

# Nuo "Ivy" Liu

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**PhD candidate with research interest in single-cell technologies, computational methods and precision medicine with applications to infectious disease and cancer research**

## Education

### Massachusetts Institute of Technology (MIT)

Cambridge, MA,  
USA

Ph.D. candidate in Computational and Systems Biology (CSB), GPA: 4.9/5.0

Fall 2020-Present

Advisor: Prof. Alex K. Shalek

### Harvey Mudd College

Claremont, CA,  
USA

B.S. in Mathematical and Computational Biology, GPA: 3.95/4.0

September  
2016-May 2020

- Graduated with High Distinction, Honors in Biology, Honors in Computer Science
- Humanities concentration in *Economics*
- Dean's List for all previous applicable semesters

## Awards and Honors

2023-24	David H. Koch Graduate Fellowship,	Koch Institute, Massachusetts Institute of Technology
2020	Computer Science Class of '94 Award, recognizes graduates with outstanding record in a combination of coursework, research and service Finalist for the <i>CRA Outstanding Undergraduate Researcher Awards</i> , recognizes undergraduate students in North American colleges and universities who show outstanding research potential in an area of computing research	CS Department, Harvey Mudd College
2020		Computing Research Association
2019	W.A. Brandenburger Biology Prize, awarded annually to a senior biology major for outstanding performance and promise in the field of biology	Biology Department, Harvey Mudd College
2019	First-Tier Traveling Fellowship,	17th Asia Pacific Bioinformatics Conference
2017	CRC Handbook Prize, awarded for outstanding performance in chemistry in the first year	Chemistry Department, Harvey Mudd College

## Research Experience

### Massachusetts Institute of Technology

Cambridge, MA

GRADUATE RESEARCHER ADVISED BY **DR. ALEX K. SHALEK**

Jun 2021- present

- Developed a broadly applicable experimental and computational framework for scaling up phenotypic screens on *ex vivo* models (Liu\*, Kattan\*, Mead\*, Kummerlove\* et al., *Nature Biotechnology*, 2024).
- Leveraging single-cell profiling and meta-analyses, identified molecular and cellular differences between healthy and tuberculosis (TB)-diseased human lung tissue, including a central role for myofibroblast-like populations in TB pathogenesis and lung remodeling (Manuscript in preparation)
  - *Collaborator*: Al Leslie (AHRI, South Africa)
- Use single-cell transcriptomics to understand functional mechanism for the effect of long-term growth hormone administration on early metabolic dysfunction-associated steatotic liver disease (MASLD, or NAFLD) patients (Manuscript in preparation)
  - *Collaborators*: Georg Lauer (MGH), Laura Dichtel (MGH)

### Westlake University

Hangzhou, China

SUMMER RESEARCH INTERN ADVISED BY **DR. TIANNAN GUO**

Jul-Aug 2020

- Built and trained a LSTM-based deep learning model on pan-human tissues using fragment sequence and charge state to predict ion mobility value (Pearson's  $r > 0.98$ )
- Predicted ion mobility values for mouse liver proteomics data generated using two non-timsTOF equipments (Thermo Orbitrap, tripleTOF), compared library search results using ion mobility-supplemented libraries and timsTOF library

SENIOR THESIS RESEARCHER ADVISED BY **DR. ELIOT BUSH**

- Year-long thesis research under the Biology Department titled *Reconstructing Gene Family Evolution in Microbes Using DTLOR Algorithm*
- Explored ways to break down a family of genes into distinct groups with similar syntenic information
- Extend the Duplication Transfer Loss model to include new events to reconstruct the evolutionary history of prokaryotic organisms more comprehensively

**Baylor College of Medicine**

Houston, TX  
Summer 2019

SUMMER RESEARCH INTERN ADVISED BY **DR. PAVEL SUMAZIN**

- Researched on phylogeny Inference from Gene Expression Profiles of Multiple Sections per Tumor at the Department of Pediatrics
- Designed a method that estimates cell-type specific expression from bulk tumor profiles using a hierarchical approach that exploits a Linear Programming solution to reconstruct the transcriptional evolution of tumors

**Baylor College of Medicine**

Houston, TX  
Summer 2018

SUMMER RESEARCH INTERN ADVISED BY **DR. CRISTIAN COARFA**

- Worked on RNA-Seq, microarray and gene enrichment analysis
- Built and trained a Convolutional Neural Network to predict epigenetic remarking events in rat liver genome under environmental influence
- Extracted *de novo* DNA motifs related to epigenetic reprogramming using trained model

**Harvey Mudd College**

Claremont, CA  
Summer 2017

SUMMER RESEARCH INTERN ADVISED BY **DR. RAN LIBESKIND-HADAS, DR. YI-CHIEH WU**

- Extended the dynamic programming algorithm for phylogenetic tree reconciliation under Duplication-Loss-Coalescence(DLC) evolution model to optimize Pareto-optimal solutions
- Tested the correctness of the algorithm and built tool to visualize the event cost landscape
- Showed the reconciliation algorithm is robust to event costs and inferred event support across optimal reconciliations

**Harvey Mudd College**

Claremont, CA  
Spring 2017

SUMMER RESEARCH INTERN ADVISED BY **DR. CATHERINE MCFADDEN**

- Investigated feasibility of using 28S rDNA for genetic barcoding to differentiate species within coral genus *Sinularia*
- Utilized computational tools to edit sequencing results and built gene tree
- Research resulted in promise for using 28S rDNA barcoding to the less economical whole-genome sequencing in coral species identification

## Publication

- **Liu, N.**<sup>#</sup>, Mbano I. M.<sup>#</sup>, Wardsworth II, M. H., Asowata, O. E., Nyquist, S., Nargan, K., Ramsuran, D., Karim, F., Hughes, T. K., Bromley, J. D., Chambers, M. J., Krause, R., Tezera, L. B., Reichmann, M. T., Kløverpris, H. N., Dullabh, K. J., Madansein, R., Steyn, A. J. C., Berger, B., Elkington, P., Shalek, A. K., Leslie, A. Single-cell RNA-sequencing highlights the central role of fibroblasts in tuberculosis-infected human lung tissue (In preparation; <sup>#</sup>Co-first authors).
- **Liu, N.**<sup>#</sup>, Kattan, W. E.<sup>#</sup>, Mead, B. E.<sup>#</sup>, Kummerlowe, C.<sup>#</sup>, Cheng, T., Cheah, J. H., Soule, C. K., Peters, J., Lowder, K. E., Blainey, P. C., Hahn, W. C., Cleary, B., Bryson, B., Winter, P. S., Raghavan, S., & Shalek, A. K. (2024). *Scalable, compressed phenotypic screening using pooled perturbations*, **Nature Biotechnology**, 2024 (<sup>#</sup>Co-first authors).
- **Liu, N.**, Gonzalez, T. A., Fischer, J., Hong, C., Johnson, M., Mawhorter, R., Mugnatto, F., Soh, R., Somji, S., Wirth, J. S., Libeskind-Hadas, R., & Bush, E. C. (2023). xenoGI 3: Using the DTLOR model to reconstruct the evolution of gene families in clades of microbes. **BMC Bioinformatics**, 24(1), 295.
- Raghavan, S., Winter, P. S., Navia, A. W., Williams, H. L., DenAdel, A., Lowder, K. E., Galvez-Reyes, J., Kalekar, R. L., Mulugeta, N., Kapner, K. S., Raghavan, M. S., Borah, A. A., **Liu, N.**, Väyrynen, S. A., Costa, A. D., Ng, R. W. S., Wang, J., Hill, E. K., Ragon, D. Y., ... Shalek, A. K. (2021). Microenvironment drives cell state, plasticity, and drug response in pancreatic cancer. **Cell**, 184(25), 6119-6137.e26.
- H. Du, Y. S. Ong, M. Knittel, R. Mawhorter, **Liu, N.**, G. Gross, R. Tojo, R. Libeskind-Hadas, & Y.-C. Wu. (2021). Multiple Optimal Reconciliations Under the Duplication-Loss-Coalescence Model. **IEEE/ACM Transactions on Computational Biology and Bioinformatics**, 18(6), 2144–2156.
- Liu, J., Mawhorter, R., **Liu, N.**, Santichaivekin, S., Bush, E., & Libeskind-Hadas, R. (2021). Maximum parsimony reconciliation in the DTLOR model. **BMC Bioinformatics**, 22(10), 394.
- Carothers, M., Gardi, J., Gross, G., Kuze, T., **Liu, N.**, Plunkett, F., Qian, J., & Wu, Y.-C. (2020). An Integer Linear Programming Solution for the Most Parsimonious Reconciliation Problem under the Duplication-Loss-Coalescence Model. **Proceedings of the 11th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics**.
- Mawhorter, R., **Liu, N.**, Libeskind-Hadas, R., & Wu, Y.-C. (2019). Inferring Pareto-optimal reconciliations across multiple event costs under the duplication-loss-coalescence model. **BMC Bioinformatics**, 20(20), 639.

## Seminars and conference presentations

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Oct. 2025	Invited talk titled <b>Compressed phenotypic screening empowers scalable biological discovery</b> , MIT CSB program retreat	Kennebunkport, ME
May. 2024	Selected oral presentation titled <b>Compressed phenotypic screening empowers scalable biological discovery</b> , Single-Cell Genomics Conference GRC	Les Diablerets, Switzerland
Feb. 2024	Presentation on research project <b>Compressed Screening: High-throughput measurement and perturbation of tissues and tissue-derived cellular models</b> , Microsoft Research New England Project ex vivo internal workshop	Cambridge, MA, USA
Oct. 2023	Poster presentation on research project <b>Single-cell Profiling of Tuberculosis-Infected Human Lung</b> , MIT Computational and Systems Biology program retreat	Kennebunkport, ME, USA
Jul. 2022	Presentation on research project <b>Putative drivers of cellular plasticity in glioblastoma</b> , NCI Human Tumor Atlas Network (HTAN) internal meeting	Cambridge, MA, USA
Nov. 2019	Presentation on research project <b>"Reconstructing Gene Family Evolution in Microbes Using DTOR Algorithm"</b> , Senior thesis proposal presentation	Claremont, CA, USA
Jul. 2019	Presentation on research project <b>"Tumor Phylogeny Inference from Gene Expression Profiles of Multiple Tumor Mixture Samples"</b> , Baylor College of Medicine SMART program final symposium	Houston, TX, USA
Jan. 2019	Selected oral presentation titled <b>"Multiple Optimal Reconciliations under the Duplication-Loss-Coalescence Model"</b> , 17th Asia and Pacific Bioinformatics Conference	Wuhan, China
Jul. 2018	Presentation on project project <b>"Predicting de novo Motifs Using Convolutional Neural Network"</b> , Baylor College of Medicine SMART program final symposium	Houston, TX, USA

## Teaching, mentoring and outreach

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### Mentoring at Shalek Lab

#### MASSACHUSETTS INSTITUTE OF TECHNOLOGY

- Ankit Basak, Chemistry graduate Student
- Sam Lizotte (Ragon Institute RISE summer intern), high school student from Brockton High School - 2024
- Sarish Ray (Ragon Institute RISE summer intern), undergraduate student from UMass Amherst - 2024
- Amy Huang, rotation student - 2024
- Eric Gai, rotation student - 2023
- Hannah Ramcharan, rotation student - 2022

### Teaching Assistant

#### MASSACHUSETTS INSTITUTE OF TECHNOLOGY

Served as TA for Modern Biostatistics (7.093) and Modern Computational Biology (7.094). Designed and led weekly recitations and office hours, and worked with instructors to design course materials and graded problem sets and exams

### Teaching volunteer

#### MIT SPARK PROGRAM

Worked with two other graduate students to devise a two-part course on immunology for 30+ local 7th and 8th grade students

### Trainer

#### 2024 HCA ASIA SINGLE-CELL OMICS WORKSHOP AT MAHIDOL UNIVERSITY

Designed teaching materials and held lectures and labs for computational training sessions on single-cell analysis for a one-week workshop with participants across Asia

Cambridge, MA  
Spring 2022

Cambridge, MA  
March 2022

Thailand  
June 2024

## Additional Experience

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### MIT-China Innovation and Entrepreneurship Forum

#### CO-PRESIDENT, DIRECTOR OF PLANNING TEAM

Worked on planning online fireside chats, invited talks and day-long annual forum during pandemic. Built a consistent program of events for MIT and local students and young professionals to learn about technology and innovation and identify entrepreneurial potentials

Cambridge, MA  
2020 - 2023

### CSB Application Assistance Program

#### EXECUTIVE BOARD, SECRETARY, FUND MANAGER

Helped establish the application assistance program for the Computational and Systems Biology PhD program at MIT. Secured Grad Student Experience Grant from Office of Graduate Education at MIT to kick-start the first year of the program.

Cambridge, MA  
2021-2022