UNIVERSITY OF ROCHESTER SCHOOL OF MEDICINE & DENTISTRY CURRICULUM VITAE

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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; *currently Data Scientist Consultant, Massachusetts General Hospital* |
| 2016 – 2017 | Isar Nassiri, Ph.D.; Primary Mentor; *currently Bioinformatician, University of Oxford* |

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;
     currently Business Analytics Associate at Management Science Associates, Inc.
2015 – 2017   Lauren Kemperman, University of Rochester;
     currently Data Scientist at Sikorsky Aircraft
2015 – 2017   Jeffrey Hrebenach, University of Rochester;
     currently Software Development Engineer at Amazon
2016 (summer)   Alida Mooney, State University of New York at Geneseo
2016 – 2017   Winslow Powers, University of Rochester;
     currently Bioinformatics Analyst at Dana Farber Cancer Center
2016 – 2018   Jonavelle Cuerdo, University of Rochester
2017 – present   Benjamin Hsu, University of Rochester
2017 – present   Qidi Yang, 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); *chair, Thesis Defense Committee*

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 Phsiology, 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
09/01/2017 – 08/30/2022; 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

12/13/2011 – 12/12/2018; 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
09/30/2015 – 06/30/2020
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

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   Harnassing 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 Approches 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. doi: 10.1158/0008-5472.CAN-17-1123.

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**°, 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° (2014). On Non-Detects in qPCR Data, Bioinformatics, 30(16):2310-2316.

16. Haider B, Baras AS, **McCall MN**°, 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**°, 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° (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[†]° (2013). ChIP-PED enhances the analysis of ChIP-seq and ChIP-chip data, Bioinformatics, 29(9):1182-1189.

20. **McCall MN**[†]° (2013). Estimation of Gene Regulatory Networks, Journal of Postdoctoral Research, 1(1):60-69.

21. Bravo HC[†]°, 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° (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° (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°, 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**°, 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[†]°, **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[†]° (2011). Thawing Frozen Robust Multi-array Analysis (fRMA), BMC Bioinformatics, 12:369.

28. **McCall MN**, Murakami PN, Lukk M, Huber W, Irizarry RA[†]° (2011). Assessing Affymetrix GeneChip Microarray Quality, BMC Bioinformatics, 12:137.

29.   **McCall MN**, Uppal K, Jaffee HA, Zilliox MJ[†], and Irizarry RA[†°] (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.