

UNIVERSITY OF ROCHESTER SCHOOL OF MEDICINE & DENTISTRY CURRICULUM VITAE

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Date of Birth: 01/08/1982

Citizenship: USA

CURRENT POSITIONS

Associate 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 – 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 – present Associate Professor, Department of Biostatistics & Computational Biology, University of Rochester School of Medicine & Dentistry, Rochester, NY

2019 – present Associate 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

2018 – present Member, Environmental Health Sciences Center, 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,

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| 2008 | Johns Hopkins School of Public Health 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

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|----------------|--|
| 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 – 2018 | Member, Biostatistics and Computational Biology Faculty Search Committee |
| 2018 – present | Member, Biostatistics and Computational Biology Computing Committee |
| 2018 – present | Member, Biostatistics and Computational Biology Curriculum Committee |
| 2019 – present | Member, Internal Advisory Board / Executive Committee for NIH T32 ES007271 |

UR Extra-Departmental

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| 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 | Reviewer, University Research Awards |
| 2019 | Reviewer, SAC Incubator Awards |
| 2019 | Reviewer, UNYTE Pipeline-to-Pilot Program |
| 2017 – present | Member, Center for Biomedical Informatics and Wilmot Cancer Institute Faculty Search Committee |
| 2018 – present | Member, Biomedical Informatics Curriculum Committee |
| 2019 – present | Member, Bioinformatics Working Group Planning Committee |
| 2019 – present | Participant, Driving our Future: Culture, Climate and Leadership in the Sciences |
| 2019 – present | Member, Wilmot Cancer Institute Scientific Leadership Committee |
| 2019 – present | Co-director, Wilmot Cancer Institute Biostatistics and Bioinformatics Shared Resource |

Local/Regional

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| 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

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|----------------|---|
| 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 – 2019 | Reviewer, CTSI Novel Biostatistical and Epidemiologic Methodology pilot program |
| 2018 | Reviewer, NIH Biodata Management and Analysis (BDMA) Study Section |
| 2018 – 2019 | Member, Bioconductor Conference (BioC2019) Organizing Committee |
| 2019 | Invited Session Organizer, Symposium on Data Science & Statistics |
| 2019 – 2020 | Member, Bioconductor Conference (BioC2020) Organizing Committee |

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

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|----------------|---|
| 2015 – 2019 | Valeriia Sherina, Statistics Ph.D. Program; Thesis Advisor (co-advisor: Dr. Tanzy Love) |
| 2018 – present | David Burton, Statistics Ph.D. Program |
| 2018 – present | Zachary Brehm, Statistics Ph.D. Program |

Graduate Research Assistants

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|---------------|--|
| 2015 – 2018 | Yun Zhang, Statistics Ph.D. Program |
| 2016 (fall) | Kejia Wang, Statistics M.A. Program |
| 2017 (summer) | Jeremiah Jones, Statistics Ph.D. Program |
| 2019 (summer) | Erik Vonkaenel, Statistics Ph.D. Program |
| 2019 (fall) | Bokai Wang, Statistics Ph.D. Program |

Rotation Students

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|---------------|---|
| 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 |

Undergraduate Students

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|----------------|---|
| 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 | Jonaville 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 – present | Yuewei Fei, University of Rochester |

2019 – present Daniel Munoz Huerta, University of Rochester
2019 – present Michael Lansford, University of Rochester

High School Students

2017 (summer) Fatima Umar, Pittsford Schools
2017 (summer) Raymond Feng, Pittsford Schools
2019 (summer) Lillian Stolberg, 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 – 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 – present IND419, Introduction to Quantitative Biology (two to three lectures)
2016 – 2017 BST494/BST430, Statistical Computing (course designer and instructor)
2018 – present BST487, Seminar in Statistical Literature (topic supervisor)
2019 BST494, Genomic Data Analysis (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 Ph.D. Program); *chair, Thesis Defense Committee*
2018 – present 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 – present Jiatong Sui (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, APJ Renal Physiology, Bioinformatics, Biometrics, Biotechniques, biOverlay, 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, Science, Scientific Reports, Statistical Applications in Genetics and Molecular Biology, 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.

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.

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 U54 CA228110 (PI: Rahman)

WNY Center for Research on Flavored Tobacco Products

09/01/2018 – 06/30/2023; Percent Effort: 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 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

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| 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

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| 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 |

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| Sept 2014 | Transcriptomics and Integrated Genomics Meeting, Rochester, NY On Non-Detects in qPCR Data |
| Mar 2015 | Transcriptomics and Integrated Genomics Meeting, Rochester, NY Overview of McCall Group Research |
| Apr 2015 | Transcriptomics and Integrated Genomics Meeting, Rochester, NY Incorporating Uncertainty in the Estimation of Gene Regulatory Networks |
| Apr 2015 | Center for Integrated Research Computing Symposium Series, Rochester, NY Challenges in Translational Genomics |
| Dec 2015 | Workshop sponsored by the Graduate Student Society, Rochester, NY Mechanics of RNA-Seq Data Analysis Using R |
| Oct 2016 | Workshop sponsored by the Center for Professional Development, Rochester, NY Sources of Variation in GTEx Lung Tissue Expression Data |
| Jan 2017 | Lung Biology Research Seminar Series, Rochester, NY Incorporating Uncertainty in the Estimation of Gene Regulatory Networks |
| Mar 2017 | Bioinformatics Cluster, Rochester, NY Sources and Effects of Transcriptomic Heterogeneity |
| Dec 2017 | Center for Biomedical Informatics, Rochester, NY What can we learn from co-expression analyses? |
| Feb 2019 | Transcriptomics and Integrated Genomics Meeting, Rochester, NY Co-expression analysis of complex tissues PhD Applicant Weekend, Rochester, NY |

Invited Presentations: National & International

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| 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 Webinar organized by the Center for the Integration of Research, Teaching and Learning |
| May 2019 | Case Studies in Interoperability: From Generic Classes To Specific Functions Symposium on Data Science & Statistics, Bellevue, WA |

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>
[ENAR Distinguished Student Paper Award to V. Sherina]
2. **Kemperman L*** and **McCall MN^{†°}** (2017). *miRcomp-Shiny*: Interactive assessment of qPCR-based microRNA quantification and quality control algorithms. F1000Research. 6:2046.
3. **Zhang Y***, **Cuerdo J***, Halushka MK, **McCall MN^{†°}** (2018). The effect of tissue composition on gene co-expression. bioRxiv. doi: <https://doi.org/10.1101/492223>
4. Nieuwenhuis TO, Yang S, Pillalamarri V, Arking D, Rosenberg AZ, **McCall MN[°]**, Halushka MK[†] (2019). Basal Contamination of Bulk Sequencing: Lessons from the GTEx dataset. bioRxiv. doi: <https://doi.org/10.1101/602367>
5. Wang L, Chu CY, **McCall MN**, Slaunwhite C, Holden-Wiltse J, Corbett A, Falsey AR, Topham DJ, Caserta MT, Mariani TJ, Walsh EE, and Qiu X (2019). Airway Gene-Expression Classifiers for Respiratory Syncytial Virus (RSV) Disease Severity in Infants. bioRxiv. doi: <https://doi.org/10.1101/628701>
6. Chu CY, Qiu X, **McCall MN**, Wang L, Corbett A, Holden-Wiltse J, Slaunwhite C, Wang Q, Anderson C, Grier A, Gill SR, Pryhuber GS, Falsey AR, Topham DJ, Caserta MT, Walsh EE, Mariani TJ (2019). Insufficiency in airway interferon activation defines clinical severity to infant RSV infection. bioRxiv. doi: <https://doi.org/10.1101/641795>
7. **Hsu B***, **Sherina V***, **McCall MN^{†°}** (2019). Auto-regressive modeling and diagnostics for qPCR amplification. bioRxiv. doi: <https://doi.org/10.1101/665596>

Peer-Reviewed Journal Articles

1. Wang YT, Lim Y, **McCall MN[°]**, Huang KT, Haynes CM, Nehrke KW, Brookes PS[†] (2019). Cardioprotection by the mitochondrial unfolded protein response requires ATF5. American Journal of Physiology-Heart and Circulatory Physiology, 317(2):H472-H478.
2. Walsh EE[†], Mariani TJ, Chu C, Grier A, Gill SR, Qiu X, Wang L, Jeanne HW, Corbett A, Thakar J, Benoodt L, **McCall MN**, Topham DJ, Falsey AR, Caserta MT (2019). Aims, study design and enrollment results from the Assessing Predictors of Infant Respiratory Syncytial Virus Effects and Severity (AsPIRES) study. JMIR Research Protocols, 8(6):e12907.
3. Spinelli P, Latchney SE, Reed JM, Fields A, Baier BS, **Lu X***, **McCall MN[°]**, Murphy SP, Mak W, Susiarjo M[†] (2018). Identification of the novel Idol imprinted locus and its potential epigenetic role in pregnancy loss. Human Molecular Genetics, 28(4):662-674.
4. **Nassiri I*** and **McCall MN^{†°}** (2018). Systematic exploration of cell morphological phenotypes associated with a transcriptomic query. Nucleic Acids Research, 46(19):e116.
5. 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.
6. 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.
7. Halushka MK[†], Fromm B, Peterson KJ, **McCall MN[°]** (2018). Big Strides in Cellular MicroRNA Expression. Trends in Genetics. 34(3):165-167.

8. **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.
9. Li N, **McCall MN**, Wu Z^{†°} (2017). Establishing Informative Prior for Gene Expression Variance from Public Databases. *Statistics in Biosciences*. 9(1):160-177.
10. 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.
11. **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.
12. **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.
13. **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.
14. 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.
15. 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.
16. 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.
17. 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.
18. **McCall MN**[†], McMurray H, Land H, Almudevar A[°] (2014). On Non-Detects in qPCR Data, *Bioinformatics*, 30(16):2310-2316.
19. 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.
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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.