

Nikhil Milind

Education

Stanford University

PH.D. IN GENETICS
NSF GRFP Fellow

PALO ALTO, CALIFORNIA
SEPTEMBER 2022 - JUNE 2028 (EXPECTED)

University of Cambridge

M.PHIL. IN BIOLOGICAL SCIENCES
Wellcome Sanger Institute
Churchill Scholar

CAMBRIDGE, UNITED KINGDOM
SEPTEMBER 2021 - AUGUST 2022

North Carolina State University

B.S. IN GENETICS • B.S. IN COMPUTER SCIENCE • MINOR IN MATHEMATICS
Biological Sciences Honors Program • Engineering Honors Program
Park Scholar • Goldwater Scholar • Phi Beta Kappa • Summa Cum Laude

RALEIGH, NORTH CAROLINA
AUGUST 2017 - MAY 2021

Research Experience

M.Phil. Student

DAVENPORT LAB, HUMAN GENETICS, WELLCOME SANGER INSTITUTE

CAMBRIDGE, UNITED KINGDOM
OCTOBER 2021 - PRESENT

Transcriptomic Analysis of Sepsis Cohort

I am using quantitative phenotypes developed from gene co-expression modules from whole blood leukocytes to identify module quantitative trait loci (mQTL). These variants are associated with broad variation in gene expression and identify *trans* factors in a disease context.

Colocalization and Fine Mapping of Molecular QTL

I am colocalizing expression quantitative trait loci (eQTL) detected in leukocytes with protein quantitative trait loci (pQTL) in plasma from the same cohort. I am also colocalizing eQTL with our set of mQTL. I am using statistical fine mapping approaches to identify credible sets for these molecular QTL.

Functional Annotation of Molecular QTL Variants

I am using publicly-available epigenomic datasets of primary blood cell types in stimulated and unstimulated conditions to better understand biological mechanisms underlying the effects of these QTL variants.

Undergraduate Research Assistant

AYLOR LAB, BIOLOGICAL SCIENCES, NORTH CAROLINA STATE UNIVERSITY

RALEIGH, NORTH CAROLINA
OCTOBER 2017 - MAY 2021

Meta-Analysis of RNA-Seq in Multiparental Mouse Populations

I curated publicly-available data from four separate studies involving mice from the Collaborative Cross (CC) and Diversity Outbred (DO) populations. I developed a custom RNA-seq pipeline to align the data for samples with mosaic genomes. I identified eQTL in liver tissue based on allele-specific gene expression derived from the RNA-seq alignment.

Meta-Analysis of Expression Quantitative Trait Loci

I conducted a meta-analysis of two pre-Collaborative Cross mouse studies to identify shared modules of expression quantitative trait loci (eQTL). Mice from the two studies were exposed to dust mite allergen and Influenza A respectively. I performed weighted correlation network analysis and categorized previously mapped eQTL to better understand the genetic architecture of context-specific regulatory elements.

Quantitative Trait Locus Mapping

I mapped clinical phenotypes measured in a Diversity Outbred mouse cohort. I used a Hidden Markov Model to reconstruct haplotype probabilities for the mice. I mapped clinical phenotypes, such as body weight and blood glucose, to identify QTL associated with changes in diet.

Research Intern

CARTER LAB, THE JACKSON LABORATORY

BAR HARBOR, MAINE

JUNE 2018 - AUGUST 2019

Mapping of Composite Phenotypes in Alzheimer's Disease (May 2019 - August 2019)

I finished the analysis of three human Late-Onset Alzheimer's Disease cohorts that I started the previous summer. I mapped quantitative traits developed from molecular subtypes in a genome-wide association study. I explored new techniques including Mendelian Randomization and Bayesian Networks.

Weighted Network Correlation Analysis of Metabolomics Data (May 2019 - August 2019)

I performed weighted network correlation analysis using WGCNA on metabolomics data. This process was used to identify modules of co-abundant metabolites.

Identifying Molecular Subtypes in Alzheimer's Disease (June 2018 - August 2018)

I developed a computational methodology to refine harmonized co-expression modules that were generated for three human Late-Onset Alzheimer's Disease cohorts. I used these modules to cluster decedents into subtypes based on their molecular profiles.

Research Intern

CHURCHILL LAB, THE JACKSON LABORATORY

DURHAM, NORTH CAROLINA

AUGUST 2016 - MAY 2017

QTL and Bayesian Network Analysis of Mouse Obesity Cohort

I identified the effects of *Fbn1* and its downstream products on glucose and energy metabolism. I utilized linkage mapping tools to determine the relationship between *Fbn1* and other genes in the pathway. I learned about causal network analysis and mediation analysis.

Professional Experience

Committee Chair and Software Developer

WEB COMMITTEE, SERVICE RALEIGH

RALEIGH, NORTH CAROLINA

SEPTEMBER 2017 - MAY 2021

Service Raleigh is an annual citywide day of service, where volunteers from the university and surrounding community unite to undertake a variety of projects, each of which provides much needed assistance to local organizations. I was responsible for communicating needs from the executive team and delegating tasks to my committee members. I developed new features for the organization's website. I work with a professional version control system (git/GitHub) and develop in Python/JavaScript.

Intern Software Developer for Senior Design Project

SAS, RTP, NORTH CAROLINA

RALEIGH, NORTH CAROLINA

AUGUST 2020 - NOVEMBER 2020

I developed a Natural Language Processing (NLP) methodology with the assistance of our sponsors at SAS. Our project, named GIST, classifies data files using an open-source taxonomy, identifies keywords in the data, and generates a business purpose for the data. Our open-source implementation is built in Python.

Research Skills

Analysis of Omics Data

- RNA-seq alignment and processing.
- ATAC-seq alignment and processing.
- Gene weighted co-expression network analysis.

Genetic Mapping of Traits

- Quantitative trait locus mapping in mouse mapping populations.
- Single-variant association mapping in human cohorts.

Statistics and Machine Learning

- Implementing machine learning models.
- Performing statistical tests and quantifying uncertainty.

Computational Analysis and Visualization

- Extensive experience in using the R programming language to perform data analysis in a biological context.
- Experience in using the Python programming language to build machine learning models.
- Visualizing complex data using tools in the R programming language.
- Using Python, Java, Javascript, and the C++ programming languages for general purpose programming.

Software Engineering and High-Performance Computing

- Experience working on large software engineering projects (iterative workflow and agile management).
- Workflow management with Nextflow and experience with multiple high-performance computing environments.
- Familiarity with version management systems (Git and GitHub) and Unix operating system.

Relevant Coursework

B.S. Genetics, North Carolina State University

Genome Science • Introduction to Machine Learning in Biology • Population, Quantitative, and Evolutionary Genetics • Quantitative Biology • Personal Genomics • Human and Biomedical Genetics • Molecular Genetics • Developmental Genetics

B.S. Computer Science, North Carolina State University

Automated Learning and Data Analysis • Computational Methods in Molecular Biology • Uncertainty Quantification • Introduction to Artificial Intelligence • Software Engineering • Data Structures • C and Software Tools • Concepts in Operating Systems • Computer Organization and Assembly • Introduction to Probability • Linear Algebra

Extracurricular Activities

Student Conduct Board Member

RALEIGH, NORTH CAROLINA

STUDENT CONDUCT BOARD, NORTH CAROLINA STATE UNIVERSITY

OCTOBER 2017 - MAY 2021

I was responsible for reviewing potential violations of the Code of Student Conduct and educating students about the rules, policies, and regulations of the Code.

Park Scholar

RALEIGH, NORTH CAROLINA

NORTH CAROLINA STATE UNIVERSITY

AUGUST 2017 - MAY 2021

NC State University's Park Scholarship is a highly selective, full merit scholarship awarded on the basis of outstanding accomplishments and potential in scholarship, leadership, service, and character. I participated in a four-year, executive-style leadership academy; diversity training; a year-long civic engagement project; and intensive learning laboratories exploring leadership challenges regionally and nationally.

Publications

Wells A, Barrington WT, Dearth S, **Milind N**, Carter GW, Threadgill DW, et al. Independent and Interactive Effects of Genetic Background and Sex on Tissue Metabolomes of Adipose, Skeletal Muscle, and Liver in Mice. 2022 Apr 8;12(4):337. <https://doi.org/10.3390/metabo12040337>

Milind N, Preuss C, Haber A, Ananda G, Mukherjee S, John C, et al. Transcriptomic stratification of late-onset Alzheimer's cases reveals novel genetic modifiers of disease pathology. PLOS Genetics. 2020 Jun 3;16(6):e1008775. <https://doi.org/10.1371/journal.pgen.1008775>

Presentations

Milind N, Burnham KL, Lee W, Mi Y, Goh C, Hinds CJ, Knight JC, Davenport EE. Multi-omics integration to characterise mechanisms of molecular QTL from a sepsis cohort. Poster session presented at: The Biology of Genomes; 2022 May; Cold Spring Harbor, NY.

Milind N, Burnham KL, Lee W, Mi Y, Goh C, Hinds CJ, Knight JC, Davenport EE. Multi-omics integration to characterise mechanisms of molecular QTL from a sepsis cohort. Talk presented at: European Mathematical Genetics Meeting; 2022 Apr; Cambridge, UK.

Milind N, Gillespie K, Aylor DL. Transcriptomic Meta-Analysis of Murine Lung Response in the Collaborative Cross. Poster session presented at: State of North Carolina Undergraduate Research and Creativity Symposium; 2019 Nov; Durham, NC.

Milind N, Preuss C, Fine A, Logsdon B, Carter G. Deciphering quantitative phenotypes in complex diseases using gene co-expression modules. Poster session presented at: State of North Carolina Undergraduate Research and Creativity Symposium; 2018 Nov; Raleigh, NC.

Fellowships

NATIONAL

2021 **Recipient**, National Science Foundation Graduate Research Fellowship ALEXANDRIA, VA

The NSF GRFP recognizes and supports outstanding graduate students in NSF-supported STEM disciplines who are pursuing research-based master's and doctoral degrees at accredited US institutions.

2021 **Recipient**, Churchill Scholarship CAMBRIDGE, UNITED KINGDOM

The Churchill Scholarship provides funding to American students for a year of Master's study at the University of Cambridge, based at Churchill College. The program was set up at the request of Sir Winston Churchill in order to fulfill his vision of US-UK scientific exchange with the goal of advancing science and technology on both sides of the Atlantic, helping to ensure our future prosperity and security.

2019 **Recipient**, Barry Goldwater Scholarship ALEXANDRIA, VA

The Goldwater Scholarship Program, one of the oldest and most prestigious national scholarships in the natural sciences, engineering, and mathematics in the United States, seeks to identify and support college sophomores and juniors who show exceptional promise of becoming this Nation's next generation of research leaders in these fields.

2017 **Recipient**, Park Scholarship RALEIGH, NC

The Park Scholarship is a four-year scholarship awarded on the basis of outstanding accomplishments and potential in scholarship, leadership, service, and character.

Honors and Awards

INTERNATIONAL

2021 **Finalist**, Gates-Cambridge Scholarship CAMBRIDGE, UK

2017 **1st Place**, International Mathematical Modeling Competition BOSTON, MA

NATIONAL

2020 **Recipient**, Genetics Society of America Undergraduate Travel Award WASHINGTON, DC

2017 **1st Place**, Mathematical Competition in Modeling DURHAM, NC

2017 **1st Place**, High School Mathematical Competition in Modeling DURHAM, NC

UNIVERSITY

2021 **Recipient**, Department of Biological Sciences Outstanding Research Award RALEIGH, NC

2021 **Recipient**, Donald L. Bitzer Creativity Award RALEIGH, NC

2021 **Recipient**, Department of Computer Science Senior Award for Leadership RALEIGH, NC

2019 **Recipient**, Student Conduct Board Member of the Year RALEIGH, NC

2018 **Recipient**, Web Committee Member of the Year RALEIGH, NC