

# 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**, Cambridge, Massachusetts, USA Jun 2022 – Present  
Principal Researcher  
Senior Researcher Sep 2020 – Jun 2022

**Brown University**, School of Public Health, Providence, Rhode Island, USA Jul 2024 – Present  
Distinguished Senior Fellow in Biostatistics  
Associate Professor of Biostatistics Jul 2022 – Jul 2024  
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. Pattillo 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. Pattillo Smith, S. Shahamatdar, W. Cheng, S. Zhang, J. Paik, M. Graff, C. Haiman, T.C. Matisse, 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*. **15**(5): 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*. **19**(5): e1011162.
- [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*. **13**(8): jkad118.
- [30] H. Adam#, F. Yin, M. Hu, N. Tenenholz, **L. Crawford**, L. Mackey, and A. Koenecke (2023). Should I stop or should I go: early stopping with heterogeneous populations. *Advances in Neural Processing Systems (NeurIPS)*. **36**: 15799-15832. (Spotlight Paper).
- [31] E.T. Winn-Nuñez#, M. Griffin, and **L. Crawford**# (2024). A simple approach for local and global variable importance in nonlinear regression models. *Computational Statistics & Data Analysis*. **194**: 107914.
- [32] J. Wrobel#, E.C. Hector, **L. Crawford**, L. D'Agostino McGowan, N. da Silva, J. Goldsmith, S. Hicks, M. Kane, Y. Lee, V. Mayrin, C.J. Paciorek, T. Usher, and J. Wolfson (2024). Partnering with authors to enhance reproducibility at JASA. *Journal of the American Statistical Association*. **119**(546): 795-797. (Invited Comment).
- [33] S. Pattillo Smith\*, G. Darnell\*, D. Udwin, J. Stamp, A. Harpak, S. Ramachandran†, and **L. Crawford**†# (2024). Discovering non-additive heritability using additive GWAS summary statistics. *eLife*. **13**: e90459.
- [34] H. Xie, **L. Crawford**†#, and A. Conard†# (2024). Multioviz: an interactive platform for *in silico* perturbation and interrogation of gene regulatory networks. *BMC Bioinformatics*. **25**: 249.
- [35] K. Li#, C. Chaguza, J. Stamp, Y.T. Chew, N.F.G. Chen, D. Ferguson, S. Pandya, N. Kerantzas, W. Schulz, Yale SARS-CoV-2 Genomic Surveillance Initiative, A.M. Hahn, C.B. Ogbunugafor, V.E. Pitzer, **L. Crawford**, D.M. Weinberger, and N.D. Grubaugh# (2024). Genome-wide association study between SARS-CoV-2 single nucleotide polymorphisms and virus copies during infections. *PLOS Computational Biology*. **20**(9): e1012469.
- [36] K. Meng#, J. Wang, **L. Crawford**, and A. Eloyan. Randomness and statistical inference of shapes via the smooth Euler characteristic transform. *Journal of the American Statistical Association*. In Press.
- [37] N. Liu\*, W.E. Kattan\*, B.E. Mead\*, C. Kummerlowe\*, T. Cheng, S. Ingabire, J.H. Cheah, C.K. Soule, A.Vrcic, J.K. McIninch, S. Triana, M. Guzman, T.T. Dao, J.M. Peters, K.E. Lowder, **L. Crawford**, A.P. Amini, P.C. Blainey, W.C. Hahn, B. Cleary, B. Bryson, P.S. Winter†, S. Raghavan†, and A.K. Shalek†#. Scalable, compressed phenotypic screening using pooled perturbations. *Nature Biotechnology*.

- [38] I.E. Kim, Jr., C. Oduor, J. Stamp, M.A. Luftig, A.M. Moormann, **L. Crawford**†#, and J.A. Bailey†#. Incorporation of Epstein-Barr viral variation implicates significance of LMP1 in survival prediction and prognostic subgrouping in Burkitt lymphoma. *International Journal of Cancer*. In Press.
- [39] A. DenAdel, M.L. Ramseier, A. Navia, A.K. Shalek, S. Raghavan†, P.S. Winter†, A.P. Amini†, and **L. Crawford**†#. A knockoff calibration method to avoid over-clustering in single-cell RNA-sequencing. *American Journal of Human 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. Puvindran, 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#, M. Ji, J. Wang, K. Ding, H. Kirveslahti, A. Eloyan, and **L. Crawford**. Statistical inference on grayscale images via the Euler-Radon transform. *arXiv*. 2308.14249.
- [7] K.Z. Kedzierska#, **L. Crawford**†, A.P. Amini†, and A.X. Lu†#. Assessing the limits of zero-shot foundation models in single-cell biology. *bioRxiv*. 2023.10.16.561085.
- [8] E.T. Winn-Nuñez#, H. Witt, D. Bhaskar, R.Y. Huang, J.S. Reichner, I.Y. Wong, and **L. Crawford**#. Generative modeling of biological shapes and images using a probabilistic  $\alpha$ -shape sampler. *bioRxiv*. 2024.01.09.574919.
- [9] C. Nwizu, M. Hughes, M.L. Ramseier, A. Navia, A.K. Shalek, N. Fusi, S. Raghavan†, P.S. Winter†, A.P. Amini†#, and **L. Crawford**†#. Scalable nonparametric clustering with unified marker gene selection for single-cell RNA-seq data. *bioRxiv*. 2024.02.11.579839.
- [10] P.S. Winter\*#, M.L. Ramseier\*, A.W. Navia\*, S. Saksena, H. Strouf, N. Senhaji, A. DenAdel, M. Mirza, H.H. An, L. Bilal, P. Dennis, C.S. Leahy, K. Shigemori, J. Galves-Reyes, Y. Zhang, F. Powers, N. Mulugeta, A.J. Gupta, N. Calistri, A. Van Scoyk, K. Jones, H. Liu, K.E. Stevenson, S. Ren, M.R. Luskin, C.P. Couturier, A.P. Amini, S. Raghavan, R.J. Kimmerling, M.M. Stevens, **L. Crawford**, D.M. Weinstock, S.R. Manalis†, A.K. Shalek†#, and M.A. Murakami†#. Mutation and cell state compatibility is required and targetable in Ph+ acute lymphoblastic leukemia minimal residual disease. *bioRxiv*. 2024.06.06.597767.
- [11] S. Surasinghe, S.N. Manivannan, S.V. Scarpino, **L. Crawford**, and C.B. Ogbunugafor#. Structural causal influence (SCI) captures the forces of social inequality in models of disease dynamics. *arXiv*. 2409.09096.
- [12] W. Sloneker#, S. Patel, M. Wang, **L. Crawford**, and R. Singh. BetaExplainer: a probabilistic method to explain graph neural networks. *arXiv*. 2412.11964.
- [13] A. DenAdel, M. Hughes, A. Thoutam, A. Gupta, A.W. Navia, N. Fusi, S. Raghavan†, P.S. Winter†, A.P. Amini†#, and **L. Crawford**†#. Evaluating the role of pre-training dataset size and diversity on single-cell foundation model performance. *bioRxiv*. 2024.12.13.628448.
- [14] A.M. Wong# and **L. Crawford**#. Rethinking cancer drug synergy prediction: a call for standardization in machine learning applications. *bioRxiv*. 2024.12.24.630216.

- [15] J. Stamp#, S. Pattillo Smith, D. Weinreich, and **L. Crawford#**. Sparse modeling of interactions enables fast detection of genome-wide epistasis in biobank-scale studies. *bioRxiv*. 2025.01.11.632557.
- [16] X. Liu#, **L. Crawford**, and S. Ramachandran. ML-MAGES: a machine learning framework for multivariate genetic association analyses with genes and effect size shrinkage. *bioRxiv*. 2025.02.11.637655.

#### NON-REFEREED PAPERS

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

#### SOFTWARE

- [1]  **$\alpha$ -Shape Sampler**: Pipeline for Generating 2D and 3D Biological Shapes and Images
- [2] **BAKR**: Bayesian Approximate Kernel Regression
- [3] **BANNs**: Biologically Annotated Neural Networks
- [4] **ESNN**: Ensemble of Single-Effect Neural Networks
- [5] **gene- $\epsilon$** : A Recalibrated Hypothesis Test for Sets of SNP-Level Summary Statistics
- [6] **GOALS**: The GLObal And Local Score
- [7] **Grid-LMM**: Fast and Flexible Linear Mixed Models for Genetic Association Studies
- [8] **HEBAE**: Hierarchical Empirical Bayes Autoencoder
- [9] **i-LDSC**: Interaction-LD Score Regression
- [10] **MAPIT**: The MArginal ePIstasis Test
- [11] **MAPIT-R**: The MArginal ePIstasis Test for Regions and SNP-Sets
- [12] **MegaLMM**: Mega-scale Linear Mixed Models for Multivariate Genomic Prediction
- [13] **Multioviz**: An Interactive Platform for Analyzing Gene Regulatory Networks
- [14] **mvMAPIT**: The Multivariate MArginal ePIstasis Test
- [15] **NCLUSION**: Nonparametric Clustering of Single-cell Populations
- [16] **RATE**: RelATive cEntrality Measures for Variable Prioritization
- [15] **recall**: Calibrated Clustering with Artificial Variables
- [18] **SECT**: The Smooth Euler Characteristic Transform
- [19] **SINATRA**: Pipeline for Sub-Image Analysis and Feature Selection on 3D Shapes
- [20] **SINATRA Pro**: Protein Structure and Conformation Analysis using Topological Summary Statistics
- [21] **SME**: The Sparse Marginal Epistasis Test
- [22] **Tropix**: Tropical Sufficient Statistics for Persistent Homology

#### AWARDS & FELLOWSHIPS

Clark Atlanta University 40 Under 40 Young Alumni Achievement Award	2023
Committee of Presidents of Statistical Societies (COPSS) Emerging Leader Award	2023
International Association for Intelligent Biology and Medicine (IAIBM) 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 Dissertation 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) NIH/NIGMS Title: <i>COBRE Center for Central Nervous System Function</i> Role: Core B Co-Investigator	09/01/18 – 09/08/20
2U10CA180794 (PIs Gray and Gatsonis) NIH/NCI/Dana Farber Cancer Institute Title: <i>ECOG-ACRIN Network Group Statistics and Data Management Center</i> Role: Biostatistician	03/01/19 – 09/08/20
W81XWH-18-1-018 (PI Somarelli) DoD/PCRP Title: <i>Targeting the p38/Snail/PD-L1 axis in Hormone-therapy Resistance and Metastasis</i> Role: Co-Investigator	09/01/18 – 08/31/21
P20GM109035 (PI Rand) NIH/NIGMS Title: <i>COBRE Center for Computational Biology of Human Disease</i> Project Title: <i>Deep learning Methods for Fine Mapping and Discovery in Genomic Association Studies</i> Role: Principal Investigator of Project	03/01/19 – 02/28/21
FG-2019-11622 (PI Crawford) Alfred P. Sloan Foundation Research Fellowship Title: <i>Interpretable Machine Learning Methods for Genome-wide Association Mapping</i> Role: Principal Investigator	09/15/19 – 09/14/21
2020-71387 (PI Crawford) David & Lucille Packard Foundation Fellowship for Science and Engineering Role: Principal Investigator	10/15/20 – 10/14/25
1R35GM138032-01 (PI Crawford) NIH/NIGMS Title: <i>Interpretable Machine Learning for Characterizing Broad-sense Heritability in Complex Traits and Rare Diseases</i> Role: Principal Investigator	Deferred

**INVITED  
TALKS**

<b>AS ASSOCIATE PROFESSOR / PRINCIPAL RESEARCHER</b>	
Yale University, Department of Biostatistics Seminar Series, New Haven, CT	2025
ENAR Spring Meeting, Invited Session, New Orleans, LA	2025
Columbia University, Department of Biostatistics Seminar Series, New York, NY	2025
Columbia University, Genomics@Columbia Seminar Series, Virtual	2025
UCLA, Department of Computational Medicine Seminar Series, Los Angeles, CA	2025
Flatiron Institute, Center for Computational Biology Seminar, New York, NY	2025
Carnegie Mellon-University of Pittsburgh, Computational Biology Seminar Series, Pittsburgh, PA	2024
NDiSTEM Conference, Modern Mathematics Workshop, Phoenix, AZ	2024
University of Pennsylvania, The Wharton School Statistics Seminar, Philadelphia, PA	2024

Joint Statistical Meetings, Invited Paper Session, Portland, OR	2024
Biology of Genomes, Computational and Statistical Genomics Session, Cold Spring Harbor, NY	2024
University of Tennessee Health Science Center, Biostatistics Seminar Series, Virtual	2024
Joint Mathematical Meetings, AMS Special Session, San Francisco, CA	2024
Johns Hopkins University, Department of Applied Mathematics and Statistics Seminar, Baltimore, MD	2023
University of Southern California, QCB Seminar Series, Los Angeles, CA	2023
Grace Hopper Celebration, Data Science Lecture, Orlando, FL	2023
Babson College, MAST Seminar Series, Babson Park, MA	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, Virtual	2022
University of Cambridge, MRC Biostatistics Unit Seminar, Cambridge, Virtual	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
<b>AS ASSISTANT PROFESSOR / SENIOR RESEARCHER</b>	
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, Virtual	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, Virtual	2022
University of Pennsylvania, Bioinformatics Seminar Series, Virtual	2022
Toronto Bioinformatics Users Group (TorBUG) Seminar Series, Virtual	2022
Joint Mathematical Meetings, AMS Special Session, Seattle, WA	2022
Winston-Salem State University, Math and Stats Club, Virtual	2021
University of Chicago, Department of Statistics Colloquium, Virtual	2021
Penn State, ICDS Symposium, Keynote Speaker, Virtual Meeting	2021
Cornell University, Plant Breeding and Genetic Seminar Series, Virtual	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, Virtual	2021
New York University and ETH Zürich, Math and Data (MAD+) Seminar, Virtual Meeting	2021
Columbia University, DSI Distinguished Speaker Series, Virtual	2021
ProbGen, Quantitative Genetics and Association Mapping Session, Virtual Meeting	2021

University of Michigan, Dept. of Biostatistics Seminar, Virtual	2021
Princeton University, Quantitative and Computational Biology Seminar Series, Virtual	2021
Johns Hopkins University, Dept. of Biostatistics Seminar Series, Virtual	2021
NeurIPS, Topological Data Analysis and Beyond Workshop, Virtual Meeting	2020
University of Colorado, Biostatistics Seminar Series, Virtual	2020
University of Wisconsin-Madison, Dept. of Statistics Seminar, Virtual	2020
University of North Carolina, Dept. of Biostatistics Seminar, Virtual	2020
University of Pennsylvania, The Wharton School Statistics Seminar, Virtual	2020
Rochester Institute of Technology, Mathematical Modeling Seminar, Virtual	2020
The Black Women in Computational Biology Network, Seminar Series, Virtual Meeting	2020
Joint Statistical Meetings, Biometrics Invited Session, Virtual	2020
Stanford University, Statistics Department Seminar, Virtual	2020
Brown University, Rhode Island IDeA Symposium (Invited Science Talk), Virtual	2020
University of Arkansas for Medical Sciences, Biomedical Informatics Seminar, Virtual	2020
Microsoft Research New England, Colloquium 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); Institute of Mathematical Statistics (IMS); International Society for Bayesian Analysis (ISBA)

**SERVICE ACTIVITIES**

**EDITORIAL SERVICE**

*Biostatistics* (Associate Editor) 2021 – Present  
*Journal of the American Statistical Association* (AE of Reproducibility) 2018 – Present

**EXTERNAL SERVICE**

National Academies Frontiers of Statistics Committee 2024 – Present

ENAR Regional Committee (RECOM)	2024 – Present
COPSS-NISS Leadership Webinar Series Organizing Committee	2024 – Present
IMS Outreach Committee	2023 – Present
ENAR Fostering Diversity in Biostatistics Workshop (Planning Committee)	2022 – Present
ISBA Section on Biostats and Pharma (Treasurer)	2021 – 2023
ENAR Regional Advisory Board	2020 – 2022

**PROFESSIONAL SERVICE**

Committee of Presidents of Statistical Societies (COPSS) Emerging Leader Award Role: Committee Member	2025
ENAR Spring Meeting, New Orleans, LA Role: Awards Committee (RECOM Representative)	2025
Banff International Research Station (BIRS), Alberta, Canada Statistical, Computational, Translational, and Ethical Challenges in Biobank Data Analysis Role: Co-Organizer	2024
Biology of Genomes, Cold Spring Harbor, NY Session: Computational and Statistical Genomics Role: Co-Chair	2024
ENAR Spring Meeting, Baltimore, MD Role: Program Committee	2024
Advances in the Genetic Architecture of Complex Human Traits Workshop, Washington, D.C. National Human Genome Research Institute Role: Scientific Organizing Committee	2023
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 Session: Quantitative Genetics and Association Mapping Role: Co-Chair	2021
Intelligent Systems for Molecular Biology (ISMB), Virtual Meeting European Conference on Computational Biology (ECCB), Virtual Meeting Role: Proceedings Program Committee	2021

**REVIEWER SERVICE**

*American Journal of Human Genetics; Annals of Applied Statistics; Bioinformatics; Biostatistics; BMC Bioinformatics; Conference on Neural Information Processing Systems (NeurIPS); Genes; Genome Research; 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 Cardiovascular Research; Nature Genetics; Nature Methods; Nature Protocols; 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
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**DOCTORAL STUDENTS**

Alan DenAdel (Computational Biology)	Present
Cecile Meier-Scherling (Computational Biology; Co-advisee)	Present
Chibuikem Nwizu (Computational Biology)	Present
Whitney Sloneker (Computational Biology; Co-advisee)	Present
Julian Stamp (Computational Biology)	Present
Ria Vinod (Computational Biology)	Present
Alexandra Wong (Computational Biology)	Present
Emily Winn-Nuñez (Applied Mathematics)	2024
Dana Udwin (Biostatistics)	2023
Ashley Conard (Computational Biology)	2022
Wai Shing Tang (Physics)	2022
Wei Cheng (Computational Biology; Co-advisee)	2022

**DOCTORAL DISSERTATION COMMITTEES**

Courtney Shearer ( <b>External:</b> Harvard University)	Present
Anushka Narayanan (Earth, Environmental, and Planetary Sciences)	Present
Robert Zielinski (Biostatistics)	Present
Alyandra Zhang (Cognitive Linguistic & Psychological Sciences)	Present
Haobo Yang (Chemistry)	Present
Vivek Ramanan (Computational Biology)	Present
Jiaqi Zhang (Computer Science)	Present

Nick Machnik ( <b>External:</b> Institute of Science and Technology Austria)	2024
Rachel Gaither (Epidemiology)	2024
Dilum Aluthge (Computational Biology)	2024
Isaac Kim (Computational Biology)	2024
Qing Wu (Computational Biology)	2023
Pinar Demetci (Computational Biology)	2023
Kun Meng (Biostatistics)	2022
Topi Paananen ( <b>External:</b> 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**

Tara Amruther (Biostatistics)	2024
Colin Small (Biotechnology)	2023
Alexander Li (Biostatistics)	2021
Isaac Zhao (Biostatistics)	2019
Bruce Wang (Data Science Institute)	2018

**UNDERGRADUATE HONORS THESIS ADVISING**

Ryan Huang (Computer Science)	Present
Helen Xie (Computer Science)	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**

Ajay Nadig (Harvard)	2024
Anay Gupta (Georgia Tech)	2024
Kasia Kedzierska (Oxford)	2023
Zeinab Navidi (University of Toronto)	2023
Giovanni Palla (Helmholtz Munich)	2023
Avish Vijayaraghavan (Imperial College London)	2023
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

