCNE1* D85N Polymorphism as a Possible Modulator of Drug-induced Torsades de Pointes. *Circ Cardiovasc Genet*. 2011 11; (1) PMID: 22100668, PMCID: PMC3237759
119. Grady BJ, Samuels DC, Robbins GK, Selph D, Canter JA, Pollard RB, Haas DW, Shafer R, Kalams SA, Murdock DG, **Ritchie MD**, Hulgán T for the ACTG 384 and DACS 250 study teams. Mitochondrial Genomics and CD4T-cell Count Recovery after Antiretroviral Therapy Initiation in AIDS Clinical Trials Group Study 384. *Journal of Acquired Immune Deficiency Syndromes*, 2011 Dec 1;58(4):363-70. PMID: 21792066, PMCID: PMC320417
120. Birdwell KA, Grady B, Choi L, Xu H, Bian A, Denny JC, Jiang M, Vranic G, Basford M, Cowan JD, Richardson DM, Robinson MP, Ikizler TA, **Ritchie MD**, Stein CM, Hass DW. Use of a DNA Biobank Linked to Electronic Medical Records to Characterize Pharmacogenomic Predictors of Tacrolimus Dose Requirement in Kidney Transplant Recipients. *Pharmacogenetics and Genomics*. 2012 Jan;22(1):32-42 PMID: 22108237, PMCID: PMC3237759
121. Fullerton S, Wolf W, Brothers K, Clayton E, Crawford D, Denny J, Greenland P, Koenig B, Leppig K, Lindor L, McARTHUR C, McGuire A, Mc Peek Hinz G, Mirel D, Ramos E, **Ritchie MD**, Smith M, Waudby C, Burke W, Jarvik G. Return of Individual Research Results from Genome-wide Association Studies: Experience of the Electronic Medical Records & Genomics (eMERGE) Network. *Genetics in Medicine*. 2012 Apr;14(4):424-31 PMID: 22361898, PMCID: PMC3297180
122. **Ritchie MD**, Rowan S, Kucera G, Stubblefield T, Blair M, Carter S, Roden DM, Darbar D. J Chromosome 4q25 variants are genetic modifiers of rare ion channel mutations associated with

Curriculum Vitae: Marylyn DeRiggi Ritchie

- familial atrial fibrillation. *Am Coll Cardiol*. 2012 Sep 25;60(13):1173-81 [PMID: 22818067](#), [PMCID: PMC3448817](#)
123. Ramirez AH, Shi Y, Schildcrout JS, Delaney JT, Xu H, Oetjens MT, Zuvich RL, Basford MA, Bowton E, Jiang M, Speltz P, Zink R, Cowan J, Pulley JM, **Ritchie MD**, Masys DR, Roden DM, Crawford DC, Denny JC. Predicting warfarin dosage in European-Americans and African-Americans using DNA samples linked to an electronic health record. *A Pharmacogenomics*. 2012 Mar;13(4):407-18. Epub 2012 Feb 13. [PMID: 22329724](#), [PMCID: PMC3361510](#)
124. Buchanan CC, Torstenson ES, Bush WS, **Ritchie MD**. A comparison of cataloged variation between International HapMap Consortium and 1000 Genomes Project data. *J Am Med Inform Assoc*. 2012 Mar-Apr;19(2):289-94. [PMID: 22319179](#), [PMCID: PMC3277631](#)
125. Zuvich RL, Armstrong LL, Bielinski SJ, Bradford Y, Carlson CS, Crawford DC, Crenshaw AT, de Andrade M, Doheny KF, Haines JL, Hayes MG, Jarvik GP, Jiang L, Kullo IJ, Li R, Ling H, Manolio TA, Matsumoto ME, McCarty A, McDavid AN, Mirel DB, Olson LM, Paschall JE, Pugh EW, Rasmussen LV, Rasmussen-Torvik LJ, Turner SD, Wilke RA, **Ritchie MD**. Pitfalls of merging GWAS data: lessons learned in the eMERGE network and quality control procedures to maintain high data quality. *Genet Epidemiol*. 2011 Dec;35(8):887-98. doi: 10.1002/gepi.20639. [PMID: 22125226](#), [PMCID: PMC3592376](#)
126. Ellinor PT, Lunetta KL, Albert CM, Gudbjartsson DF, Glazer NL, **Ritchie MD**, Smith AV, Arking DE, Müller M, Krijthe BP, Lubitz SA, Bis JC, Chung MK, Dörr M, Ozaki K, Roberts JD, Smith JG, Holm H, Pfeufer A, Sinner MF, Smith NL, Smith JD, Rienstra M, Rice KM, Van Wagoner DR, Magnani JW, Wakili R, Clauss S, Arnar DO, Rotter JI, Steinbeck G, Launer LJ, Davies RW, Borkovich M, Harris TB, Lin H, Völker U, Völzke H, Milan DJ, Hofman A, Boerwinkle E, Chen LY, Soliman E, Voight BF, Li G, Chakravarti A, Kubo M, Tedrow U, Rose LM, Ridker PM, Conen D, Tsunoda T, Furukawa T, Sotoodehnia N, Xu S, Kamatani N, Levy DL, Nakamura Y, Parvez B, Thorsteinsdottir U, Muhammad R, Psaty BM, Meitinger T, Perz S, Wichmann H-E, Witteman JCM, Kao WHL, Kathiresan S, Roden DM, Kong A, Uitterlinden AG, Rivadeneira F, McKnight B, Sjögren M, Gollob MH, Melander O, Tanaka T, Stricker BHCh, Felix SB, Alonso A, Gudnason V, Darbar D, Barnard J, Stefansson K, Heckbert SR, Chasman D, Benjamin EJ, Kääb S. Meta-Analysis in the AFGen Consortium Identifies Seven Novel Loci for Atrial Fibrillation. *Nature Genetics*. 2012 Apr 29;44(6):670-5 [PMID: 22544366](#), [PMCID: PMC3366038](#)
127. Ding K, Shameer K, Jouni H, Masys DR, Jarvik GP, Kho AN, **Ritchie MD**, McCarty CA, Chute CG, Manolio TA, Kullo IJ. Genetic Loci Implicated in Erythroid Differentiation and Cell Cycle Regulation are Associated with Red Blood Cell Traits. *Mayo Clin Proc*. 2012 May;87(5):461-74. [PMID: 22560525](#), [PMCID: PMC3538470](#)
128. Stranger BE, Björkegren J, Dolan ME, **Ritchie MD**. Systems and genome-wide approaches unite to provide a route to personalized medicine. *Genome Med*. 2012 Mar 30;4(3):29. [PMID: 22494390](#), [PMCID: PMC3446279](#)
129. Peters U, North KE, Sethupathy P, Buyske S, Haessler J, Fesinmeyer MD, Jackson RD, Kuller L, Rajkovic A, Lim U, Cheng I, Schumacher F, Wilkens L, Li R, Monda K, Ehret G, Nguyen KH, Cooper R, Lewis CE, Leppert M, Irvin MR, Gu CC, Houston D, Bůžková P, **Ritchie MD**, Matisse TC, Le Marchand L, Hindorff LA, Crawford DC, Haiman CA, Kooperberg CL. A systematic mapping approach of 16q12.2/FTO and BMI in over 20,000 African Americans narrows in on the underlying functional variation: results from the Population Architecture using Genomics and Epidemiology (PAGE) Study. *PLoS Genetics*, 2013 January; 9(1): e1003171. [PMID: 23341774](#), [PMCID: PMC3547789](#)
130. Holzinger ER, Grady B, **Ritchie MD**, Ribaldo HJ, Acosta EP, Morse GD, Gulick RM, Robbins GK, Clifford DB, Daar ES, McLaren P, Hass DW. Genome-Wide Association Study of Plasma Efavirenz Pharmacokinetics in AIDS clinical Trials Group Protocols implicates several CYP2B6

- variants. *Pharmacogenetics and Genomics*. 2012 Dec;22(12):858-67. [PMID: 23080225](#), [PMCID: PMC3614365](#)
131. Holzinger ER, Hulan T, Ellis RJ, Samuels DC, **Ritchie MD**, Haas DW, Kallianpur AR, Bloss CS, Clifford DB, Collier AC, Gelman BB, Marra CM, McArthur JC, McCutchan JA, Morgello S, Simpson DM, Franklin DR, Rosario D, Selph D, Letendre S, Grant I, for the CHARTER group. Mitochondrial DNA variation and HIV-associated sensory neuropathy in CHARTER. *Journal of Neurovirology*, 2012 Dec;18(6):511-20. [PMID: 23073667](#), [PMCID: PMC3587171](#)
132. S.A. Pendergrass, K. Brown-Gentry, S. Dudek, E.S. Torstenson, R. Goodloe, J.L. Ambite, C.L. Avery, S. Buyske, P. Bůžková, C. Cai, E. Deelman, M.D. Fesinmeyer, C. Haiman G. Heiss, L.A. Hindorff, C.-N. Hsu; R. D. Jackson; C. Kooperberg, L. LeMarchand, Y. Lin, T. C. Matise, K.R. Monroe, L. Moreland, A. Reiner, R. Wallace, L. R. Wilkens, D.C. Crawford, **M.D. Ritchie**. Phenome-Wide Association Study (PheWAS) for Detection of Pleiotropy within the Population Architecture Using Genomics and Epidemiology (PAGE) Network. *PLoS Genetics*, 2013 January; 9(1): e1003087. [PMID: 23382687](#), [PMCID: PMC3561060](#)
133. Graff, Mariaelisa; Gordon-Larsen, Penny; Lim, Unhee; Fowke, Jay; Love, Shelly-Ann; Fesinmeyer, Megan; Wilkens, Lynne; Vertilus, Shawyntee; **Ritchie, Marylyn**; Prentice, Ross; Pankow, James; Monroe, Kristine; Manson, JoAnn; Marchand, Loic; Kuller, Lewis; Kolonel, Laurence; Hong, Ching; Henderson, Brian; Haessler, Jeff; Gross, Myron; Goodloe, Robert; Franceschini, Nora; Carlson, Christopher; Buyske, Steven; Buzkova, Petra; Hindorff, Lucia; Matise, Tara; Crawford, Dana; Haiman, Chris; Peters, Ulrike; North, Kari. The Influence of Obesity related SNPs on BMI across the Life Course: the PAGE Study, *Diabetes*. 2013 Jan 8. [PMID: 23300277](#), [PMC ID: PMC3636619](#)
134. Crosslin DR, McDavid A, Weston N, Zheng X, Hart E, de Andrade M, Kullo IJ, McCarty CA, Doheny KF, Pugh E, Kho A, Hayes MG, **Ritchie MD**, Saip A, Crawford DC, Crane PK, Newton K, Carrell DS, Gallego CJ, Nalls MA, Li R, Mirel DB, Crenshaw A, Couper DJ, Tanaka T, van Rooij FJ, Chen MH, Smith AV, Zakai NA, Yango Q, Garcia M, Liu Y, Lumley T, Folsom AR, Reiner AP, Felix JF, Dehghan A, Wilson JG, Bis JC, Fox CS, Glazer NL, Cupples LA, Coresh J, Eiriksdottir G, Gudnason V, Bandinelli S, Frayling TM, Chakravarti A, van Duijn CM, Melzer D, Levy D, Boerwinkle E, Singleton AB, Hernandez DG, Longo DL, Witteman JC, Psaty BM, Ferrucci L, Harris TB, O'Donnell CJ, Ganesh SK; CHARGE Hematology Working Group, Larson EB, Carlson CS, Jarvik GP; The electronic Medical Records and Genomics (eMERGE) Network. Genetic variation associated with circulating monocyte count in the eMERGE Network. *Hum Mol Genet*. 2013 May 15;22(10):2119-27. Epub 2013 Jan 12. [PMID: 23314186](#), [PMCID: PMC3633369](#)
135. Fesinmeyer MD, North KE, Lim U, Buzková P, Crawford DC, Haessler J, Gross MD, Fowke JH, Goodloe R, Love SA, Graff M, Carlson CS, Kuller LH, Matise TC, Hong CP, Henderson BE, Allen M, Rohde RR, Mayo P, Schnetz-Boutaud N, Monroe KR, **Ritchie MD**, Prentice RL, Kolonel LN, Manson JE, Pankow J, Hindorff LA, Franceschini N, Wilkens LR, Haiman CA, Marchand L, Peters U. Effects of smoking on the genetic risk of obesity: the population architecture using genomics and epidemiology study. *BMC Med Genet*. 2013 Jan 11;14(1):6. [PMID: 23311614](#), [PMCID: PMC3564691](#)
136. Kim D, Kim S, Risacher SL, Shen L, **Ritchie MD**, Weiner MW, Saykin AJ, Nho K; the Alzheimer's Disease Neuroimaging Initiative (ADNI). A Graph-Based Integration of Multimodal Brain Imaging Data for the Detection of Early Mild Cognitive Impairment (E-MCI). *Multimodal Brain Image Anal* (2013). 2013; 8159:159-169. [PMID: 25383392](#), [PMCID: PMC4224282](#)
137. Spencer KL, Malinowski J, Carty CL, Franceschini N, Fernández-Rhodes L, Young A, Cheng I, **Ritchie MD**, Haiman CA, Wilkens L, Chunyuanwu, Matise TC, Carlson CS, Brennan K, Park A, Rajkovic A, Hindorff LA, Buyske S, Crawford DC. Genetic variation and reproductive timing: African American women from the Population Architecture using Genomics and

Curriculum Vitae: Marylyn DeRiggi Ritchie

- Epidemiology (PAGE) Study. *PLoS One*. 2013;8(2):e55258. doi: 10.1371/journal.pone.0055258. Epub 2013 Feb 12. PMID: 23424626, PMCID: PMC3570525
138. Rasmussen-Torvik LJ, Pacheco JA, Wilke RA, Thompson WK, **Ritchie MD**, Kho AN, Muthalagu A, Hayes MG, Armstrong LL, Scheftner DA, Wilkins JT, Zuvich RL, Crosslin D, Roden DM, Denny JC, Jarvik GP, Carlson CS, Kullo IJ, Bielinski SJ, McCarty CA, Li R, Manolio TA, Crawford DC, Chisholm RL. High density GWAS for LDL cholesterol in African Americans using electronic medical records reveals a strong protective variant in APOE. *Clin Transl Sci*. 2012 Oct;5(5):394-9. doi: 10.1111/j.1752-8062.2012.00446.x. Epub 2012 Aug 23. PMID: 23067351, PMCID: PMC3521536
139. Fesinmeyer MD, North KE, **Ritchie MD**, Lim U, Franceschini N, Wilkens LR, Gross MD, Bůžková P, Glenn K, Qibrera PM, Fernández-Rhodes L, Li Q, Fowke JH, Li R, Carlson CS, Prentice RL, Kuller LH, Manson JE, Matisse TC, Cole SA, Chen CT, Howard BV, Kolonel LN, Henderson BE, Monroe KR, Crawford DC, Hindorff LA, Buyske S, Haiman CA, Le Marchand L, Peters U. Genetic Risk Factors for BMI and Obesity in an Ethnically Diverse Population: Results from the Population Architecture Using Genomics and Epidemiology (PAGE) Study. *Obesity* (Silver Spring). 2013 Apr;21(4):835-46. doi: 10.1002/oby.20268. PM 23712987, PMC 3482415
140. Schildcrout JS*, Denny JC*, Bowton E, Gregg W, Pulley JM, Basford MA, Cowan J, Ramirez AH, Crawford DC, **Ritchie MD**, Peterson JF, Masys DR, Wilke R, Roden DM. Optimizing drug outcomes with pharmacogenomics: A case for preemptive genotyping. *Clin Pharmacol Ther*. 2012 Aug;92(2):235-42. doi: 10.1038/clpt.2012.66. Epub 2012 Jun 27. PMID: 22739144, PMCID: PMC3785311
141. Pendergrass SA, Dudek SM, Crawford DC, **Ritchie MD**. Visually integrating and exploring high throughput Phenome-Wide Association Study (PheWAS) results using PheWAS-View. *BioData Min*. 2012 Jun 8;5(1):5. PMID: 22682510, PMC ID: PMC3476448
142. Pendergrass SA, Verma SS, Holzinger ER, Moore CB, Wallace JR, Dudek SM, Huggins W, Kitchner T, Waudby C, Berg R, McCarty CA, **Ritchie MD**. Next-Generation Analysis of Cataracts: Determining Knowledge Driven Gene-Gene Interactions Using Biofilter, and Gene-Environment Interactions Using the PhenX Toolkit. *Pacific Symposium on Biocomputing* 18:147-158(2013) PMID 23424120, PMCID: PMC3615413
143. Crawford DC, Goodloe R, Brown-Gentry K, Wilson S, Roberson J, Gillani NB, **Ritchie MD**, Dilks HH, Bush WS. Characterization of the Metabochip in Diverse Populations from the International HapMap Project in the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) Project. *Pacific Symposium on Biocomputing* 18:188-199(2013) PMID: 23424124, PMCID: PMC3584704
144. Moore CB, Wallace JR, Frase AT, Pendergrass SA, **Ritchie MD**. Using BioBin to Explore Rare Variant Population Stratification. *Pacific Symposium on Biocomputing* 18:332-343(2013) PMID: 23424138, PMCID: PMC3638724
145. Bush WS, Boston J, Pendergrass SA, Dumitrescu L, Goodloe R, Brown-Gentry K, Wilson S, McClellan R Jr, Torstenson E, Basford MA, Spencer KL, **Ritchie MD**, Crawford DC. Enabling High-Throughput Genotype-Phenotype Associations in the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) Project as Part of the Population Architecture Using Genomics and Epidemiology (PAGE) Study. *Pacific Symposium on Biocomputing* 18:373-384(2013) PMID: 23424142, PMCID: PMC3579641
146. Holzinger ER, Dudek SM, Frase AT, Krauss RM, Medina MW, **Ritchie MD**. ATHENA: A Tool for Meta-Dimensional Analysis Applied to Genotypes and Gene Expression Data to Predict HDL Cholesterol Levels. *Pacific Symposium on Biocomputing* 18:385-396(2013) PMID: 23424143, PMCID: PMC3587764

Curriculum Vitae: Marylyn DeRiggi Ritchie

147. Moore CB, Wallace JR, Frase AT, Pendergrass SA, **Ritchie MD**. BioBin: A bioinformatics tool for automating the binning of rare variants using publicly available biological knowledge. *BMC Medical Genomics*. 2013; 6(Suppl 2): S6. [PMID: 23819467](#), [PMCID: PMC3654874](#)
148. **Ritchie MD**, Deny JC, Zuvich RL, Crawford DC, Schildcrout JS, Bastarache L, Ramirez AH, Mosley JD, Pulley JM, Basford MA, Bradford Y, Rasmussen LV, Pathak J, Chute CG, Kullo IJ, McCarty C, Chisholm RL, Kho AN, Carlson CS, Larson EB, Jarvik GP, Sotoodehnia N, Manolio TA, Li R, Masys DR, Haines JL, Roden DM. Genome- and phenome-wide analysis of cardiac conduction identifies markers of arrhythmia risk. *Circulation*, 2013. [PMID: 23463857](#), [PMCID: PMC3713791](#)
149. McGeachie MJ, Stahl EA, Himes BE, Pendergrass SA, Lima JJ, Irvin CG, Peters SP, **Ritchie MD**, Plenge RM, Tantisira KG. Polygenic Heritability Estimates in Pharmacogenetics: Focus on Asthma and Related Phenotypes. *Pharmacogenet Genomics*. 2013 Jun;23(6):324-328. [PMID: 23532052](#), [PMCID: PMC3767309](#)
150. Gottesman O, Kuivaniemi H, Tromp G, Faucett WA, Li R, Manolio TA, Sanderson SC, Kannry J, Zinberg R, Basford MA, Brilliant M, Carey DJ, Chisholm RL, Chute CG, Connolly JJ, Crosslin D, Denny JC, Gallego CJ, Haines JL, Hakonarson H, Harley J, Jarvik GP, Kohane I, Kullo IJ, Larson EB, McCarty C, Ritchie MD, Roden DM, Smith ME, Böttinger EP, Williams MS; eMERGE Network. The Electronic Medical Records and Genomics (eMERGE) Network: past, present, and future. *Genet Med*. 2013 Oct;15(10):761-71. doi: 10.1038/gim.2013.72. Epub 2013 Jun 6. Review. [PMID: 23743551](#), [PMCID: PMC3795928](#)
151. Park SL, Cheng I, Pendergrass SA, Kucharska-Newton AM, Lim U, Ambite JL, Caberto CP, Monroe KR, Schumacher F, Hindorff LA, Oetjens MT, Wilson S, Goodloe RJ, Love SA, Henderson BE, Kolonel LN, Haiman CA, Crawford DC, North KE, Heiss G, **Ritchie MD**, Wilkens LR, Le Marchand L. Association of the FTO Obesity Risk Variant rs8050136 With Percent Energy Intake from Fat in Multiple Ethnic/Racial Populations: The PAGE Study. *American Journal of Epidemiology*, in press (2013). [PMID: 23820787](#), [PMCID: PMC3755639](#)
152. Jeff JM, **Ritchie MD**, Denny JC, Kho AN, Ramirez AH, Crosslin D, Armstrong L, Basford MA, Wolf WA, Pacheco JA, Chisholm RL, Roden DM, Hayes G, Crawford DC. Generalization of Variants Identified by Genome-wide Association Studies for ECG Traits in African Americans. *Ann Hum Genet*. 2013 Mar 28. doi: 10.1111/ahg.12023. [PMID: 23534349](#), [PMCID: PMC3743946](#)
153. Zhang L, Franceschini N, Buzkova P, Wassel CL, Roman MJ, North KE, Crawford DC, Boston J, Brown-Gentry KD, Cole SA, Deelman E, Goodloe R, Heiss G, Jenny NS, Jorgensen NW, Matisse TC, McClellan Jr BE, **Ritchie MD**, Wilson S, Kao WHL. Lack of Associations of Coronary Heart Disease Risk Genetic Variants and Subclinical Atherosclerosis in Four U.S. Populations: the Population Architecture using Genomics and Epidemiology (PAGE) Study. *Atherosclerosis*. 2013 Jun;228(2):390-9. doi: 10.1016/j.atherosclerosis.2013.02.038. Epub 2013 Mar 13. [PMID: 23587283](#), [PMCID: PMC 3717342](#)
154. Ding K, de Andrade M, Manolio T, Crawford D, Rasmussen-Torvik L, **Ritchie M**, Denny J, Masys D, Jouni H, Pacheco J, Kho A, Roden D, Chisholm R, Kullo I, Genetic Variants That Confer Resistance to Malaria are Associated with Red Blood Cell Traits in African Americans: An Electronic Medical Record-Based Genome Wide Association Study. *G3 (Bethesda)*. 2013 5; [PMID: 23696099](#), [PMCID: PMC3704235](#)
155. Oetjens M, Denny J, **Ritchie M**, Gillani N, Richardson D, Restrepo N, Pulley J, Dilks H, Basford M, Bowton E, Masys D, Wilke R, Roden D, Crawford D, Assessment of a pharmacogenomic marker panel in a polypharmacy population identified from electronic medical records. *Pharmacogenomics*. 2013 05; 14(7): 735-44. [PMID: 23651022](#), [PMCID: PMC3725600](#)
156. Girirajan S, Johnson R, Tassone F, Balciuniene J, Katiyar N, Fox K, Baker C, Srikanth A, Yeoh K, Khoo S, Nauth T, Hansen R, **Ritchie M**, Hertz-Picciotto I, Eichler E, Pessah I, Selleck

Curriculum Vitae: Marylyn DeRiggi Ritchie

- S, Global increases in both common and rare copy number load associated with autism. *Hum. Mol. Genet.* 2013 4; (2): [PMID: 23535821](#), [PMCID: PMC3690969](#)
157. McDavid A, Crane P, Newton KM, Crosslin D, McCormik W, Weston N, Ehrlich K, Hart E, Harrison R, Kukul WA, Rottscheit C, Peissing P, Stefanski E, McCartha CA, Suvich RL, **Ritchie MD**, Schellenberg G, deAndrade M, Kullo I, Li R, Mirel D, Crenshaw A, Bowed JD, Li G, Tsuang D, McCurry S, Teri L, Larson E, Jarvik GP, Carlson CS. Enhancing the Power of Genetic Association Studies through the Use of Silver Standard Cases Derived from Electronic Medical Records. *PLoS One.* 2013 Jun 10;8(6):e63481. [PMID: 23762230](#), [PMCID: PMC3677889](#)
158. Hulan T, Stein JH, Cotter BR, Murdock DG, **Ritchie MD**, Dube MP, Gerschenson M, Haas DW, and Torriani FJ. Mitochondrial DNA Variation and Changes in Adiponectin and Endothelial Function in HIV-infected Adults after Antiretroviral Therapy Initiation. *AIDS Res Hum Retroviruses* 2013 Aug 14. [Epub ahead of print]. [PMID: 23944767](#) [PMCID: PMC3785797](#)
159. **Ritchie MD**. Erratum to: 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.* 132:1437. [PMID: 22923055](#), [PMCID: PMC3432217](#)
160. Shameer K, Denny JC, Ding K, Jouni H, Crosslin DR, de Andrade M, Chute CG, Peissig P, Pacheco JA, Li R, Bastarache L, Kho AN, **Ritchie MD**, Masys DR, Chisholm RL, Larson EB, McCarty CA, Roden DM, Jarvik GP, Kullo IJ. A genome- and phenome-wide association study to identify genetic variants influencing platelet count and volume and their pleiotropic effects. *Hum Genet.* 2013 Sep 12. [PMID: 24026423](#), [PMCID: PMC3880605](#)
161. Pare G, Kubo M, Byrd JB, McCarty CA, Woodard-Grice A, Teo KK, Anand SS, Zuvich RL, Bradford Y, Ross S, Nakamura Y, **Ritchie M**, Brown NJ. Genetic variants associated with angiotensin-converting enzyme inhibitor-associated angioedema. *Pharmacogenet Genomics.* 2013 Sep;23(9):470-8. doi: 10.1097/FPC.0b013e328363c137. [PMID: 23838604](#), [PMCID: PMC3904664](#)
162. Moore CB, Wallace JR, Wolfe DJ, Frase AT, Pendergrass SA, Weiss KM, Ritchie MD. Low frequency variants, collapsed based on biological knowledge, uncover complexity of population stratification in 1000 genomes project data. *PLoS Genet.* 2013 Dec;9(12):e1003959. doi: 10.1371/journal.pgen.1003959. Epub 2013 Dec 26. [PMID: 24385916](#), [PMCID: PMC3873241](#)
163. Holzinger ER, Dudek SM, Frase AT, Pendergrass SA, **Ritchie MD**. ATHENA: the analysis tool for heritable and environmental network associations. *Bioinformatics.* 2014 Mar 1;30(5):698–705 [PMID: 24149050](#) [PMCID: PMC3933870](#)
164. Hall MA, Dudek SM, Goodloe R, Crawford DC, Pendergrass SA, Peissig P, Brilliant M, McCarty CA, Ritchie MD. Environment-wide association study (ewas) for type 2 diabetes in the marshfield personalized medicine research project biobank. *Pac Symp Biocomput.* 19:200-211. [PMID: 24297547](#), [PMCID: PMC4037237](#)
165. Behr ER, **Ritchie MD**, Tanaka T, Käab S, Crawford DC, Nicoletti P, Floratos A, Sinner MF, Kannankeril PJ, Wilde AA, Bezzina CR, Schulze-Bahr E, Zumhagen S, Guicheney P, Bishopric NH, Marshall V, Shakir S, Dalageorgou C, Bevan S, Jamshidi Y, Bastiaenen R, Myerburg RJ, Schott JJ, Camm AJ, Steinbeck G, Norris K, Altman RB, Tatonetti NP, Jeffery S, Kubo M, Nakamura Y, Shen Y, George AL Jr, Roden DM. Genome wide analysis of drug-induced torsades de pointes: lack of common variants with large effect sizes. *PLoS One.* 2013 Nov 6;8(11):e78511. doi: 10.1371/journal.pone.0078511. [PMID: 24223155](#), [PMCID: PMC3819377](#)
166. Denny JC, Bastarache L, **Ritchie MD**, Carroll RJ, Zink R, Mosley JD, Field JR, Pulley JM, Ramirez AH, Bowton E, Basford MA, Carrell DS, Peissig PL, Kho AN, Pacheco JA, Rasmussen LV, Crosslin DR, Crane PK, Pathak J, Bielinski SJ, Pendergrass SA, Xu H, Hindorff LA, Li R, Manolio TA, Chute CG, Chisholm RL, Larson EB, Jarvik GP, Brilliant MH, McCarty CA, Kullo

Curriculum Vitae: Marylyn DeRiggi Ritchie

- IJ, Haines JL, Crawford DC, Masys DR, Roden DM. Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. *Nat Biotechnol.* 31:1102-1111. PMID: 24270849, PMCID: PMC3969265
167. Wolfe D, Dudek S, **Ritchie MD**, Pendergrass SA. Visualizing genomic information across chromosomes with PhenoGram. *BioData Min.* 2013 Oct 16;6(1):18. PMID: 24131735, PMCID: PMC4015356
168. Gong J, Schumacher F, Lim U, Hindorff LA, Haessler J, Buyske S, Carlson CS, Rosse S, Bůžková P, Fornage M, Gross M, Pankratz N, Pankow JS, Schreiner PJ, Cooper R, Ehret G, Gu CC, Houston D, Irvin MR, Jackson R, Kuller L, Henderson B, Cheng I, Wilkens L, Leppert M, Lewis CE, Li R, Nguyen KD, Goodloe R, Farber-Eger E, Boston J, Dilks HH, **Ritchie MD**, Fowke J, Pooler L, Graff M, Fernandez-Rhodes L, Cochrane B, Boerwinkle E, Kooperberg C, Matisse TC, Le Marchand L, Crawford DC, Haiman CA, North KE, Peters U. Fine Mapping and Identification of BMI Loci in African Americans. *Am J Hum Genet.* 2013 Oct 3;93(4):661-71. PMID: 24094743, PMCID: PMC3791273
169. Carlson CS, Matisse TC, North KE, Haiman CA, Fesinmeyer MD, Buyske S, Schumacher FR, Peters U, Franceschini N, **Ritchie MD**, Duggan DJ, Spencer KL, Dumitrescu L, Eaton CB, Thomas F, Young A, Carty C, Heiss G, Le Marchand L, Crawford DC, Hindorff LA, Kooperberg CL; PAGE Consortium. Generalization and dilution of association results from European GWAS in populations of non-European ancestry: the PAGE study. *PLoS Biol.* 2013 Sep;11(9):e1001661. Epub 2013 Sep 17. PMID: 24068893, PMCID: PMC3775722
170. Pendergrass SA, Frase A, Wallace J, Wolfe D, Katiyar N, Moore C, **Ritchie MD**. Genomic analyses with biofilter 2.0: knowledge driven filtering, annotation, and model development. *BioData Min.* 2013 Dec 30;6(1):25. PMID: 24378202, PMCID: PMC3917600
171. Kim D, Shin H, Sohn KA, Verma A, **Ritchie MD**, Kim JH. Incorporating inter-relationships between different levels of genomic data into cancer clinical outcome prediction. *Methods.* Epub 2014 Feb 18. pii: S1046-2023(14)00033-4. doi: 10.1016/j.ymeth.2014.02.003. PMID: 24561168, PMC ID:PMC4664202
172. Chhibber A, Mefford J, Stahl EA, Pendergrass SA, Baldwin RM, Owzar K, Li M, Winer EP, Hudis CA, Zembutsu H, Kubo M, Nakamura Y, McLeod HL, Ratain MJ, Shulman LN, **Ritchie MD**, Plenge RM, Witte JS, Kroetz DL. Polygenic inheritance of paclitaxel-induced sensory peripheral neuropathy driven by axon outgrowth gene sets in CALGB 40101 (Alliance). *Pharmacogenomics J.* 2014 Aug;14(4):336-42. doi: 10.1038/tpj.2014.2. Epub 2014 Feb 11. PMID: 24513692, PMCID: PMC4111770
173. Kim D, Li R, Dudek SM, **Ritchie MD**. ATHENA: Identifying interactions between different levels of genomic data associated with cancer clinical outcomes using grammatical evolution neural network. *BioData Min.* 2013 Dec 20;6(1):23. doi: 10.1186/1756-0381-6-23. PMID: 24359638, PMCID: PMC3912499
174. Mosley JD, Van Driest SL, Larkin EK, Weeke PE, Witte JS, Wells QS, Karnes JH, Guo Y, Bastarache L, Olson LM, McCarty CA, Pacheco JA, Jarvik GP, Carrell DS, Larson EB, Crosslin DR, Kullo IJ, Tromp G, Kuivaniemi H, Carey DJ, **Ritchie MD**, Denny JC, Roden DM. Mechanistic phenotypes: an aggregative phenotyping strategy to identify disease mechanisms using GWAS data. *PLoS ONE.* 2013 Dec 12;8(12):e81503. PMID: 24349080, PMCID: PMC3861317
175. McCarty CA, Berg R, Rottscheit CM, Waudby CJ, Kitchner T, Brilliant M, **Ritchie MD**. Validation of PhenX measures in the personalized medicine research project for use in gene/environment studies. *BMC Med Genomics.* 2014 Jan 14;7:3. doi: 10.1186/1755-8794-7-3. PMID: 24423110, PMCID: PMC3896802

Curriculum Vitae: Marylyn DeRiggi Ritchie

176. Jeff JM, Armstrong LL, **Ritchie MD**, Denny JC, Kho AN, Basford MA, Wolf WA, Pacheco JA, Li R, Chisholm RL, Roden DM, Hayes MG, Crawford DC. Admixture mapping and subsequent fine-mapping suggests a biologically relevant and novel association on chromosome 11 for type 2 diabetes in African Americans. *PLoS ONE*. 2014 Mar 3;9(3):e86931. doi: 10.1371/journal.pone.0086931. eCollection 2014. PMID: 24595071, PMCID: PMC3940426
177. McCarty CA, Huggins W, Aiello AE, Bilder RM, Hariri A, Jernigan TL, Newman E, Sanghera DK, Strauman TJ, Zeng Y, Ramos EM, Junkins HA, PhenX RISING network. PhenX RISING: real world implementation and sharing of PhenX measures. *BMC Med Genomics*. 2014 Mar 20;7:16. doi: 10.1186/1755-8794-7-16. PMID:24650325, PMCID: 3994539
178. Johnson DH, Venuto C, **Ritchie MD**, Morse GD, Daar ES, McLaren PJ, Haas DW. Genomewide association study of atazanavir pharmacokinetics and hyperbilirubinemia in AIDS Clinical Trials Group protocol A5202. *Pharmacogenet Genomics*. 2014 Apr;24(4):195–203. doi: 10.1097/FPC.0000000000000034. PMID: 24557078, PMCID: PMC4059003
179. Sun X, Lu Q, Mukheerjee S, Crane PK, Elston R, **Ritchie MD**. Analysis pipeline for the epistasis search - statistical versus biological filtering. *Front Genet*. 2014 Apr 30;5:106. doi: 10.3389/fgene.2014.00106. eCollection 2014. PMID: 24817878, PMCID: PMC4012196
180. Arking DE, Pulit SL, Crotti L, van der Harst P, Munroe PB, Koopmann TT, Sotoodehnia N, Rossin EJ, Morley M, Wang X, Johnson AD, Lundby A, Gudbjartsson DF, Noseworthy PA, Eijgelsheim M, Bradford Y, Tarasov KV, Dörr M, Müller-Nurasyid M, Lahtinen AM, Nolte IM, Smith AV, Bis JC, Isaacs A, Newhouse SJ, Evans DS, Post WS, Waggott D, Lyytikäinen LP, Hicks AA, Eisele L, Ellinghaus D, Hayward C, Navarro P, Ulivi S, Tanaka T, Tester DJ, Chatel S, Gustafsson S, Kumari M, Morris RW, Naluai AT, Padmanabhan S, Kluttig A, Strohmer B, Panayiotou AG, Torres M, Knoflach M, Hubacek JA, Slowikowski K, Raychaudhuri S, Kumar RD, Harris TB, Launer LJ, Shuldiner AR, Alonso A, Bader JS, Ehret G, Huang H, Kao WH, Strait JB, Macfarlane PW, Brown M, Caulfield MJ, Samani NJ, Kronenberg F, Willeit J; CARE Consortium; COGENT Consortium, Smith JG, Greiser KH, Meyer Zu Schwabedissen H, Werdan K, Carella M, Zelante L, Heckbert SR, Psaty BM, Rotter JI, Kolcic I, Polašek O, Wright AF, Griffin M, Daly MJ; DCCT/EDIC, Arnar DO, Hólm H, Thorsteinsdóttir U; eMERGE Consortium, Denny JC, Roden DM, Zuvich RL, Emilsson V, Plump AS, Larson MG, O'Donnell CJ, Yin X, Bobbo M, D'Adamo AP, Iorio A, Sinagra G, Carracedo A, Cummings SR, Nalls MA, Jula A, Kontula KK, Marjamaa A, Oikarinen L, Perola M, Porthan K, Erbel R, Hoffmann P, Jöckel KH, Kälisch H, Nöthen MM; HRGEN Consortium, den Hoed M, Loos RJ, Thelle DS, Gieger C, Meitinger T, Perz S, Peters A, Prucha H, Sinner MF, Waldenberger M, de Boer RA, Franke L, van der Vleuten PA, Beckmann BM, Martens E, Bardai A, Hofman N, Wilde AA, Behr ER, Dalageorgou C, Giudicessi JR, Medeiros-Domingo A, Barc J, Kyndt F, Probst V, Ghidoni A, Insolia R, Hamilton RM, Scherer SW, Brandimarto J, Margulies K, Moravec CE, Greco M FD, Fuchsberger C, O'Connell JR, Lee WK, Watt GC, Campbell H, Wild SH, El Mokhtari NE, Frey N, Asselbergs FW, Mateo Leach I, Navis G, van den Berg MP, van Veldhuisen DJ, Kellis M, Krijthe BP, Franco OH, Hofman A, Kors JA, Uitterlinden AG, Witteman JC, Kedenko L, Lamina C, Oostra BA, Abecasis GR, Lakatta EG, Mulas A, Orrú M, Schlessinger D, Uda M, Markus MR, Völker U, Snieder H, Spector TD, Arnlöv J, Lind L, Sundström J, Syvänen AC, Kivimäki M, Kähönen M, Mononen N, Raitakari OT, Viikari JS, Adamkova V, Kiechl S, Brion M, Nicolaidis AN, Paulweber B, Haerting J, Dominiczak AF, Nyberg F, Whincup PH, Hingorani AD, Schott JJ, Bezzina CR, Ingelsson E, Ferrucci L, Gasparini P, Wilson JF, Rudan I, Franke A, Mühleisen TW, Pramstaller PP, Lehtimäki TJ, Paterson AD, Parsa A, Liu Y, van Duijn CM, Siscovick DS, Gudnason V, Jamshidi Y, Salomaa V, Felix SB, Sanna S, **Ritchie MD**, Stricker BH, Stefansson K, Boyer LA, Cappola TP, Olsen

Curriculum Vitae: Marylyn DeRiggi Ritchie

- JV, Lage K, Schwartz PJ, Käab S, Chakravarti A, Ackerman MJ, Pfeufer A, de Bakker PI, Newton-Cheh C. Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nat Genet.* 2014 Aug;46(8):826-36. doi: 10.1038/ng.3014. Epub 2014 Jun 22. PMID: 24952745, PMCID: PMC4124521
181. Rasmussen-Torvik LJ, Stallings SC, Gordon AS, Almoguera B, Basford MA, Bielinski SJ, Brautbar A, Brilliant MH, Carrell DS, Connolly JJ, Crosslin DR, Doheny KF, Gallego CJ, Gottesman O, Kim DS, Leppig KA, Li R, Lin S, Manzi S, Mejia AR, Pacheco JA, Pan V, Pathak J, Perry CL, Peterson JF, Prows CA, Ralston J, Rasmussen LV, **Ritchie MD**, Sadhasivam S, Scott SA, Smith M, Vega A, Vinks AA, Volpi S, Wolf WA, Bottinger E, Chisholm RL, Chute CG, Haines JL, Harley JB, Keating B, Holm IA, Kullo IJ, Jarvik GP, Larson EB, Manolio T, McCarty CA, Nickerson DA, Scherer SE, Williams MS, Roden DM, Denny JC. Design and Anticipated Outcomes of the eMERGE-PGx Project: A Multicenter Pilot for Preemptive Pharmacogenomics in Electronic Health Record Systems. *Clin Pharmacol Ther.* 2014 Jun 24. doi: 10.1038/clpt.2014.137. [Epub ahead of print]. PMID: 24960519, PMCID: PMC4169732
182. Kraja AT, Chasman DI, North KE, Reiner AP, Yanek LR, Kilpeläinen TO, Smith JA, Dehghan A, Dupuis J, Johnson AD, Feitosa MF, Tekola-Ayele F, Chu AY, Nolte IM, Dastani Z, Morris A, Pendergrass SA, Sun YV, **Ritchie MD**, Vaez A, Lin H, Ligthart S, Marullo L, Rohde R, Shao Y, Ziegler MA, Im HK; Cross Consortia Pleiotropy (XC-Pleiotropy) Group; Cohorts for Heart and Aging Research in Genetic Epidemiology (CHARGE); Genetic Investigation of Anthropometric Traits (GIANT) Consortium; Global Lipids Genetics Consortium (GLGC); Meta-Analyses of Glucose; Insulin-related traits Consortium (MAGIC); Global BPgen (GBPG) Consortium; ADIPOGen Consortium; Women's Genome Health Study (WGHS); Howard University Family Study (HUFs), Schnabel RB, Jørgensen T, Jørgensen ME, Hansen T, Pedersen O, Stolk RP, Snieder H, Hofman A, Uitterlinden AG, Franco OH, Ikram MA, Richards JB, Rotimi C, Wilson JG, Lange L, Ganesh SK, Nalls M, Rasmussen-Torvik LJ, Pankow JS, Coresh J, Tang W, Linda Kao WH, Boerwinkle E, Morrison AC, Ridker PM, Becker DM, Rotter JI, Kardina SL, Loos RJ, Larson MG, Hsu YH, Province MA, Tracy R, Voight BF, Vaidya D, O'Donnell CJ, Benjamin EJ, Alizadeh BZ, Prokopenko I, Meigs JB, Borecki IB. Pleiotropic genes for metabolic syndrome and inflammation. *Mol Genet Metab.* 2014 Aug;112(4):317-38. doi: 10.1016/j.ymgme.2014.04.007. Epub 2014 May 9. PMID: 24981077, PMCID: PMC4122618
183. Crawford DC, Crosslin DR, Tromp G, Kullo IJ, Kuivaniemi H, Hayes MG, Denny JC, Bush WS, Haines JL, Roden DM, McCarty CA, Jarvik GP, **Ritchie MD**. eMERGEing progress in genomics-the first seven years. *Front Genet.* 2014 Jun 17;5:184. doi: 10.3389/fgene.2014.00184. eCollection 2014. PMID: 24987407, PMCID: PMC4060012
184. Kim D, Joung JG, Sohn KA, Shin H, Park YR, **Ritchie MD**, Kim JH. Knowledge boosting: a graph-based integration approach with multi-omics data and genomic knowledge for cancer clinical outcome prediction. *J Am Med Inform Assoc.* 2014 Jul 7. doi: 10.1136/amiajnl-2013-002481. PMID: 25002459, PMCID: PMC4433357
185. Ciesielski TH, Pendergrass SA, White MJ, Kodaman N, Sobota RS, Huang M, Bartlett J, Li J, Pan Q, Gui J, Selleck SB, Amos CI, **Ritchie MD**, Moore JH, Williams SM. Diverse convergent evidence in the genetic analysis of complex disease: coordinating omic, informatic, and experimental evidence to better identify and validate risk factors. *BioData Min.* 2014 Jun 30;7:10. doi: 10.1186/1756-0381-7-10. PMID: 25071867, PMCID: PMC4112852
186. Cronin RM, Field JR, Bradford Y, Shaffer CM, Carroll RJ, Mosley JD, Bastarache L, Edwards TL, Hebring SJ, Lin S, Hindorff LA, Crane PK, Pendergrass SA, **Ritchie MD**, Crawford DC,

Curriculum Vitae: Marylyn DeRiggi Ritchie

- Pathak J, Bielinski SJ, Carrell DS, Crosslin DR, Ledbetter DH, Carey DJ, Tromp G, Williams MS, Larson EB, Jarvik GP, Peissig PL, Brilliant MH, McCarty CA, Chute CG, Kullo IJ, Bottinger E, Chisholm R, Smith ME, Roden DM, Denny JC. Phenome-wide association studies demonstrating pleiotropy of genetic variants within FTO with and without adjustment for body mass index. *Front Genet.* 2014 Aug 5;5:250. doi: 10.3389/fgene.2014.00250. PMID: 25177340, PMCID: PMC4134007.
187. Kim D, Li R, Dudek SM, Frase AT, Pendergrass SA, **Ritchie MD**. Knowledge-driven genomic interactions: an application in ovarian cancer. *BioData Min.* 2014 Sep 9;7:20. doi: 10.1186/1756-0381-7-20. eCollection 2014. PMID: 25214892, PMCID: PMC4161273.
188. Namjou B, Marsolo K, Carroll RJ, Denny JC, **Ritchie MD**, Verma SS, Lingren T, Porollo A, Cobb BL, Perry C, Kottyan LC, Rothenberg ME, Thompson SD, Holm IA, Kohane IS, Harley JB. Phenome-wide association study (PheWAS) in EMR-linked pediatric cohorts, genetically links PLCL1 to speech language development and IL5-IL13 to Eosinophilic Esophagitis. *Front Genet.* 2014 Nov 18;5:401. doi: 10.3389/fgene.2014.00401. eCollection 2014. PMID: 25477900, PMCID: PMC4235428.
189. Hall MA, Verma A, Brown-Gentry KD, Goodloe R, Boston J, Wilson S, McClellan B, Sutcliffe C, Dilks HH, Gillani NB, Jin H, Mayo P, Allen M, Schnetz-Boutaud N, Crawford DC, **Ritchie MD**, Pendergrass SA. Detection of Pleiotropy through a Phenome-Wide Association Study (PheWAS) of Epidemiologic Data as Part of the Environmental Architecture for Genes Linked to Environment (EAGLE) Study. *PLoS Genet.* 2014 Dec 4;10(12):e1004678. doi: 10.1371/journal.pgen.1004678. eCollection 2014 Dec. PMID: 25474351, PMCID: PMC4256091
190. Malinowski JR, Denny JC, Bielinski SJ, Basford MA, Bradford Y, Peissig PL, Carrell D, Crosslin DR, Pathak J, Rasmussen L, Pacheco J, Kho A, Newton KM, Li R, Kullo IJ, Chute CG, Chisholm RL, Jarvik GP, Larson EB, McCarty CA, Masys DR, Roden DM, de Andrade M, **Ritchie MD**, Crawford DC. Genetic Variants Associated with Serum Thyroid Stimulating Hormone (TSH) Levels in European Americans and African Americans from the eMERGE Network. *PLoS One.* 2014 Dec 1;9(12):e111301. doi: 10.1371/journal.pone.0111301. eCollection 2014. PMID: 25436638, PMCID: PMC4249871.
191. Crosslin DR, Tromp G, Burt A, Kim DS, Verma SS, Lucas AM, Bradford Y, Crawford DC, Armasu SM, Heit JA, Hayes MG, Kuivaniemi H, **Ritchie MD**, Jarvik GP, de Andrade M; electronic Medical Records and Genomics (eMERGE) Network. Controlling for population structure and genotyping platform bias in the eMERGE multi-institutional biobank linked to electronic health records. *Front Genet.* 2014 Nov 4;5:352. doi: 10.3389/fgene.2014.00352. eCollection 2014. PMID: 25414722, PMCID: PMC4220165.
192. Chen HS, Hutter CM, Mechanic LE, Amos CI, Bafna V, Hauser ER, Hernandez RD, Li C, Liberles DA, McAllister K, Moore JH, Paltoo DN, Papanicolaou GJ, Peng B, **Ritchie MD**, Rosenfeld G, Witte JS, Gillanders EM, Feuer EJ. Genetic simulation tools for post-genome wide association studies of complex diseases. *Genet Epidemiol.* 2015 Jan;39(1):11-9. doi: 10.1002/gepi.21870. Epub 2014 Nov 4. PMID: 25371374, PMCID: PMC4270837.
193. **Ritchie MD**, Verma SS, Hall MA, Goodloe RJ, Berg RL, Carrell DS, Carlson CS, Chen L, Crosslin DR, Denny JC, Jarvik G, Li R, Linneman JG, Pathak J, Peissig P, Rasmussen LV, Ramirez AH, Wang X, Wilke RA, Wolf WA, Torstenson ES, Turner SD, McCarty CA. Electronic medical records and genomics (eMERGE) network exploration in cataract: several new potential susceptibility loci. *Mol Vis.* 2014 Sep 19;20:1281-95. eCollection 2014. PMID: 25352737, PMCID: PMC4168835.

Curriculum Vitae: Marylyn DeRiggi Ritchie

194. Barrie ES, Weinshenker D, Verma A, Pendergrass SA, Lange LA, **Ritchie MD**, Wilson JG, Kuivaniemi H, Tromp G, Carey DJ, Gerhard GS, Brilliant MH, Hebring SJ, Cubells JF, Pinsonneault JK, Norman GJ, Sadee W. Regulatory Polymorphisms in Human DBH Affect Peripheral Gene Expression and Sympathetic Activity. *Circ Res*. 2014 Dec 5;115(12):1017-25. doi: 10.1161/CIRCRESAHA.116.304398. Epub 2014 Oct 17. PMID: 25326128, PMCID: PMC58174.
195. Crosslin DR, Carrell DS, Burt A, Kim DS, Underwood JG, Hanna DS, Comstock BA, Baldwin E, de Andrade M, Kullo IJ, Tromp G, Kuivaniemi H, Borthwick KM, McCarty CA, Peissig PL, Doheny KF, Pugh E, Kho A, Pacheco J, Hayes MG, **Ritchie MD**, Verma SS, Armstrong G, Stallings S, Denny JC, Carroll RJ, Crawford DC, Crane PK, Mukherjee S, Bottinger E, Li R, Keating B, Mirel DB, Carlson CS, Harley JB, Larson EB, Jarvik GP. Genetic variation in the HLA region is associated with susceptibility to herpes zoster. *Genes Immun*. 2014 Oct 9;0. doi: 10.1038/gene.2014.51. PMID: 25297839, PMCID: PMC4308645.
196. Wood AR, Esko T, Yang J, Vedantam S, Pers TH, Gustafsson S, Chu AY, Estrada K, Luan J, Kutalik Z, Amin N, Buchkovich ML, Croteau-Chonka DC, Day FR, Duan Y, Fall T, Fehrmann R, Ferreira T, Jackson AU, Karjalainen J, Lo KS, Locke AE, Mägi R, Mihailov E, Porcu E, Randall JC, Scherag A, Vinkhuyzen AA, Westra HJ, Winkler TW, Workalemahu T, Zhao JH, Absher D, Albrecht E, Anderson D, Baron J, Beekman M, Demirkan A, Ehret GB, Feenstra B, Feitosa MF, Fischer K, Fraser RM, Goel A, Gong J, Justice AE, Kanoni S, Kleber ME, Kristiansson K, Lim U, Lotay V, Lui JC, Mangino M, Mateo Leach I, Medina-Gomez C, Nalls MA, Nyholt DR, Palmer CD, Pasko D, Pechlivanis S, Prokopenko I, Ried JS, Ripke S, Shungin D, Stancáková A, Strawbridge RJ, Sung YJ, Tanaka T, Teumer A, Trompet S, van der Laan SW, van Setten J, Van Vliet-Ostaptchouk JV, Wang Z, Yengo L, Zhang W, Afzal U, Arnlöv J, Arscott GM, Bandinelli S, Barrett A, Bellis C, Bennett AJ, Berne C, Blüher M, Bolton JL, Böttcher Y, Boyd HA, Bruinenberg M, Buckley BM, Buyske S, Caspersen IH, Chines PS, Clarke R, Claudi-Boehm S, Cooper M, Daw EW, De Jong PA, Deelen J, Delgado G, Denny JC, Dhonukshe-Rutten R, Dimitriou M, Doney AS, Dörr M, Eklund N, Eury E, Folkersen L, Garcia ME, Geller F, Giedraitis V, Go AS, Grallert H, Grammer TB, Gräßler J, Grönberg H, de Groot LC, Groves CJ, Haessler J, Hall P, Haller T, Hallmans G, Hannemann A, Hartman CA, Hassinen M, Hayward C, Heard-Costa NL, Helmer Q, Hemani G, Henders AK, Hillege HL, Hlatky MA, Hoffmann W, Hoffmann P, Holmen O, Houwing-Duistermaat JJ, Illig T, Isaacs A, James AL, Jeff J, Johansen B, Johansson Å, Jolley J, Juliusdottir T, Junttila J, Kho AN, Kinnunen L, Klopp N, Kocher T, Kratzer W, Lichtner P, Lind L, Lindström J, Lobbens S, Lorentzon M, Lu Y, Lyssenko V, Magnusson PK, Mahajan A, Maillard M, McArdle WL, McKenzie CA, McLachlan S, McLaren PJ, Menni C, Merger S, Milani L, Moayyeri A, Monda KL, Morken MA, Müller G, Müller-Nurasyid M, Musk AW, Narisu N, Nauck M, Nolte IM, Nöthen MM, Oozageer L, Pilz S, Rayner NW, Renstrom F, Robertson NR, Rose LM, Roussel R, Sanna S, Scharnagl H, Scholtens S, Schumacher FR, Schunkert H, Scott RA, Sehmi J, Seufferlein T, Shi J, Silventoinen K, Smit JH, Smith AV, Smolonska J, Stanton AV, Stirrups K, Stott DJ, Stringham HM, Sundström J, Swertz MA, Syvänen AC, Tayo BO, Thorleifsson G, Tyrer JP, van Dijk S, van Schoor NM, van der Velde N, van Heemst D, van Oort FV, Vermeulen SH, Verweij N, Vonk JM, Waite LL, Waldenberger M, Wennauer R, Wilkens LR, Willenborg C, Wilsgaard T, Wojczynski MK, Wong A, Wright AF, Zhang Q, Arveiler D, Bakker SJ, Beilby J, Bergman RN, Bergmann S, Biffar R, Blangero J, Boomsma DI, Bornstein SR, Bovet P, Brambilla P, Brown MJ, Campbell H, Caulfield MJ, Chakravarti A, Collins R, Collins FS, Crawford DC, Cupples LA, Danesh J, de Faire U, den Ruijter HM, Erbel R, Erdmann J, Eriksson JG, Farrall M, Ferrannini E, Ferrières J, Ford I, Forouhi NG, Forrester T, Gansevoort RT, Gejman PV, Gieger C, Golay A, Gottesman O, Gudnason V, Gyllenstein U, Haas DW, Hall AS, Harris TB, Hattersley AT, Heath AC,

Curriculum Vitae: Marylyn DeRiggi Ritchie

- Hengstenberg C, Hicks AA, Hindorff LA, Hingorani AD, Hofman A, Hovingh GK, Humphries SE, Hunt SC, Hypponen E, Jacobs KB, Jarvelin MR, Jousilahti P, Jula AM, Kaprio J, Kastelein JJ, Kayser M, Kee F, Keinanen-Kiukkaanniemi SM, Kiemeny LA, Kooner JS, Kooperberg C, Koskinen S, Kovacs P, Kraja AT, Kumari M, Kuusisto J, Lakka TA, Langenberg C, Le Marchand L, Lehtimäki T, Lupoli S, Madden PA, Männistö S, Manunta P, Marette A, Matise TC, McKnight B, Meitinger T, Moll FL, Montgomery GW, Morris AD, Morris AP, Murray JC, Nelis M, Ohlsson C, Oldehinkel AJ, Ong KK, Ouwehand WH, Pasterkamp G, Peters A, Pramstaller PP, Price JF, Qi L, Raitakari OT, Rankinen T, Rao DC, Rice TK, **Ritchie M**, Rudan I, Salomaa V, Samani NJ, Saramies J, Sarzynski MA, Schwarz PE, Sebert S, Sever P, Shuldiner AR, Sinisalo J, Steinthorsdottir V, Stolk RP, Tardif JC, Tönjes A, Tremblay A, Tremoli E, Virtamo J, Vohl MC; Electronic Medical Records and Genomics (eMEMERGE) Consortium; MIGen Consortium; PAGEGE Consortium; LifeLines Cohort Study, Amouyel P, Asselbergs FW, Assimes TL, Bochud M, Boehm BO, Boerwinkle E, Bottinger EP, Bouchard C, Cauchi S, Chambers JC, Chanock SJ, Cooper RS, de Bakker PI, Dedoussis G, Ferrucci L, Franks PW, Froguel P, Groop LC, Haiman CA, Hamsten A, Hayes MG, Hui J, Hunter DJ, Hveem K, Jukema JW, Kaplan RC, Kivimäki M, Kuh D, Laakso M, Liu Y, Martin NG, März W, Melbye M, Moebus S, Munroe PB, Njølstad I, Oostra BA, Palmer CN, Pedersen NL, Perola M, Pérusse L, Peters U, Powell JE, Power C, Quertermous T, Rauramaa R, Reinmaa E, Ridker PM, Rivadeneira F, Rotter JI, Saaristo TE, Saleheen D, Schlessinger D, Slagboom PE, Snieder H, Spector TD, Strauch K, Stumvoll M, Tuomilehto J, Uusitupa M, van der Harst P, Völzke H, Walker M, Wareham NJ, Watkins H, Wichmann HE, Wilson JF, Zanen P, Deloukas P, Heid IM, Lindgren CM, Mohlke KL, Speliotes EK, Thorsteinsdottir U, Barroso I, Fox CS, North KE, Strachan DP, Beckmann JS, Berndt SI, Boehnke M, Borecki IB, McCarthy MI, Metspalu A, Stefansson K, Uitterlinden AG, van Duijn CM, Franke L, Willer CJ, Price AL, Lettre G, Loos RJ, Weedon MN, Ingelsson E, O'Connell JR, Abecasis GR, Chasman DI, Goddard ME, Visscher PM, Hirschhorn JN, Frayling TM. Defining the role of common variation in the genomic and biological architecture of adult human height. *Nat Genet.* 2014 Nov;46(11):1173-86. doi: 10.1038/ng.3097. Epub 2014 Oct 5. PMID: 25282103, PMCID: PMC250049.
197. Restrepo NA, Spencer KL, Goodloe R, Garrett TA, Heiss G, Bůžková P, Jorgensen N, Jensen RA, Matise TC, Hindorff LA, Klein BE, Klein R, Wong TY, Cheng CY, Cornes BK, Tai ES, **Ritchie MD**, Haines JL, Crawford DC. Genetic determinants of age-related macular degeneration in diverse populations from the PAGE study. *Invest Ophthalmol Vis Sci.* 2014 Sep 9;55(10):6839-50. doi: 10.1167/iovs.14-14246. PMID: 25205864, PMCID: PMC4214207.
198. Ng MC, Shriner D, Chen BH, Li J, Chen WM, Guo X, Liu J, Bielinski SJ, Yanek LR, Nalls MA, Comeau ME, Rasmussen-Torvik LJ, Jensen RA, Evans DS, Sun YV, An P, Patel SR, Lu Y, Long J, Armstrong LL, Wagenknecht L, Yang L, Snively BM, Palmer ND, Mudgal P, Langefeld CD, Keene KL, Freedman BI, Mychaleckyj JC, Nayak U, Raffel LJ, Goodarzi MO, Chen YD, Taylor HA Jr, Correa A, Sims M, Couper D, Pankow JS, Boerwinkle E, Adeyemo A, Doumatey A, Chen G, Mathias RA, Vaidya D, Singleton AB, Zonderman AB, Igo RP Jr, Sedor JR; FIND Consortium, Kabagambe EK, Siscovick DS, McKnight B, Rice K, Liu Y, Hsueh WC, Zhao W, Bielak LF, Kraja A, Province MA, Bottinger EP, Gottesman O, Cai Q, Zheng W, Blot WJ, Lowe WL, Pacheco JA, Crawford DC; **eMERGE Consortium**; DIAGRAM Consortium, Grundberg E; MuTHER Consortium, Rich SS, Hayes MG, Shu XO, Loos RJ, Borecki IB, Peyser PA, Cummings SR, Psaty BM, Fornage M, Iyengar SK, Evans MK, Becker DM, Kao WH, Wilson JG, Rotter JI, Sale MM, Liu S, Rotimi CN, Bowden DW; MEta-analysis of type 2 Diabetes in African Americans Consortium. Meta-analysis of genome-wide association studies in African Americans provides insights into the genetic architecture of type 2 diabetes. *PLoS Genet.* 2014

199. Jeff JM, Brown-Gentry K, Goodloe R, **Ritchie MD**, Denny JC, Kho AN, Armstrong LL, McClellan B Jr, Mayo P, Allen M, Jin H, Gillani NB, Schnetz-Boutaud N, Dilks HH, Basford MA, Pacheco JA, Jarvik GP, Chisholm RL, Roden DM, Hayes MG, Crawford DC. Replication of SCN5A Associations with Electrocardio-graphic Traits in African Americans from Clinical and Epidemiologic Studies. *Evol Comput Mach Learn Data Min Bioinform*. 2014;2014:939-951. doi: 10.1007/978-3-662-45523-4_76. PMID: 25590050; PMCID: PMC4290789.
200. Verma SS, de Andrade M, Tromp G, Kuivaniemi H, Pugh E, Namjou-Khales B, Mukherjee S, Jarvik GP, Kottyan LC, Burt A, Bradford Y, Armstrong GD, Derr K, Crawford DC, Haines JL, Li R, Crosslin D, **Ritchie MD**. Imputation and quality control steps for combining multiple genome-wide datasets. *Front Genet*. 2014 Dec 11;5:370. doi: 10.3389/fgene.2014.00370. eCollection 2014. PMID: 25566314, PMCID: PMC4263197.
201. Pendergrass SA, Verma SS, Hall MA, Holzinger ER, Moore CB, Wallace JR, Dudek SM, Huggins W, Kitchner T, Waudby C, Berg R, Mccarty CA, **Ritchie MD**. Next-generation analysis of cataracts: determining knowledge driven gene-gene interactions using biofilter, and gene-environment interactions using the Phenx Toolkit*. *Pac Symp Biocomput*. 2015:495-505. doi: PMID: 25741542
202. Locke AE, Kahali B, Berndt SI, Justice AE, Pers TH, Day FR, Powell C, Vedantam S, Buchkovich ML, Yang J, Croteau-Chonka DC, Esko T, Fall T, Ferreira T, Gustafsson S, Kutalik Z, Luan J, Mägi R, Randall JC, Winkler TW, Wood AR, Workalemahu T, Faul JD, Smith JA, Hua Zhao J, Zhao W, Chen J, Fehrmann R, Hedman ÅK, Karjalainen J, Schmidt EM, Absher D, Amin N, Anderson D, Beekman M, Bolton JL, Bragg-Gresham JL, Buyske S, Demirkan A, Deng G, Ehret GB, Feenstra B, Feitosa MF, Fischer K, Goel A, Gong J, Jackson AU, Kanoni S, Kleber ME, Kristiansson K, Lim U, Lotay V, Mangino M, Mateo Leach I, Medina-Gomez C, Medland SE, Nalls MA, Palmer CD, Pasko D, Pechlivanis S, Peters MJ, Prokopenko I, Shungin D, Stančáková A, Strawbridge RJ, Ju Sung Y, Tanaka T, Teumer A, Trompet S, van der Laan SW, van Setten J, Van Vliet-Ostapchouk JV, Wang Z, Yengo L, Zhang W, Isaacs A, Albrecht E, Ärnlöv J, Arscott GM, Attwood AP, Bandinelli S, Barrett A, Bas IN, Bellis C, Bennett AJ, Berne C, Blagieva R, Blüher M, Böhringer S, Bonnycastle LL, Böttcher Y, Boyd HA, Bruinenberg M, Caspersen IH, Ida Chen YD, Clarke R, Daw EW, de Craen AJ, Delgado G, Dimitriou M, Doney AS, Eklund N, Estrada K, Eury E, Folkersen L, Fraser RM, Garcia ME, Geller F, Giedraitis V, Gigante B, Go AS, Golay A, Goodall AH, Gordon SD, Gorski M, Grabe HJ, Grallert H, Grammer TB, Gräßler J, Grönberg H, Groves CJ, Gusto G, Haessler J, Hall P, Haller T, Hallmans G, Hartman CA, Hassinen M, Hayward C, Heard-Costa NL, Helmer Q, Hengstenberg C, Holmen O, Hottenga JJ, James AL, Jeff JM, Johansson Å, Jolley J, Juliusdottir T, Kinnunen L, Koenig W, Koskenvuo M, Kratzer W, Laitinen J, Lamina C, Leander K, Lee NR, Lichtner P, Lind L, Lindström J, Sin Lo K, Lobbens S, Lorbeer R, Lu Y, Mach F, Magnusson PK, Mahajan A, McArdle WL, McLachlan S, Menni C, Merger S, Mihailov E, Milani L, Moayyeri A, Monda KL, Morken MA, Mulas A, Müller G, Müller-Nurasyid M, Musk AW, Nagaraja R, Nöthen MM, Nolte IM, Pilz S, Rayner NW, Renstrom F, Rettig R, Ried JS, Ripke S, Robertson NR, Rose LM, Sanna S, Scharnagl H, Scholtens S, Schumacher FR, Scott WR, Seufferlein T, Shi J, Vernon Smith A, Smolonska J, Stanton AV, Steinthorsdottir V, Stirrups K, Stringham HM, Sundström J, Swertz MA, Swift AJ, Syvänen AC, Tan ST, Tayo BO, Thorand B, Thorleifsson G, Tyrer JP, Uh HW, Vandenput L, Verhulst FC, Vermeulen SH, Verweij N, Vonk JM, Waite LL, Warren HR, Waterworth D, Weedon MN, Wilkens LR, Willenborg C, Wilsgaard T, Wojczynski MK, Wong A, Wright AF, Zhang Q; LifeLines Cohort

Curriculum Vitae: Marylyn DeRiggi Ritchie

Study, Brennan EP, Choi M, Dastani Z, Drong AW, Eriksson P, Franco-Cereceda A, Gådin JR, Gharavi AG, Goddard ME, Handsaker RE, Huang J, Karpe F, Kathiresan S, Keildson S, Kiryluk K, Kubo M, Lee JY, Liang L, Lifton RP, Ma B, McCarroll SA, McKnight AJ, Min JL, Moffatt MF, Montgomery GW, Murabito JM, Nicholson G, Nyholt DR, Okada Y, Perry JR, Dorajoo R, Reinmaa E, Salem RM, Sandholm N, Scott RA, Stolk L, Takahashi A, Tanaka T, Van't Hooft FM, Vinkhuyzen AA, Westra HJ, Zheng W, Zondervan KT; ADIPOGen Consortium; AGEN-BMI Working Group; CARDIOGRAMplusC4D Consortium; CKDGen Consortium; GLGC; ICBP; MAGIC Investigators; MuTHER Consortium; MIGen Consortium; PAGE Consortium; ReproGen Consortium; GENIE Consortium; International Endogene Consortium, Heath AC, Arveiler D, Bakker SJ, Beilby J, Bergman RN, Blangero J, Bovet P, Campbell H, Caulfield MJ, Cesana G, Chakravarti A, Chasman DI, Chines PS, Collins FS, Crawford DC, Cupples LA, Cusi D, Danesh J, de Faire U, den Ruijter HM, Dominiczak AF, Erbel R, Erdmann J, Eriksson JG, Farrall M, Felix SB, Ferrannini E, Ferrières J, Ford I, Forouhi NG, Forrester T, Franco OH, Gansevoort RT, Gejman PV, Gieger C, Gottesman O, Gudnason V, Gyllensten U, Hall AS, Harris TB, Hattersley AT, Hicks AA, Hindorff LA, Hingorani AD, Hofman A, Homuth G, Hovingh GK, Humphries SE, Hunt SC, Hyppönen E, Illig T, Jacobs KB, Jarvelin MR, Jöckel KH, Johansen B, Jousilahti P, Jukema JW, Jula AM, Kaprio J, Kastelein JJ, Keinanen-Kiukaanniemi SM, Kiemeny LA, Knekt P, Kooner JS, Kooperberg C, Kovacs P, Kraja AT, Kumari M, Kuusisto J, Lakka TA, Langenberg C, Le Marchand L, Lehtimäki T, Lyssenko V, Männistö S, Marette A, Matise TC, McKenzie CA, McKnight B, Moll FL, Morris AD, Morris AP, Murray JC, Nelis M, Ohlsson C, Oldehinkel AJ, Ong KK, Madden PA, Pasterkamp G, Peden JF, Peters A, Postma DS, Pramstaller PP, Price JF, Qi L, Raitakari OT, Rankinen T, Rao DC, Rice TK, Ridker PM, Rioux JD, **Ritchie MD**, Rudan I, Salomaa V, Samani NJ, Saramies J, Sarzynski MA, Schunkert H, Schwarz PE, Sever P, Shuldiner AR, Sinisalo J, Stolk RP, Strauch K, Tönjes A, Trégouët DA, Tremblay A, Tremoli E, Virtamo J, Vohl MC, Völker U, Waeber G, Willemsen G, Witteman JC, Zillikens MC, Adair LS, Amouyel P, Asselbergs FW, Assimes TL, Bochud M, Boehm BO, Boerwinkle E, Bornstein SR, Bottinger EP, Bouchard C, Cauchi S, Chambers JC, Chanock SJ, Cooper RS, de Bakker PI, Dedoussis G, Ferrucci L, Franks PW, Froguel P, Groop LC, Haiman CA, Hamsten A, Hui J, Hunter DJ, Hveem K, Kaplan RC, Kivimäki M, Kuh D, Laakso M, Liu Y, Martin NG, März W, Melbye M, Metspalu A, Moebus S, Munroe PB, Njølstad I, Oostra BA, Palmer CN, Pedersen NL, Perola M, Pérusse L, Peters U, Power C, Quertermous T, Rauramaa R, Rivadeneira F, Saaristo TE, Saleheen D, Sattar N, Schadt EE, Schlessinger D, Slagboom PE, Snieder H, Spector TD, Thorsteinsdottir U, Stumvoll M, Tuomilehto J, Uitterlinden AG, Uusitupa M, van der Harst P, Walker M, Wallaschofski H, Wareham NJ, Watkins H, Weir DR, Wichmann HE, Wilson JF, Zanen P, Borecki IB, Deloukas P, Fox CS, Heid IM, O'Connell JR, Strachan DP, Stefansson K, van Duijn CM, Abecasis GR, Franke L, Frayling TM, McCarthy MI, Visscher PM, Scherag A, Willer CJ, Boehnke M, Mohlke KL, Lindgren CM, Beckmann JS, Barroso I, North KE, Ingelsson E, Hirschhorn JN, Loos RJ, Speliotes EK. Genetic studies of body mass index yield new insights for obesity biology. *Nature*. 2015 Feb 12;518(7538):197-206. doi: 10.1038/nature14177. PMID: 25673413, PMCID: PMC4382211.

203. Shungin D, Winkler TW, Croteau-Chonka DC, Ferreira T, Locke AE, Mägi R, Strawbridge RJ, Pers TH, Fischer K, Justice AE, Workalemahu T, Wu JM, Buchkovich ML, Heard-Costa NL, Roman TS, Drong AW, Song C, Gustafsson S, Day FR, Esko T, Fall T, Kutalik Z, Luan J, Randall JC, Scherag A, Vedantam S, Wood AR, Chen J, Fehrmann R, Karjalainen J, Kahali B, Liu CT, Schmidt EM, Absher D, Amin N, Anderson D, Beekman M, Bragg-Gresham JL, Buyske S, Demirkan A, Ehret GB, Feitosa MF, Goel A, Jackson AU, Johnson T, Kleber ME, Kristiansson K, Mangino M, Mateo Leach I, Medina-Gomez C, Palmer CD, Pasko D,

Curriculum Vitae: Marylyn DeRiggi Ritchie

Pechlivanis S, Peters MJ, Prokopenko I, Stančáková A, Ju Sung Y, Tanaka T, Teumer A, Van Vliet-Ostaptchouk JV, Yengo L, Zhang W, Albrecht E, Ärnlöv J, Arscott GM, Bandinelli S, Barrett A, Bellis C, Bennett AJ, Berne C, Blüher M, Böhringer S, Bonnet F, Böttcher Y, Bruinenberg M, Carba DB, Caspersen IH, Clarke R, Daw EW, Deelen J, Deelman E, Delgado G, Doney AS, Eklund N, Erdos MR, Estrada K, Eury E, Friedrich N, Garcia ME, Giedraitis V, Gigante B, Go AS, Golay A, Grallert H, Grammer TB, Gräßler J, Grewal J, Groves CJ, Haller T, Hallmans G, Hartman CA, Hassinen M, Hayward C, Heikkilä K, Herzig KH, Helmer Q, Hillege HL, Holmen O, Hunt SC, Isaacs A, Ittermann T, James AL, Johansson I, Juliusdottir T, Kalafati IP, Kinnunen L, Koenig W, Kooner IK, Kratzer W, Lamina C, Leander K, Lee NR, Lichtner P, Lind L, Lindström J, Lobbens S, Lorentzon M, Mach F, Magnusson PK, Mahajan A, McArdle WL, Menni C, Merger S, Mihailov E, Milani L, Mills R, Moayyeri A, Monda KL, Mooijaart SP, Mühleisen TW, Mulas A, Müller G, Müller-Nurasyid M, Nagaraja R, Nalls MA, Narisu N, Glorioso N, Nolte IM, Olden M, Rayner NW, Renstrom F, Ried JS, Robertson NR, Rose LM, Sanna S, Scharnagl H, Scholtens S, Sennblad B, Seufferlein T, Sitlani CM, Vernon Smith A, Stirrups K, Stringham HM, Sundström J, Swertz MA, Swift AJ, Syvänen AC, Tayo BO, Thorand B, Thorleifsson G, Tomaschitz A, Troffa C, van Oort FV, Verweij N, Vonk JM, Waite LL, Wennauer R, Wilsgaard T, Wojczynski MK, Wong A, Zhang Q, Hua Zhao J, Brennan EP, Choi M, Eriksson P, Folkersen L, Franco-Cereceda A, Gharavi AG, Hedman ÅK, Hivert MF, Huang J, Kanoni S, Karpe F, Keildson S, Kiryluk K, Liang L, Lifton RP, Ma B, McKnight AJ, McPherson R, Metspalu A, Min JL, Moffatt MF, Montgomery GW, Murabito JM, Nicholson G, Nyholt DR, Olsson C, Perry JR, Reinmaa E, Salem RM, Sandholm N, Schadt EE, Scott RA, Stolk L, Vallejo EE, Westra HJ, Zondervan KT; ADIPOGen Consortium; CARDIOGRAMplusC4D Consortium; CKDGen Consortium; GEFOS Consortium; GENIE Consortium; GLGC; ICBP; International Endogene Consortium; LifeLines Cohort Study; MAGIC Investigators; MuTHER Consortium; PAGE Consortium; ReproGen Consortium, Amouyel P, Arveiler D, Bakker SJ, Beilby J, Bergman RN, Blangero J, Brown MJ, Burnier M, Campbell H, Chakravarti A, Chines PS, Claudi-Boehm S, Collins FS, Crawford DC, Danesh J, de Faire U, de Geus EJ, Dörr M, Erbel R, Eriksson JG, Farrall M, Ferrannini E, Ferrières J, Forouhi NG, Forrester T, Franco OH, Gansevoort RT, Gieger C, Gudnason V, Haiman CA, Harris TB, Hattersley AT, Heliövaara M, Hicks AA, Hingorani AD, Hoffmann W, Hofman A, Homuth G, Humphries SE, Hyppönen E, Illig T, Jarvelin MR, Johansen B, Jousilahti P, Jula AM, Kaprio J, Kee F, Keinanen-Kiukaanniemi SM, Kooner JS, Kooperberg C, Kovacs P, Kraja AT, Kumari M, Kuulasmaa K, Kuusisto J, Lakka TA, Langenberg C, Le Marchand L, Lehtimäki T, Lyssenko V, Männistö S, Marette A, Matisse TC, McKenzie CA, McKnight B, Musk AW, Möhlenkamp S, Morris AD, Nelis M, Ohlsson C, Oldehinkel AJ, Ong KK, Palmer LJ, Penninx BW, Peters A, Pramstaller PP, Raitakari OT, Rankinen T, Rao DC, Rice TK, Ridker PM, **Ritchie MD**, Rudan I, Salomaa V, Samani NJ, Saramies J, Sarzynski MA, Schwarz PE, Shuldiner AR, Staessen JA, Steinthorsdottir V, Stolk RP, Strauch K, Tönjes A, Tremblay A, Tremoli E, Vohl MC, Völker U, Vollenweider P, Wilson JF, Wittteman JC, Adair LS, Bochud M, Boehm BO, Bornstein SR, Bouchard C, Cauchi S, Caulfield MJ, Chambers JC, Chasman DI, Cooper RS, Dedoussis G, Ferrucci L, Froguel P, Grabe HJ, Hamsten A, Hui J, Hveem K, Jöckel KH, Kivimäki M, Kuh D, Laakso M, Liu Y, März W, Munroe PB, Njølstad I, Oostra BA, Palmer CN, Pedersen NL, Perola M, Pérusse L, Peters U, Power C, Quertermous T, Rauramaa R, Rivadeneira F, Saaristo TE, Saleheen D, Sinisalo J, Slagboom PE, Snieder H, Spector TD, Thorsteinsdottir U, Stumvoll M, Tuomilehto J, Uitterlinden AG, Uusitupa M, van der Harst P, Veronesi G, Walker M, Wareham NJ, Watkins H, Wichmann HE, Abecasis GR, Assimes TL, Berndt SI, Boehnke M, Borecki IB, Deloukas P, Franke L, Frayling TM, Groop LC, Hunter DJ, Kaplan RC, O'Connell JR, Qi L, Schlessinger D, Strachan DP, Stefansson K, van Duijn CM, Willer CJ, Visscher PM, Yang J, Hirschhorn JN, Zillikens MC, McCarthy MI, Speliotes EK,

Curriculum Vitae: Marylyn DeRiggi Ritchie

- North KE, Fox CS, Barroso I, Franks PW, Ingelsson E, Heid IM, Loos RJ, Cupples LA, Morris AP, Lindgren CM, Mohlke KL. New genetic loci link adipose and insulin biology to body fat distribution. *Nature*. 2015 Feb 12;518(7538):187-96. doi: 10.1038/nature14132. PMID: 25673412, PMCID: PMC4338562.
204. Kim D, Li R, Dudek SM, Wallace JR, **Ritchie MD**. Binning somatic mutations based on biological knowledge for predicting survival: an application in renal cell carcinoma. *Pac Symp Biocomput*. 2015:96-107. PMID: 25592572, PMCID: PMC4299944.
205. **Ritchie MD**, de Andrade M, Kuivaniemi H. The foundation of precision medicine: integration of electronic health records with genomics through basic, clinical, and translational research. *Front Genet*. 2015 Mar 17;6:104. doi: 10.3389/fgene.2015.00104. *eCollection* 2015. PMID: 25852745, PMCID: PMC4362332.
206. Hall MA, Verma SS, Wallace J, Lucas A, Berg RL, Connolly J, Crawford DC, Crosslin DR, de Andrade M, Doheny KF, Haines JL, Harley JB, Jarvik GP, Kitchner T, Kuivaniemi H, Larson EB, Carrell DS, Tromp G, Vrabec TR, Pendergrass SA, McCarty CA, **Ritchie MD**. Biology-Driven Gene-Gene Interaction Analysis of Age-Related Cataract in the eMERGE Network. *Genet Epidemiol*. 2015 Jul;39(5):387-84. doi: 10.1002/gepi.21902. Epub 2015 May 17. PMID: 25982363, PMCID: PMC4550090
207. Moore CB, Verma A, Pendergrass S, Verma SS, Johnson DH, Daar ES, Gulick RM, Haubrich R, Robbins GK, **Ritchie MD**, Haas DW. Phenome-wide Association Study Relating Pretreatment Laboratory Parameters With Human Genetic Variants in AIDS Clinical Trials Group Protocols. *Open Forum Infect Dis*. 2015 Jan 9;2(1):ofu113. doi: 10.1093/ofid/ofu113. *eCollection* 2015 Jan. PMID: 25884002, PMCID: PMC4396430.
208. Crosslin DR, Robertson PD, Carrell DS, Gordon AS, Hanna DS, Burt A, Fullerton SM, Scrol A, Ralston J, Leppig K, Hartzler A, Baldwin E, Andrade Md, Kullo IJ, Tromp G, Doheny KF, **Ritchie MD**, Crane PK, Nickerson DA, Larson EB, Jarvik GP. Prospective participant selection and ranking to maximize actionable pharmacogenetic variants and discovery in the eMERGE Network. *Genome Med*. 2015 Jul 3;7(1):67. doi: 10.1186/s 13073-015-0181-z. *eCollection* 2015. PMID: 26221186, PMCID: PMC4517371
209. Crawford DC, Goodloe R, Farber-Eger E, Boston J, Pendergrass SA, Haines JL, **Ritchie MD**, Bush WS. Leveraging Epidemiologic and Clinical Collections for Genomic Studies of Complex Traits. *Hum Hered*. 2015; 79(3-4):137-46. Doi: 10.1159/000381805. Epub 2015 Jul 28. PMID: 26201699, PMCID: PMC4528966
210. Pendergrass SA, Verma A, Okula A, Hall MA, Crawford DC, **Ritchie MD**. Phenome-Wide Association Studies: Embracing Complexity for Discovery. *Hum Hered*. 2015;79(3-4):111-23. Doi: 10.1159/000381851. Epub 2015 Jul 28. PMID: 26201697
211. Mosley JD, Shaffer CM, Van Driest SL, Weeke PE, Wells QS, Karnes JH, Velez Edwards DR, Wei WQ, Teixeira PL, Bastarache L, Crawford DC, Li R, Manolio TA, Bottinger EP, McCarty CA, Linneman JG, Brilliant MH, Pacheco JA, Thompson W, Chisholm RL, Jarvik GP, Crosslin DR, Carrell DS, Baldwin E, Ralston J, Larson EB, Grafton J, Scrol A, Jouni H, Kullo IJ, Tromp G, Borthwick KM, Kuivaniemi H, Carey DJ, **Ritchie MD**, Bradford Y, Verma SS, Chute CG, Veluchamy A, Siddiqui MK, Palmer CN, Doney A, MahmoudPour SH, Maitland-van der Zee AH, Morris AD, Denny JC, Roden DM. A genome-wide association study identifies variants in KCNIP4 associated with ACE inhibitor-induced cough. *Pharmacogenomics j*. 2015 Jul 14. doi: 10.1038/tpj.2015.51. [Epub ahead of print] PMID: 26169577, PMCID: PMC4713364

Curriculum Vitae: Marylyn DeRiggi Ritchie

212. Freitag DF, Butterworth AS, Willeit P, Howson JM, Burgess S, Kaptoge S, Young R, Ho WK, Wood AM, Sweeting M, Spackman S, Staley JR, Ramond A, Harshfield E, Nielsen SF, Grande P, Lange LA, Bown MJ, Jones GT, Scott RA, Bevan S, Porcu E, Thorleifsson G, Zeng L, Kessler T, Do R, Nikpay M, Zhang W, Hopewell JC, Kleber M, Delgado GE, Nelson CP, Goel A, Bis JC, Dehghan A, Ligthart S, Smith AV, Qu L, van 't Hof FN, de Bakker PI, Baas AF, van Rij A, Tromp G, Kuivaniemi H, Ritchie MD, Verma SS, Crawford DC, Malinowski J, de Andrade M, Kullo IJ, Peissig PL, McCarty CA, Böttlinger EP, Gottesman O, Crosslin DR, Carrell DS, Rasmussen-Torvik LJ, Pacheco JA, Huang J, Timpson NJ, Kettunen J, Ala-Korpela M, Mitchell GF, Parsa A, Wilkinson IB, Gorski M, Li Y, Franceschini N, Keller MF, Ganesh SK, Langefeld CD, Bruijn L, Brown MA, Evans DM, Baltic S, Ferreira MA, Baurecht H, Weidinger S, Franke A, Lubitz SA, Müller-Nurasyid M, Felix JF, Smith NL, Sudman M, Thompson SD, Zeggini E, Panoutsopoulou K, Nalls MA, Singleton A, Polychronakos C, Bradfield JP, Hakonarson H, Easton DF, Thompson D, Tomlinson IP, Dunlop M, Hemminki K, Morgan G, Eisen T, Goldschmidt H, Allan JM, Henrion M, Whiffin N, Wang Y, Chubb D, Houlston RS, Iles MM, Bishop DT, Law MH, Hayward NK, Luo Y, Nejentsev S, Barbalic M, Crossman D, Sanna S, Soranzo N, Markus HS, Wareham NJ, Rader DJ, Reilly M, Assimes T, Harris TB, Hofman A, Franco OH, Gudnason V, Tracy R, Psaty BM, Farrall M, Watkins H, Hall AS, Samani NJ, März W, Clarke R, Collins R, Kooner JS, Chambers JC, Kathiresan S, McPherson R, Erdmann J, Kastrati A, Schunkert H, Stefánsson K, Walston JD, Tybjærg-Hansen A, Alam DS, Majumder AA, Di Angelantonio E, Chowdhury R, Nordestgaard BG, Saleheen D, Thompson SG, Danesh J. Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. *Lancet Diabetes Endocrinol.* 2015 Apr;3(4):243-53. doi: 10.1016/S2213-8587(15)00034-0. Epub 2015 Feb 26. PMID: 25726324
PMCID: PMC4648058
213. Kim D, Li R, Dudek SM, **Ritchie MD**. Predicting censored survival data based on the interactions between meta-dimensional omics data in breast cancer. *J Biomed Inform.* 2015 Aug;56:220-8. doi: 10.1016/j.jbi.2015.05.019. PMID: 26048077, PMCID: PMC4550096
214. Pendergrass SA, **Ritchie MD**. Phenome-Wide Association Studies: Leveraging Comprehensive Phenotypic and Genotypic Data for Discovery. *Curr Genet Med Rep.* 2015 Jun 1;3(2):92-100. PMID: 26146598, PMCID: PMC4489156
215. Namjou B, Marsolo K, Lingren T, **Ritchie MD**, Verma SS, Cobb BL, Perry C, Kitchner TE, Brilliant MH, Peissig PL, Borthwick KM, Williams MS, Grafton J, Jarvik GP, Holm IA, Harley JB. A GWAS Study on Liver Function Test Using eMERGE Network Participants. *PLoS One.* 2015 Sep 28;10(9):e0138677. doi: 10.1371/journal.pone.0138677. PMID: 2641371, PMCID: PMC4586138
216. Li YR, van Setten J, Verma SS, Lu Y, Holmes MV, Gao H, Lek M, Nair N, Chandrupatla H, Chang B, Karczewski KJ, Wong C, Mohebnasab M, Mukhtar E, Phillips R, Tragante V, Hou C, Steel L, Lee T, Garifallou J, Guettouche T, Cao H, Guan W, Himes A, van Houten J, Pasquier A, Yu R, Carrigan E, Miller MB, Schladt D, Akdere A, Gonzalez A, Llyod KM, McGinn D, Gangasani A, Michaud Z, Colasacco A, Snyder J, Thomas K, Wang T, Wu B, Alzahrani AJ, Al-Ali AK, Al-Muhanna FA, Al-Rubaish AM, Al-Mueilo S, Monos DS, Murphy B, Olthoff KM, Wijmenga C, Webster T, Kamoun M, Balasubramanian S, Lanktree MB, Oetting WS, Garcia-Pavia P, MacArthur DG, de Bakker PI, Hakonarson H, Birdwell KA, Jacobson PA, **Ritchie MD**, Asselbergs FW, Israni AK, Shaked A, Keating BJ. Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. *Genome Med.* 2015 Oct 1;7:90. doi: 10.1186/s13073-015-0211-x. PMID: 26423053, PMCID: PMC4589899
217. Keating BJ, van Setten J, Jacobson PA, Holmes MV, Verma SS, Chandrupatla HR, Nair N, Gao H, Li YR, Chang BL, Wong C, Phillips R, Cole BS, Mukhtar E, Zhang W, Cao H, Mohebnasab

Curriculum Vitae: Marylyn DeRiggi Ritchie

- M, Hou C, Lee T, Steel L, Shaked O, Garifallou J, Miller MB, Karczewski KJ, Akdere A, Gonzalez A, Lloyd KM, McGinn D, Michaud Z, Colasacco A, Lek M, Fu Y, Pawashe M, Guettouche T, Himes A, Perez L, Guan W, Wu B, Schladt D, Menon M, Zhang Z, Tragante V, de Jonge N, Otten HG, de Weger RA, van de Graaf EA, Baan CC, Manintveld OC, De Vlaminc I, Piening BD, Strehl C, Shaw M, Snieder H, Klintmalm GB, O'Leary JG, Amaral S, Goldfarb S, Rand E, Rossano JW, Kohli U, Heeger P, Stahl E, Christie JD, Fuentes MH, Levine JE, Aplenc R, Schadt EE, Stranger BE, Kluijn J, Potena L, Zuckermann A, Khush K, Alzahrani AJ, Al-Muhanna FA, Al-Ali AK, Al-Ali R, Al-Rubaish AM, Al-Mueilo S, Byrne EM, Miller D, Alexander SI, Onengut-Gumuscu S, Rich SS, Suthanthiran M, Tedesco H, Saw CL, Ragoussis J, Kfoury AG, Horne B, Carlquist J, Gerstein MB, Reindl-Schwaighofer R, Oberbauer R, Wijmenga C, Palmer S, Pereira AC, Segovia J, Alonso-Pulpon LA, Comez-Bueno M, Vilches C, Jaramillo N, de Borst MH, Naesens M, Hao K, MacArthur DG, Balasubramanian S, Conlon PJ, Lord GM, **Ritchie MD**, Snyder M, Olthoff KM, Moore JH, Petersdorf EW, Kamoun M, Wang J, Monos DS, de Bakker PI, Hakonarson H, Murphy B, Lankree MB, Garcia-Pavia P, Oetting WS, Birdwell KA, Bakker SJ, Israni AK, Shaked A, Asselbergs FW. Design and Implementation of the International Genetics and Translational Research in Transplantation Network. *Transplantation*. 2015 Nov;99(11):2401-12. doi: 10.1097/TP.0000000000000913. [PMID: 26479416](#), [PMCID: PMC4623847](#)
218. De R, Verma SS, Drenos F, Holzinger ER, Holmes MV, Hall MA, Crosslin DR, Carrell DS, Hakonarson H, Jarvik G, Larson E, Pacheco JA, Rasmussen-Torvik LJ, Moore CB, Asselbergs FW, Moore JH, Ritchie MD, Keating BJ, Gilbert-Diamond D. Identifying gene-gene interactions that are highly associated with Body Mass Index using Quantitative Multifactor Dimensionality Reduction (QMDR). *BioData Min*. 2015 Dec 14;8:41. doi: 10.1186/s13040-015-0074-0. [PMID: 26674805](#), [PMCID: PMC4678717](#)
219. Van Driest SL, Wells QS, Stallings S, Bush WS, Gordon A, Nickerson DA, Kim JH, Crosslin DR, Jarvik GP, Carrell DS, Ralston JD, Larson EB, Bielinski SJ, Olson JE, Ye Z, Kullo IJ, Abul-Husn NS, Scott SA, Bottinger E, Almoguera B, Connolly J, Chiavacci R, Hakonarson H, Rasmussen-Torvik LJ, Pan V, Persell SD, Smith M, Chisholm RL, Kitchner TE, He MM, Brilliant MH, Wallace JR, Doheny KF, Shoemaker MB, Li R, Manolio TA, Callis TE, Macaya D, Williams MS, Carey D, Kapplinger JD, Ackerman MJ, **Ritchie MD**, Denny JC, Roden DM. Association of Arrhythmia-Related Genetic Variants With Phenotypes Documented in Electronic Medical Records. *JAMA*. 2016 Jan 5;315(1):47-57. doi: 10.1001/jama.2015.17701. [PMID: 26746457](#), [PMCID: PMC4758131](#)
220. Verma SS, Frase AT, Verma A, Pendergrass SA, Mahony S, Haas DW, Ritchie MD. PHENOME-WIDE INTERACTION STUDY (PheWIS) IN AIDS CLINICAL TRIALS GROUP DATA (ACTG). *Pac Symp Biocomput*. 2016;21:57-68. [PMID: 26776173](#), [PMCID: PMC4722952](#)
221. Verma A, Leader JB, Verma SS, Frase A, Wallace J, Dudek S, Lavage DR, Van Hout CV, Dewey FE, Penn J, Lopez A, Overton JD, Carey DJ, Ledbetter DH, Kirchner HL, **Ritchie MD**, Pendergrass SA. INTEGRATING CLINICAL LABORATORY MEASURES AND ICD-9 CODE DIAGNOSES IN PHENOME-WIDE ASSOCIATION STUDIES. *Pac Symp Biocomput*. 2016;21:168-79. [PMID: 26776183](#), [PMCID: PMC4718547](#)
222. Basile AO, Wallace JR, Peissig P, McCarty CA, Brilliant M, **Ritchie MD**. KNOWLEDGE DRIVEN BINNING AND PHEWAS ANALYSIS IN MARSHFIELD PERSONALIZED MEDICINE RESEARCH PROJECT USING BIOBIN. *Pac Symp Biocomput*. 2016;21:249-60. [PMID: 26776191](#), [PMCID: PMC4824557](#)
223. Kim D, Lucas A, Glessner J, Verma SS, Bradford Y, Li R, Frase AT, Hakonarson H, Peissig P, Brilliant M, **Ritchie MD**. BIOFILTER AS A FUNCTIONAL ANNOTATION PIPELINE FOR

Curriculum Vitae: Marylyn DeRiggi Ritchie

- COMMON AND RARE COPY NUMBER BURDEN. *Pac Symp Biocomput.* 2016;21:357-68. PMID: 26776200, PMCID: PMC4722964
224. Hohman TJ, Bush WS, Jiang L, Brown-Gentry KD, Torstenson ES, Dudek SM, Mukherjee S, Naj A, Kunkle BW, **Ritchie MD**, Martin ER, Schellenberg GD, Mayeux R, Farrer LA, Pericak-Vance MA, Haines JL, Thornton-Wells TA; Alzheimer's Disease Genetics Consortium. Discovery of gene-gene interactions across multiple independent data sets of late onset Alzheimer disease from the Alzheimer Disease Genetics Consortium. *Neurobiol Aging.* 2016 Feb;38:141-50. doi: 10.1016/j.neurobiolaging.2015.10.031. PMID: 26827652, PMCID: PMC4735733
225. Bush WS, Crosslin DR, Owusu-Obeng A, Wallace J, Almoguera B, Basford MA, Bielinski SJ, Carrell DS, Connolly JJ, Crawford D, Doheny KF, Gallego CJ, Gordon AS, Keating B, Kirby J, Kitchner T, Manzi S, Mejia AR, Pan V, Perry CL, Peterson JF, Prows CA, Ralston J, Scott SA, Scrol A, Smith M, Stallings SC, Veldhuizen T, Wolf W, Volpi S, Wiley K, Li R, Manolio T, Bottinger E, Brilliant MH, Carey D, Chisholm RL, Chute CG, Haines JL, Hakonarson H, Harley JB, Holm IA, Kullo IJ, Jarvik GP, Larson EB, McCarty CA, Williams MS, Denny JC, Rasmussen-Torvik LJ, Roden DM, **Ritchie MD**. Genetic variation among 82 pharmacogenes: The PGRNseq data from the eMERGE network. *Clin Pharmacol Ther.* 2016 Aug;100(2):160-9. doi: 10.1002/cpt.350. PMID: 26857349, PMCID: PMC5010878
226. Simonti CN, Vernot B, Bastarache L, Bottinger E, Carrell DS, Chisholm RL, Crosslin DR, Hebringer SJ, Jarvik GP, Kullo IJ, Li R, Pathak J, **Ritchie MD**, Roden DM, Verma SS, Tromp G, Prato JD, Bush WS, Akey JM, Denny JC, Capra JA. The phenotypic legacy of admixture between modern humans and Neandertals. *Science.* 2016 Feb 12;351(6274):737-41. doi: 10.1126/science.aad2149. PMID: 26912863, PMCID: PMC4849557
227. Dewey FE, Gusarova V, O'Dushlaine C, Gottesman O, Trejos J, Hunt C, Van Hout CV, Habegger L, Buckler D, Lai KM, Leader JB, Murray MF, **Ritchie MD**, Kirchner HL, Ledbetter DH, Penn J, Lopez A, Borecki IB, Overton JD, Reid JG, Carey DJ, Murphy AJ, Yancopoulos GD, Baras A, Gromada J, Shuldiner AR. Inactivating Variants in ANGPTL4 and Risk of Coronary Artery Disease. *N Engl J Med.* 2016 Mar 24;374(12):1123-33. doi: 10.1056/NEJMoa1510926. PMID: 26933753, PMCID: PMC4900689
228. Williams MS, **Ritchie MD**, Payne PR. Interdisciplinary training to build an informatics workforce for precision medicine. *Appl Transl Genom.* 2015 Aug 4;6:28-30. doi: 10.1016/j.atg.2015.07.003. PMID: 27054076, PMCID: PMC4803783
229. Butkiewicz M, Cooke Bailey JN, Frase A, Dudek S, Yaspan BL, **Ritchie MD**, Pendergrass SA, Haines JL. Pathway analysis by randomization incorporating structure-PARIS: an update. *Bioinformatics.* 2016 Aug 1;32(15):2361-3. doi: 10.1093/bioinformatics/btw130. PMID: 27153576, PMCID: PMC4965631
230. Li R, Dudek SM, Kim D, Hall MA, Bradford Y, Peissig PL, Brilliant MH, Linneman JG, McCarty CA, Bao L, **Ritchie MD**. Identification of genetic interaction networks via an evolutionary algorithm evolved Bayesian network. *BioData Min.* 2016 May 10;9:18. doi: 10.1186/s13040-016-0094-4. PMID: 27168765, PMCID: PMC4862166
231. Oetjens MT, Bush WS, Denny JC, Birdwell K, Kodaman N, Verma A, Dilks HH, Pendergrass SA, **Ritchie MD**, Crawford DC. Evidence for extensive pleiotropy among pharmacogenes. *Pharmacogenomics.* 2016 Jun;17(8):853-66. doi: 10.2217/pgs-2015-0007. PMID: 27249515, PMCID: PMC5352965
232. Hall MA, Moore JH, **Ritchie MD**. Embracing Complex Associations in Common Traits: Critical Considerations for Precision Medicine. *Trends Genet.* 2016 Aug;32(8):470-84. doi: 10.1016/j.tig.2016.06.001. Review. PMID: 27392675
233. van 't Hof FN, Ruigrok YM, Lee CH, Ripke S, Anderson G, de Andrade M, Baas AF, Blankensteijn JD, Böttlinger EP, Bown MJ, Broderick J, Bijlenga P, Carrell DS, Crawford DC,

Curriculum Vitae: Marylyn DeRiggi Ritchie

- Crosslin DR, Ebeling C, Eriksson JG, Fornage M, Foroud T, von Und Zu Fraunberg M, Friedrich CM, Gaál EI, Gottesman O, Guo DC, Harrison SC, Hernesniemi J, Hofman A, Inoue I, Jääskeläinen JE, Jones GT, Kiemeny LA, Kivisaari R, Ko N, Koskinen S, Kubo M, Kullo IJ, Kuivaniemi H, Kurki MI, Laakso A, Lai D, Leal SM, Lehto H, LeMaire SA, Low SK, Malinowski J, McCarty CA, Milewicz DM, Mosley TH, Nakamura Y, Nakaoka H, Niemelä M, Pacheco J, Peissig PL, Pera J, Rasmussen-Torvik L, **Ritchie MD**, Rivadeneira F, van Rij AM, Santos-Cortez RL, Saratzis A, Slowik A, Takahashi A, Tromp G, Uitterlinden AG, Verma SS, Vermeulen SH, Wang GT; Aneurysm Consortium; Vascular Research Consortium of New Zealand., Han B, Rinkel GJ, de Bakker PI. Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. *J Am Heart Assoc*. 2016 Jul 14;5(7). pii: e002603. doi: 10.1161/JAHA.115.002603. PMID: 2741816, PMCID: PMC5015357
234. Verma A, Basile AO, Bradford Y, Kuivaniemi H, Tromp G, Carey D, Gerhard GS, Crowe JE Jr, **Ritchie MD**, Pendergrass SA. Phenome-Wide Association Study to Explore Relationships between Immune System Related Genetic Loci and Complex Traits and Diseases. *PLoS One*. 2016 Aug 10;11(8):e0160573. doi: 10.1371/journal.pone.0160573. PMID: 27508393, PMCID: PMC4980020
235. Verma A, Verma SS, Pendergrass SA, Crawford DC, Crosslin DR, Kuivaniemi H, Bush WS, Bradford Y, Kullo I, Bielinski SJ, Li R, Denny JC, Peissig P, Hebring S, De Andrade M, **Ritchie MD**, Tromp G. eMERGE Phenome-Wide Association Study (PheWAS) identifies clinical associations and pleiotropy for stop-gain variants. *BMC Med Genomics*. 2016 Aug 12;9 Suppl 1:32. doi: 10.1186/s12920-016-0191-8. PMID: 27535653, PMCID: PMC4989894
236. Moore CC, Basile AO, Wallace JR, Frase AT, **Ritchie MD**. A biologically informed method for detecting rare variant associations. *BioData Min*. 2016 Aug 30;9(1):27. doi: 10.1186/s13040-016-0107-3. PMID: 27582876, PMCID: PMC5006419
237. Verma SS, Cooke Bailey JN, Lucas A, Bradford Y, Linneman JG, Hauser MA, Pasquale LR, Peissig PL, Brilliant MH, McCarty CA, Haines JL, Wiggs JL, Vrabec TR, Tromp G, **Ritchie MD**; eMERGE Network.; NEIGHBOR Consortium. Epistatic Gene-Based Interaction Analyses for Glaucoma in eMERGE and NEIGHBOR Consortium. *PLoS Genet*. 2016 Sep 13;12(9):e1006186. doi: 10.1371/journal.pgen.1006186. PMID: 27623284, PMCID: PMC5021356
238. De R, Verma SS, Holzinger E, Hall M, Burt A, Carrell DS, Crosslin DR, Jarvik GP, Kuivaniemi H, Kullo IJ, Lange LA, Lanktree MB, Larson EB, North KE, Reiner AP, Tragante V, Tromp G, Wilson JG, Asselbergs FW, Drenos F, Moore JH, **Ritchie MD**, Keating B, Gilbert-Diamond D. Identifying gene-gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. *Hum Genet*. 2017 Feb;136(2):165-178. doi: 10.1007/s00439-016-1738-7. PMID: 27848076
239. Yoneyama S, Yao J, Guo X, Fernandez-Rhodes L, Lim U, Boston J, Buzková P, Carlson CS, Cheng I, Cochran B, Cooper R, Ehret G, Fornage M, Gong J, Gross M, Gu CC, Haessler J, Haiman CA, Henderson B, Hindorff LA, Houston D, Irvin MR, Jackson R, Kuller L, Leppert M, Lewis CE, Li R, Le Marchand L, Matise TC, Nguyen KD, Chakravarti A, Pankow JS, Pankratz N, Pooler L, **Ritchie MD**, Bien SA, Wassel CL, Chen YD, Taylor KD, Allison M, Rotter JI, Schreiner PJ, Schumacher F, Wilkens L, Boerwinkle E, Kooperberg C, Peters U, Buyske S, Graff M, North KE. Generalization and fine mapping of European ancestry-based central adiposity variants in African ancestry populations. *Int J Obes (Lond)*. 2017 Feb;41(2):324-331. doi: 10.1038/ijo.2016.207. PMID: 27867202, PMCID: PMC5296276
240. Verma SS, Lucas AM, Lavage DR, Leader JB, Metpally R, Krishnamurthy S, Dewey F, Borecki I, Lopez A, Overton J, Penn J, Reid J, Pendergrass SA, Breitwieser G, **Ritchie MD**. IDENTIFYING GENETIC ASSOCIATIONS WITH VARIABILITY IN METABOLIC HEALTH AND BLOOD COUNT LABORATORY VALUES: DIVING INTO THE

- QUANTITATIVE TRAITS BY LEVERAGING LONGITUDINAL DATA FROM AN EHR. *Pac Symp Biocomput.* 2016;22:533-544. PMID: 27897004
241. Jones GT, Tromp G, Kuivaniemi H, Gretarsdottir S, Baas AF, Giusti B, Strauss E, Van't Hof FN, Webb TR, Erdman R, **Ritchie MD**, Elmore JR, Verma A, Pendergrass S, Kullo IJ, Ye Z, Peissig PL, Gottesman O, Verma SS, Malinowski J, Rasmussen-Torvik LJ, Borthwick KM, Smelser DT, Crosslin DR, de Andrade M, Ryer EJ, McCarty CA, Böttinger EP, Pacheco JA, Crawford DC, Carrell DS, Gerhard GS, Franklin DP, Carey DJ, Phillips VL, Williams MJ, Wei W, Blair R, Hill AA, Vasudevan TM, Lewis DR, Thomson IA, Krysa J, Hill GB, Roake J, Merriman TR, Oszkinis G, Galora S, Saracini C, Abbate R, Pulli R, Pratesi C, Saratzis A, Verissimo AR, Bumpstead S, Badger SA, Clough RE, Cockerill G, Hafez H, Scott DJ, Futers TS, Romaine SP, Bridge K, Griffin KJ, Bailey MA, Smith A, Thompson MM, van Bockxmeer FM, Matthiasson SE, Thorleifsson G, Thorsteinsdottir U, Blankensteijn JD, Teijink JA, Wijmenga C, de Graaf J, Kiemeny LA, Lindholt JS, Hughes A, Bradley DT, Stirrups K, Golledge J, Norman PE, Powell JT, Humphries SE, Hamby SE, Goodall AH, Nelson CP, Sakalihasan N, Courtois A, Ferrell RE, Eriksson P, Folkersen L, Franco-Cereceda A, Eicher JD, Johnson AD, Betsholtz C, Ruusalepp A, Franzén O, Schadt EE, Björkegren JL, Lipovich L, Drolet AM, Verhoeven EL, Zebregs CJ, Geelkerken RH, van Sambeek MR, van Sterkenburg SM, de Vries JP, Stefansson K, Thompson JR, de Bakker PI, Deloukas P, Sayers RD, Harrison SC, van Rij AM, Samani NJ, Bown MJ. Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. *Circ Res.* 2017 Jan 20;120(2):341-353. doi: 10.1161/CIRCRESAHA.116.308765. PMID: 27899403, PMCID: PMC5253231
242. Schmidt AF, Swerdlow DI, Holmes MV, Patel RS, Fairhurst-Hunter Z, Lyall DM, Hartwig FP, Horta BL, Hyppönen E, Power C, Moldovan M, van Iperen E, Hovingh GK, Demuth I, Norman K, Steinhagen-Thiessen E, Demuth J, Bertram L, Liu T, Coassin S, Willeit J, Kiechl S, Willeit K, Mason D, Wright J, Morris R, Wanamethee G, Whincup P, Ben-Shlomo Y, McLachlan S, Price JF, Kivimaki M, Welch C, Sanchez-Galvez A, Marques-Vidal P, Nicolaides A, Panayiotou AG, Onland-Moret NC, van der Schouw YT, Matullo G, Fiorito G, Guarrera S, Sacerdote C, Wareham NJ, Langenberg C, Scott R, Luan J, Bobak M, Malyutina S, Pajak A, Kubinova R, Tamosiunas A, Pikhart H, Husemoen LL, Grarup N, Pedersen O, Hansen T, Linneberg A, Simonsen KS, Cooper J, Humphries SE, Brilliant M, Kitchner T, Hakonarson H, Carrell DS, McCarty CA, Kirchner HL, Larson EB, Crosslin DR, de Andrade M, Roden DM, Denny JC, Carty C, Hancock S, Attia J, Holliday E, O'Donnell M, Yusuf S, Chong M, Pare G, van der Harst P, Said MA, Eppinga RN, Verweij N, Snieder H; LifeLines Cohort study group., Christen T, Mook-Kanamori DO, Gustafsson S, Lind L, Ingelsson E, Pazoki R, Franco O, Hofman A, Uitterlinden A, Dehghan A, Teumer A, Baumeister S, Dörr M, Lerch MM, Völker U, Völzke H, Ward J, Pell JP, Smith DJ, Meade T, Maitland-van der Zee AH, Baranova EV, Young R, Ford I, Campbell A, Padmanabhan S, Bots ML, Grobbee DE, Froguel P, Thuillier D, Balkau B, Bonnefond A, Cariou B, Smart M, Bao Y, Kumari M, Mahajan A, Ridker PM, Chasman DI, Reiner AP, Lange LA, **Ritchie MD**, Asselbergs FW, Casas JP, Keating BJ, Preiss D, Hingorani AD; UCLEB consortium., Sattar N. PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. *Lancet Diabetes Endocrinol.* 2017 Feb;5(2):97-105. doi: 10.1016/S2213-8587(16)30396-5. PMID: 27908689, PMCID: PMC5266795
243. Dewey FE, Murray MF, Overton JD, Habegger L, Leader JB, Fetterolf SN, O'Dushlaine C, Van Hout CV, Staples J, Gonzaga-Jauregui C, Metpally R, Pendergrass SA, Giovanni MA, Kirchner HL, Balasubramanian S, Abul-Husn NS, Hartzel DN, Lavage DR, Kost KA, Packer JS, Lopez AE, Penn J, Mukherjee S, Gosalia N, Kanagaraj M, Li AH, Mitnaul LJ, Adams LJ, Person TN, Praveen K, Marcketta A, Lebo MS, Austin-Tse CA, Mason-Suares HM, Bruse S, Mellis S, Phillips R, Stahl N, Murphy A, Economides A, Skelding KA, Still CD, Elmore JR, Borecki IB, Yancopoulos GD, Davis FD, Faucett WA, Gottesman O, **Ritchie MD**, Shuldiner AR, Reid JG,

Curriculum Vitae: Marylyn DeRiggi Ritchie

- Ledbetter DH, Baras A, Carey DJ. Distribution and clinical impact of functional variants in 50,726 whole-exome sequences from the DiscovEHR study. *Science*. 2016 Dec 23;354(6319). pii: aaf6814. doi: 10.1126/science.aaf6814. PMID: 28008009
244. Abul-Husn NS, Manickam K, Jones LK, Wright EA, Hartzel DN, Gonzaga-Jauregui C, O'Dushlaine C, Leader JB, Lester Kirchner H, Lindbuchler DM, Barr ML, Giovanni MA, **Ritchie MD**, Overton JD, Reid JG, Metpally RP, Wardeh AH, Borecki IB, Yancopoulos GD, Baras A, Shuldiner AR, Gottesman O, Ledbetter DH, Carey DJ, Dewey FE, Murray MF. Genetic identification of familial hypercholesterolemia within a single U.S. health care system. *Science*. 2016 Dec 23;354(6319). pii: aaf7000. doi: 10.1126/science.aaf7000. PMID: 28008010
245. Kim D, Li R, Lucas A, Verma SS, Dudek SM, **Ritchie MD**. Using knowledge-driven genomic interactions for multi-omics data analysis: metadimensional models for predicting clinical outcomes in ovarian carcinoma. *J Am Med Inform Assoc*. 2016 Dec 31. pii: ocw165. doi: 10.1093/jamia/ocw165. [Epub ahead of print] PMID: 28040685, PMCID: PMC5391734
246. Verma A, Bradford Y, Verma SS, Pendergrass SA, Daar ES, Venuto C, Morse GD, **Ritchie MD**, Haas DW. Multiphenotype association study of patients randomized to initiate antiretroviral regimens in AIDS Clinical Trials Group protocol A5202. *Pharmacogenet Genomics*. 2017 Mar;27(3):101-111. doi: 10.1097/FPC.0000000000000263. PMID: 28099408, PMCID: PMC5285297
247. Shan Y, Tromp G, Kuivaniemi H, Smelser DT, Verma SS, **Ritchie MD**, Elmore JR, Carey DJ, Conley YP, Gorin MB, Weeks DE. Genetic risk models: Influence of model size on risk estimates and precision. *Genet Epidemiol*. 2017 Feb 15. doi: 10.1002/gepi.22035. [Epub ahead of print] PMID: 28198095
248. Heit JA, Armasu SM, McCauley BM, Kullo IJ, Sicotte H, Pathak J, Chute CG, Gottesman O, Bottinger EP, Denny JC, Roden DM, Li R, **Ritchie MD**, de Andrade M. Identification of unique venous thromboembolism-susceptibility variants in African-Americans. *Thromb Haemost*. 2017 Feb 16. doi: 10.1160/TH16-08-0652. [Epub ahead of print] PMID: 28203683
249. Dumitrescu L, **Ritchie MD**, Denny JC, El Rouby NM, McDonough CW, Bradford Y, Ramirez AH, Bielinski SJ, Basford MA, Chai HS, Peissig P, Carrell D, Pathak J, Rasmussen LV, Wang X, Pacheco JA, Kho AN, Hayes MG, Matsumoto M, Smith ME, Li R, Cooper-DeHoff RM, Kullo IJ, Chute CG, Chisholm RL, Jarvik GP, Larson EB, Carey D, McCarty CA, Williams MS, Roden DM, Bottinger E, Johnson JA, de Andrade M, Crawford DC. Genome-wide study of resistant hypertension identified from electronic health records. *PLoS One*. 2017 Feb 21;12(2):e0171745. doi: 10.1371/journal.pone.0171745. PMID: 28222112, PMCID: PMC5319785
250. Haggerty CM, James CA, Calkins H, Tichnell C, Leader JB, Hartzel DN, Nevius CD, Pendergrass SA, Person TN, Schwartz M, **Ritchie MD**, Carey DJ, Ledbetter DH, Williams MS, Dewey FE, Lopez A, Penn J, Overton JD, Reid JG, Lebo M, Mason-Suares H, Austin-Tse C, Rehm HL, Delisle BP, Makowski DJ, Mehra VC, Murray MF, Fornwalt BK. Electronic health record phenotype in subjects with genetic variants associated with arrhythmogenic right ventricular cardiomyopathy: a study of 30,716 subjects with exome sequencing. *Genet Med*. 2017 May 4. doi: 10.1038/gim.2017.40. PMID: 28471438
251. Kim D, Volk H, Girirajan S, Pendergrass S, Hall MA, Verma SS, Schmidt RJ, Hansen RL, Ghosh D, Ludena-Rodriguez Y, Kim K, **Ritchie MD**, Hertz-Picciotto I, Selleck SB. The joint effect of air pollution exposure and copy number variation on risk for autism. *Autism Res*. 2017 Apr 27. doi: 10.1002/aur.1799. PMID: 28448694
252. Fernández-Rhodes L, Gong J, Haessler J, Franceschini N, Graff M, Nishimura KK, Wang Y, Highland HM, Yoneyama S, Bush WS, Goodloe R, **Ritchie MD**, Crawford D, Gross M, Fornage M, Buzkova P, Tao R, Isasi C, Avilés-Santa L, Daviglus M, Mackey RH, Houston D, Gu CC, Ehret G, Nguyen KH, Lewis CE, Leppert M, Irvin MR, Lim U, Haiman CA, Le Marchand L,

Curriculum Vitae: Marylyn DeRiggi Ritchie

- Schumacher F, Wilkens L, Lu Y, Bottinger EP, Loos RJ, Sheu WH, Guo X, Lee WJ, Hai Y, Hung YJ, Absher D, Wu IC, Taylor KD, Lee IT, Liu Y, Wang TD, Quertermous T, Juang JJ, Rotter JI, Assimes T, Hsiung CA, Chen YI, Prentice R, Kuller LH, Manson JE, Kooperberg C, Smokowski P, Robinson WR, Gordon-Larsen P, Li R, Hindorff L, Buyske S, Matise TC, Peters U, North KE. Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. *Hum Genet.* 2017 Apr 8. doi: 10.1007/s00439-017-1787-6. [PMID: 28391526](#)
253. Greene CS, Garmire LX, Gilbert JA, **Ritchie MD**, Hunter LE. Celebrating parasites. *Nat Genet.* 2017 Mar 30;49(4):483-484. doi: 10.1038/ng.3830. No abstract available. [PMID: 28358134](#)
254. Holzinger ER, Verma SS, Moore CB, Hall M, De R, Gilbert-Diamond D, Lanktree MB, Pankratz N, Amuzu A, Burt A, Dale C, Dudek S, Furlong CE, Gaunt TR, Kim DS, Riess H, Sivapalaratnam S, Tragante V, van Iperen EPA, Brautbar A, Carrell DS, Crosslin DR, Jarvik GP, Kuivaniemi H, Kullo IJ, Larson EB, Rasmussen-Torvik LJ, Tromp G, Baumert J, Cruickshanks KJ, Farrall M, Hingorani AD, Hovingh GK, Kleber ME, Klein BE, Klein R, Koenig W, Lange LA, März W, North KE, Charlotte Onland-Moret N, Reiner AP, Talmud PJ, van der Schouw YT, Wilson JG, Kivimaki M, Kumari M, Moore JH, Drenos F, Asselbergs FW, Keating BJ, **Ritchie MD**. Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. *BioData Min.* 2017 Jul 24;10:25. doi: 10.1186/s13040-017-0145-5. eCollection 2017. [PMID: 28770004](#)
255. Li R, Kim D, **Ritchie MD**. Methods to analyze big data in pharmacogenomics research. *Pharmacogenomics.* 2017 Jun;18(8):807-820. doi: 10.2217/pgs-2016-0152. Epub 2017 Jun 14. [PMID: 28612644](#)
256. Kim D, Basile AO, Bang L, Horgusluoglu E, Lee S, Ritchie MD, Saykin AJ, Nho K. Knowledge-driven binning approach for rare variant association analysis: application to neuroimaging biomarkers in Alzheimer's disease. *BMC Med Inform Decis Mak.* 2017 May 18;17(Suppl 1):61. doi: 10.1186/s12911-017-0454-0. [PMID: 28539126](#)
257. Dewey FE, Gusarova V, Dunbar RL, O'Dushlaine C, Schurmann C, Gottesman O, McCarthy S, Van Hout CV, Bruse S, Dansky HM, Leader JB, Murray MF, Ritchie MD, Kirchner HL, Habegger L, Lopez A, Penn J, Zhao A, Shao W, Stahl N, Murphy AJ, Hamon S, Bouzelmat A, Zhang R, Shumel B, Pordy R, Gipe D, Herman GA, Sheu WHH, Lee IT, Liang KW, Guo X, Rotter JI, Chen YI, Kraus WE, Shah SH, Damrauer S, Small A, Rader DJ, Wulff AB, Nordestgaard BG, Tybjaerg-Hansen A, van den Hoek AM, Princen HMG, Ledbetter DH, Carey DJ, Overton JD, Reid JG, Sasiela WJ, Banerjee P, Shuldiner AR, Borecki IB, Teslovich TM, Yancopoulos GD, Mellis SJ, Gromada J, Baras A. Genetic and Pharmacologic Inactivation of ANGPTL3 and Cardiovascular Disease. *N Engl J Med.* 2017 Jul 20;377(3):211-221. doi: 10.1056/NEJMoal1612790. Epub 2017 May 24. [PMID: 28538136](#)
258. Rasmussen-Torvik LJ, Almoguera B, Doheny KF, Freimuth RR, Gordon AS, Hakonarson H, Hawkins JB, Husami A, Ivacic LC, Kullo IJ, Linderman MD, Manolio TA, Obeng AO, Pellegrino R, Prows CA, Ritchie MD, Smith ME, Stallings SC, Wolf WA, Zhang K, Scott SA. Concordance between Research Sequencing and Clinical Pharmacogenetic Genotyping in the eMERGE-PGx Study. *J Mol Diagn.* 2017 Jul;19(4):561-566. doi: 10.1016/j.jmoldx.2017.04.002. Epub 2017 May 11. [PMID: 28502727](#)
259. Hall MA, Wallace J, Lucas A, Kim D, Basile AO, Verma SS, McCarty CA, Brilliant MH, Peissig PL, Kitchner TE, Verma A, Pendergrass SA, Dudek S, Moore JH, **Ritchie MD**. PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. *Nature Communications,* 2017 Oct 27;8(1):1167 [PMID: 29079728](#), [PMCID: PMC5660079](#)

Curriculum Vitae: Marylyn DeRiggi Ritchie

260. McAllister K, Mechanic LE, Amos C, Aschard H, Blair IA, Chatterjee N, Conti D, Gauderman WJ, Hsu L, Hutter CM, Jankowska MM, Kerr J, Kraft P, Montgomery SB, Mukherjee B, Papanicolaou GJ, Patel CJ, Ritchie MD, Ritz BR, Thomas DC, Wei P, Witte JS. Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. *Am J Epidemiol.* 2017 Oct 1;186(7):753-761. [PMID: 28978193](#)
261. Ritchie MD, Davis JR, Aschard H, Battle A, Conti D, Du M, Eskin E, Fallin MD, Hsu L, Kraft P, Moore JH, Pierce BL, Bien SA, Thomas DC, Wei P, Montgomery SB. Incorporation of Biological Knowledge Into the Study of Gene-Environment Interactions. *Am J Epidemiol.* 2017 Oct 1;186(7):771-777. [PMID: 28978191](#)
262. Basile AO, Byrska-Bishop M, Wallace J, Frase A, and **Ritchie MD**. Novel features and enhancements in BioBin, a tool for the biologically inspired binning and association analysis of rare variants. *Bioinformatics.* 2017 Sep 14. [PMID: 28968757](#).
263. Mechanic LE, Lindström S, Daily KM, Sieberts SK, Amos CI, Chen HS, Cox NJ, Dathe M, Feuer EJ, Guertin MJ, Hoffman J, Liu Y, Moore JH, Myers CL, **Ritchie MD**, Schildkraut J, Schumacher F, Witte JS, Wang W, Williams SM; U4C Challenge Participants; U4C Challenge Data Contributors, Gillanders EM. Up For A Challenge (U4C): Stimulating innovation in breast cancer genetic epidemiology. *PLoS Genet.* 2017 Sep 28;13(9):e1006945. [PMID: 28957327](#). [PMCID: PMC5619686](#)
264. Veturi Y, **Ritchie MD**. How powerful are summary-based methods for identifying expression-trait associations under different genetic architectures? *Pac Symp Biocomput.* 2018; 23:228-239. [PMID: 29218884](#). [PMCID: PMC5785784](#)
265. Li B, Verma SS, Veturi YC, Verma A, Bradford Y, Haas DW, **Ritchie MD**. Evaluation of PrediXcan for prioritizing GWAS associations and predicting gene expression. *Pac Symp Biocomput.* 2018;23:448-459. [PMID: 29218904](#). [PMCID: PMC5749400](#)
266. Buchanan AH, Manickam K, Meyer MN, Wagner JK, Hallquist MLG, Williams JL, Rahm AK, Williams MS, Chen ZE, Shah CK, Garg TK, Lazzeri AL, Schwartz MLB, Lindbuchler DM, Fan AL, Leeming R, Servano PO 3rd, Smith AL, Vogel VG, Abul-Husn NS, Dewey FE, Lebo MS, Mason-Suares HM, **Ritchie MD**, Davis FD, Carey DJ, Feinberg DT, Faucett WA, Ledbetter DH, Murray MF. Early cancer diagnoses through BRCA1/2 screening of unselected adult biobank participants. *Genet Med.* 2017 Oct 26. [PMID: 29261187](#)
267. Nielsen JB, Fritsche LG, Zhou W, Teslovich TM, Holmen OL, Gustafsson S, Gabrielsen ME, Schmidt EM, Beaumont R, Wolford BN, Lin M, Brummett CM, Preuss MH, Refsgaard L, Bottinger EP, Graham SE, Surakka I, Chu Y, Skogholt AH, Dalen H, Boyle AP, Oral H, Herron TJ, Kitzman J, Jalife J, Svendsen JH, Olesen MS, Njølstad I, Løchen ML, Baras A, Gottesman O, Marcketta A, O'Dushlaine C, **Ritchie MD**, Wilsgaard T, Loos RJF, Frayling TM, Boehnke M, Ingelsson E, Carey DJ, Dewey FE, Kang HM, Abecasis GR, Hveem K, Willer CJ. Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. *Am J Hum Genet.* 2018 Jan 4;102(1):103-115. [PMID: 29290336](#)
268. Volpi S, Bult CJ, Chisholm RL, Deverka PA, Ginsburg GS, Jacob HJ, Kasapi M, McLeod HL, Roden DM, Williams MS, Green ED, Rodriguez LL, Aronson S, Cavallari LH, Denny JC, Dressler LG, Johnson JA, Klein TE, Leeder JS, Piquette-Miller M, Perera M, Rasmussen-Torvik LJ, Rehm HL, **Ritchie MD**, Skaar TC, Wagle N, Weinshilboum R, Weitzel KW, Wildin R, Wilson J, Manolio TA, Relling MV. Research Directions in the Clinical Implementation of Pharmacogenomics: An Overview of US Programs and Projects. *Clin Pharmacol Ther.* 2018 Feb 20. doi: 10.1002/cpt.1048. [PMID:29460415](#).
269. Verma SS, Josyula N, Verma A, Zhang X, Veturi Y, Dewey FE, Hartzel DN, Lavage DR, Leader J, **Ritchie MD**, Pendergrass SA. Rare variants in drug target genes contributing to

Curriculum Vitae: Marylyn DeRiggi Ritchie

- complex diseases, phenome-wide. *Sci Rep.* 2018 Mar 15;8(1):4624. doi: 10.1038/s41598-018-22834-4. [PMID:29545597](#); [PMCID:PMC5854600](#)
270. Verma A, Lucas A, Verma SS, Zhang Y, Josyula N, Khan A, Hartzel DN, Lavage DR, Leader J, **Ritchie MD**, Pendergrass SA. PheWAS and Beyond: The Landscape of Associations with Medical Diagnoses and Clinical Measures across 38,662 Individuals from Geisinger. *Am J Hum Genet.* 2018 Mar 19. pii: S0002-9297(18)30062-4. doi: 10.1016/j.ajhg.2018.02.017. [PMID:29606303](#)
271. Verma A, Bradford Y, Dudek SM, Verma SS, Pendergrass SA, **Ritchie MD**. A simulation study investigating power of Phenome-Wide Association Studies. *BMC Bioinformatics*, 2018 Apr 4;19(1):120. doi: 10.1186/s12859-018-2135-0. [PMID:29618318](#)

Papers Submitted

1. **Ritchie MD**, Van Steen K, Gusareva E. Dimensionality reduction in Genome-Wide Association Interaction Studies (GWAIS): practical considerations. *Annals of Translational Medicine*, *accepted*.
2. Li R, Kim D, Wheeler HE, Dudek SM, Dolan EM, **Ritchie MD**. Integration of genetic and functional genomics data to uncover chemotherapeutic induced cytotoxicity. *The Pharmacogenomics Journal*, *accepted*
3. Miller JE, Metpally RP, Person TN, Krishnamurthy SB, Dasari VR, Lavage DR, Cook AM, Smith AL, Nash J, Carey DJ, **Ritchie MD**, Kim D, Gogoi R. on behalf of the DiscovEHR collaboration. Systematic characterization of germline variants from the DiscovEHR study Endometrial Carcinoma population. Submitted

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](#)
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](#)

Curriculum Vitae: Marylyn DeRiggi Ritchie

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
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

Non-Peer Reviewed Papers/Chapters

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

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 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: 7th European Conference, Proceedings EvoBIO 2009*. Springer publishing (2009).
 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: 8th 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).

ABSTRACT CONTRIBUTED PRESENTATIONS

2003 “Optimization of Neural Networks using Genetic Programming to Improve Detection and Modeling of Gene-Gene Interactions in Studies of Human

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 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)
- 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)

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 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)
- 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)

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 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)
- 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)

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 2004 “Genome-Wide Association Studies: Challenges, Strategies, and MDR,” Vanderbilt University Genetic Interest Group Seminar Series, Nashville, TN (Host: Kelly McDermott)
- 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 Lisciandra, 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)
- 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)

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 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
- 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

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 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.
- 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

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 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
- 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

Curriculum Vitae: Marylyn DeRiggi Ritchie

- 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
- 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 “TBD”, Informing Environmental Health Decisions Through Data Integration Workshop, National Academy of Science, Washington DC, Host: Ben Wender

Curriculum Vitae: Marylyn DeRiggi Ritchie

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 “TBD”, Copenhagen Novo Nordisk Foundation (NNF) symposium. Copenhagen, Denmark. Host: Ramneek Gupta

2018 “TBD” Keynote at Penn 2nd annual precision medicine symposium, Philadelphia PA, Host: David Roth