

CURRICULUM VITAE**Eric F. Lock, Ph.D.**Website: <http://ericfrazierlock.com/>**IDENTIFYING INFORMATION****Academic Rank**

Tenured Associate Professor of Biostatistics

Education

Degree	Institution	Date Degree Granted
B.A.	Hamilton College Mathematics	2006
Ph.D.	University of North Carolina Statistics Advisors: Andrew B. Nobel and J.S. Marron	2012

Positions/Employment

University of Minnesota, Twin Cities

Associate Professor 2020-present

Assistant Professor 2014-2020

Duke University

Postdoctoral Associate 2012-2014

Current Membership in Professional Organizations

Delta Omega Honorary Society in Public Health

Sigma Xi

Phi Beta Kappa

American Statistical Association (ASA)

Institute of Mathematical Statistics (IMS)

International Biometric Society, Eastern North America Region (ENAR)

Society for Industrial and Applied Mathematics (SIAM)

HONORS AND AWARDS FOR RESEARCH/CREATIVE WORK, TEACHING, PUBLIC ENGAGEMENT, AND SERVICE

Delta Omega Honorary Society in Public Health, Spring 2019

Teaching Award, UNC Department of Statistics and Operations Research, Fall 2011

Wassily Hoeffding Award, Outstanding First Year Student in Statistics, UNC, Fall 2008

Sigma Xi Inductee, Spring 2006

Phi Beta Kappa Inductee, Spring 2006

Huntington Memorial Mathematical Prize Scholarship, Hamilton College, Fall 2005

Deans List (Spring 2003, Fall 2003, Spring 2004, Fall 2004, Fall 2005, Spring 2006)

Top Senior, Pi Mu Epsilon regional high school mathematics competition, Spring 2002

RESEARCH, SCHOLARSHIP, AND CREATIVE WORK

Publications

§ = mentored or supervised student author

* = senior or corresponding author

Refereed Journal Articles

1. §CT Rohloff, N Kohli, **EF Lock**. Identifiability and estimability of Bayesian linear and nonlinear crossed random effects models. *British Journal of Mathematical and Statistical Psychology*, doi: 10.1111/bmsp.12334, 2024.
2. BJ Sandri, §J Kim, GR Lubach, **EF Lock**, E Ennis-Czerniak, PJ Kling, MK Georgieff, CL Coe, RB Rao. Prognostic Performance of Hematological and Serum Iron and Metabolite Indices for Detection of Early Iron Deficiency Induced Metabolic Brain Dysfunction in Infant Rhesus Monkey. *The Journal of Nutrition*, doi: 10.1016/j.tjnut.2023.10.031, 2023.
3. §J Wang, ***EF Lock**. Multiple Augmented Reduced Rank Regression for Pan-Cancer Analysis. *Biometrics*, 80 (1): ujad002, 2024.
4. B Sandri, K Ennis-Czerniak, P Kanajam, W Frey, **EF Lock**, R Rao. Intranasal Insulin Treatment Partially Corrects the Altered Gene Expression Profile in the Hippocampus of Developing Rats with Perinatal Iron Deficiency. *American Journal of Physiology-Regulatory, Integrative and Comparative Physiology*, 325 (4): R423-R432, 2023.
5. WJ Bosl, MB Enlow, **EF Lock**, CA Nelson. A biomarker discovery framework for childhood anxiety. *Frontiers in Psychiatry*, 14: 1158569, 2023.
6. AK Baldomero, DM MacDonald, §A Kaplan, **EF Lock**, MH Cho, R Bowler, L Gillenwater, KM Kunisaki, CH Wendt. Bilirubin-associated single nucleotide

polymorphism (SNP) and respiratory health outcomes: a Mendelian randomization study. *Respiratory Research*, 24: 190, 2023.

7. §J Kim, BJ Sandri, RB Rao, *EF Lock. Bayesian predictive modeling of multi-source multi-way data. *Computational Statistics and Data Analysis*, 186: 107783, 2023.
8. KA Peterson, CS Carlin, LI Solberg, §J Normington, EF Lock. Care Management Processes Important for High Quality Diabetes Care. *Diabetes Care*, 46 (10):1762–1769, 2023.
9. Y Peralta, N Kohli, P Kendeou, ML Davison, EF Lock. Modeling the Interrelation of Reading and Mathematics Achievement Trajectories: Is their Development Intertwined? *Reading and Writing*, doi: 10.1007/s11145-023-10442-2, 2023.
10. DM MacDonald, §S Samorodnitsky, CH Wendt, JV Baker, G Collins, M Kruk, EF Lock, R Paredes, S Poongulali, DO Weise, A Winston, R Wood, KM Kunisaki. Pneumoproteins and biomarkers of inflammation and coagulation do not predict rapid lung function decline in people living with HIV. *Scientific Reports*, 13: 4749, 2023.
11. §S Samorodnitsky, EF Lock, M Kruk, A Morris, JM Leung, KM Kunisaki, TJ Griffin, CH Wendt. Lung proteome and metabolome endotype in HIV-associated obstructive lung disease. *ERJ Open Research*, 9 (2), 2023.
12. RB Rao, G Lubach, K Ennis-Czerniak, EF Lock, P Kling, MK Georgieff, C Coe. Reticulocyte Hemoglobin Equivalent has Comparable Predictive Accuracy as Conventional Serum Iron Indices for Predicting Iron Deficiency and Anemia in a Nonhuman Primate Model of Infantile Iron Deficiency. *Journal of Nutrition*, 153 (1):148-157, 2023.
13. §B Guo, LE Eberly, PG Henry, C Lenglet, and *EF Lock. Multiway sparse distance weighted discrimination. *Journal of Computational and Graphical Statistics*, 32 (2): 730-743, 2023.
14. B Sandri, §J Kim, G Lunach, EF Lock, C Guerrero, L Higgings, T Markowski, P Kling, M Georgieff, C Coe, R Rao. Tandem mass tag proteomic and untargeted metabolomic profiling reveals altered serum and CSF biochemical datasets in iron deficient monkeys. *Data in Brief*, 45: 108591, 2022.
15. CH Wendt, §S Samorodnitsky, EF Lock, M Kruk, A Morris, JM Leung, KM Kunisaki, TJ Griffin. The lung and plasma metabolome in HIV-associated obstructive lung disease. *Journal of Acquired Immune Deficiency Syndrome*, 91(3):312-318, 2022.
16. §EF Palzer, C Wendt, R Bowler, CP Hersh, SE Safo, and *EF Lock. sJIVE: Supervised joint and individual variation explained. *Computational Statistics and Data Analysis*, 175: 107547, 2022.
17. §S Samorodnitsky, KA Hoadley, and *EF Lock. A Hierarchical Spike-and-Slab Model for Pan-Cancer Survival Using Pan-Omic Data. *BMC Bioinformatics*, 23: 235, 2022.
18. N Georgiou-Karistianis, LA Corben, K Reetz, IM Adanyeguh, M Corti, DK Deelchand, MB Delatycki, I Dogan, R Evans, J Farmer, MC França, W Gaetz, IH Harding, KS

- Harris, S Hersch, R Joules, JJ Joers, ML Krishnan, M Lax, **EF Lock**, D Lynch, T Mareci, SM Gamage, M Pandolfo, M Papoutsis, T Rezende, TPL Roberts, JT Rosenberg, S Romanzetti, JB Schulz, T Schilling, A Schwarz, S Subramony, B Yao, S Zicha, C Lenglet, and PG Henry. A natural history study to track brain and spinal cord changes in individuals with Friedreich's ataxia: TRACK-FA study protocol. *Plos One*, 17 (11): e0269649, 2022.
19. **EF Lock**. Bayesian Distance Weighted Discrimination. *Journal of Computational and Graphical Statistics*, 31 (4): 1177-1188, 2022.
 20. S Priya, MB Burns, T Ward, RAT Mars, B Adamowicz, **EF Lock**, PC Kashyap, D Knights, R Blekhman. Shared and disease-specific host gene-microbiome associations across human diseases. *Nature Microbiology*, 7: 780-795, 2022.
 21. B Sandri, SJ Kim, G Lunach, **EF Lock**, C Guerrero, L Higgings, T Markowski, P Kling, M Georgieff, C Coe, R Rao. Multiomic Profiling of Iron Deficient Infant Monkeys Reveals Alterations in Neurologically Important Biochemicals in Serum and CSF Prior to the Onset of Anemia. *American Journal of Physiology-Regulatory, Integrative and Comparative Physiology*, 322 (6): R486-500, 2022.
 22. **EF Lock**, SJ Park, and KA Hoadley. Bidimensional linked matrix factorization for pan-omics pan-cancer analysis. *Annals of Applied Statistics*, 16 (1): 193-215, 2022.
 23. SJ Normington, **EF Lock**, TA Murray, CS Carlin. Bayesian variable selection in hierarchical difference-in-differences models. *Statistical Methods in Medical Research*, 31 (1): 169-183, 2022.
 24. SY Peralta, N Kohli, **EF Lock**, ML Davison. Bayesian modeling of associations in bivariate piecewise linear mixed-effects models. *Psychological Methods*, 27 (1): 44-64, 2022.
 25. **EF Lock**, and D Bandopadhyay. Bayesian nonparametric multiway regression for clustered binomial data. *Stat*, 10 (1): e378, 2021.
 26. BJ Sandri, GR Lubach, **EF Lock**, PJ Kling, MK Georgieff, CL Coe, RB Rao. Correcting Iron Deficiency Anemia with Iron Dextran Alters the Serum Metabolomic Profile of the Infant Rhesus Monkey. *American Journal of Clinical Nutrition*, 113 (4): 915-923, 2021.
 27. AM Siddappa, GM Quiggle, **EF Lock**, and RB Rao. Predictors of severe intraventricular hemorrhage in preterm infants under 29-weeks gestation. *Journal of Maternal and Fetal Neonatal Medicine*, 34(2): 195-200, 2021.
 28. DJ Beisang, K Smith, A Gilbertson, A Bunyemov, J Herrera, **EF Lock**, E Racila, C Forster, CA Henke, and PB Bitterman. Single-cell sequencing identifies pathogenic mesenchymal progenitor cells in the IPF lung. *Scientific Reports*, 10:11162, 2020.
 29. SS Samorodnitsky, KA Hoadley, and ***EF Lock**. A Pan-Cancer and Polygenic Bayesian Hierarchical Model for the Effect of Somatic Mutations on Survival. *Cancer Informatics*, 19:1176935120907399, 2020.

30. BJ Sandri, GR Lubach, **EF Lock**, MK Georgieff, PJ King, CL Coe, and RB Rao. Early-Life Iron Deficiency and Its Natural Resolution Are Associated with Altered Serum Metabolomic Profiles in Infant Rhesus Monkeys, *The Journal of Nutrition*, 150 (4): 685–693, 2020.
31. §J Park and ***EF Lock**. Integrative Factorization of Bidimensionally Linked Matrices. *Biometrics*, 76(1): 61-74, 2020.
32. §A Kaplan, ***EF Lock**, and M Fiecas. Bayesian GWAS with structured and non-local priors. *Bioinformatics*, 76 (1): 17-25, 2020.
33. §H Zhu, G Li, and **EF Lock**. Generalized Integrative Principal Component Analysis for Multi-Type Data with Block-Wise Missing Structure. *Biostatistics*, 21(2): 302-318, 2020.
34. §J Normington, **EF Lock**, C Carlin, K Peterson, and BP Carlin. A Bayesian difference-in-difference framework for the impact of primary care redesign on diabetes outcomes. *Statistics in Public Policy*, 6 (1): 55-66, 2019.
35. §MJ O’Connell and ***EF Lock**. Linked Matrix Factorization. *Biometrics*, 75(2): 582-592, 2018.
36. **EF Lock**. Tensor-on-tensor regression. *Journal of Computational and Graphical Statistics*, 27(3): 638-647, 2018.
37. **EF Lock**, N Kohli, and §M Bose. Detecting Multiple Random Changepoints in Bayesian Piecewise Growth Mixture Models. *Psychometrika*, 83(3), 733-750, 2018.
38. BJ Sandri, §A Kaplan, SW Hodgson, M Peterson, S Avdulov, LA Higgins, T Markowski, P Yang, AH Limper, TJ Griffin, P Bitterman, **EF Lock**, and CH Wendt. Multi-Omic Molecular Profiling of Lung Cancer Risk in Chronic Obstructive Pulmonary Disease. *European Respiratory Journal*, 52(1): 1702665, 2018.
39. **EF Lock** and G Li. Supervised multiway factorization. *Electronic Journal of Statistics*, 12 (1): 1150-1180, 2018.
40. R Rao, K Ennis, G Lubach, **EF Lock**, M Georgieff, and C Coe. Metabolomic Analysis of CSF Indicates Brain Metabolic Impairment Precedes Hematological Indices of Anemia in the Iron-Deficient Infant Monkey. *Nutritional Neuroscience*, 21(1): 40-48, 2018.
41. §A Kaplan and ***EF Lock**. Prediction with Dimension Reduction of Multiple Molecular Data Sources for Patient Survival. *Cancer Informatics*, 16: 1-11, 2017.
42. §T Lyu, ***EF Lock**, and LE Eberly. Discriminating sample groups with multi-way data. *Biostatistics*, 18 (3): 434-450, 2017.
43. **EF Lock** and DB Dunson. Bayesian Genome- and Epigenome-wide Association Studies with Gene-Level Dependence. *Biometrics*, 73 (3): 1018-1028, 2017.
44. §MJ O’Connell and ***EF Lock**. R.JIVE for exploration of multi-source molecular data. *Bioinformatics*, 32(18): 2877-2879, 2016.

45. **EF Lock** and DB Dunson. Shared kernel Bayesian screening. *Biometrika*, 102 (4): 829-842, 2015.
46. **EF Lock**, CA Markunas, K Soldano, H Cope, G Grant, H Fuchs, DB Dunson, SG Gregory and AE Ashley-Koch. Joint eQTL Assessment of Whole Blood and Dura Mater Tissue from Individuals with Chiari Type I Malformation. *BMC Genomics*, 16(1):11, 2015.
47. J Kuligowski, D Perez-Guaita, A Sánchez-Illana, Z Leon, M De La Guardia, M Vento, **EF Lock**, and G Quintas. Multi-source metabolomic data analysis using Joint and Individual Variation Explained (JIVE). *Analyst*, 140 (13): 4521-4529, 2015.
48. MS McKinney, AW Beaven, A Moffitt, JL Smith, **EF Lock**, D Jima, J Healy, G Li, A Greenough, CL Love, XY Yang, DB Dunson, HK Lysterly, L Bernal-Mizrachi, RD Gascoyne, S Dave. *Blood*, 124 (21) 271, 2014.
49. CA Markunas, **EF Lock**, CC Ding, K Soldano, H Cope, DS Enterline, G Grant, H Fuchs, AE Ashley-Koch, and SG Gregory. Identification of Chiari Type I Malformation subtypes using whole genome expression profiles and cranial base morphometrics. *BMC Medical Genomics*, 7(1): 39, 2014.
50. J Zhang, D Jima, Q Liu, A Moffitt, M Czader, Y Fedoriw, K Richards, Z Sun, C Love, P Scotland, **EF Lock**, S Levy, DB Dunson, and S Dave. The genomic landscape of mantle cell lymphoma is related to the epigenetically determined chromatin state of normal B cells. *Blood*, 123(19): 2988-2996, 2014.
51. **EF Lock** and DB Dunson. Bayesian consensus clustering. *Bioinformatics*, 29 (20): 2610-2616, 2013.
52. **EF Lock**, KA Hoadley, JS Marron, and AB Nobel. Joint and Individual Variation Explained (JIVE) for integrated analysis of multiple datatypes. *Annals of Applied Statistics*, 7(1): 523-542, 2013.
53. DM Reif, M Sypa, **EF Lock**, FA Wright, A Wilson, T Cathey, RR Judson, and I Rusyn. ToxPi GUI: An interactive visualization tool for transparent integration of data from diverse sources of evidence. *Bioinformatics*, 29(3): 402-403, 2013.
54. **EF Lock**, N Abdo, O Kosyk, SH OShae, R Huang, M Xia, YH Zhou, A Sedykh, A Tropsha, CP Austin, RR Tice, FA Wright, and I Rusyn. Quantitative high-throughput screening for chemical toxicity in a population-based in vitro model. *Toxicological Sciences*, 126(2):578-588, 2012.
55. BU Bradford, **EF Lock**, O Kosyk, S Kim, T Uehara, D Harbourt, M DeSimone, DW Threadgill, V Tryndyak, IP Pogribny, L Bleyly, DR Koop, and I Rusyn. Inter-strain differences in the liver effects of trichloroethylene in a multi-strain panel of inbred mice. *Toxicological Sciences*, 120(1), 2010.
56. **EF Lock**, R Ziemiecki, D Dittmer, and JS Marron. Efficiency clustering for low-density microarrays and its application to QPCR. *BMC Bioinformatics*, 11:386, 2010.

57. S Yeo, J Cisewski, **EF Lock**, and JS Marron. Exploratory analysis of exercise adherence patterns with sedentary pregnant women. *Nursing Research*, 59(4): 280-287, 2010.
58. RM Frongillo, **EF Lock**, and DM Brown. Symmetric fractal trees in three dimensions. *Chaos, Solitons & Fractals*, 32(2): 284-295, 2007.

Invited discussion articles

1. **EF Lock**, AB Nobel, and JS Marron. Comment: Population Value Decomposition, a framework for the analysis of image populations. *Journal of the American Statistical Association*, 106(495), 2011.

Book Chapters

1. **EF Lock** and AB Nobel. Exploratory methods to integrate multisource data. In GC Tseng, D Ghosh & XJ Zhou (Eds), *Integrating Omics Data*, pp. 242-268. Cambridge University Press, Cambridge, UK. 2015.

Books or Monographs

1. RH Lock, PF Lock, KL Morgan, **EF Lock**, and DF Lock. Statistics: Unlocking the Power of Data, 3rd Edition. John Wiley & Sons, Hoboken, NJ, 2020.
2. RH Lock, PF Lock, KL Morgan, **EF Lock**, and DF Lock. Statistics: Unlocking the Power of Data, 2nd Edition. John Wiley & Sons, Hoboken, NJ, 2017.
3. RH Lock, PF Lock, KL Morgan, **EF Lock**, and DF Lock. Statistics: Unlocking the Power of Data. John Wiley & Sons, Hoboken, NJ, 2012.

Grants and Contracts

Current

1. **Title:** Tensor Array Methods for RNA-Seq Analysis
Source: NIH NHGRI R01
Role: UMN Subcontract Principal Investigator
PI: Gen Li (University of Michigan)
Period: 2020-2025
Effort: 11% annual FTE
Subcontract award: \$250,000
2. **Title:** Identifying Biomarkers from Multi-Source, Multi-Way Data
Source: NIH NIGMS R01
Role: Principal Investigator
Period: 2019-2024
Effort: 40% annual FTE (5% in 2024)
Award: \$1,000,000
3. **Title:** Human Microbiome Compendium: large-scale curation and processing of human microbiome datasets
Source: NIH NLM R01

Role: UMN Subcontract Principal Investigator

PI: Ran Blekhman (University of Chicago)

Period: 2022-2025

Effort: 5% annual FTE

Subcontract Award: \$81,000/YR

4. **Title:** Comprehensive Proteomic Classifier for the Molecular Characterization of Pulmonary Sarcoidosis
Source: NIH NHLBI R01
Role: Co-Investigator
PI: Maneesh Bhargava (UMN)
Period: 2021-2025
Effort: 5% annual FTE
Award: \$3,905,293
5. **Title:** TRACK FA: Multi-site natural history study in Friedreich's Ataxia
Source: Friedreich's Ataxia Research Alliance
Role: Co-Investigator
PI: Pierre-Gilles Henry (UMN)
Period: 2021-2025
Effort: 16% annual FTE
Award: \$1,749,077
6. **Title:** Milk-Omics: Systems Biology of Human Milk and Its Links to Maternal and Infant Health
Source: NIH NICHD R01
Role: Co-investigator
PIs: Ellen Demerath (UMN)
Period: 2022-2026
Effort: 10% annual FTE
Award: \$732,226.00 (YR 1)
7. **Title:** Multi-Omics Multimodal longitudinal imaging of brain and cervical cord as an ALS disease biomarker using microstructure statistics and morphometry.
Source: DHHS Food & Drug Administration (FDA)
Role: Co-investigator
PIs: Pramod Pisharady (UMN)
Period: 2023-2027
Effort: 5% annual FTE
Award: \$1,599,721.00

Completed

1. **Title:** Sphingolipids in HIV-associated Chronic Obstructive Pulmonary Disease
Source: NIH NHLBI R01
Role: Co-investigator
PIs: Christine Wendt (UMN)
Period: 2018-2023
Effort: 10% annual FTE

Award: \$2,341,415

2. **Title:** Detection and Correction of Iron Deficiency Induced Abnormal Brain Metabolism
Source: NIH NICHD R01
Role: Co-investigator
PI: Raghu Rao (UMN)
Period: 2017-2022
Effort: 8% annual FTE
Award: \$2,201,393
3. **Title:** Biomarkers of Bilirubin Toxicity
Source: Pediatrics Cross-Divisional Grant Program
Role: Biostatistician
PI: Katie Satrom (UMN)
Period: 2020-2022
Effort: 10% annual FTE
Award: \$100,000
4. **Title:** Bidimensional integration for pan-omics pan-cancer analysis
Source: NIH NCI R21
Role: Principal investigator
Period: 2018-2020
Effort: 22% annual FTE
Award: \$332,193
5. **Title:** Evaluating Natural Experiments in Healthcare to Improve Diabetes Prevention and Treatment
Source: NIH NIDDK R18
Role: Co-investigator
PI: Kevin Peterson (UMN)
Period: 2016-2020
Effort: 10% annual FTE
Award: \$2,600,000
6. **Title:** Biomarkers for Multi-Source, Multi-Way Data
Source: NIH Clinical and Translational Science Institute at UMN, KL2
Role: Principal Investigator
Period: September 2015 – August 2018
Effort: 75% annual FTE
Award: \$100,000 salary support and \$25,000 research costs per year
7. **Title:** Methods Development for the Integration of Multi-way Array Datasets
Source: Grant in Aid of Scholarship, Artistry and Scholarship
Role: PI and sole author of proposal
Period: January 2015 – May 2016
Award: \$33,902

Software Development

1. **BayesianPGMM:** An R package to infer a Bayesian piecewise growth mixture model with linear segments.
2. **MultiwayRegression:** An R package to predict one multi-way array (e.g., a tensor) from another multi-way array.
3. **MultiwayClassification:** An R package to perform linear classification for data with multi-way structure.
4. **BayesianScreening:** An R package to screen for group differences in high-dimensional data using Bayesian nonparametrics.
5. **JIVE.R:** an R package to perform the joint and individual variation explained (JIVE) method for integrating multiple high-dimensional datasets and visualize the results.
6. Bayesian consensus clustering (BCC): Publicly available, documented R functions to implement the BCC method for clustering multi-source data.
7. Primer efficiency analysis (PEA): Publicly available, documented R functions to account for variability among different quantitative polymerase chain-reaction (qPCR) technologies.

Presentations, Posters, and Exhibits

Invited Presentations

1. “Integrative Regression and Factorization of Multi-Omics Multi-Cohort Data.” CFE-CMStatistics in Berlin, Germany (presented virtually), December 2023.
2. “Integrative regression and factorization of bidimensionally linked matrices.” EcoSta2023 in Tokyo, Japan (presented virtually), August 2023.
3. “Tensor classification methods for multi-way biological data.” Classification Society Annual Meeting, Rochester, NY June 2023.
4. “Classification from multi-region molecular data”, Statistical Methods in Imaging meeting, Minneapolis, MN, May 2023.
5. “Integrative Regression and Factorization of Multi-Omics Multi-Cohort Data.” JSM in Washington, D.C., August 2022.
6. “Integrative factorization of bidimensionally linked matrices.” TRICAP 2022, France.
7. “Bidimensional linked matrix decomposition for pan-omics pan-cancer analysis.” Texas A&M University, April 2022.
8. “Bidimensional linked matrix decomposition for pan-omics pan-cancer analysis.” Binghamton University, September 2021.
9. “Bidimensional linked matrix decomposition for pan-omics pan-cancer analysis.” ICSA Applied Statistics online Symposium, September 2021.

10. "Bidimensional linked matrix decomposition for pan-omics pan-cancer analysis." Florida State University, January 2021.
11. "Bidimensional linked matrix decomposition for pan-omics pan-cancer analysis." JSM Virtual, August 2020.
12. "Bidimensional linked matrix decomposition for pan-omics pan-cancer analysis." University of North Carolina at Chapel Hill, January 2020.
13. "Bidimensional linked matrix decomposition for pan-omics pan-cancer analysis." University of Michigan at Ann Arbor, January 2020
14. "Tensor-on-tensor regression." CMStatistics Conference in London, December 2019.
15. "Bidimensional linked matrix decomposition for pan-omics pan-cancer analysis." University of Texas at Austin, December 2019.
16. "Integrative Factorization of Bidimensionally Linked Matrices." iBright conference at MD Anderson Cancer Center in Houston, TX, November 2019.
17. "Integrative Factorization of Bidimensionally Linked Matrices." Joint Statistical Meetings in Denver, CO, August 2019.
18. "Tensor-on-tensor regression." ICSA Applied Statistics Symposium in Raleigh, NC, June 2019.
19. "Linked matrix factorization." ASA Data Science Symposium in Seattle, June, 2019
20. "Tensor-on-tensor regression." SLDS / nonparametric conference in New York City, June, 2018.
21. "Tensor-on-tensor regression." CMStatistics conference in Pisa, Italy, December, 2018.
22. "Tensor-on-tensor regression." Texas A&M University, March, 2018.
23. "Tensor-on-tensor regression." ICSA Applied Statistics Symposium in Chicago, June, 2017.
16. "Bayesian Screening for Group Differences in High-Throughput Data." Columbia University, December, 2016.
17. "Integrative Analysis of High-Throughput Toxicity Screening Data." Joint Statistical Meetings in Chicago, August, 2016.
18. "Exploratory Factorization of Multi-Source Data." ICSA Applied Statistics Symposium in Atlanta, June, 2016.
19. "Bayesian Screening for Group Differences in High-Throughput Data." Iowa State University, November, 2015.

20. "Subtyping from Multi-Source High-Throughput Data." iBright Conference, MD Anderson Cancer Center, November 2015.
21. "Exploratory Integrative Analysis of Multi-Source Genomic Data." Johns Hopkins University, September, 2015.
22. "Shared Kernel Bayesian Screening." Department of Statistics, UMN, November 2014.
23. "Integrated Analysis of Multi-Source Biological Data." Department of Plant Biology, UMN, October 2014.
24. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." EXTREEMS-QED colloquium, College of William & Mary, April 2014.
25. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." Cornell University, February 2014.
26. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." Emory University, February 2014.
27. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." University of Minnesota, February 2014.
28. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." Washington State University, February 2014.
29. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." University of South Carolina, January 2014.
30. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." University of Michigan, January 2014.
31. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." University of Notre Dame, January 2014.
32. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." Colorado State University, January 2014.
33. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." University of Florida, January 2014.
34. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." University of Chicago, January 2014.
35. "Sparse low-rank models for the integration of multiple data types." Invited presentation. ASA-IMS Joint Statistical Meetings in Montreal, 2013.
36. "Genetic Dissection of Chiari Type I Malformation." Invited presentation. American Syringomyelia and Chiari Annual Conference in Los Angeles, CA, July 2013.
37. "Joint and Individual Variation Explained (JIVE) for Integrated Analysis of Multiple

Datatypes.” Florida State University, February 2012.

38. “Joint and Individual Variation Explained (JIVE) for Integrated Analysis of Multiple Datatypes.” UMASS-Amherst, February 2012.
39. “Joint and Individual Variation Explained (JIVE) for Integrated Analysis of Multiple Datatypes.” MD Anderson Cancer Center, February 2012.
40. “Joint and Individual Variation Explained (JIVE) for Integrated Analysis of Multiple Datatypes.” Wake Forest University, January 2012.

Contributed Presentations

1. “Supervised Multiway Factorization.” Contributed poster presentation. ENAR Spring Meeting in Washington, DC, March 2017.
2. “Detecting Multiple Random Knots in Bayesian Piecewise Growth Mixture Models.” International Meeting of the Psychometric Society in Asheville, NC, July, 2016.
3. “Bayesian Clustering of Multi-Source Data.” Topic-contributed presentation. ASA-IMS Joint Statistical Meetings in Seattle, WA, August 2015.
4. “Bayesian Screening for Group Differences in Methylation Array Data.” Contributed presentation. Eastern North American Region of the International Biometrics Society conference in Miami, FL, March 2015.
5. “Bayesian Screening for Group Differences in Methylation Array Data.” Contributed presentation. Statistical Modeling and Analysis of Epigenetics Workshop at SAMSI, Raleigh, NC, March 2015.
6. “Bayesian Consensus Clustering.” Topic-contributed presentation. ASA-IMS Joint Statistical Meetings in Boston, MA, August 2014.
7. “Technology for teaching bootstraps and randomizations”, with RH Lock, PF Lock, DF Lock and KF Lock. Breakout Session. United States Conference on Teaching Statistics in Raleigh, NC, May 2011 & May 2013.
8. “Using randomization methods to build conceptual understanding of statistical inference,” with RH Lock, PF Lock, DF Lock and KF Lock. Minicourse. Presented at AMS-MAA Joint Mathematics Meetings, January 2012 & January 2013.
9. “Low-rank modeling across multiple high-dimensional datasets”. Topic-contributed presentation. ASA-IMS Joint Statistical Meetings in San Diego, CA, August 2012.
10. “Joint and Individual Variation Explained (JIVE) for Integrated Analysis of Multiple Datatypes.” Topic-contributed presentation. ASA-IMS Joint Statistical Meetings in Miami, FL, August 2011.
11. “Fractal Trees in Three Dimensions”. Contributed presentation. Hudson River Undergraduate Mathematics Conference in Westfield, MA, April 2006.

TEACHING AND CURRICULUM DEVELOPMENT**University of Minnesota****Courses taught**

PUBH8442 Bayesian Decision Theory and Data Analysis (Spring 2015, Spring 2016, Spring 2017, and Spring 2018, Spring 2019, Spring 2020, Spring 2021, Spring 2022, Spring 2023)

PUBH7401 Fundamentals of Biostatistical Inference (Fall 2018)

Duke University**Courses taught**

STA101 Data Analysis and Statistical Inference (co-taught Spring 2013)

University of North Carolina**Courses taught**

STOR155 Introduction to Statistics (Spring 2009, Fall 2011)

Linear Algebra Boot camp (Summer 2011, Summer 2010)

NIH T32 Training Grant Faculty

1. Associate Director, Statistical Genetics and Genomics NIGMS T32, 2023 – Present
2. Mentor, An Interdisciplinary Training Program to Transform Graduate Education in Genetics and Genomics NIGMS T32, 2021 – Present
3. Mentor, Training in Lung Science NHLBI T32, 2018 – Present
4. Mentor, Statistical Genetics and Genomics NIGMS T32, 2016-2023

ADVISING AND MENTORING**University of Minnesota**

Name	Degree Program	Major	Date of completion	Role
Michael Anderson	PhD	Biostatistics	Active	Academic Advisor
Wenhao Cao	PhD	Biostatistics	2023	Academic Advisor
Charles Broadbent	PhD	Computer Science	Active	Doctoral Committee
Bingxin Zhao	PhD	Statistics	Active	Doctoral Committee
Haoxiang Li	PhD	Statistics	Active	Doctoral Committee
Oh-Ran Kwon	PhD	Statistics	2023	Doctoral Committee
Sithara Vivek	PhD	BICB	2023	Doctoral Committee
Rik Lamm	PhD	Ed. Psych	2022	Doctoral Committee

Sambhawa Priya	PhD	BICB	2021	Doctoral Committee
Jun Young Park	PhD	Biostatistics	2020	Doctoral Committee
Jack Pattee	PhD	Biostatistics	2020	Doctoral Committee
Yadira Peralta	PhD	Ed. Psych	2018	Doctoral Committee
Jaron Arbet	PhD	Biostatistics	2018	Doctoral Committee
Tianmeng Lyu	PhD	Biostatistics	2018	Doctoral Committee
Brandon Coombes	PhD	Biostatistics	2016	Doctoral Committee
Abhirup Datta	PhD	Biostatistics	2016	Doctoral Committee
Zhiyu Kang	PhD	Biostatistics	Active	Dissertation Advisor
Jiuzhou Wang	PhD	Biostatistics	Active	Dissertation Advisor
Jonathan Kim	PhD	Biostatistics	2023	Dissertation Advisor
Sarah Samorodnitsky	PhD	Biostatistics	2023	Dissertation Advisor
Elise Palzer	PhD	Biostatistics	2022	Dissertation Advisor
Adam Kaplan	PhD	Biostatistics	2021	Dissertation Advisor
Bin Guo	PhD	Biostatistics	2021	Dissertation Advisor
James Normington	PhD	Biostatistics	2019	Dissertation Advisor
Michael O'Connell	PhD	Biostatistics	2018	Dissertation Advisor
<i>Master's Students</i>				
Cheng-Chang Wu	Masters	Biostatistics	Active	Project Director
Yiyao Jin	Masters	Biostatistics	2022	Project Director
Yuxin Guo	Masters	Biostatistics	2021	Project Director
Wenhao Cao	Masters	Biostatistics	2020	Project Director
Sungtae Kim	Masters	Biostatistics	2019	Advisor / Project Director
Adam Kaplan	Masters	Biostatistics	2017	Advisor / Project Director
Elizabeth Duffy	Masters	Biostatistics	2015	Project Director

Other Institutions

Reviewer for Arnaud Gloaguen's PhD Defense, Laboratoire des Signaux et Systèmes, Université Paris-Saclay, Paris, France, 2020.

SERVICE AND PUBLIC OUTREACH

Service to The Profession:

Grant review experience

1. Reviewer for UMN Interdisciplinary Graduate Fellowship (IDF), Fall 2023
2. Reviewer for NIH NCI Informatics Technologies for Cancer Research (R21 and U01) Special Emphasis Panel, Fall 2023
3. Reviewer for NIH National Cancer Institute R21 & R03 Special Emphasis Panel, Fall 2022
4. Reviewer for NIH-sponsored CTSI TL1 Program at UMN, Spring 2021
5. Reviewer for NIH National Cancer Institute P01 Special Emphasis Panel, Fall 2021
6. Reviewer for NIH-sponsored CTSI TL1 Program at UMN, Spring 2021
7. Ad-hoc reviewer for the National Science Foundation, Fall 2015

Journal Editor Experience

1. Guest Editor, *PLOS Computational Biology*, Spring 2022
2. Associate Editor, *Biometrics*, 2022-present
3. Associate Editor, *Biostatistics*, 2022-present

Journal Reviewer Experience

1. *American Journal of Human Genetics*
2. *Annals of Applied Statistics*
3. *Artificial Intelligence Review*
4. *Bioinformatics*
5. *Biometrics*
6. *Biometrika*
7. *Biostatistics*
8. *Cancer Research*
9. *Computational Statistics and Data Analysis*
10. *Entropy*
11. *IEEE Transactions on Neural Networks and Learning Systems*
12. *IEEE Transactions on Computational Biology and Bioinformatics*
13. *IEEE Transactions on Pattern Analysis and Machine Intelligence*
14. *Journal of the American Statistical Association*
15. *Journal of Chemometrics*
16. *Journal of Computational and Graphical Statistics*
17. *Journal of Machine Learning Research*
18. *Journal of Multivariate Analysis*
19. *Nature Communications*
20. *Pattern Recognition*
21. *PLOS Computational Biology*
22. *PLOS ONE*
23. *Scientific Reports*
24. *Statistica Sinica*
25. *Statistics in Medicine*
26. *Technometrics*
27. *The American Statistician*
28. *The Journal of Agricultural, Biological, and Environmental Statistics*

Other Review Experience

Evaluator, Banff International Research Station (BIRS) Program, Fall 2016

Professional Committees

1. Membership Engagement Committee, Section on Statistical Genetics and Genomics, American Statistical Association (ASA SSGG), 2021-2023.
2. Chair of ASA SSGG MEC communications subcommittee (2023)
3. Eastern North American (ENAR) Regional Advisory Board for the International Biometric society (appointed for term 2018-2020)
4. Chair of social media subcommittee for ENAR RAB, 2020.

5. Program committee member for the ENAR Spring Meeting in Atlanta, GA, March 2018

Organization of conferences, workshops, panels, symposia

1. Program committee member for the ENAR Spring Meeting in Atlanta, GA, March 2018
2. Organizer of invited session "Advancing the Analysis of Multiway (Tensor) Data", ENAR Spring Meeting in Atlanta, GA, March 2018
3. Chair of session "Multi-platform Data Integration: Network and Prediction", ASA-IMS Joint Statistical Meetings in Chicago, IL, August 2016
4. Co-organizer of session "Next Generation Matrix Decompositions: Methods and Applications," with V Zipunnikov. ASA-IMS Joint Statistical Meetings in San Diego, CA, August 2012

Service to The University/College/Department

University of Minnesota

Collegiate Service

Member, SPH Faculty Consultative Committee (2021-present)

Co-organizer, SPH Assistant Professor Lunch (2019-2020)

Affiliated member, Public Health Practice (2015-present)

Judge, SPH Research Day (2015, 2018)

Division Service

Exam committee (2014-2015; Chair, 2023-2024)

Faculty search committee (member, 2015-2016 & 2019-2020; Chair, 2022-2023)

Diversity, Climate and Inclusion Committee (2019-)

Administrator search committee member (2020-2021)

Reading room coordinator (2014-2021)

Curriculum committee (2016-2020)

Seminar committee (member, 2014; chair, 2015-2017)

Exam committee (2014-2015)