Nathan Riley Summers LaPierre

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RECENT POSITIONS

Postdoctoral Scholar and Fellow　　　　　　　　　Aug. 2022 - Present
Department of Human Genetics, University of Chicago
Labs of Xin He and Matthew Stephens
(Scholar, Aug. 2022 - May 2023; Fellow, June 2023 - Present)

Graduate Student Researcher　　　　　　　　　Sep. 2016 - June 2022
Department of Computer Science, University of California, Los Angeles
Labs of Eleazar Eskin and Wei Wang

EDUCATION

PhD in Computer Science, June 2022
University of California, Los Angeles

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 (*magna cum laude*)
George Mason University

PUBLICATIONS

For all research software, please see: https://github.com/nlapier2/

P. B. Chen, R. Chen, **N. LaPierre**, et al, "Complementation testing identifies genes mediating effects at quantitative trait loci underlying fear-related behavior," *Cell Genomics*, vol. 4, no. 5, pp. 100545, May 2024. PubMed PMID: 38697120.

M. Alser, ..., **N. LaPierre**, ..., "Packaging and containerization of computational methods," *Nature Protocols*, vo. 19, no. 9, pp. 2529-2539, Apr. 2024. PubMed PMID: 38565959.

N. LaPierre and Harold Pimentel, "Accounting for Isoform Expression in eQTL Mapping Substantially Increases Power," *PLOS Computational Biology*, 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 Informatics*, 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: Mendelian randomization; GWAS & statistical fine mapping; alignment; assembly; metagenomics; common software such as 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 Berkelely 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

Security Engineering Intern   Summers 2013-2015
Sony Corporation of America
- 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