

# Nathan Riley Summers LaPierre

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<b>CURRENT POSITION</b>	<i>Postdoctoral Research Fellow</i> Department of Medical Oncology Dana-Farber Cancer Institute Lab of Alexander Gusev	Mar. 2025 - Present
<b>OTHER RECENT POSITIONS</b>	<i>Postdoctoral Scholar and Fellow</i> Department of Human Genetics University of Chicago Labs of Xin He and Matthew Stephens	Aug. 2022 - Mar. 2025
<b>EDUCATION</b>	PhD in Computer Science, June 2022 University of California, Los Angeles Labs of Eleazar Eskin and Wei Wang	
	M.S. in Computer Science, March 2019 – 3.74 GPA University of California, Los Angeles	
	B.S. in Applied Computer Science, December 2015 – 3.86 GPA ( <i>magna cum laude</i> ) George Mason University	
<b>RECENT COMPETITION RESULTS</b>	Arc Institute Virtual Cell Challenge (Nov. 2025) 1st in Pearson Correlation, 10th in Generalist Rankings, 38th Overall (out of 1265+ total entrants in validation and final rounds)	
<b>PUBLICATIONS</b>	For all research software, please see: <a href="https://github.com/nlapier2/">https://github.com/nlapier2/</a> Google Scholar: <a href="https://scholar.google.com/citations?user=EVMceKUAAAJ&amp;hl=en">https://scholar.google.com/citations?user=EVMceKUAAAJ&amp;hl=en</a>	
	Z. Lu, Y. Ding, <b>N. LaPierre</b> , et al, “Integrating perturbational screens, eQTL, and GWAS data identifies mediating genes for complex traits,” <i>medRxiv</i> , Jan. 2026.	
	A. Khan, J. Bagley, <b>N. LaPierre</b> , et al, “Differing Genetics of Saline and Cocaine SelfAdministration in the Hybrid Mouse Diversity Panel,” <i>Genes, Brain and Behavior</i> , vol. 24, no. 3, pp. e70029, June 2025.	
	P. B. Chen, R. Chen, <b>N. LaPierre</b> , et al, “Complementation testing identifies genes mediating effects at quantitative trait loci underlying fear-related behavior,” <i>Cell Genomics</i> , vol. 4, no. 5, pp. 100545, May 2024. PubMed PMID: 38697120.	
	M. Alser, ..., <b>N. LaPierre</b> , ..., “Packaging and containerization of computational methods,” <i>Nature Protocols</i> , vo. 19, no. 9, pp. 2529-2539, Apr. 2024. PubMed PMID: 38565959.	
	<b>N. LaPierre</b> and Harold Pimentel, “Accounting for Isoform Expression in eQTL Mapping Substantially Increases Power,” <i>PLOS Computational Biology</i> , vol. 20,	

no. 2, pp. e1011857, Feb. 2024. PubMed PMID: 38346082. PubMed Central PMCID: PMC10890775.

A. Khan, J. Bagley, **N. LaPierre**, et al, "Genetic pathways regulating the longitudinal acquisition of cocaine self-administration in inbred and recombinant inbred mice," *Cell Reports*, vol. 42, no. 8, pp. 112856, Aug. 2023. PubMed PMID: 37481717; PubMed Central PMCID: PMC10530068.

**N. LaPierre\***, B. Fu\*, S. Turnbull, E. Eskin, and S. Sankararaman, "Leveraging family data to design Mendelian Randomization that is provably robust to population stratification," *Genome Research*, vol. 33, pp. 1032-1041, July 2023. PubMed PMID: 37197991; PubMed Central PMCID: PMC10538495.

B. Fuqua, ... **N. LaPierre**, ..., "The Genetic Architecture of Dietary Iron Overload and Associated Pathology in Mice," *bioRxiv*, June 2023.

J. Karlin, L. Gai, **N. LaPierre**, et al, "Ensemble neural network model for detecting thyroid eye disease using external photographs," *British Journal of Ophthalmology*, Sep. 2022. PubMed PMID: 36126104.

F. Meyer, ... **N. LaPierre**, ..., "Critical Assessment of Metagenome Interpretation—the second round of challenges," *Nature Methods*, vol. 19, pp. 429440, Apr. 2022. PubMed PMID: 35396482; PubMed Central PMCID: PMC9007738.

C. Cinelli, **N. LaPierre**, B. L. Hill, S. Sankararaman, and E Eskin, "Robust Mendelian randomization in the presence of residual population stratification, batch effects and horizontal pleiotropy," *Nature Communications*, vol. 13, no 1., pp. 1093, Mar. 2022. PubMed PMID: 35232963; PubMed Central PMCID: PMC8888767.

**N. LaPierre\***, K. Taraszka\*, H. Huang, R. He, F. Hormozdiari, and E. Eskin, "Identifying Causal Variants by Fine Mapping Across Multiple Studies," *PLOS Genetics*, vol. 17, no. 9, pp. e1009733, Sept. 2021. PubMed PMID: 34543273; PubMed Central PMCID: PMC8491908.

J. Bloom et al (many authors), "Massively scaled-up testing for SARS-CoV-2 RNA via next-generation sequencing of pooled and barcoded nasal and saliva samples," *Nature Biomedical Engineering*, vol. 5, no. 7, pp. 657-665, July 2021. PubMed PMID: 34211145.

**N. LaPierre**, M. Alser, E. Eskin, D. Koslicki\*, and S. Mangul\*, "Metalign: Efficient alignment-based metagenomic profiling via containment min hash," *Genome Biology*, vol. 21, pp. e242, Sep. 2020. PubMed PMID: 32912225; PubMed Central PMCID: PMC7488264.

**N. LaPierre**, R. Egan, W. Wang, and Z. Wang, "De novo Nanopore read quality improvement using deep learning," *BMC Bioinformatics*, vol. 20, no. 1, pp. e552, Dec. 2019. PubMed PMID: 31694525; PubMed Central PMCID: PMC6833143.

**N. LaPierre**, C. Ju, G. Zhou, and W. Wang, "MetaPheno: A Critical Evaluation of Deep Learning and Machine Learning in Metagenome-Based Disease Prediction," *Methods*, vol. 166, pp. 74-82, Aug. 2019. PubMed PMID: 30885720; PubMed Central PMCID: PMC6708502.

**N. LaPierre\***, S. Mangul\*, M. Alser, I. Mandric, N.C. Wu, D. Koslicki, and E.

Eskin, “MiCoP: Microbial Community Profiling method capable of detecting low abundance viral and fungal organisms in metagenomic samples,” *BMC Genomics*, vol. 20, no. 5, pp. e423, June 2019. PubMed PMID: 31167634; PubMed Central PMCID: PMC6551237.

M. A. Rahman, **N. LaPierre**, H. Rangwala, and D. Barbara, “Metagenome sequence clustering with hash-based canopies,” *Journal of bioinformatics and computational biology*, vol. 15, no. 6, pp.1740006, Oct. 2017. PubMed PMID: 29113561.

M. A. Rahman, **N. LaPierre**, and H. Rangwala, “Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL),” *IEEE/ACM transactions on computational biology and bioinformatics*, Oct. 2017. PubMed PMID: 28981422.

**N. LaPierre**, M. A. Rahman, and H. Rangwala, “CAMIL: Clustering and Assembly with Multiple Instance Learning for Phenotype Prediction,” in *IEEE International Conference on Bioinformatics and Biomedicine*, Shenzhen, China, 2016.

**N. LaPierre** and H. Rangwala, “Predicting Clinical Phenotype using OTU-based Metagenome Representation,” in *IEEE International Conference on Data Mining Workshop on Biological Data Mining and its Applications in Healthcare*, Atlantic City, New Jersey, 2015, pp. 156-163.

(\* Authors contributed equally)

## CONFERENCE TALKS

“Pleiotropy-robust methods for high-dimensional multivariable Mendelian randomization,” in *STATGEN 2024: Conference on Statistics in Genomics and Genetics*, May 2024.

“Leveraging family data to design Mendelian Randomization that is provably robust to population stratification,” in *International Conference on Research in Computational Molecular Biology (RECOMB)*, Apr. 2023.

“Metalign: Efficient alignment-based metagenomic profiling via containment min hash,” in *Intelligent Systems for Molecular Biology (ISMB) HitSeq*, virtual, July 2020.

“Identifying Causal Variants by Fine Mapping Across Multiple Studies” in *International Conference on Research in Computational Molecular Biology (RECOMB)*, virtual, June 2020.

“Metalign: Efficient alignment-based metagenomic profiling via containment min hash,” in *RECOMB-Seq*, virtual, June 2020.

“CAMIL: Clustering and Assembly with Multiple Instance Learning for Phenotype Prediction” in *IEEE International Conference on Bioinformatics and Biomedicine*, December 2016.

“Predicting Clinical Phenotype using OTU-based Metagenome Representation” in *IEEE International Conference on Data Mining workshop on Biological Data Mining and its Applications in Healthcare*, November 2015.

## CONFERENCE POSTERS

“Accounting for Isoform Expression in eQTL Mapping,” in *CSHL Genome Information*

matics, virtual, Nov. 2021.

“Identifying Causal Variants by Fine Mapping Across Multiple Studies” in American Society for Human Genetics Annual Meeting, October 2019.

“MiniScrub: de novo long read scrubbing using approximate alignment and deep learning” in Amazon Web Services - UCLA Computational Medicine Symposium, February 2019.

“MiniScrub: de novo long read scrubbing using approximate alignment and deep learning” in American Society for Human Genetics Annual Meeting, October 2018.

“MiCoP: Microbial Community Profiling method capable of detecting low abundance viral and fungal organisms in metagenomic samples” in American Society for Human Genetics Annual Meeting, October 2017.

“Developing a Computational Pipeline for Metagenomic State Classification with Feature Engineering” in Volgenau School of Engineering Undergraduate Research Celebration, April 2015

- Won Outstanding Undergraduate Research Project Award for poster

## FUNDING AND AWARDS

Fellowships and Merit-Based Scholarships

- NIH T32 HL007605 - *Research Training in Respiratory Biology*, July 2023-2024, University of Chicago
- *ModEling and uNdersTanding human behaviOR (MENTOR) NSF Training Grant*, 2018-19 academic year at UCLA
- NIH T32 Doctoral Training Fellowship, 2016-18 academic years at UCLA
- Bersoff Endowed Scholarship, Outstanding Academic Achievement, Awarded twice in 2015 and 2014
- SWIFT Scholarship, Outstanding Academic Achievement, Awarded in 2015

Selected Honors

- Honorable Mention in NSF Graduate Research Fellowship, 2015-16
- Outstanding Undergraduate Student Award, given to overall best undergraduate student in Computer Science at George Mason University, May 2016
- Outstanding Academic Achievement Award, given for outstanding performance in Computer Science, May 2016
- Outstanding Undergraduate Research Project for presentation of my research project at Volgenau School of Engineering Undergraduate Research Symposium, April 2015
- Outstanding Undergraduate Teaching Assistant for two semesters of excellence as a teaching assistant, April 2015
- Dean’s List every semester

Technical Competitions

- Top 5 at VTHacks, a software development competition at Virginia Tech with over 45 teams, April 2014
- 2nd Place in the Technical Innovation Challenge, a week-long competition at George Mason University to design a viable software product, jointly refereed by Computer Science and Business Departments, October 2014

## TEACHING EXPERIENCE

Graduate Teaching Assistant

Spring 2020

CS/BIOINFO 122/222 - Algorithms in Bioinformatics, Computer Science Department, UCLA

Graduate Teaching Assistant Winter 2020  
CS/BIOINFO 124/224 - Machine Learning in Genomics, Computer Science Department, UCLA

Undergraduate Teaching Assistant Fall 2014 - Spring 2015  
CS 306 - Computer Law and Ethics, Computer Science Department, George Mason University

- Received Outstanding Undergraduate Teaching Assistant Award
- Assisted students with legal research, writing, and oral communication
- Responsible for grading student assignments worth 25% of their grade; one of the only Undergraduate Teaching Assistants entrusted with this responsibility

**VOLUNTEERING, ORGANIZATIONS, AND LEADERSHIP** Diversity, Equity, and Inclusion Committee – University of Chicago Departments of Human Genetics and Genetics, Genomics, & Systems Biology 2023 - present

- Participated in monthly discussions to plan and organize events and resources promoting DEI initiatives for the HG and GGSB departments
- Currently revising a yearly survey to be sent out to survey the DEI “climate” in these departments

Student-Run Computing and Technology (SRCT) 2013 - 2016  
• Student organization at George Mason University that works on software projects and competitions to benefit the university and broader local community  
• Secretary and Member of Executive Board, Fall 2015 Semester

Executive Curriculum Planner and Mentor, Community Programming Initiative George Mason University Honors College and SRCT 2014 - 2015  
• Volunteer effort to teach basic programming to local 5th-8th grade students  
• Planned and developed parts of the curriculum for the sessions, such as designing games and hints to help the students create them  
• Mentored the elementary and middle school students during the sessions

**COMPUTATIONAL SKILLS** Languages / Scripting: Fluent in Python, R, Bash; past experience with C(++) and Java

Deep Learning Frameworks: PyTorch, Keras

Other Technologies: Git, Docker, LaTeX

Bioinformatics experience: Single cell RNA-seq and Perturb-seq; Mendelian randomization; GWAS & statistical fine mapping; alignment; assembly; metagenomics; common software such as Scanpy, AnnData, Plink, Bedtools, Samtools, Bcftools, etc; SGE and Slurm grid/cluster computing systems

Machine Learning Algorithms: Deep Learning, Linear & Logistic Regression, SVMs, Random Forests, etc

Operating Systems: Linux, Windows, macOS

**INTERNSHIPS** Graduate Student Researcher Summer 2017  
DOE Joint Genome Institute / Lawrence Berkeley National Lab

- Developed a method that uses a Convolutional Neural Network (Deep learning method) to improve Oxford Nanopore long read quality *de novo*
- Method improves both read accuracy and downstream *de novo* assembly
- Helped pioneer use of deep learning within the lab

- Wrote secure and scalable software and worked with Big Data in order to help analyze, detect, and prevent attacks on Sony's networks
- Used Python, Javascript (Node, Express, Meteor), MongoDB, X/HTML, CSS
- Developed a workplace communications system using Meteor.js; solo project
- Assisted in the development of a web application based on a searchable database system using Node.js, Express.js, and MongoDB
- Assisted in the development of a network forensics system; wrote backend python scripts and XML web layouts