

## UNIVERSITY OF ROCHESTER SCHOOL OF MEDICINE & DENTISTRY 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  
Associate Professor of Biomedical Genetics  
Program Director, Statistics PhD Program  
Co-director, Wilmot Cancer Institute Biostatistics and Bioinformatics Shared Resource  
Co-chair, GIDS Working Group on Life Sciences and Biomedical Data Science  
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 – 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  
2015 – Affiliated Faculty, The Goergen Institute for Data Science  
University of Rochester, Rochester, NY  
2017 – Affiliated Faculty, Center for Biomedical Informatics  
University of Rochester Medical Center, Rochester, NY

## **HOSPITAL & 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)
- 2009 – ASA Biometrics Section
- 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 – 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 – 2023 Member, Provost Fellowship Review Committee  
 2022 Chair, Provost Fellowship Review 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 Reviewer, CTSI Novel Biostatistical and Epidemiologic Methodology pilot program  
 2018 Reviewer, NIH Biodata Management and Analysis (BDMA) Study Section  
 2018 – Member, Bioconductor Conference Organizing Committee  
 2019 – 2020 Chair, Bioconductor Conference (BioC2020) Competitive Program  
 2019 Invited Session Organizer, Symposium on Data Science & Statistics

**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

Graduate Students

2015 – 2019 Valeriia Sherina, Statistics Ph.D. Program  
Thesis Advisor (co-advisor: Dr. Tanzy Love)

2018 – Zachary Brehm, Statistics Ph.D. Program; Thesis Advisor

2020 – Erik Vonkaenel, Statistics Ph.D. Program; Thesis Advisor

2021 – Hannah Swan, Statistics Ph.D. Program; Thesis Advisor

Graduate Research Assistants

2015 – 2018 Yun Zhang, Statistics Ph.D. Program

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 – Sami Leon, 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

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 –	Maisa Maliha, Dickinson College

### 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 –	IND419, Introduction to Quantitative Biology (two to five lectures)
2016 – 2017	BST494/BST430, Statistical Computing (course designer and instructor)
2018 –	BST487, Seminar in Statistical Literature (topic supervisor)
2019, 2021, 2023	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)

### **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); <i>Chair Thesis Defense Committee</i>
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 – Abhinav Mittal (Biophysics, Structural & Computational Biology Ph.D. Program)  
2022 – Dakarai Esgdaille (Genetics, Development, and Stem Cells 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 Systems, Database, Epigenomics, F1000Research, Gene, Genome Biology, 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, 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 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.

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.

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.

## **Other Roles**

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; Percent 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<br>IEEE International Workshop on Genomic Signal Processing and Statistics,<br>Newport, RI |
| Sept 2008 | An Improved Gene Expression Barcode based on a Hierarchical Mixture Model<br>International Meeting of MGED, Riva del Garda, Italy                     |
| July 2009 | From a Single CEL File to a Gene Expression Barcode<br>Bioconductor Conference (BioC2009), Seattle, WA  |
| Mar 2010  | Gene Expression Barcodes<br>ENAR Spring Meeting, New Orleans, LA  |
| July 2011 | Thawing Frozen Robust Multi-array Analysis (fRMA)<br>Bioconductor Conference (BioC2011), Seattle, WA  |
| Aug 2011  | Assessing Microarray Quality<br>Joint Statistical Meeting, Miami Beach, FL  |
| Aug 2011  | A Computational Bayesian Approach for the Inference of Boolean Networks<br>Q-Bio Conference in Cellular Information Processing, Santa Fe, NM          |
| July 2012 | Batch effect reduction using the frma package<br>Bioconductor Conference (BioC2012), Seattle, WA  |
| Aug 2013  | Addressing Within-Subject Genomic Heterogeneity<br>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
- 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

### **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**

Sept 2008	EMERALD Workshop on Array Quality Assessment Methods International Meeting of MGED, Riva del Garda, Italy
Feb 2011	Frozen Robust Multi-array Analysis (fRMA) La Caestienne Meeting, Nismes, Belgium
Oct 2011	Microarray Preprocessing and Quality Control La Caestienne Meeting, Nismes, Belgium
Oct 2011	MicroRNA Microarray Performance Janssen Research and Development, Beerse, Belgium
Apr 2012	Batch Effects and Splice Variants La Caestienne Meeting, Nismes, Belgium
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 Caestienne Meeting, Nismes, Belgium
July 2013	A Computational Bayesian Approach to Gene Regulatory Network Estimation Bioconductor Conference (BioC2013), Seattle, WA
June 2015	Modeling qPCR Non-Detects as Missing Data qPCR and Digital PCR Congress: USA, San Diego, CA
Dec 2016	Incorporating Uncertainty in the Estimation of Gene Regulatory Networks University of Buffalo Biostatistics Seminar Series, Buffalo, NY
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
Mar 2018	How Amazing Mentors Think About Mentoring Center for the Integration of Research, Teaching and Learning, Webinar
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
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

**PUBLICATIONS**

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

**Peer-Reviewed Journal Articles****Methodological Research**

1. McMurray HR, Stern HA, Ambeskovic A, Land H, **McCall MN**<sup>°</sup> (2022). Protocol to use TopNet for gene regulatory network modeling using gene expression data from perturbation experiments. *STAR Protocols*, 3(4):101737.
2. Patil AH, **Baran A\***, **Brehm ZP\***, **McCall MN**<sup>°</sup>, Halushka MK<sup>†</sup> (2022). A curated human cellular microRNAome based on 196 primary cell types. *GigaScience*, 11.

3. **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<sup>†</sup>, Mariani TJ<sup>†</sup> (2021). A systems genomics approach uncovers molecular associates of RSV severity. *PLoS Computational Biology*, 17(12):e1009617.
4. McMurray HR, Ambeskovic A, Newman LA, Aldersley J, Balakrishnan V, Smith B, Stern HA, Land H<sup>†</sup>, **McCall MN<sup>†</sup>** (2021). Gene network modeling via TopNet reveals functional dependencies between diverse tumor-critical mediator genes. *Cell Reports*, 37(12):110136.
5. **Zhang Y\***, **Cuerdo J\***, Halushka MK, **McCall MN<sup>†</sup>** (2021). The effect of tissue composition on gene co-expression. *Briefings in Bioinformatics*, 22(1):127-139.
6. **Hsu B\***, **Sherina V\***, **McCall MN<sup>†</sup>** (2020). Autoregressive modeling and diagnostics for qPCR amplification. *Bioinformatics*, 36(22-23):5386-5391.
7. **Sherina V\***, McMurray HR, **Powers W\***, Land H, Love TMT, and **McCall MN<sup>†</sup>** (2020). Multiple imputation and direct estimation for qPCR data with non-detects. *BMC Bioinformatics*, 21:545.  
[ENAR Distinguished Student Paper Award to V. Sherina]
8. **Nassiri I\*** and **McCall MN<sup>†</sup>** (2018). Systematic exploration of cell morphological phenotypes associated with a transcriptomic query. *Nucleic Acids Research*, 46(19):e116.
9. Halushka MK<sup>†</sup>, Fromm B, Peterson KJ, **McCall MN<sup>†</sup>** (2018). Big Strides in Cellular MicroRNA Expression. *Trends in Genetics*, 34(3):165-167.
10. **McCall MN<sup>†</sup>**, 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<sup>†</sup> (2017). Toward the human cellular microRNAome. *Genome Research*, 27(10):1769-1781.
11. Li N, **McCall MN**, Wu Z<sup>†</sup> (2017). Establishing Informative Prior for Gene Expression Variance from Public Databases. *Statistics in Biosciences*, 9(1):160-177.
12. **McCall MN<sup>†</sup>**, Illei PB, Halushka MK<sup>†</sup> (2016). Complex Sources of Variation in Tissue Expression Data: Analysis of the GTEx Lung Transcriptome. *The American Journal of Human Genetics*, 99(3):624-635.
13. **Xie QY\***, Almudevar A, Whitney-Miller CL, Barry CT, **McCall MN<sup>†</sup>** (2016). A microRNA biomarker of hepatocellular carcinoma recurrence following liver transplantation accounting for within-patient heterogeneity. *BMC Medical Genomics*, 9(1):18.
14. **McCall MN<sup>†</sup>**, Baras AS, Crits-Christoph A, Ingersoll R, McAlexander MA, Witwer KW, Halushka MK (2016). A benchmark for microRNA quantification algorithms using the OpenArray platform. *BMC Bioinformatics*, 17(1):138.
15. Verbist BM, Verheyen GR, Vervoort L, Crabbe M, Beerens D, Bosmans C, Jaensch S, Osselaer S, Talloen W, Van den Wyngaert I, Van Hecke G, Wuyts D, **Qstar Consortium**, Van Goethem F, Gohlmann HW (2015). Integrating High-Dimensional Transcriptomics and Image Analysis Tools into Early Safety Screening: Proof of Concept for a New Early Drug Development Strategy, *Chemical Research in Toxicology*, 28(10):1914-25.
16. Verbist B, Klambauer G, Vervoort L, Talloen W, **Qstar Consortium**, Shkedy Z, Thas O, Bender A, Gohlmann HWH, Hochreiter S (2015). Using transcriptomics to guide lead optimization in drug discovery projects: Lessons learned from the QSTAR project, *Drug Discovery Today*, Volume 20, Issue 5, Pages 505-513.

17. Ravindranath AC, Perualila-Tan N, Kasim A, Drakakis G, Liggi S, Brewerton SC, Mason D, Bodkin MJ, Evans DA, Bhagwat A, Talloen W, Gohlmann HW, **Qstar Consortium**, Shkedy Z, Bender A (2015). Connecting gene expression data from connectivity map and in silico target predictions for small molecule mechanism-of-action analysis, *Molecular Biosystems*, 11(1):86-96.
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#### Pre-prints / Non-Peer-Reviewed Journal Articles

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7.

### **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

#### **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.