

Wesley Lawrence Crouse

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Education

PhD, Bioinformatics and Computational Biology, University of North Carolina at Chapel Hill, NC,
Fall 2019. Mentors: Dr. Samir Kelada and Dr. William Valdar.

BA, Economics and Mathematics, Minor in History, University of North Carolina at Chapel Hill, NC,
Spring 2011.

Professional Experience

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| 2021 – Present | Department of Human Genetics, The University of Chicago, Chicago, IL.

<u>Postdoctoral Scholar</u> – Supervised by Xin He and Matthew Stephens. Developing and applying statistical methods for prioritizing causal genes and tissues in transcriptome-wide association studies. |
| 2020 – 2021 | Department of Genetics, University of North Carolina at Chapel Hill, NC.

<u>Postdoctoral Research Associate</u> – Supervised by Samir Kelada, Terry Furey, and William Valdar. Developed Bayesian model selection approach for mediation analysis. Assessed differential gene expression and chromatin accessibility in response to ozone exposure in mouse airway macrophages. Applied correlation network and mediation analysis to gene expression in rat adipose. |
| 2014 – 2019 | Department of Genetics, University of North Carolina at Chapel Hill, NC.

<u>Graduate Research Assistant</u> – Supervised by Samir Kelada and William Valdar. Developed Bayesian nonparametric approach for haplotype-based genetic association. Designed simulation-based power analyses for QTL mapping in a multiparental population. |
| 2011 – 2014 | RTI International, Research Triangle Park, NC.

<u>Associate Economist</u> – Public Health and Economics Program. Conducted literature reviews and performed statistical analyses for CDC-contracted research. |

2009 (Summer) The Motley Fool, Washington, D.C.

Intern – CAPS Department. Developed software to track returns for quantitative hedge fund. Analyzed performance of stock recommendation services.

Teaching Experience

2015, 2017 (Summer) How to Learn to Code, University of North Carolina at Chapel Hill, NC.

Instructor – “Introduction to R.” Student-organized course for graduate students without prior programming experience. Lectured and developed curriculum.

2015 (Fall) Curriculum in Bioinformatics and Computational Biology, University of North Carolina at Chapel Hill, NC.

Teaching Assistant – “BCB 720 Introduction to Statistical Modeling.” Required course for BCB graduate students. Held office hours, graded assignments, and lectured.

2010 (Summer) Morehead Planetarium and Science Center, Chapel Hill, NC.

Counselor – Summer Science Camps. Led elementary and middle school students through experiential learning curricula in astronomy and physics.

Honors and Awards

BA with Highest Honors and Distinction
Morehead-Cain Scholar
Phi Beta Kappa
Dean’s List—7 of 8 undergraduate semesters

Technical Skills

Most experienced – R, Stan, Excel
Some experience – Bash, Python
Used in the past – Stata, VBA

Preprints and Working Papers

Zhao S*, **Crouse W***, Qian S, Luo K, Stephens M, He X (under review) Adjusting for genetic confounders in transcriptome-wide association studies leads to reliable detection of causal genes. *bioRxiv*. <https://doi.org/10.1101/2022.09.27.509700>

Aygün N, Liang D, **Crouse W**, Keele G, Love M, Stein J (under review) Inferring cell-type-specific causal gene regulatory networks during human neurogenesis. *bioRxiv*. <https://doi.org/10.1101/2022.04.25.488920>

Peer-Reviewed Publications

Le T, **Crouse W**, Keele G, Holl K, Seshie O, Tschannen M, Craddock A, Das S, Szalanczy A, McDonald B, Grzybowski M, Klotz J, Sharma N, Geurts A, Key C, Hawkins G, Valdar W, Mott R, Solberg Woods L (2022) Genetic mapping of multiple metabolic traits identifies novel genes for adiposity, lipids and insulin secretory capacity in outbred rats. *Diabetes* 72(1):135-148. <https://doi.org/10.2337/db22-0252>

Crouse W*, Keele G*, Gastonguay M, Churchill G, Valdar W (2022) A Bayesian Model Selection Approach to Mediation Analysis. *PLOS Genetics* 18(5): e1010184. <https://doi.org/10.1371/journal.pgen.1010184>

Crouse W*, Das S*, Le T, Keele G, Holl K, Seshie O, Craddock L, Sharma N, Comeau M, Langefeld C, Hawkins G, Mott R, Valdar W, Solberg Woods L (2022) Transcriptome-wide Analyses of Adipose Tissue in Outbred Rats Reveal Genetic Regulatory Mechanisms Relevant for Human Obesity. *Physiological Genomics* 54(6): 206-219. <https://doi.org/10.1152/physiolgenomics.00172.2021>
▪ Excellence in Research award (top 6 articles from 11/2021-11/2022); June 2022 APSselect collection

Tovar A*, **Crouse W***, Smith G, Thomas J, Keith B, McFadden K, Moran T, Furey T, Kelada S (2022) Integrative Analysis Reveals Mouse Strain-Dependent Responses to Acute Ozone Exposure Associated with Airway Macrophage Transcriptional Activity. *American Journal of Physiology - Lung Cellular and Molecular Physiology* 322(1): L33-L49. <https://doi.org/10.1152/ajplung.00237.2021>

Crouse W, Kelada S, Valdar W (2020) Inferring the Allelic Series at QTL in Multiparental Populations. *Genetics* 216(4): 957-983. <https://doi.org/10.1534/genetics.120.303393>.
▪ Selected by editors for 2020 Spotlight collection; highlight in December 2020 issue

Tovar A, Smith G, Thomas J, **Crouse W**, Harkema J, Kelada S (2020) Transcriptional Profiling of the Murine Airway Response to Acute Ozone Exposure. *Toxicological Sciences* 173(1): 114-130. <https://doi.org/10.1093/toxsci/kfz219>

Keele G*, **Crouse W***, Kelada S, Valdar W (2019) Determinants of QTL Mapping Power in the Realized Collaborative Cross. *G3: Genes, Genomes, Genetics* 9(5): 1707-1727. <https://doi.org/10.1534/g3.119.400194>

- Subramanian S, Tangka F, Ekwueme D, Trogon J, **Crouse W**, Royalty J (2015) Explaining Variation Across Grantees in Breast and Cervical Cancer Screening Proportions in the NBCCEDP. *Cancer Causes and Control* 26(5): 689-95. <https://doi.org/10.1007/s10552-015-0569-5>
- Hoerger T, **Crouse W**, Zhuo X, Gregg E, Albright A, Zhang P (2015): Medicare's Intensive Behavioral Therapy for Obesity: An Exploratory Cost-Effectiveness Analysis. *American Journal of Preventive Medicine* 48(4): 419-25. <https://doi.org/10.1016/j.amepre.2014.11.008>
- Ekwueme D, Subramanian S, Trogon J, Miller J, Royalty J, Li C, Tangka F, Guy G, **Crouse W**, Thompson H, Gardner J (2014) Cost of Services Provided by the National Breast and Cervical Cancer Early Detection Program. *Cancer* 120(S16): 2604-611. <https://doi.org/10.1002/cncr.28816>
- Trogon J, Ekwueme D, Subramanian S, **Crouse W** (2013) Economies of Scale in Federally-Funded State-Organized Public Health Programs: Results from the National Breast and Cervical Cancer Early Detection Program. *Health Care Management Science* 17(4): 321-30. <https://doi.org/10.1007/s10729-013-9261-z>
- Wittenborn J, Zhang X, Feagan C, **Crouse W**, Shrestha S, Kemper A, Hoerger T, Saaddine J (2013) The Economic Burden of Vision Loss and Eye Disorders among the United States Population Younger than 40 Years. *Ophthalmology* 120(9): 1728-735. <https://doi.org/10.1016/j.ophtha.2013.01.068>

Presentations

- Crouse W***, Zhao S*, Luo K, Qian S, Stephens M, He X (2022, October): "Adjusting for genetic confounders leads to reliable detection of causal genes from transcriptome-wide association studies." Poster presentation at American Society of Human Genetics Annual Meeting in Los Angeles, CA.
- Zhao S*, **Crouse W***, Luo K, Stephens M, He X (2022, May): "An extended fine-mapping framework to identify causal genes from transcriptome-wide association studies." Virtual poster presentation at Biology of Genomes in Cold Spring Harbor, NY.
- Crouse W**, Kelada S, Valdar W (2019, February): "Tree-Based Inference of Multiallelism via Bayesian Regression." Oral presentation at the Gordon Research Seminar and Conference on Quantitative Genetics and Genomics in Lucca, Italy.
- Crouse W**, Kelada S, Valdar W (2019, February): "Tree-Based Inference of Multiallelism via Bayesian Regression." Oral presentation at the Gordon Research Seminar and Conference on Quantitative Genetics and Genomics in Lucca, Italy.
- Crouse W**, Kelada S, Valdar W (2019, February): "Tree-Based Inference of Multiallelism via Bayesian Regression." Oral presentation at the Gordon Research Seminar and Conference on Quantitative Genetics and Genomics in Lucca, Italy.

Crouse W, Kelada S, Valdar W (2018, May): “Tree-Based Inference of Multiallelism via Bayesian Regression.” Poster presentation at the Population, Evolutionary and Quantitative Genetics Conference in Madison, WI.

Crouse W, Kelada S, Valdar W (2017, June): “Tree-Based Inference of Multiallelism via Bayesian Regression.” Oral presentation at the Complex Trait Community Meeting in Memphis, TN.

Crouse W, Kelada S, Valdar W (2017, February): “Tree-Based Inference of Multiallelism via Bayesian Regression.” Poster presentation at the Gordon Research Seminar and Conference on Quantitative Genetics and Genomics in Galveston, TX.

Crouse W, Kelada S, Valdar W (2016, June): “Bayesian Inference of the Allelic Series at Quantitative Trait Loci in Multiparent Populations.” Poster presentation at the International Conference on Quantitative Genetics 5 in Madison WI.

Crouse W, Valdar W, Kelada S (2015, June): “Efficient Detection of Trans-eQTL in Incipient Lines of the Collaborative Cross.” Poster presentation at the Complex Trait Community Meeting in Portland, OR.

Crouse W, Valdar W, Kelada S (2015, March): “Efficient Detection of Trans-eQTL in Incipient Lines of the Collaborative Cross.” Poster presentation at the Population-Based Rodent Resources for Environmental Health Sciences Meeting in Durham, NC.

Other Works

Crouse W (2011): Victim Identification and Dishonest Behavior. Unpublished honors thesis, University of North Carolina at Chapel Hill.

Research Support

T32 ES007126 05/15/2020 – 02/15/2021 9.0 calendar months
Pre- and Postdoctoral Training in Toxicology

T32 GM067553 08/01/2015 – 04/30/2015 9.0 calendar months
Predoctoral Training Program in Bioinformatics and Computational Biology

Professional Service

2007 - 2011 Campus Y, University of North Carolina at Chapel Hill, Chapel Hill, NC.

Director of Programming, Special Projects Coordinator, First-Year Member at Large. Largest social justice organization on UNC campus. Assessed new project applications for the Campus Y umbrella. Overhauled process for new project applications. Provided feedback and capacity building for existing projects.