

# Nathan LaPierre

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## EDUCATION

PhD in Computer Science, 2016 - June 2022 (Expected)  
University of California, Los Angeles

M.S. in Computer Science, 3.74 GPA, March 2019  
University of California, Los Angeles

B.S. in Applied Computer Science, 3.86 GPA (*magna cum laude*), December 2015  
George Mason University

## PUBLICATIONS

**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.

F. Meyer et al (many authors), "Critical Assessment of Metagenome Interpretation—the second round of challenges," *bioRxiv*, July 2021.

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, Sep. 2020.

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," *bioRxiv*, Oct. 2020.

**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.

**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.

**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.

**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.

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.

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.

**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)

**PRESENTATIONS** (Upcoming) “Accounting for Isoform Expression in eQTL Mapping,” in *CSHL Genome Informatics*, virtual, Nov. 2021.

“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), June 2020.

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

“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.

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

- Won a conference travel grant sponsored by NSF

“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 14, 2015

- Won a travel grant from the Undergraduate Student Travel Fund of the Office of Student Scholarship, Creative Activities, and Research at GMU

“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

## RESEARCH EXPERIENCE

### *PhD Student*

University of California, Los Angeles

September 2016 - Present

- Working with Professors Wei Wang, Eleazar Eskin, and Harold Pimentel
- Developed a method for identifying causal variants (statistical fine mapping) by leveraging information from multiple studies using a Bayesian approach
- Developing multiple Mendelian Randomization methods providing sensitivity analysis and robustness to confounding from population structure
- Contributed to the effort to develop & deploy a saliva-based COVID-19 test (“Swab-Seq”) that is now deployed campus-wide at UCLA
- Developing a method for isoform-aware eQTL mapping
- Developed multiple published methods that perform accurate abundance profiling of microbial organisms based on metagenomic reads
- Developed a method that uses deep learning to improve long sequencing read quality, in collaboration with scientists from the Joint Genome Institute
- Two-time teaching assistant (courses: Computational Genetics and Machine Learning in Genetics), given an average rating of 8 out of 9 by my students
- Mentored four undergraduate summer students, two of whom are now PhD students

### *Graduate Research Assistant (GRA) / Student Researcher*

George Mason University

January - August 2016 (June-August as GRA)

- Worked with Professor Huzefa Rangwala
- Developed CAMIL, a pipeline that uses multiple instance learning techniques based on whole metagenome shotgun sequence reads to predict whether or not a patient has a disease.
- CAMIL paper accepted into IEEE BIBM 2016 (19% acceptance rate).
- Second author of paper on using canopy clustering and locality sensitive hashing to reduce clustering time for biological datasets.

### *Predicting Clinical Phenotype using OTU-based Metagenome Representation*

George Mason University

January 2015 - November 2015

- Worked with Professor Huzefa Rangwala
- Developed a computational pipeline that uses clustering and classification methods to quickly and accurately predict whether a patient has a disease based on a case/control metagenomic dataset
- Paper accepted for publication, and poster presentation won Outstanding Undergraduate Project Award (see publications and presentations sections)

## WORK EXPERIENCE

### *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

### *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

**TEACHING  
EXPERIENCE**

*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

**AWARDS,  
FELLOWSHIPS,  
SCHOLARSHIPS**

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

Fellowships and Merit-Based Scholarships

- *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

Honors Societies and Organizations

- *Honors College* at George Mason University
- *Alpha Lambda Delta Honor Society*
- *Golden Key International Honour Society*

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

- VOLUNTEER EXPERIENCE** 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:* Python, R, C, Matlab/Octave, bash  
*Deep Learning Frameworks:* Keras, TensorFlow, PyTorch  
*Other Technologies:* Git, Docker, LaTeX  
*Operating Systems:* Linux, Windows, macOS  
*Experience with:*
- Machine Learning Algorithms: Deep Learning, Linear Regression, Logistic Regression, SVMs, Random Forests, etc
  - Machine Learning Applications: Clustering, Classification, Bioinformatics
  - Bioinformatics methods experience: statistical fine mapping, alignment, assembly, read error correction, metagenomics, abundance profiling
  - SGE and Slurm grid/cluster computing systems
- MEMBERSHIPS AND LEADERSHIP** *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