Lorin Crawford

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EDUCATION

Duke University, Durham, North Carolina, USA   Aug 2013 – May 2017
Ph.D. in Statistical Science
Co-Advisors: Sayan Mukherjee, Ph.D. and Kris C. Wood, Ph.D.
Thesis: Bayesian Kernel Models for Statistical Genetics and Cancer Genomics

Clark Atlanta University, Atlanta, Georgia, USA   Aug 2009 – May 2013
B.S. in Mathematics
Advisor: Fisseha Abebe, Ph.D.
Valedictorian/*Summa Cum Laude* (Cumulative GPA: 4.0/4.0)

PROFESSIONAL EXPERIENCE

Microsoft Research New England, Cambridge, Massachusetts, USA
Principal Researcher   Jun 2022 – Present
Senior Researcher   Sep 2020 – Jun 2022

Brown University, School of Public Health, Providence, Rhode Island, USA
Associate Professor of Biostatistics   Jul 2022 – Present
RGSS Assistant Professor of Biostatistics   Jul 2019 – Jul 2022
Assistant Professor of Biostatistics   Jul 2017 – Jul 2019

PUBLICATIONS

REFEREED PAPERS (*CO-FIRST AUTHORS; †CO-SENIOR AUTHORS; #CORRESPONDING AUTHOR(S); ADVISEE)

[1] **L. Crawford**, V. Ponomarenko#, J. Steinberg, and M. Williams (2014). Accepted elasticity in local arithmetic congruence monoids. *Results in Mathematics*. **66**: 227-245.

[2] G.R. Anderson, S.E. Wardell, M. Cakir, **L. Crawford**, J.C. Leeds, D.P. Nussbaum, P.S. Shankar, R.S. Soderquist, E.M. Stein, J.P. Tingley, P.S. Winter, E.K. Zeiser-Misenheimer, H.M. Alley, A. Yllanes, V. Haney, K.L. Blackwell, S.J. McCall, D.P. McDonnell, and K.C. Wood# (2016). PIK3CA mutations enable selective targeting of a breast tumor lineage survival dependency through MTOR-mediated control of MCL-1 translation. *Science Translational Medicine*. **8**: 369ra175.

[3] G.R. Anderson*, P.S. Winter*, K.H. Lin, D.P. Nussbaum, M. Cakir, E.M. Stein, R. Soderquist, **L. Crawford**, J.C. Leeds, R. Newcomb, P. Stepp, C. Yip, S.E. Wardell, J.P. Tingley, M. Ali, M. Xu, M. Ryan, S.J. McCall, A. McRee, C.M. Counter, C.J. Der, and K.C Wood# (2017). A landscape of therapeutic cooperativity in KRAS mutant cancers reveals principles for controlling tumor evolution. *Cell Reports*. **20**(4): 999-1015.

[4] **L. Crawford**#, P. Zeng, S. Mukherjee, and X. Zhou# (2017). Detecting epistasis with the marginal epistasis test in genetic mapping studies of quantitative traits. *PLOS Genetics*. **13**(7): e1006869.

[5] K.R. Singleton*, **L. Crawford***, E. Tsui, H.E. Manchester, O. Maertens, X. Liu, M.V. Liberti, A.N. Magpusao, E.M. Stein, J.P. Tingley, D.T. Frederick, G.M. Boland, K.T. Flaherty, S.J. McCall, C. Krepler, K. Sproesser, M. Herlyn, D.J. Adams, J.W. Locasale, K. Cichowski, S. Mukherjee, and K.C. Wood# (2017). Melanoma therapeutic strategies that select against resistance by exploiting MYC-driven evolutionary convergence. *Cell Reports*. **21**(10): 2796-2812.

[6] R. Soderquist, **L. Crawford**, E. Liu, M. Lu, A. Agarwal, G.R. Anderson, K.H. Lin, P.S. Winter, M. Cakir, and K.C. Wood# (2018). Systematic mapping of BCL-2 gene dependencies in cancer reveals molecular determinants of BH3 mimetic sensitivity. *Nature Communications*. **9**(1): 3513.

[7] **L. Crawford**#, K.C. Wood, X. Zhou#, and S. Mukherjee# (2018). Bayesian approximate kernel regression with variable selection. *Journal of the American Statistical Association*. **113**(524): 1710-1721.

[8] D.E. Runcie# and **L. Crawford** (2019). Fast and general-purpose linear mixed models for genome-wide genetics. *PLOS Genetics*. **15**(2): e1007978.

[9] A. Monod#, S. Kališnik, J.Á. Patiño-Galindo, and **L. Crawford** (2019). Tropical sufficient statistics for persistent homology with a parametric application to infectious viral disease. *SIAM Journal on Applied Algebra and Geometry*. **3**(2): 337-371.

[10] **L. Crawford**#, S.R. Flaxman, D.E. Runcie, and M. West (2019). Variable prioritization in nonlinear black box methods: a genetic association case study. *Annals of Applied Statistics*. **13**(2): 958-989.

[11] T. Borgovan#, **L. Crawford**, C. Nwizu, and P. Quesenberry (2019). Stem cells and extracellular vesicles: biological regulators of physiology and disease. *American Journal of Physiology-Cell Physiology*. **317**(2): C155-C166.

[12] K.H. Lin, J.C. Rutter, A. Xie, E.T. Winn, B. Pardieu, R. Dal Bello, Y.R. Ahn, Z. Dai, R.T. Sobhan, G.R. Anderson, K.R. Singleton, A.E. Decker, P.S. Winter, J.W. Locasale, **L. Crawford**, A. Puissant#, and K.C. Wood# (2020). Using antagonistic pleiotropy to design a chemotherapy-induced evolutionary trap. *Nature Genetics*. **52**: 408-417.

[13] W. Cheng, S. Ramachandran#, and **L. Crawford**# (2020). Estimation of non-null SNP effect size distributions enables the detection of enriched genes underlying complex traits. *PLOS Genetics*. **16**(6): e1008855.

[14] J.S. Sadick, **L. Crawford**, H.C. Cramer, C. Franck, S.A. Liddelow, and E.M. Darling# (2020). Generating cell type-specific protein signatures from non-symptomatic and diseased tissues. *Annals of Biomedical Engineering*. **48**: 2218-2232.

[15] **L. Crawford**#, A. Monod#, A.X. Chen, S. Mukherjee, and R. Rabadán (2020). Predicting clinical outcomes in glioblastoma: an application of topological and functional data analysis. *Journal of the American Statistical Association*. **115**(531): 1139-1150.

[16] B.A. Borden, Y. Baca, J. Xiu, F. Tavora, I. Winer, B.A. Weinberg, A.M. VanderWalde, S. Darabi, W.M. Korn, A.P. Mazar, F.J. Giles, **L. Crawford**, H. Safran, W.S. El-Deiry, and B.A. Carneiro# (2021). The landscape of glycogen synthase kinase-3 beta (GSK-3b) genomic alterations in cancer. *Molecular Cancer Therapeutics*. **20**(1): 183-190.

[17] A.N. Spierer#, J.A. Mossman, S.P. Smith, **L. Crawford**, S. Ramachandran, and D.M. Rand# (2021). Natural variation in the regulation of neurodevelopmental genes modifies flight performance in *Drosophila*. *PLOS Genetics*. **17**(3): e1008887.

[18] B. Wang*, T. Sudijono*, H. Kirveslahti*, T. Gao, D.M. Boyer, S. Mukherjee†, and **L. Crawford**†# (2021). A statistical pipeline for identifying physical features that differentiate classes of 3D shapes. *Annals of Applied Statistics*. **15**(2): 638-661.

[19] D.E. Runcie#, J. Qu, H. Cheng, and **L. Crawford** (2021). Mega-scale linear mixed models for genomic predictions with thousands of traits. *Genome Biology*. **22**: 213.

[20] P. Demetci*, W. Cheng*, G. Darnell, X. Zhou, S. Ramachandran, and **L. Crawford**# (2021). Multi-scale inference of genetic architecture using biologically annotated neural networks. *PLOS Genetics*. **17**(8): e1009754.

[21] M. Kamariza#, **L. Crawford**#, D. Jones#, and H.K. Finucane# (2021). Misuse of the term "trans-ethnic" in genomics research. *Nature Genetics*. **50**: 1520-1521.

[22] S. Raghavan*, P.S. Winter*#, A.W. Navia*, H.L. Williams*, A. DenAdel, R.L. Kalekar, J. Galvez-Reyes, K.E. Lowder, J. Galvez-Reyes, R.L. Kalekar, N. Mulugeta, K.S. Kapner, M.S. Raghavan, A.A. Borah, N. Liu, S.A. Väyrynen, A. Dias Costa, R.W.S. Ng, J. Wang, E.K. Hill, D.Y. Ragon, L.K. Brais, A.M. Jaeger, L.F. Spurr, Y.Y. Li, A.D. Cherniack, M.A. Booker, E.F. Cohen, M.Y. Tolstorukov, I. Wakiro, A. Rotem, B.E. Johnson, J.M. McFarland, E.T. Sicinska, T.E. Jacks, R.J. Sullivan, T.E. Clancy, K. Perez, D.A. Rubinson, K. Ng, J.M. Cleary, **L. Crawford**, S.R. Manalis, J.A. Nowak, B.R. Wolpin†, W.C. Hahn†, A.J. Aguirre†#, and A.K. Shalek†# (2021). Microenvironment drives cell state, plasticity, and drug response in pancreatic cancer. *Cell*. **184**(25): 6119-6137.

[23] S.P. Smith, S. Shahamatdar, W. Cheng, S. Zhang, J. Paik, M. Graff, C. Haiman, T.C. Matise, K.E. North, U. Peters, E. Kenny, C. Gignoux, G. Wojcik, **L. Crawford**†, and S. Ramachandran†# (2022). Enrichment analyses identify shared associations for 25 quantitative traits in over 600,000 individuals from seven diverse ancestries. *American Journal of Human Genetics*. **109**: 871-884.

[24] W.S. Tang*, G.M. da Silva*, H. Kirveslahti, E. Skeens, B. Feng, T. Sudijono, K.K. Yang, S. Mukherjee, B. Rubenstein†, and **L. Crawford**†# (2022). A topological data analytic approach for discovering biophysical signatures in protein dynamics. *PLOS Computational Biology*. **18**(5): e1010045.

[25] W. Cheng#, S. Ramachandran, and **L. Crawford**# (2022). Uncertainty quantification in variable selection for genetic fine-mapping using Bayesian neural networks. *iScience*. **25**(7): 104553. (Spotlight Talk at the 10th RECOMB Satellite on Computational Methods in Genetics).

[26] B.L. Trippe#, B. Huang, E.A. DeBenedictis, B. Coventry, N. Bhattacharya, K.K. Yang, D. Baker, and **L. Crawford**# (2022). Randomized gates eliminate bias in sort-seq assays. *Protein Science*. **31**(9): e4401.

[27] A. Conard*, A. DenAdel*, and **L. Crawford**# (2023). A spectrum of explainable and interpretable machine learning approaches for genomic studies. *WIREs Computational Statistics*. e1617.

[28] C. Rios-Martinez, N. Bhattacharya, A.P. Amini, **L. Crawford**, and K.K. Yang# (2023). Deep self-supervised learning for biosynthetic gene cluster detection and product classification. *PLOS Computational Biology*. In Press.

[29] J. Stamp#, A. DenAdel, D. Weinreich, and **L. Crawford**# (2023). Leveraging the genetic correlation between traits improves the detection of epistasis in genome-wide association studies. *G3: Genes, Genomes, Genetics*. In Press.

PREPRINTS (*CO-FIRST AUTHORS; †CO-SENIOR AUTHORS; #CORRESPONDING AUTHOR(S); ADVISEE)

[1] **L. Crawford**# and X. Zhou#. Genome-wide marginal epistatic association mapping in case-control studies. *bioRxiv*. 374983.

[2] J. Ish-Horowicz*, D. Udwin*, K. Scharfstein, S.R. Flaxman, S.L. Filippi#, and **L. Crawford**#. Interpreting deep neural networks through variable importance. *arXiv*. 1901.09839.

[3] K.E. Ware, S. Gupta, J. Eng, G. Kemeny, B.J. Puviindran, W.C. Foo, **L. Crawford**, R.G. Almquist, D. Runyambo, B.C. Thomas, M.U. Sheth, A. Agarwal, M. Pierobon, E.F. Petricoin, D.L. Corcoran, J. Freedman, S.R. Patierno, T. Zhang, S. Gregory, Z. Sychev, J.M. Drake, A.J. Armstrong#, J.A. Somarelli#. Convergent evolution of p38/MAPK activation in hormone resistant prostate cancer mediates pro-survival, immune evasive, and metastatic phenotypes. *bioRxiv*. 2020.04.22.050385.

[4] W. Cheng, G. Darnell, S. Ramachandran, and **L. Crawford**#. Generalizing variational autoencoders with hierarchical empirical Bayes. *arXiv*. 2007.10389.

[5] M.C. Turchin#, G. Darnell, **L. Crawford**#, and S. Ramachandran#. Pathway analysis within multiple human ancestries reveals novel signals for epistasis in complex traits. *bioRxiv*. 2020.09.24.312421.

[6] K. Meng#, J. Wang, **L. Crawford**, and A. Eloyan. Randomness and statistical inference of shapes via the smooth Euler characteristic transform. *arXiv*. 2204.12699.

[7] G. Darnell*, S.P. Smith*, D. Udwin, S. Ramachandran†, and **L. Crawford**†#. Partitioning tagged non-additive genetic effects in summary statistics provides evidence of pervasive epistasis in complex traits. *bioRxiv*. 2022.07.21.501001.

[8] E.T. Winn-Nuñez#, M. Griffin, and **L. Crawford**#. A simple approach for local and global variable importance in nonlinear regression models. *arXiv*. 2302.02024.

NON-REFEREED PAPERS

[1] At the intersection of machine learning, biology, and health: an interview with Lorin Crawford (2021). *Communications Biology*. **4**(1): 32. [Link]

SOFTWARE

[1] **BAKR**: Bayesian Approximate Kernel Regression

[2] **BANNs**: Biologically Annotated Neural Networks

[3] **ESNN**: Ensemble of Single-Effect Neural Networks

[4] **gene-ε**: A Recalibrated Hypothesis Test for Sets of SNP-Level Summary Statistics

[5] **GOALS**: The GlObal And Local Score

[6] **Grid-LMM**: Fast and Flexible Linear Mixed Models for Genetic Association Studies

[7] **HEBAE**: Hierarchical Empirical Bayes Autoencoder

[8] **MAPIT**: The MArginal ePIstasis Test

[9] **MAPIT-R**: The MArginal ePIstasis Test for Regions and SNP-Sets

[10] **MegaLMM**: Mega-scale Linear Mixed Models for Multivariate Genomic Prediction

[11] **MELD**: Marginal Epistatic LD Score Regression

[12] **mvMAPIT**: The Multivariate MArginal ePIstasis Test

[13] **RATE**: RelATive cEntrality Measures for Variable Prioritization

[14] **SECT**: The Smooth Euler Characteristic Transform

[15] **SINATRA**: Pipeline for Sub-Image Analysis and Feature Selection on 3D Shapes

[16] **SINATRA Pro**: Protein Structure and Conformation Analysis using Topological Summary Statistics

[17] **Tropix**: Tropical Sufficient Statistics for Persistent Homology

AWARDS &	Committee of Presidents of Statistical Societies (COPSS) Emerging Leader Award	2023
FELLOWSHIPS	International Conference on Intelligent Biology and Medicine (ICIBM) Eminent Scholar Award	2023
	Mathematical Association of America & National Association of Mathematicians Lecturer	2022
	Kavli Fellow of the National Academy of Sciences, Frontiers of Science Symposium	2021
	Cell Press: 1000 Inspiring Black Scientists in America	2021
	David & Lucille Packard Foundation Fellowship for Science and Engineering	2020
	Mathematically Gifted & Black: Black History Month Honoree	2020
	The Root: 100 Most Influential African Americans in 2019	2019
	Endowed Named Assistant Professorship	2019
	Alfred P. Sloan Research Fellowship	2019
	Forbes 30 Under 30 Class of 2019: Science	2019
	Leonard J. Savage Thesis Award in Applied Methodology	2018
	National Science Foundation (NSF) Graduate Research Fellowship	2015
	Duke University Dean Graduate Fellowship	2013
	Isabella T. Jenkins Outstanding Academic Achievement Award	2013
	J.J. Dennis Endowed Undergraduate Fellowship	2012
	Clark Atlanta University Provost Scholarship	2009

SPONSORED RESEARCH

P20GM103645 (PI Sanes)   09/01/18 – 09/08/20
NIH/NIGMS
Title: *COBRE Center for Central Nervous System Function*
Role: Core B Co-Investigator

2U10CA180794 (PIs Gray and Gatsonis)   03/01/19 – 09/08/20
NIH/NCI/Dana Farber Cancer Institute
Title: *ECOG-ACRIN Network Group Statistics and Data Management Center*
Role: Biostatistician

W81XWH-18-1-018 (PI Somarelli)   09/01/18 – 08/31/21
DoD/PCRP
Title: *Targeting the p38/Snail/PD-L1 axis in Hormone-therapy Resistance and Metastasis*
Role: Co-Investigator

P20GM109035 (PI Rand)   03/01/19 – 02/28/21
NIH/NIGMS
Title: *COBRE Center for Computational Biology of Human Disease*
Project Title: *Deep learning Methods for Fine Mapping and Discovery in Genomic Association Studies*
Role: Principal Investigator of Project

FG-2019-11622 (PI Crawford)   09/15/19 – 09/14/21
Alfred P. Sloan Foundation Research Fellowship
Title: *Interpretable Machine Learning Methods for Genome-wide Association Mapping*
Role: Principal Investigator

2020-71387 (PI Crawford)   10/15/20 – 10/14/25
David & Lucille Packard Foundation Fellowship for Science and Engineering
Role: Principal Investigator

1R35GM138032-01 (PI Crawford)   Deferred
NIH/NIGMS
Title: *Interpretable Machine Learning for Characterizing Broad-sense Heritability in Complex Traits and Rare Diseases*
Role: Principal Investigator

INVITED TALKS

AS ASSOCIATE PROFESSOR / PRINCIPAL RESEARCHER

University of Southern California, QCB Seminar Series, Los Angeles, CA	2023
International Conference on Intelligent Biology and Medicine, Eminent Scholar, Tampa Bay, FL	2023
Mount Sinai, Charles Bronfman Institute for Personalized Medicine (CBIPM) Seminar, NYC, NY	2023
ICLR, Machine Learning & Global Health Network Workshop, Hybrid, Kigali, Rwanda	2023
Applied Algebraic Topology Research Network, Online Seminar Series, Virtual	2023
UMass Chan Medical School, Department of Systems Biology Seminar, Worcester, MA	2023
IMSI, Randomness in Topology and its Applications Workshop, Chicago, IL	2023
Cedars-Sinai, Computational Biomedicine Grand Rounds Seminar, Los Angeles, CA	2023
NCI, Division of Cancer Epidemiology and Genetics, Biostatistics Branch Seminar Series, Virtual	2023
Johns Hopkins University, Statistical Genetics Working Group Seminar, Virtual	2022
Stanford University, Department of Biomedical Data Science, Biostatistics Workshop, Palo Alto, CA	2022
Georgia Institute of Technology, School of Biological Sciences Seminar, Atlanta, GA	2022
University of Rhode Island, Department of Computer Science and Statistics Seminar, Kingston, RI	2022
University of Oxford, Applied Topology Seminar, Oxford, England, UK	2022
University of Cambridge, MRC Biostatistics Unit Seminar, Cambridge, England, UK	2022
University of California Santa Cruz, Department of Statistics Seminar, Virtual	2022
SIAM Conference on Mathematics of Data Science, San Diego, CA	2022
Joint Statistical Meetings, Biometrics Invited Session, Washington, D.C.	2022
SIAM Annual Meeting, Plenary Speaker, Pittsburgh, PA	2022

AS ASSISTANT PROFESSOR / SENIOR RESEARCHER

Bayesian Young Statisticians Meeting (BAYSM), Plenary Speaker, Montréal, Québec, CA	2022
WNAR/IMS/JR Meeting, IMS Invited Session, Virtual	2022
Population, Evolutionary, and Quantitative Genetics (PEQG), Pacific Grove, CA	2022
NES/MAA Spring Meeting, Plenary Talk, Haddam, CT	2022
FASEB, The Cell Signaling in Cancer Conference: From Mechanisms to Therapy, New Orleans, LA	2022
Yale University, CBDS Distinguished Speaker Seminar Series, New Haven, CT	2022
Duke University, Department of Statistical Sciences Seminar Series, Durham, NC	2022
KS/MAA Fall Meeting, Plenary Talk, Atchison, KS	2022
Conference on Health, Inference, and Learning (CHIL), Keynote Speaker, Virtual	2022
Brown University, Provost's By Faculty For Faculty Lecture Series, Providence, RI	2022
University of Chicago, Department of Human Genetics Seminar Series, Chicago, IL	2022
University of Pennsylvania, Bioinformatics Seminar Series, Philadelphia, PA	2022

Toronto Bioinformatics Users Group (TorBUG) Seminar Series, Toronto, Ontario, CA	2022
Joint Mathematical Meetings, AMS Special Session, Seattle, WA	2022
Winston-Salem State University, Math and Stats Club, Winston-Salem, NC	2021
University of Chicago, Department of Statistics Colloquium, Chicago, IL	2021
Penn State, ICDS Symposium, Keynote Speaker, University Park, PA	2021
Cornell University, Plant Breeding and Genetic Seminar Series, Ithaca, NY	2021
Atlanta University Center Data Science Symposium, Keynote Speaker, Virtual Meeting	2021
Joint Statistical Meetings, Biometrics Invited Session, Virtual Meeting	2021
SMB, Data-Driven Modeling and Analysis in Mathematical Biology, Virtual Meeting	2021
Great Lakes Bioinformatics Conference, Keynote Speaker, Virtual Meeting	2021
ICLR, Geometrical and Topological Representation Learning Workshop, Virtual Meeting	2021
IMSI, Topological Data Analysis Workshop, Chicago, IL	2021
New York University and ETH Zürich, Math and Data (MAD+) Seminar, Virtual Meeting	2021
Columbia University, DSI Distinguished Speaker Series, New York, NY	2021
ProbGen, Quantitative Genetics and Association Mapping Session, Cold Spring Harbor, NY	2021
University of Michigan, Dept. of Biostatistics Seminar, Ann Arbor, MI	2021
Princeton University, Quantitative and Computational Biology Seminar Series, Princeton, NJ	2021
Johns Hopkins University, Dept. of Biostatistics Seminar Series, Baltimore, MD	2021
NeurIPS, Topological Data Analysis and Beyond Workshop, Virtual Meeting	2020
University of Colorado, Biostatistics Seminar Series, Aurora, CO	2020
University of Wisconsin-Madison, Dept. of Statistics Seminar, Madison, WI	2020
University of North Carolina, Dept. of Biostatistics Seminar, Chapel Hill, NC	2020
University of Pennsylvania, The Wharton School Statistics Seminar, Philadelphia, PA	2020
Rochester Institute of Technology, Mathematical Modeling Seminar, Rochester, NY	2020
The Black Women in Computational Biology Network, Seminar Series, Virtual Meeting	2020
Joint Statistical Meetings, Biometrics Invited Session, Philadelphia, PA	2020
Stanford University, Statistics Department Seminar, Palo Alto, CA	2020
Brown University, Rhode Island IDeA Symposium (Invited Science Talk), Providence, RI	2020
University of Arkansas for Medical Sciences, Biomedical Informatics Seminar, Little Rock, AR	2020
Microsoft Research New England, Seminar Series, Cambridge, MA	2020
ENAR Spring Meeting, Invited Session, Nashville, TN	2020
Brown University and Lifespan, Populations Science Group Meeting, Providence, RI	2020
Duke University, Sloan Research Summit (Keynote Speaker), Durham, NC	2020
University of Massachusetts Amherst, Statistics and Probability Seminar, Amherst, MA	2020
NES/MAA Fall Meeting, Plenary Talk, Wellesley, MA	2019
Broad Institute of MIT and Harvard, Models, Inference & Algorithms Seminar, Cambridge, MA	2019
Duke University, Computational Biology Seminar, Durham, NC	2019
Joint Statistical Meetings, IMS Invited Session, Denver, CO	2019
WNAR/IMS/JR Meeting, IMS Invited Session, Portland, OR	2019
33rd New England Statistics Symposium (NESS), Hartford, CT	2019
UC Irvine, Dept. of Statistics Seminar, Irvine, CA	2019
Brown University, Center for Computational Biology of Human Disease Seminar, Providence, RI	2019
ENAR Spring Meeting, IMS Invited Session, Philadelphia, PA	2019
University of Connecticut, Dept. of Statistics Seminar, Storrs, CT	2018
University of Michigan, Dept. of Biostatistics Seminar, Ann Arbor, MI	2018
Harvard University, Data Science Initiative Conference, Cambridge, MA	2018
Brown University, Pattern Theory Seminar Series, Providence, RI	2018
ISBA World Meeting, Edinburgh, Scotland, UK	2018
College of the Holy Cross, Pi Mu Epsilon (PME) Colloquium, Worcester, MA	2018
ENAR Spring Meeting, Geometry and Topology in Statistical Inference Workshop, Atlanta, GA	2018
42nd SIAM-SEAS, Statistical Topological Data Analysis Mini Symposium, Chapel Hill, NC	2018
ICERM, NSF TRIPODS: Geometry and Topology of Data Workshop, Providence, RI	2017
NeurIPS, Synergies in Geometric Data Analysis Workshop, Long Beach, CA	2017
Brown University, Data Science Initiative Seminar, Providence, RI	2017
Brown University, Center for Computational Molecular Biology Seminar, Providence, RI	2017

Brown University, Applied Topology and Geometry Seminar, Providence, RI	2017
SIAM AG'17, Statistics and Applied Algebraic Topology Workshop, Atlanta, GA	2017

PROFESSIONAL AFFILIATIONS

American Statistical Association (ASA); Genetics Society of America (GSA); International Biometric Society Eastern North American Region (IBS ENAR); International Society for Bayesian Analysis (ISBA)

SERVICE ACTIVITIES

EDITORIAL SERVICE

Biostatistics (Associate Editor)	2021 – Present
Journal of the American Statistical Association (AE of Reproducibility for A&CS)	2018 – Present

EXTERNAL SERVICE

ENAR Fostering Diversity in Biostatistics Workshop (Planning Committee)	2022 – Present
ISBA Section on Biostats and Pharma (Treasurer)	2021 – 2023
IBS ENAR Regional Advisory Board	2020 – 2022

PROFESSIONAL SERVICE

ENAR Spring Meeting, Baltimore, MD Role: Program Committee	2024
New England Statistical Society (NESS) Conference, Boston, MA Role: Keynote Panel Organizing Committee	2023
The Junior Section of the International Society of Bayesian Analysis Blackwell-Rosenbluth Award Scientific Committee Role: Chair	2022
Conference on Neural Information Processing Systems (NeurIPS), New Orleans, LA Workshop: Learning Meaningful Representations of Life Role: Organizing Committee	2022
Conference on Neural Information Processing Systems (NeurIPS), New Orleans, LA Role: Workshop Proposal Reviewer	2022
35th New England Statistics Symposium (NESS), Storrs, CT MassMutual Student Paper Award Role: Review Committee	2022
Joint Statistical Meetings (JSM), Washington, D.C. Session: Imaging and Clinical Biomarkers in Neurodegenerative Disease Role: Co-Organizer	2022
Population, Evolutionary, and Quantitative Genetics (PEQG), Pacific Grove, CA Role: Session Chair	2022
Intelligent Systems for Molecular Biology (ISMB), Virtual Meeting Role: Proceedings Program Committee	2022
Conference on Neural Information Processing Systems (NeurIPS), Virtual Meeting Workshop: Learning Meaningful Representations of Life Role: Organizing Committee	2021
The Junior Section of the International Society of Bayesian Analysis Blackwell-Rosenbluth Award Scientific Committee Role: Vice Chair	2021

Probabilistic Modeling in Genomics (ProbGen), Virtual Meeting	2021

Session: Quantitative Genetics and Association Mapping
Role: Co-Chair

Intelligent Systems for Molecular Biology (ISMB), Virtual Meeting	2021

European Conference on Computational Biology (ECCB), Virtual Meeting
Role: Proceedings Program Committee

REVIEWER SERVICE

American Journal of Human Genetics; *Annals of Applied Statistics*; *Bioinformatics*; *Biostatistics*; *BMC Bioinformatics*; *Conference on Neural Information Processing Systems (NeurIPS)*; *Genes*; *Intelligent Systems for Molecular Biology (ISMB)*; *International Conference on Artificial Intelligence and Statistics (AISTATS)*; *International Conference on Machine Learning (ICML)*; *Journal of the American Statistical Association*; *Journal of Animal Science*; *Journal of Computational and Graphical Statistics*; *Journal of Machine Learning Research*; *Journal of Multivariate Analysis*; *Nature Communications*; *Nature Genetics*; *New England Journal of Medicine*; *PLOS Genetics*; *Research in Computational Molecular Biology (RECOMB); Transactions of Mathematics and Its Applications*

INSTITUTIONAL SERVICE (BROWN UNIVERSITY)

Center for Computational Molecular Biology: Executive Steering Committee	2022 – Present
Data Science Initiative (DSI) Campus Advisory Board	2021 – Present
Center for Computational Molecular Biology: PhD Admissions Committee	2017 – Present
Goldwater Scholarship Nomination Committee	2019 – 2020
School of Public Health: Operational Planning Committee	2019 – 2020
Department of Biostatistics: PhD Admissions Committee	2018 – 2020
Department of Biostatistics: Seminar Series Organizer	2018 – 2020
Department of Biostatistics: Communications Committee	2017 – 2020
Department of Biostatistics: Academic Programs Committee	2017 – 2020

MENTORSHIP ACTIVITIES

POSTDOCTORAL FELLOWS

Greg Darnell (Co-advisee)	2019 – 2020

DOCTORAL STUDENTS

Alan DenAdel (Computational Biology)	Present
Cecile Meier-Scherling (Computational Biology; Co-advisee)	Present
Chibuikem Nwizu (Computational Biology)	Present
Julian Stamp (Computational Biology)	Present
Ria Vinod (Computational Biology)	Present
Emily Winn-Nuñez (Applied Mathematics)	Present
Alexandra Wong (Computational Biology)	Present
Dana Udwin (Biostatistics)	2022
Ashley Conard (Computational Biology)	2022
Wai Shing Tang (Physics)	2022
Wei Cheng (Computational Biology; Co-advisee)	2022

DOCTORAL DISSERTATION COMMITTEES

Rob Zielinski (Biostatistics)	Present
Alysandra Zhang (Cognitive Linguistic & Psychological Sciences)	Present
Rachel Gaither (Epidemiology)	Present
Isaac Kim (Computational Biology)	Present
Dilum Aluthge (Computational Biology)	Present
Qing Wu (Computational Biology)	Present
Haobo Yang (Chemistry)	Present
Vivek Ramanan (Computational Biology)	Present
Jiaqi Zhang (Computer Science)	Present

Pinar Demetci (Computational Biology) 2023
Kun Meng (Biostatistics) 2022
Topi Paananen (Aalto University - Finland) 2022
Samuel Smith (Computational Biology) 2022
Haobo Yang (Chemistry) 2022
Adrienne Parsons (Molecular Pharmacology, Physiology, and Biotechnology) 2021
Dhananjay Bhaskar (Biomedical Engineering) 2021
Sahar Shahamatdar (Computational Biology) 2021

MASTERS THESIS ADVISING

Colin Small (Biotechnology) 2023
Alexander Li (Biostatistics) 2021
Isaac Zhao (Biostatistics) 2019
Bruce Wang (Data Science Initiative) 2018

UNDERGRADUATE HONORS THESIS ADVISING

Helen Xie (Undeclared) Present

Lee Ding (Applied Math) 2022
Erin Bugbee (Statistics) 2020
Gabrielle Ferra (Applied Math-Biology) 2020
Kayla Scharfstein (Applied Math-Computer Science) 2020
Zachary Kaplan (Applied Math) 2019
Timothy Sudijono (Applied Math) 2019

MICROSOFT RESEARCH INTERNS

Fatemeh Afrasiabi (UMass Boston) 2022
Dan Yuan (U Washington) 2022
Brian Trippe (MIT) 2021
Yaniv Yacoby (Harvard) 2021

COURSES TAUGHT

PHP0100 - First Year Seminar: Statistics is Everywhere
PHP2601 - Linear Models
PHP2605 - Generalized Linear Models
PHP2950 - Doctoral Seminar in Public Health

[*CV compiled on 2023-06-02*]