CURRICULUM VITAE

Matthew N. McCall, Ph.D.
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Date of Birth: 01/08/1982   **Citizenship:** USA
Pronouns: he/him/his

CURRENT POSITIONS
Associate Professor of Biostatistics & Computational Biology and of Biomedical Genetics
Program Director, Statistics PhD Program
Co-director, Wilmot Cancer Institute Biostatistics and Bioinformatics Shared Resource
Associate Director, Environmental Health Biostatistics Training Grant
University of Rochester School of Medicine & Dentistry, Rochester, NY

EDUCATION
2000 – 2004   B.S., Statistics
              University of Michigan, Ann Arbor, MI
2009 – 2010   M.H.S., Bioinformatics
              Johns Hopkins Bloomberg School of Public Health, Baltimore, MD
2005 – 2010   Ph.D., Biostatistics
              Johns Hopkins Bloomberg School of Public Health, Baltimore, MD

POST-DEGREE TRAINING
2010 – 2013   Postdoctoral Fellowship
              University of Rochester School of Medicine & Dentistry, Rochester, NY
2013 – 2014   Postdoctoral Associate
              University of Rochester School of Medicine & Dentistry, Rochester, NY

FACULTY APPOINTMENTS
2014 – 2018   Assistant Professor, Department of Biostatistics & Computational Biology
              University of Rochester School of Medicine & Dentistry, Rochester, NY
2014 – 2018   Assistant Professor, Department of Biomedical Genetics
              University of Rochester School of Medicine & Dentistry, Rochester, NY
2019 – 2024   Associate Professor, Department of Biostatistics & Computational Biology
              University of Rochester School of Medicine & Dentistry, Rochester, NY
2019 –   Associate Professor, Department of Biomedical Genetics
              University of Rochester School of Medicine & Dentistry, Rochester, NY
2024 –   Associate Professor with Unlimited Tenure,
              Department of Biostatistics & Computational Biology
              University of Rochester School of Medicine & Dentistry, Rochester, NY
2015 –   Affiliated Faculty, The Goergen Institute for Data Science
              University of Rochester, Rochester, NY

ADMINISTRATIVE APPOINTMENTS

2019 –   Co-director, Wilmot Cancer Institute Biostatistics and Bioinformatics
               Shared Resource, University of Rochester Medical Center, Rochester, NY
2019 –   Co-chair, GIDS Working Group on Life Sciences and Biomedical Data
               Science, University of Rochester, Rochester, NY
2020 – 2022   Associate Program Director, Statistics PhD Program
               University of Rochester Medical Center, Rochester, NY
2023 –   Associate Director, Environmental Health Biostatistics Training Grant
               NIH T32 ES007271, University of Rochester Medical Center, Rochester, NY
2023 –   Program Director, Statistics PhD Program
               University of Rochester Medical Center, Rochester, NY

HONORS AND AWARDS

2004   Honors College Concentration in Statistics with Highest Distinction,
               University of Michigan, Ann Arbor, MI
2004   Phi Beta Kappa
               University of Michigan, Ann Arbor, MI
2004 – 2005   Intramural Research Training Award Fellow
               NIH/NHGRI, Cancer Genetics Branch
2005 – 2007   Trainee, NIH Training Grant in the Epidemiology and Biostatistics of Aging,
               Johns Hopkins Bloomberg School of Public Health, Baltimore, MD
2007 – 2010   Trainee, NIH Training Grant in Biostatistics for Genetics/Genomics,
               Johns Hopkins Bloomberg School of Public Health, Baltimore, MD
2008   Travel Award, International Meeting of the Microarray and Gene Expression Data
               Society, Riva del Garda, Italy
2009 & 2010   Teaching Assistant Recognition Award Nominee
               Johns Hopkins Bloomberg School of Public Health, Baltimore, MD
2010   Helen Abbey Award for Excellence in Teaching
               Johns Hopkins Bloomberg School of Public Health, Baltimore, MD
2010 – 2013   Trainee, NIH Training Grant in Experimental Therapy Models,
               University of Rochester School of Medicine & Dentistry, Rochester, NY
2011   Conference Fellowship, q-bio Conference on Cellular Information Processing
               Santa Fe, NM
2011   Conference Scholarship, Bioconductor Conference (BioC2011)
               Seattle, WA
2015   Graduate Student Society Advocacy Award
               University of Rochester School of Medicine & Dentistry, Rochester, NY

ACADEMIC & PROFESSIONAL ORGANIZATIONS

2009 –   American Statistical Association (ASA)
2009 –   The International Biometric Society, Eastern North American Region (ENAR)
2014 –   Rochester Chapter of the ASA
2015 –   ASA Section on Statistics in Genomics and Genetics
2020 –   Math Alliance

COMMITTEES & OTHER ADMINISTRATIVE SERVICE

UR Department of Biostatistics & Computational Biology

2015 – 2017	Chair, Biostatistics and Computational Biology Departmental Seminar Series
2015 –	Member, Bioinformatics Concentration Curriculum Committee
2016 –	Member, Statistics Graduate Admissions Committee
2016 – 2022	Member, Biostatistics and Computational Biology Faculty Search Committee
2018 –	Member, Biostatistics and Computational Biology Computing Committee
2018 –	Member, Biostatistics and Computational Biology Curriculum Committee
2019 –	Member, Internal Advisory Board / Executive Committee for NIH T32 ES007271

UR Extra-Departmental

2015 – 2016	Co-chair, Data Science Colloquium Series
2015 – 2019	Judge, Graduate Student Society Poster Competition
2016 – 2018	Member, CTSI Informatics Education Cluster
2017, 2019 – 2021	Reviewer, University Research Awards
2017 – 2019	Member, Center for Biomedical Informatics and Wilmot Cancer Institute Faculty Search Committee
2018 – 2019	Member, Biomedical Informatics Curriculum Committee
2018 –	Member, Environmental Health Sciences Center
2018 –	Member, Wilmot Cancer Institute
2019	Reviewer, SAC Incubator Awards
2019	Reviewer, UNYTE Pipeline-to-Pilot Program
2019 – 2020	Member, Bioinformatics Working Group Planning Committee
2019 – 2020	Participant, Driving our Future: Culture, Climate and Leadership in the Sciences
2019 –	Member, Wilmot Cancer Institute Scientific Leadership Committee
2021 – 2022	Member, Sproull Fellowship Review Committee
2021 – 2024	Member, Provost Fellowship Review Committee
2022	Chair, Provost Fellowship Review Committee
2023 –	Alternate, Standing Conduct Panel
2023	Reviewer, GIDS Seed Funding Program
2024	Reviewer, WCI Wilmot Team Science Pilot Funding Program
2024	Observer, MEDSAC Steering Committee

Local/Regional

2018 – 2019	Member, UP-STAT Organizing Committee
2018	Member, UP-STAT Data Analytics Committee
2016, 2018, 2019	Session Chair, UP-STAT Conference
2018 – 2019	Judge, UP-STAT Conference Student Research Awards

National

2012 – 2013	Judge, ASA/NCTM Statistical Project Competition
2017 – 2019	NIH Early Career Reviewer Program
2018, 2019, 2020, 2022	Reviewer, CTSI Novel Biostatistical and Epidemiologic Methodology pilot program
2018	Reviewer, NIH Biodata Management and Analysis BDMA Study Section

2018 – 2024	Member, Bioconductor Conference Organizing Committee
2019 – 2020	Chair, Bioconductor Conference (BioC2020) Competitive Program
2019	Invited Session Organizer, Symposium on Data Science & Statistics
2023	Reviewer, NIH Genomics, Computational Biology and Technology GCAT Study Section
2024	Reviewer, NIH Analytics and Statistics for Population Research Panel A ASPA Study Section

EDUCATIONAL CONTRIBUTIONS
Research Mentoring
Research Assistant Professors

2022 – 2023	Seong-Hwan Jun, Ph.D.; Primary Mentor

Postdoctoral Fellows

2014 – 2015	Qingyan Lilly Xie, Ph.D.; Primary Mentor
2016 – 2017	Isar Nassiri, Ph.D.; Primary Mentor
2020 – 2021	Hongying Sun, Ph.D.; Primary Mentor
2023 –	Ernesto Luis Aparicio Puerta, Ph.D.; Primary Mentor

Graduate Students

2015 – 2019	Valeriia Sherina, Statistics Ph.D. Program; Thesis Advisor (co-advisor: Dr. Tanzy Love)
2015 – 2018	Yun Zhang, T32 Program; Program Mentor
2018 – 2023	Zachary Brehm, Statistics Ph.D. Program; Thesis Advisor
2020 – 2023	Erik Vonkaenel, Statistics Ph.D. Program; Thesis Advisor
2021 –	Hannah Swan, Statistics Ph.D. Program; Thesis Advisor
2023 –	Ludia J. Pack, GIDS-REM Program; Program Mentor
2023 –	Ricardo Lopez Candelaria, T32 Program; Program Mentor
2024 –	Elijah Soh, GIDS-REM Program; Program Mentor

Graduate Research Assistants

2016 (fall)	Kejia Wang, Statistics M.A. Program
2017 (summer)	Jeremiah Jones, Statistics Ph.D. Program
2018 – 2022	David Burton, Statistics Ph.D. Program
2019 (fall)	Bokai Wang, Statistics Ph.D. Program
2020 – 2024	Sami Leon, Statistics Ph.D. Program
2023 (summer)	Christian Hammond, Statistics Ph.D. Program
2024 (summer)	Meherab Hossain, Statistics Ph.D. Program
2024 – 2025	Xinzhu (Claire) Wang, Statistics Ph.D. Program

Rotation Students

2015 (fall)	Bokai Wang, Statistics Ph.D. Program
2018 (spring)	Mukta Palshikar Biophysics, Structural & Computational Biology Ph.D. Program
2019 (spring)	Abhinav Mittal Biophysics, Structural & Computational Biology Ph.D. Program

2023 (spring)	Jing Guo, Genetics Ph.D. Program
2024 (spring)	Thandolwethu Shabangu, Microbiology & Immunology Ph.D. Program

Undergraduate Students

2015 (summer)	Lindsey Barden, University of North Carolina at Chapel Hill
2015 (summer)	Allison Maier, State University of New York at Geneseo
2015 (summer)	Scott Onestak, University of Rochester
2015 – 2017	Lauren Kemperman, University of Rochester
2015 – 2017	Jeffrey Hrebenach, University of Rochester
2016 (summer)	Alida Mooney, State University of New York at Geneseo
2016 – 2017	Winslow Powers, University of Rochester
2016 – 2018	Jonavelle Cuerdo, University of Rochester
2017 – 2019	Benjamin Hsu, University of Rochester
2018 (fall)	Oleg Demus, University of Rochester
2017 – 2019	Qidi Yang, University of Rochester
2018 – 2019	Kailey Ferger, University of Rochester
2019 (summer)	Joshua Dennis, University of Rochester
2019 (fall)	Daniel Munoz Huerta, University of Rochester
2019 – 2021	Yuewei Fei, University of Rochester
2019 – 2021	Michael Lansford, University of Rochester
2019 – 2021	Benyu Zhou, University of Rochester
2020 – 2021	Frank Gonzalez, University of Rochester
2022 – 2023	Maisa Maliha, Dickinson College
2023 (fall)	Claire English, University of Rochester
2023 – 2024	Monish Shah, University of Rochester
2024 –	Youjia Zhang, University of Rochester

High School Students

2017 (summer)	Fatima Umar, Pittsford Schools
2017 (summer)	Raymond Feng, Pittsford Schools
2019 (summer)	Lillian Stolberg, Pittsford Schools
2022 (summer)	Ivan Wiandt, Pittsford Schools

Classroom Teaching

2012	BST520, Current Topics in Bioinformatics (course co-designer and co-instructor)
2014	BST512, Advanced Bayesian Inference with an Emphasis on Computation (one lecture)
2014	BST432, Introduction to Bioinformatics (one lecture)
2014 – 2018	IND501, Ethics and Professional Integrity in Research (small group facilitator)
2015	GEN508, Genomics and Systems Biology (two lectures)
2015	GEN504, Genetics Seminar (one lecture)
2015	BST550, Genomic Data Analysis Using R/Bioconductor (course designer and instructor)
2016 – 2023	IND419, Introduction to Quantitative Biology (two to five lectures)

2016, 2017, 2023	BST494/BST430, Statistical Computing (course designer and instructor)
2018 – 2023	BST487, Seminar in Statistical Literature (topic supervisor)
2019, 2021, 2023, 2024, 2025	BST494/BST434, Genomic Data Analysis (course designer and instructor)
2020	BST570, Statistical Analysis of Cell Mixtures (course designer and instructor)
2022	BST550, Genomic Data Science (course designer and instructor)
2023	Scientific Reasoning in Medicine (one lecture)

Short Courses & Workshops

2015	Challenges in Translational Genomics (course designer and instructor)
2015	Mechanics of RNA-Seq Data Analysis Using R (course instructor)
2018	Grad STEM for All Summer Program (instructor and program mentor)
2018	Genomic Data Analysis Workshop (course designer and instructor)

Thesis Committee Service

2014 – 2017	Justin Komisarof (Genetics, Development, and Stem Cells Ph.D. Program)
2016 – 2018	Yun Zhang (Statistics Ph.D. Program)
2017 – 2020	Rohith Palli (Biophysics, Structural & Computational Biology Ph.D. Program)
2017	Adan Becerra (Epidemiology Ph.D. Program); *Chair Thesis Defense Committee*
2017 – 2023	Adam Cornwell (Genetics, Development, and Stem Cells Ph.D. Program)
2017 – 2022	Derek Crowe (Genetics, Development, and Stem Cells Ph.D. Program)
2018 – 2020	Matthew Turner (Genetics, Development, and Stem Cells Ph.D. Program)
2018	Kyle Berger (Biophysics, Structural & Computational Biology Ph.D. Program) *Chair Thesis Defense Committee*
2019 – 2021	Jiatong Sui (Statistics Ph.D. Program)
2021 – 2024	Abhinav Mittal (Biophysics, Structural & Computational Biology Ph.D. Program)
2022 –	Dakarai Esgdaille (Biomedical Genetics and Genomics)
2023 –	Ruoqiao Wang (Biomedical Genetics and Genomics)
2023 – 2024	Sami Leon (Statistics Ph.D. Program)
2024 –	Ricardo Lopez Candelaria (Statistics Ph.D. Program)
2024 –	Joshua Marvald (Statistics Ph.D. Program)

CONSULTATIONS

2008 – 2009	University of Miami Miller School of Medicine, Miami, Florida, USA
2010 – 2011	GenomeDx Biosciences Inc, Vancouver, British Columbia, Canada
2011 – 2013	Janssen Research and Development, Beerse, Belgium
2012 – 2013	OpenAnalytics, Heist-op-den-Berg, Belgium
2013	Selventa Inc, Cambridge, Massachusetts, USA

EDITORIAL ASSIGNMENTS IN PROFESSIONAL JOURNALS

Ad hoc **reviews for:** Annals of Applied Statistics, AJP Renal Physiology, Bioinformatics, Biometrics, Biotechniques, biOverlay, BMC Bioinformatics, BMC Cancer, BMC Genomics, BMC Medical Genomics, Cancer Informatics, Cell Reports Methods, Cell Systems, Database, Epigenomics, F1000Research, Gene, Genome Biology, Genome Research, IEEE/ACM Transactions on Computational Biology and Bioinformatics, IMS Collections, iScience, Journal

of the American Statistical Association, Journal of Postdoctoral Research, Microarrays, Nature Methods, Nucleic Acids Research, NAR Genomics and Bioinformatics, PLoS Computational Biology, PLoS Genetics, PLoS One, Proceedings of the National Academy of Sciences, Science, Scientific Reports, STAR Protocols, Statistical Applications in Genetics and Molecular Biology, Statistics in Biosciences

Editorial Assignments
2012 – 2014   Editor, Journal of Postdoctoral Research
2015 – 2020   Review Editor, Frontiers in Genetics
2018 –   Associate Editor, Biostatistics

GRANTS & CONTRACTS
As Principal Investigator / Co-Principal Investigator
NIH R01 GM139928 (PI: McCall)
Statistical Methods for MicroRNA-seq Experiments
09/11/20-06/30/25; Total Award: $1,975,065
The overall objective of this application is to improve the analysis of sRNA-seq data by developing statistical methods that account for challenges specific to sRNA-seq data.

NIH R01 NS136626 (MPI: McCall and Thurston)
Statistical Methods for Confocal Microscopy Images of Microglia
03/15/24-02/28/29; Total Award: $1,925,000
The overall goal of the proposed research is to develop statistical methodology that will lead to improved analysis of microglial images and uncover the changes in morphology that are most predictive of alterations in microglial function.

NIH R25 HG012324 (MPI: Larracuente, Fay, McCall)
Genomic Intensive Data Science Research, Education and Mentorship
05/01/23-02/29/28; Total Award: $1,305,935
The Genomic Intensive Data Science Research, Education and Mentorship (GIDS-REM) program at the University of Rochester aims to increase the number of researchers with strong quantitative skills in the genomics workforce. The focus is on recruiting and retaining members of groups traditionally underrepresented in biomedical fields.

NIH R00 HG006853 (PI: McCall)
Statistical Methods for Estimation of Gene Regulatory Networks
09/01/14 - 08/31/18 (NCE); Total Award: $726,419
The overall goals of the proposed research are to improve the estimation of gene regulatory networks from perturbation experiments, by using methods that explicitly model and incorporate uncertainty in each step of the process, and to use these estimated networks to predict cellular response to intervention.

NIH K99 HG006853 (PI: McCall)
Statistical Methods for Estimation of Gene Regulatory Networks
09/10/13 - 08/31/14; Total Award: $79,893

Responsibilities: This Award provided support to obtain the expertise required to address the proposed research aims and transition to an independent research career through a combination of coursework, mentorship, and research experience.

NIH R01 HL137811 (PI: Halushka; Subcontract-PI: McCall)
Fine Dissection of Atherosclerosis Microenvironment RNA Expression
09/01/17 – 08/30/22; Annual Direct Costs to McCall Lab: $65,866/year
This project will identify genes, long noncoding RNAs and microRNAs that are involved in the development of coronary artery atherosclerosis.

NIH R01 GM083084 (PI: Irizarry; Subcontract-PI: McCall)
Preprocessing and Analysis Tools for High-Throughput Technologies
09/01/16 - 06/30/20; Annual Direct Costs to McCall Lab: $25,000/year
The goal of the proposed research is to leverage the public data repositories to gain insights into the stochastic nature of measurement and develop methods to model application-specific systematic bias and unwanted variability. The proposed research requires the use of a vast amount of publicly available data across several high-throughput platforms.

UL1 TR002001 Pilot Studies Award (PI: McCall)
Development of qPCR Methodology for Clinical Testing
08/15/16 - 05/31/17; Total Award: $35,000
The overall goals of the proposed research are: (1) to develop improved methodology to handle non-detects in qPCR data, (2) to develop a single sample version of our methodology for clinical biomarkers, and (3) to assess the applicability of our methods to microRNA transcriptome screening.

UL1 TR002001 Pilot Studies Award (PI: McCall)
Estimation of cell-type specific microRNA expression in complex tissue samples
06/01/17 - 05/31/18; Total Award: $35,000
The overall goal of the proposed research is to develop statistical deconvolution methodology to estimate the cellular composition and cell-type specific microRNA expression of tissue samples.

UL1 TR002001 Pilot Studies Award (PI: McCall)
Statistical methods to quantify imaged microglia
06/01/19 - 05/31/20; Total Award: $35,000
The overall goal of the proposed research is to improve the analysis of microglial morphology by developing statistical methods to quantify images of microglia.

Goergen Institute for Data Science Seed Funding Award (PI: McCall)
Improving deconvolution estimates through Bayesian shrinkage
10/11/22 - 10/31/23; Total Award: $20,000
The overall goal of the proposed research is to develop a shrinkage procedure based on empirical Bayes techniques to improve estimation of tissue composition.

Goergen Institute for Data Science Seed Funding Award (PI: McCall)
Estimation of Cancer-Relevant Gene Regulatory Networks from Perturb-Seq Data

10/11/23 - 10/31/24; Total Award: $20,000
The overall goal of the proposed research is to develop statistical and computational methodology to estimate gene regulatory networks (GRNs) based on thousands of gene perturbations at single cell resolution and to apply these methods to identify vulnerabilities in the GRN of cancer cells.

Goergen Institute for Data Science Seed Funding Award (MPI: Rossmann, Jun, McCall)
Development of a Metabolomics Data Analysis Pipeline
10/11/24 - 10/31/25; Total Award: $30,000
The goal of the proposed project is to develop statistical and computational methodology to analyze untargeted metabolomics data. To assess the performance of our methods and compare them to alternative approaches, we propose the generation of a large reference data set based on our expertise in chemical perturbation studies, which would represent the first experimental benchmark data set of its kind for the metabolomics field.

Other Roles
NIH R61 NS131932 (PI: Thornton)
Pharmacodynamic Biomarker of Myotonic Dystrophy
04/01/2023 – 03/31/2028; Percent Effort: 10%
The major goal of this project is to develop biomarkers of disease severity and therapeutic response in myotonic dystrophy.

NIH R01 AR083224 (PI: Zhang)
Molecular control of blood vessel types at the regenerative interface for engineering of osteogenic and angiogenic periosteum mimetic
07/01/2023 – 06/30/2028; Percent Effort: 5%
This proposal seeks to establish blood vessel subtypes and the associated molecular signatures at the osteogenic and angiogenic interface of periosteum-mediated repair. To establish the role of Slits, specifically Slit2 and/or 3, in osteogenesis and bone-specialized vessel formation at the osteogenic and angiogenic interface of periosteum-mediated repair. To establish the controlled delivery of Slits via periosteum surface coating of bone allograft for enhanced defect repair and reconstruction.

NIH R01 ES034829 (PI: Terry)
Endocrine Disrupting Chemicals and Male-biased Neurobehavioral Disorders
02/03/23 – 11/30/27; Percent Effort: 5-16%
This proposal seeks to understand how endocrine disrupting chemical (EDC) mixtures cause the brain and behavior to develop abnormally in a sex dependent fashion. Our previous research revealed that a curated EDC mixture, representative of maternal and infant exposures, targets the perinatal testosterone surge in male mice. The proposed research will define the epigenetic mechanisms of sex-dependent behavioral toxicity following androgen disruption.

Invidumed GmbH (PI: Land)
Global Cancer Database Project
01/01/18 - 12/31/23; Percent Effort: 5-20%

The URMC and INDIVUMED bioinformatics collaboration will focus on the development of a multi-dimensional analytics platform (Portal Solution) linked to a global biospecimen and clinical data resource controlled for molecular integrity, comprehensive data annotation and diversity of patient population. The Global Cancer Data Base Solution (GCDS) will result from the convergence of the Portal Solution and a global biospecimen resource, allowing for an investigator, regardless of their analytical bias (e.g. genomics, proteomics, metabolomics, immune-profiling, etc.,) to interrogate research hypothesis. The GCDS, when developed should represent the most comprehensive analytical tool to interpret and utilize cancer phenomic data linked to a dynamic and growing pool of molecular and phenomic data curated from patients on a global scale.

NIH R35 CA197562 (PI: Land)
Mediators of Cancer Cell Homeostasis: Intervention Targets Common to Diverse Types of Cancer
09/01/15 - 08/31/22; Percent Effort: 10%
The goals of this research program are to develop a rational path towards cancer interventions independent of the tumors' mutational status and with lower rates of associated disease recurrence that can be delivered to a large fraction of patients.

NIH HHSN272201200005C (PI: Topham)
NIAID Respiratory Pathogens Research Center (RPRC) at the University of Rochester
12/13/11 – 12/12/18; Percent Effort: 10%
This center's purpose is to establish, direct, and maintain the UR-RPRC, a multidisciplinary, collaborative, integrated, and iterative program focused on the conduct of research activities to understand the etiology and impact of respiratory pathogens and to develop and evaluate strategies for   their control, treatment and prevention. Specifically, we will provide and maintain a multidisciplinary team of experienced investigators and technical staff with expertise in clinical research and laboratory methods, and experience working with respiratory pathogens and the diseases they cause.

NIH R01 HL127891 (PI: Brookes)
The Role of the Mitochondrial UPR in Ischemic Protection
06/01/15 – 02/28/19; Percent Effort: 5%
This proposal aims to identify mechanisms through which the UPRmt protects C. elegans and to translate these findings to a mammalian cardiac model. Our approach will include defining mechanistic crosstalk with other signaling pathways that are also protective and will result in the identification of functional orthologs that perform similarly in mammals as ATFS-1 and HAF-1.

NIH U54 CA228110 (PI: Rahman)
WNY Center for Research on Flavored Tobacco Products
09/01/2018 – 06/30/2023; Precent Effect: 5%
We propose a Center for Research on Flavored Tobacco Products (CRoFT), the goal of which is to develop a novel framework and approaches for assessing the impact of tobacco product flavors and flavorings on consumer behavior, exposures, and health.

NIH P30 ES001247 (PI: Lawrence)
Environmental Agents as Modulators of Disease Processes
04/01/2019 – 03/31/2026; Percent Effort: 3-5%
The mission of the EHSC at Rochester is to improve public health through the generation of fundamental knowledge and elaboration of mechanisms by which chemical exposures, alone or through interaction with other modifying factors, contribute to cumulative health risk across the lifespan.

NIH R01 NS114480 (PI: Majewska)
Mechanisms that regulate microglial dynamics in the context of plasticity
01/01/2020 – 12/31/2024; Percent Effort: 5%
The goals of this research program are to investigate microglial mechanisms that govern changes in neuronal networks. This will yield information with broad implications for understanding and treating a large spectrum of human neurological disorders.

NIH T32 ES007271 (PI: Thurston)
Training in Environmental Health Biostatistics
09/30/15 – 06/30/25
I am associate director and a research mentor on this training grant; no salary support.

PRESENTATIONS
National & International Conferences

May 2005	A Novel Algorithm for Microarray Time Series Data Analysis IEEE International Workshop on Genomic Signal Processing and Statistics, Newport, RI
Sept 2008	An Improved Gene Expression Barcode based on a Hierarchical Mixture Model International Meeting of MGED, Riva del Garda, Italy
Sept 2008	EMERALD Workshop on Array Quality Assessment Methods International Meeting of MGED, Riva del Garda, Italy
July 2009	From a Single CEL File to a Gene Expression Barcode Bioconductor Conference (BioC2009), Seattle, WA
Mar 2010	Gene Expression Barcodes ENAR Spring Meeting, New Orleans, LA
Feb 2011	Frozen Robust Multi-array Analysis (fRMA) La Calestienne Meeting, Nismes, Belgium
Oct 2011	Microarray Preprocessing and Quality Control La Calestienne Meeting, Nismes, Belgium
July 2011	Thawing Frozen Robust Multi-array Analysis (fRMA) Bioconductor Conference (BioC2011), Seattle, WA
Aug 2011	Assessing Microarray Quality Joint Statistical Meeting, Miami Beach, FL
Aug 2011	A Computational Bayesian Approach for the Inference of Boolean Networks Q-Bio Conference in Cellular Information Processing, Santa Fe, NM
Apr 2012	Batch Effects and Splice Variants La Calestienne Meeting, Nismes, Belgium
July 2012	Batch effect reduction using the frma package

	Bioconductor Conference (BioC2012), Seattle, WA
Aug 2012	Summarization of Affymetrix GeneChip Probe Level Data: from RMA to fRMA
	International Biometric Conference, Kobe, Japan
Oct 2012	fRMA for Exon / Gene ST Arrays
	La Calestienne Meeting, Nismes, Belgium
July 2013	A Computational Bayesian Approach to Gene Regulatory Network Estimation
	Bioconductor Conference (BioC2013), Seattle, WA
Aug 2013	Addressing Within-Subject Genomic Heterogeneity
	Joint Statistical Meeting, Montreal, Canada
Feb 2015	A Gene Regulatory Network of Cooperation Response Genes Governs the Cancer Phenotype, Winter q-bio Meeting, Maui, HI
June 2015	Estimation of a Regulatory Network of Cooperation Response Genes in a Model of Cancer Malignancy, Statistical Learning of Biological Systems from Perturbations, Ascona, Switzerland
June 2015	Modeling qPCR Non-Detects as Missing Data
	qPCR and Digital PCR Congress: USA, San Diego, CA
May 2016	Estimation of a Regulatory Network of Cooperation Response Genes in a Model of Cancer Malignancy, Great Lakes Bioinformatics Conference, Toronto, Canada
July 2016	Complex Sources of Variation in Tissue Expression Data: Analysis of the Genotype-Tissue Expression (GTEx) Lung Transcriptome, GTEx Project Community Meeting, Stanford, CA
Aug 2017	It's all about the residuals: estimating gene networks by leveraging residual structure in multi-tissue transcriptomic data
	Joint Statistical Meeting, Baltimore, MD
May 2019	Case Studies in Interoperability: From Generic Classes To Specific Functions
	Symposium on Data Science & Statistics, Bellevue, WA
Aug 2020	Co-Expression Analysis of Complex Tissues
	Joint Statistical Meeting, Virtual Conference
August 2023	Preprocessing and analysis of microRNA-seq data
	Bioconductor Conference (BioC2023), Boston, MA

Invited Presentations: Local, Regional, & State

Apr 2008	Cross-platform comparisons using microarray spike-in data
	The Expressionist Seminar Series, Baltimore, MD
Oct 2009	Barcodes for Beginners
	The Expressionist Seminar Series, Baltimore, MD
Mar 2011	What can I do with a single microarray?
	Transcriptomics and Integrated Genomics Meeting, Rochester, NY
May 2012	Harnessing heterogeneity to improve genomic biomarkers
	Transcriptomics and Integrated Genomics Meeting, Rochester, NY
Sept 2012	Batch effects in genomic data
	Transcriptomics and Integrated Genomics Meeting, Rochester, NY
Dec 2013	Gene Regulatory Network Estimation
	Transcriptomics and Integrated Genomics Meeting, Rochester, NY
Sept 2014	On Non-Detects in qPCR Data
	Transcriptomics and Integrated Genomics Meeting, Rochester, NY

Mar 2015	Overview of McCall Group Research
	Transcriptomics and Integrated Genomics Meeting, Rochester, NY
Apr 2015	Incorporating Uncertainty in the Estimation of Gene Regulatory Networks
	Center for Integrated Research Computing Symposium Series, Rochester, NY
Apr 2015	Challenges in Translational Genomics
	Workshop sponsored by the Graduate Student Society, Rochester, NY
Dec 2015	Mechanics of RNA-Seq Data Analysis Using R
	Workshop sponsored by the Center for Professional Development, Rochester, NY
Oct 2016	Sources of Variation in GTEx Lung Tissue Expression Data
	Lung Biology Research Seminar Series, Rochester, NY
Jan 2017	Incorporating Uncertainty in the Estimation of Gene Regulatory Networks
	Bioinformatics Cluster, Rochester, NY
Mar 2017	Sources and Effects of Transcriptomic Heterogeneity
	Center for Biomedical Informatics, Rochester, NY
Dec 2017	What can we learn from co-expression analyses?
	Transcriptomics and Integrated Genomics Meeting, Rochester, NY
Feb 2019	Co-expression analysis of complex tissues
	PhD Applicant Weekend, Rochester, NY
Oct 2020	Co-expression, Deconvolution, and MicroRNAs
	CTSI Seminar Series, Rochester, NY

Invited Presentations: National & International

Oct 2011	MicroRNA Microarray Performance
	Janssen Research and Development, Beerse, Belgium
Dec 2016	Incorporating Uncertainty in the Estimation of Gene Regulatory Networks
	University of Buffalo Biostatistics Seminar Series, Buffalo, NY
Mar 2018	How Amazing Mentors Think About Mentoring
	Center for the Integration of Research, Teaching and Learning, Webinar
Sept 2020	Quantifying Uncertainty in the Estimation of Gene Regulatory Networks
	University of Pennsylvania Biostatistics Seminar Series, Virtual Seminar
Oct 2020	Quantifying Uncertainty in the Estimation of Gene Regulatory Networks
	Roswell Park Cancer Genetics and Genomics Webinar Series
June 2023	Improved Understanding of Human Health and Disease Through Genomic Data Science, UKM The National University of Malaysia, FSK Guest Lecture
July 2023	Applications of Genomic Data Science in Human Health and Disease
	National Institutes of Health Malaysia
July 2023	Statistical and Mathematical Approaches to Current Challenges in Biomedicine
	Universiti Sains Malaysia (USM), School of Mathematical Sciences
July 2023	Applications of Genomic Data Science in Human Health and Disease
	Malaysia Genome and Vaccine Institute (MGVI) at the National Institutes of Biotechnology Malaysia (NIBM), NIBM Science Talk Series
July 2023	Improved Understanding of Human Health and Disease Through Genomic Data Science, University of Malaya
June 2024	Gene regulatory networks in cancer: from targeted networks to genome scale investigation, National University of Singapore (NUS), Cancer Science Institute of Singapore

PUBLICATIONS
* denotes trainee / supervisee; ° denotes senior statistician; † denotes corresponding author(s)

Peer-Reviewed Journal Articles

Methodological Research
1. **Baran AM***, Patil AH, **Aparicio-Puerta E***, **Jun S***, Halushka MK, **McCall**†° (2025). miRglmm: a generalized linear mixed model of isomiR-level counts improves estimation of miRNA-level differential expression and uncovers variable differential expression between isomiRs. *Genome Biology, In Press.*
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7. **McCall MN**, Chu C, **Wang L***, Benoodt L, Thakar J, Corbett A, Holden-Wiltse J, Slaunwhite C, Grier A, Gill S, Falsey AR, Topham DJ, Caserta M, Walsh E, Qiu X†°, Mariani TJ† (2021). A systems genomics approach uncovers molecular associates of RSV severity. *PLoS Computational Biology*, 17(12):e1009617.
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10. **Hsu B***, **Sherina V***, **McCall MN**†° (2020). Autoregressive modeling and diagnostics for qPCR amplification. *Bioinformatics,* 36(22-23):5386-5391.
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    [ENAR Distinguished Student Paper Award to V. Sherina]
12. **Nassiri I*** and **McCall MN**†° (2018). Systematic exploration of cell morphological phenotypes associated with a transcriptomic query. *Nucleic Acids Research*, 46(19):e116.
13. Halushka MK†, Fromm B, Peterson KJ, **McCall MN**° (2018). Big Strides in Cellular MicroRNA Expression. *Trends in Genetics*, 34(3):165-167.
14. **McCall MN**°, Kim MS, Adil M, Patil AH, Lu Y, Mitchell CJ, Leal-Rojas P, Xu J, Kumar M, Dawson VL, Dawson TM, Baras AS, Rosenberg AZ, Arking DE, Burns KH,

Pandey A, Halushka MK[†] (2017). Toward the human cellular microRNAome. *Genome Research*, 27(10):1769-1781.

15. Li N, **McCall MN**, Wu Z[†°] (2017). Establishing Informative Prior for Gene Expression Variance from Public Databases. *Statistics in Biosciences*, 9(1):160-177.

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Collaborative Research

38. Knudsen-Clark AM, Mwangi D, Cazarin J, Morris K, Baker C, Hablitz LM, **McCall MN**[°], Kim M, Altman BJ[†] (2024). Circadian rhythms of macrophages are altered by the acidic pH of the tumor microenvironment. *EMBO Reports*, doi: https://doi.org/10.1101/2024.02.14.580339

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43. Strohm A, O'Connor T, Oldfield S, Young S, **Hammond C**[*], **McCall MN**[°], Dirksen R, and Majewska A[†] (2023). Cortical Microglia Dynamics Are Conserved During Voluntary Wheel Running. *Journal of Applied Physiology*, 136(1), 89-108.

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Pre-prints / Non-Peer-Reviewed Journal Articles

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Other Media: Peer-Reviewed R/Bioconductor Software Packages
1.   frma: Single microarray preprocessing and analysis
2.   frmaTools: Extension and customization of the frma package
3.   miRcomp: Tools to assess and compare miRNA expression estimation methods
4.   nondetects: Methods to model and impute non-detects in qPCR data
5.   spkTools: Methods for microarray spike-in data
6.   ternarynet: Computational Bayesian approach to ternary network estimation

Other Media: Peer-Reviewed R/Bioconductor Data Packages
1.   microRNAome: This package provides a SummarizedExperiment object of read counts for microRNAs across tissues, cell-types, and cancer cell-lines.
2.   miRcompData: Raw amplification data from a large microRNA mixture / dilution study. These data are used by the miRcomp package to assess the performance of methods that estimate expression from the amplification curves.
3-12.   <platform>frmavecs: data packages containing the frozen parameter vectors used by the frma package for 10 different microarray platforms.