

UNIVERSITY OF ROCHESTER SCHOOL OF MEDICINE & DENTISTRY CURRICULUM VITAE

Matthew N. McCall, Ph.D.

265 Crittenden Boulevard, CU 420630

Rochester, New York 14642-0630

Telephone: 585-273-3177 | Fax: 585-273-1031

E-Mail: matthew_mccall@urmc.rochester.edu

Website: <https://www.urmc.rochester.edu/biostat/people/faculty/mccall.aspx>

Date of Birth: 01/08/1982

Citizenship: USA

CURRENT POSITIONS

Assistant Professor of Biostatistics & Computational Biology

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 School of Public Health, Baltimore, MD

2005 – 2010 Ph.D., Biostatistics, Johns Hopkins 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 – present Assistant Professor, Department of Biostatistics & Computational Biology, University of Rochester School of Medicine & Dentistry, Rochester, NY

2014 – present Assistant Professor, Department of Biomedical Genetics, University of Rochester School of Medicine & Dentistry, Rochester, NY

2015 – present Affiliated Faculty, The Goergen Institute for Data Science, University of Rochester, Rochester, NY

2017 – present Affiliated Faculty, Center for Biomedical Informatics, University of Rochester Medical Center, Rochester, NY

HONORS AND AWARDS

2004 Honors College Concentration in Statistics with Highest Distinction, University of Michigan

2004 Phi Beta Kappa, University of Michigan

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 School of Public Health

2007 – 2010 Trainee, NIH Training Grant in Biostatistics for Genetics/Genomics, Johns Hopkins School of Public Health

2008 Travel Award, International Meeting of the Microarray and Gene Expression Data Society

2009 & 2010 Teaching Assistant Recognition Award Nominee, Johns Hopkins School of Public Health

2010 Helen Abbey Award for Excellence in Teaching, Johns Hopkins School of Public Health

2010 – 2013	Trainee, NIH Training Grant in Experimental Therapy Models, University of Rochester School of Medicine & Dentistry
2011	Conference Fellowship, q-bio Conference on Cellular Information Processing
2011	Conference Scholarship, Bioconductor Conference (BioC2011)
2015	Graduate Student Society Advocacy Award, University of Rochester School of Medicine & Dentistry

ACADEMIC & PROFESSIONAL ORGANIZATIONS

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

COMMITTEES & OTHER ADMINISTRATIVE SERVICE

UR Department of Biostatistics & Computational Biology

2015 – present	Member, Bioinformatics Concentration Curriculum Committee
2015 – 2017	Chair, Biostatistics and Computational Biology Departmental Seminar Series
2016 – present	Member, Statistics Graduate Admissions Committee
2016 – present	Member, Biostatistics and Computational Biology Faculty Search Committee
2018 – present	Member, Biostatistics and Computational Biology Computing Committee

UR Extra-Departmental

2015 – 2016	Co-chair, Data Science Colloquium Series
2015 – 2018	Judge, Graduate Student Society Poster Competition
2016 – present	Member, CTSI Informatics Education Cluster
2017	Reviewer, University Research Awards
2017 – 2018	Member, Center for Biomedical Informatics and Wilmot Cancer Institute Faculty Search Committee

Local/Regional

2016	Session Chair, UP-STAT 2016 Conference
2018	Member, UP-STAT 2018 Organizing Committee
2018	Member, UP-STAT 2018 Data Analytics Committee
2018	Session Chair, UP-STAT 2018 Conference
2018	Judge, UP-STAT 2018 Conference Student Research Awards
2018	Reviewer, CTSI Novel Biostatistical and Epidemiologic Methodology pilot program

National

2012 – 2013	Judge, ASA/NCTM Statistical Project Competition
2016 – present	Member, Patient-Centered Outcomes Research Institute (PCORI) reviewer community
2017 – present	NIH Early Career Reviewer Program
2018	Reviewer, NIH Biodata Management and Analysis (BDMA) Study Section

EDUCATIONAL CONTRIBUTIONS

Research Mentoring

Postdoctoral Fellows

2014 – 2015	Qingyan Lilly Xie, Ph.D.; Primary Mentor
2016 – 2017	Isar Nassiri, Ph.D.; Primary Mentor

2017 – present Carol Fries Simpson, M.D.; Department of Pediatrics Dean’s Fellowship Secondary Mentor

Graduate Students

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

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 (summer) David Burton, Statistics Ph.D. Program
 2018 (summer) Zachary Brehm, 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

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 – present Benjamin Hsu, University of Rochester
 2017 – present Qidi Yang, University of Rochester
 2018 – present Oleg Demus, University of Rochester
 2018 – present Kailey Ferger, University of Rochester

High School Students

2017 (summer) Fatima Umar, Pittsford Schools
 2017 (summer) Raymond Feng, Pittsford Schools

Classroom Teaching

2012 BST520, Current Topics in Bioinformatics (developed and taught with Dr. Almudevar)
 2014 BST512, Advanced Bayesian Inference with an Emphasis on Computation (one lecture)
 2014 BST432, Introduction to Bioinformatics (one lecture)
 2014 – present 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 – present IND419, Introduction to Quantitative Biology (two to three lectures)
 2016 – 2017 BST494/BST430, Statistical Computing (course designer and instructor)

Short Courses & Workshops

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 – present	Rohith Palli (Biophysics, Structural & Computational Biology Ph.D. Program)
2017 – present	Adam Cornwell (Genetics, Development, and Stem Cells Ph.D. Program)
2017 – present	Derek Crowe (Genetics, Development, and Stem Cells Ph.D. Program)
2017	Adan Becerra (Epidemiology); <i>chair, Thesis Defense Committee</i>
2018 – present	Xiaolu Wei (Genetics, Development, and Stem Cells Ph.D. Program)
2018 – present	Matthew Turner (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, APJ Renal Physiology, Bioinformatics, Biometrics, Biotechniques, BMC Bioinformatics, BMC Cancer, BMC Genomics, BMC Medical Genomics, Cancer Informatics, Database, Epigenomics, F1000Research, Gene, 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, PLoS Computational Biology, PLoS Genetics, PLoS One, Proceedings of the National Academy of Sciences, Statistical Applications in Genetics and Molecular Biology, Scientific Reports, Statistics in Biosciences

Editorial Assignments

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

GRANTS & CONTRACTS

As Principal Investigator / Co-Principal Investigator

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 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.

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.

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 - 12/31/19; Percent Effort: 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 T32 ES007271 (PI: Thurston)

Training in Environmental Health Biostatistics

09/30/15 – 06/30/20

I am 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
- 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
- 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
- July 2012 Batch effect reduction using the frma package
Bioconductor Conference (BioC2012), 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
- 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

- 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

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 Calestienne Meeting, Nismes, Belgium
- Oct 2011 Microarray Preprocessing and Quality Control
La Calestienne Meeting, Nismes, Belgium
- Oct 2011 MicroRNA Microarray Performance
Janssen Research and Development, Beerse, Belgium
- Apr 2012 Batch Effects and Splice Variants
La Calestienne 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 Calestienne 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
Webinar organized by the Center for the Integration of Research, Teaching and Learning

PUBLICATIONS

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

Pre-prints

1. **Sherina V***, McMurray HR, **Powers W***, Land H, Love TMT, and **McCall MN^{†°}** (2017). Statistical Approaches to Decreasing the Discrepancy of Non-detects in qPCR Data. bioRxiv. doi: <http://dx.doi.org/10.1101/231621>
2. **Kemperman L*** and **McCall MN^{†°}** (2017). *miRcomp-Shiny*: Interactive assessment of qPCR-based microRNA quantification and quality control algorithms. F1000Research. 6:2046.
3. Wang YT, Lim Y, **McCall MN[°]**, Haynes CM, Nehrke KW, Brookes PS[†] (2018). Cardioprotection by the Mitochondrial Unfolded Protein Response is Mediated by ATF5. bioRxiv. doi: <https://doi.org/10.1101/344606>

Peer-Reviewed Journal Articles

1. **Nassiri I*** and **McCall MN^{†°}** (2018). Systematic exploration of cell morphological phenotypes associated with a transcriptomic query. Nucleic Acids Research. doi: <https://doi.org/10.1093/nar/gky626>
2. Rosenberg AZ, Wright C, Fox-Talbot K, Rajpurohit A, Williams C, Porter C, Kovbasnjuk O, **McCall MN[°]**, Shin JH, Halushka MK[†] (2018). xMD-miRNA-seq to generate near in vivo miRNA expression estimates in colon epithelial cells. Scientific Reports. 8(1):9783.
3. Hill MA, Alexander WB, Guo B, Kato Y, Patra KC, O'Dell MR, **McCall MN[°]**, Whitney-Miller CL, Bardeesy N, and Hezel AF[†] (2018). Kras and Tp53 mutations cause cholangiocyte- and hepatocyte-derived cholangiocarcinoma. Cancer Research. 78(16):4445-4451.
4. Halushka MK[†], Fromm B, Peterson KJ, **McCall MN[°]** (2018). Big Strides in Cellular MicroRNA Expression. Trends in Genetics. 34(3):165-167.
5. **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.
6. Li N, **McCall MN**, Wu Z^{†°} (2017). Establishing Informative Prior for Gene Expression Variance from Public Databases. Statistics in Biosciences. 9(1):160-177.
7. Komisarof J, **McCall MN[°]**, Newman L, Bshara W, Mohler JL, Morrison C, Land H[†] (2017). A Four Gene Signature Predictive of Recurrent Prostate Cancer. Oncotarget. 8(2):3430-3440.
8. **McCall MN^{†°}**, Illei PB, Halushka MK[†] (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.
9. **Xie QY***, Almudevar A, Whitney-Miller CL, Barry CT, **McCall MN^{†°}** (2016). A microRNA biomarker of hepatocellular carcinoma recurrence following liver transplantation accounting for within-patient heterogeneity. BMC Medical Genomics. 9(1):18.
10. **McCall MN^{†°}**, 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.
11. 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.
12. 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.
 13. 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.
 14. Kent O, **McCall MN**^o, Cornish T, Halushka MK[†] (2014). Lessons from miR-143/145: The importance of cell-type localization of miRNAs, *Nucleic Acids Research*, 42(12):7528-7538.
 15. **McCall MN**[†], McMurray H, Land H, Almudevar A^o (2014). On Non-Detects in qPCR Data, *Bioinformatics*, 30(16):2310-2316.
 16. Haider B, Baras AS, **McCall MN**^o, Hertel JA, Cornish TC, Halushka MK[†] (2014). A critical evaluation of microRNA biomarkers in non-neoplastic disease, *PLoS ONE*, 9(2): e89565.
 17. **McCall MN**^o, Jaffee HA, Zelisko SJ, Sinha N, Hooiveld G, Irizarry RA, Zilliox MJ[†] (2014). The Gene Expression Barcode 3.0: improved data processing and mining tools, *Nucleic Acids Research*, 42(D1):D938-D943.
 18. Tran V, **McCall MN**[†], McMurray H, Almudevar A^o (2013). On the underlying assumptions of threshold Boolean networks as a model for genetic regulatory network behavior, *Frontiers in Genetics*, 4:263.
 19. Wu G, Yustein JT, **McCall MN**, Zilliox M, Irizarry RA, Zeller K, Dang CV, Ji H^{†o} (2013). ChIP-PED enhances the analysis of ChIP-seq and ChIP-chip data, *Bioinformatics*, 29(9):1182-1189.
 20. **McCall MN**^{†o} (2013). Estimation of Gene Regulatory Networks, *Journal of Postdoctoral Research*, 1(1):60-69.
 21. Bravo HC^{†o}, Pihur V, **McCall MN**, Irizarry RA, Leek JT (2012). Gene expression anti-profiles as a basis for accurate universal cancer signatures, *BMC Bioinformatics*, 13:272.
 22. **McCall MN**[†], Jaffee HA, Irizarry RA^o (2012). fRMA ST: Frozen robust multiarray analysis for Affymetrix Exon and Gene ST arrays, *Bioinformatics*, 28 (23): 3153-3154.
 23. **McCall MN**[†] and Almudevar A^o (2012). Affymetrix GeneChip microarray preprocessing for multivariate analyses, *Briefings in Bioinformatics*, 13(5):536-546.
 24. Barry CT[†], D'Souza M, **McCall MN**, Safadjou S, Ryan C, Kashyap R, Marroquin C, Orloff M, Almudevar A^o, Godfrey TE (2012). Micro RNA expression profiles as adjunctive data to assess the risk of hepatocellular carcinoma recurrence after liver transplantation, *American Journal of Transplantation*, 12(2):428-437.
 25. **McCall MN**^o, Kent OA, Yu J, Fox-Talbot K, Zaiman AL, Halushka MK[†] (2011). MicroRNA profiling of diverse endothelial cell types, *BMC Medical Genomics*, 4:78.
 26. Almudevar A^{†o}, **McCall MN**, McMurray H, Land H (2011). Fitting Boolean Networks from Steady State Perturbation Data, *Statistical Applications in Genetics and Molecular Biology*, 10(1): Article 47.
 27. **McCall MN** and Irizarry RA^{†o} (2011). Thawing Frozen Robust Multi-array Analysis (fRMA), *BMC Bioinformatics*, 12:369.
 28. **McCall MN**, Murakami PN, Lukk M, Huber W, Irizarry RA^{†o} (2011). Assessing Affymetrix GeneChip Microarray Quality, *BMC Bioinformatics*, 12:137.
 29. **McCall MN**, Uppal K, Jaffee HA, Zilliox MJ[†], and Irizarry RA^{†o} (2011). The Gene Expression Barcode: leveraging public data repositories to begin cataloging the human and murine transcriptomes, *Nucleic Acids Research*, 39:D1011-5.
 30. Shi L[†], Campbell G, Jones WD, ..., **McCall MN**, ..., Scherf U, Tong W, Wolfinger RD; MAQC Consortium (2010). The MicroArray Quality Control (MAQC)-II study of common practices for the

development and validation of microarray-based predictive models, *Nature Biotechnology*, 28(8):827-38.

31. **McCall MN**, Bolstad BM, and Irizarry RA[†] (2010). Frozen Robust Multi-Array Analysis (fRMA), *Biostatistics*, 11(2):242-253.
32. Sah S, **McCall MN**, Eveleigh D, Wilson M, and Irizarry RA[†] (2010). Performance Evaluation of Commercial miRNA Expression Array Platforms, *BMC Research Notes*, 3:80.
33. **McCall MN** and Irizarry RA[†] (2008). Consolidated strategy for the analysis of microarray spike-in data, *Nucleic Acids Research*, 36(17), e108.

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.