

Lucille Porter

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SUMMARY

Statistical genetics researcher completing a Ph.D. in Biostatistics in 2026, with four years of doctoral research developing and applying quantitative methods for human genetic, genomic, and multiomic data. Research includes **genetic association analysis**, fine mapping, xQTL analysis, colocalization, TWAS, and molecular trait integration for complex disease biology. Proficient in R, Linux, HPC workflows, simulation studies, **reproducible scientific computing**, documented research software, and rigorous analysis of large datasets. Manuscript preparation, scientific presentations, collaborative research, and transparent computational practices connect methodological work with interpretable biological questions. Research on context dependent regulation and aging related molecular phenotypes supports future studies of **Alzheimer's disease** and the aging brain, with a clear foundation for developing an **independent research direction**.

EDUCATION

Ph.D. in Biostatistics	2026
University of Michigan GPA: 4.0	Ann Arbor, MI
<i>Coursework: Statistical genetics, functional genomics, biostatistics, human genetic data analysis</i>	
Bachelor's Degree in Statistics	2021
University of Wisconsin Madison GPA: 4.0	Madison, WI
<i>Coursework: Statistical inference, regression analysis, probability, computational statistics</i>	

TECHNICAL SKILLS

- **Programming Languages:** R, Bash, Linux shell
- **Statistical Genetics:** Genetic association analysis, fine mapping, linkage disequilibrium
- **Functional Genomics:** xQTL analysis, eQTL analysis, TWAS
- **Molecular Data:** Transcriptomics, multiomic integration, molecular phenotypes
- **Statistical Methods:** Simulation studies, regression, multiple testing
- **Computing Systems:** Linux, HPC, scheduled computing
- **Research Software:** Documented software, reusable R functions, version control
- **Reproducibility:** Reproducible reports, provenance records, environment specifications
- **Genomic Analysis:** Quality control, genomic files, phenotype data
- **Scientific Communication:** Manuscript preparation, scientific presentations, research seminars

SKILLS

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|------------------------|------------------------------|----------------------|--------------------------|
| • R | • Genomic data analysis | • xQTL analysis | • Reproducible computing |
| • Statistical genetics | • Multiomic data integration | • Colocalization | • Documented software |
| • Functional genomics | • Association analysis | • TWAS | • Linux |
| • Human genetics | • Fine mapping | • Simulation studies | |

EXPERIENCE

Doctoral Researcher, Statistical Genetics	September 2024 - October 2026
University Research Lab	Ann Arbor, MI
Led doctoral research across statistical genetics and functional genomics , developing methods, computational workflows, and scientific outputs for human genetic and molecular phenotype studies.	
• Developed context dependent genetic regulation models, then evaluated operating characteristics through simulations and applied analyses. • Built R workflows for association analysis and fine mapping across large genomic datasets using Linux and HPC scheduling. • Integrated eQTL evidence with disease signals through colocalization analyses, documenting assumptions and diagnostic outputs for collaborators. • Implemented TWAS analyses linking predicted molecular traits with complex phenotypes and functional genomic evidence. • Maintained version controlled research software, environment specifications, and reproducible reports for auditable computational results. • Drafted manuscript methods and results, then presented statistical findings to interdisciplinary research audiences.	
Graduate Research Assistant, Multiomic Data Integration	September 2023 - August 2024
Academic Research	Ann Arbor, MI

Supported quantitative research integrating genotype, transcriptomic, and regulatory data while building reusable analysis components and simulation frameworks for complex trait studies.

- Designed genotype and **transcriptomic** integration analyses that prioritized candidate mechanisms underlying complex human traits.
- Conducted simulations varying effect size, **linkage disequilibrium**, sample size, and molecular architecture to characterize method behavior.
- Developed reusable **R functions** for harmonization, **quality control**, testing, and visualization with documented checks.
- Ran **Linux** and HPC analyses while organizing jobs, logs, outputs, and **provenance records** for genomic datasets.
- Evaluated fine mapped loci against xQTL and functional genomic evidence, guiding follow up analyses and manuscript figures.
- Presented research progress at lab meetings and forums, incorporating feedback into revised models and validation plans.

Graduate Researcher, Human Genomics Methods

September 2022 - August 2023

University Project

Ann Arbor, MI

Conducted supervised human **genomics** research, translating statistical methods into reproducible analyses of curated genotype and phenotype datasets for academic evaluation.

- Investigated genetic association methods using curated **human genotype** and phenotype datasets under faculty supervision.
- Implemented association testing and **multiple testing** procedures in R, comparing calibration and power across datasets.
- Constructed reproducible notebooks covering cleaning, exploration, model fitting, diagnostics, and interpretation for research deliverables.
- Used Linux command line tools and scheduled computing resources to process genomic files reproducibly.
- Reviewed literature on **linkage disequilibrium**, **causal variant prioritization**, and molecular QTLs to inform project design.
- Delivered written methods reports and oral presentations distinguishing findings, uncertainty, and methodological limitations.

Biostatistics Research Trainee

September 2021 - August 2022

Student Lab

Ann Arbor, MI

Completed supervised quantitative research exercises in **biostatistics** and human genetics, building practical foundations in statistical inference, genomic analysis, and reproducible computing.

- Completed supervised research exercises using human genetics examples involving probability, regression, inference, and genomic analysis.
- Programmed R simulations examining sampling variability, model assumptions, type I error, and statistical power.
- Cleaned and summarized teaching datasets containing genotype and phenotype variables with structured quality checks.
- Practiced reproducible computing through scripted workflows, organized directories, data dictionaries, and generated reports.
- Participated in journal discussions on genetic association and **functional genomics**, preparing concise technical critiques.
- Presented a supervised final analysis to graduate seminar participants, explaining evidence and methodological limitations clearly.

PROJECTS

Context Dependent Regulation Methods

 2026

Developed and evaluated statistical methods for nonlinear genetic regulation, using simulation studies and human molecular phenotype data to assess performance and interpretability.

Multimic Evidence Integration

 2024

Integrated genotype, transcriptomic, regulatory, xQTL, and disease association evidence to prioritize mechanisms underlying complex human traits.

LEADERSHIP & AWARDS

- Graduate Research Fellowship, 2024
- Outstanding Graduate Research Presentation, 2025
- Dean's List, 2020
- Graduate Quantitative Methods Peer Mentor, 2024 to 2026

CERTIFICATIONS

- Reproducible Research Practices Certificate  2023
- Linux for Scientific Computing  2022

PROFESSIONAL AFFILIATIONS

- Genomics Journal Club Coordinator, 2023 to 2025
- Graduate Quantitative Methods Peer Mentor, 2024 to 2026

LANGUAGES

- English (Native)
- Spanish (Intermediate)

ADDITIONAL INFORMATION

Work Status : Authorized to work in United States. No sponsorship required.

REFERENCES

AVAILABLE ON REQUEST