Nuo “Ivy” Liu

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PhD candidate in Computational and Systems Biology with expertise in single-cell technologies, computational methods and precision medicine with applications to infectious disease and cancer research

Education

Massachusetts Institute of Technology — *Cambridge, MA*
Ph.D. candidate in Computational and Systems Biology , GPA: 4.9/5.0 — *2020-Present*
Advisor: Prof. Alex K. Shalek

Harvey Mudd College — *Claremont, CA*
B.S. in Mathematical and Computational Biology, GPA: 3.95/4.0 — *2016-2020*

- High Distinction, Honors in Biology and Computer Science
- Humanities, Social Sciences, and the Arts (HSA) concentration in *Economics*
- Dean’s List recipient across all eligible semesters

Awards and Honors

2023-24	David H. Koch Graduate Fellowship,	*Koch Institute, MIT*
2020	Computer Science Class of ’94 Award, recognizes graduates with outstanding record in a combination of coursework, research and service	*Harvey Mudd College*
2020	Finalist for the *CRA Outstanding Undergraduate Researcher Awards*, recognizes undergraduate students in North American colleges and universities who show outstanding research potential in an area of computing research	*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** — *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)
  - *MIT News coverage*: ”A new framework to efficiently screen drugs”
  - *Nature Biotechnology Briefing*: ”A framework for expanding discovery efforts with compressed phenotypic screens ”
- 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** — *2020*

- Built and trained a LSTM-based deep learning model across human tissues using fragment sequence and charge state to predict ion mobility value (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

Harvey Mudd College — *Claremont, CA*
Senior thesis researcher advised by **Dr. Eliot Bush** — *2019-2020*

- 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 Research Intern Advised by **Dr. Pavel Sumazin** *2019*

- 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 Research Intern Advised by **Dr. Cristian Coarfa** *2018*

- 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 research intern Advised by **Dr. Ran Libeskind-Hadas**, **Dr. Yi-Chieh Wu** *2017*

- 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*

Summer research intern Advised by **Dr. Catherine McFadden** *2017*

- 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

Publications

- **Liu, N.**$^{\#}$, Mbano I. M.$^{\#}$, 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; $^{\#}$Co-first authors).
- **Liu, N.**$^{\#}$, Kattan, W. E.$^{\#}$, Mead, B. E.$^{\#}$, Kummerlowe, C.$^{\#}$,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 ($^{\#}$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). dblquoteMaximum 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

Oct. 2024	Invited talk titled ***Single-cell profiling reveals a role for tuberculosis-induced myofibroblasts in the immunopathology of infected lungs***, Ragon Institue Work-In-Progress Seminar	*Cambridge, MA*
Oct. 2024	Invited talk titled ***Compressed phenotypic screening empowers scalable biological discovery*** , MIT CSB program retreat	*Kennebunkport, ME*
May. 2024	Selected oral presentation titled ***Compressed phenotypic screening empowers scalable biological discovery*** , GRC Single-Cell Genomics Conference	*Les Diablerets, Switzerland*
Feb. 2024	Invited talk titled ***Compressed phenotypic screening empowers scalable biological discovery*** , MIT CSB program open house	*Cambridge, MA*
Feb. 2024	Presentation on research project ***Compressed Screening: High-throughput measurement and perturbatio nof tissues and tissue-derived cellular models***, Microsoft Research New England Project *ex vivo* internal workshop	*Cambridge, MA*
Oct. 2023	Poster presentation on research project ***Single-cell Profiling of Tuberculosis-Infected Human Lung***, MIT CSB program retreat	*Kennebunkport, ME*
Jul. 2022	Presentation on research project ***Putative drivers of cellular plasticity in glioblastoma***, NCI Human Tumor Atlas Network (HTAN) internal meeting	*Cambridge, MA*
Nov. 2019	Presentation on research project ”***Reconstructing Gene Family Evolution in Microbes Using DTLOR Algorithm***”, Senior thesis proposal presentation	*Claremont, CA, USA*
Jul. 2019	Presentation on research project ”***Tumor Phylogeny Inference from Gene Expression Profiles of Multiple Tumor Mixture Samples***”, Baylor College of Medicine SMART program final symposium	*Houston, TX*
Jan. 2019	Selected oral presentation titled ”***Multiple Optimal Reconciliations under the Duplication-Loss-Coalescence Model***”, *17th Asia and Pacific Bioinformatics Conference*	*Wuhan, China*
Jul. 2018	Presentation on project project”***Predicting de novo Motifs Using Convolutional Neural Network***”, Baylor College of Medicine SMART program final symposium	*Houston, TX*

Teaching, mentoring and outreach

Mentoring at Shalek Lab
MASSACHUSETTS INSTITUTE OF TECHNOLOGY

- Ankit Basak, MIT Chemistry graduate Student
- Sam Lizotte, Ragon Institute RISE summer intern - 2024
- Sarish Ray, Ragon Institute RISE summer intern - 2024
- Amy Huang, MIT CSB rotation student - 2024
- Eric Gai, MIT CSB rotation student - 2023
- Hannah Ramcharan, MIT CSB rotation student - 2022

Trainer *Thailand*
2024 HCA ASIA SINGLE-CELL OMICS WORKSHOP AT MAHIDOL UNIVERSITY *June 2024*
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

CSB Application Assistance Program *Cambridge, MA*
EXECUTIVE BOARD, SECRETARY, FUND MANAGER *2021-2022*
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.

Teaching Assistant *Cambridge, MA*
MASSACHUSETTS INSTITUTE OF TECHNOLOGY *Spring 2022*

- **Modern Biostatistics** (7.093)
- **Modern Computational Biology** (7.094)

Teaching volunteer *Cambridge, MA*
MIT SPARK PROGRAM *March 2022*
Worked with two other graduate students to devised a two-part course on immunology for 30+ local 7th and 8th grade students

Biology Academic Excellence Program Facilitator *Claremont, CA*
HARVEY MUDD COLLEGE *2019-2020*
Developed weekly workshops to help students improve their understanding of concepts in the core biology courses and teach problem solving skills.

Teaching Assistant *Claremont, CA*
HARVEY MUDD COLLEGE *2017 - 2022*

- **CS5** (Intro to CS)
- **CS60** (Principles of Computer Science)
- **CS133** (Database Systems)
- **CS158** (Machine Learning)
- **MCB118b** (Introduction to Computational Biology)

Additional Experience

MIT-China Innovation and Entrepreneurship Forum *Cambridge, MA*
CO-PRESIDENT, DIRECTOR OF PLANNING TEAM *2020 - 2023*
Oversaw event planning and execution during the pandemic, building a strong program of fireside chats and annual forums. Built a consistent program of events for MIT and local students and young professionals to learn about technology and innovation and identify entrepreneurial potentials. Co-lead the organization of annual MIT-CHIEF forum.

CSB Application Assistance Program *Cambridge, MA*
EXECUTIVE BOARD, SECRETARY, FUND MANAGER *2021-2022*
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.

MIT Graduate Student Council External Affairs Board *Cambridge, MA*
OPERATIONS AND DEVELOPMENT CO-CHAIR *2023*
Helped oversee regular operations of the EAB. This includes developing, documenting, and evaluating the methods used to engage with different types of organizations and policy stakeholders.