Gillian Chu

Email: gc3045@princeton.edu
Homepage: https://gillichu.github.io/

Education

Ph.D. Princeton University Aug 2022 – May 2027 (Expected)
Department of Computer Science
Advisor: Benjamin J. Raphael
M.A. Princeton University *Computer Science* (earned en passant) Aug 2022 – Dec 2024

M.S. University of Illinois at Urbana–Champaign Dec 2020 – Aug 2022
Program in Ecology, Evolution, and Conservation
Thesis: Phylogenetic Placement
Advisor: Professor Tandy Warnow

B.S. University of California, Berkeley Aug 2016 – Dec 2020
Department of Computer Science

H.S.D. Phillips Exeter Academy Aug 2014 – May 2016

Research Interests

Computational Biology, Computational/Statistical Genetics, Probabilistic Graphical Models.
My interests are at the intersection of computer science, statistics, and biology. I design and build tools that help us understand the evolution of complex and heterogeneous biological systems.

Academic Honors and Fellowships

- Computing Research Association – Widening Participation (CRA–WP) Conference (April 2025). *Awarded scholarship.*
- National Cancer Institute: SSACB (2024). *Awarded Best Poster Runner-up.*
- William G. Bowen Merit Fellowship (2023). *Internal Princeton fellowship.*
- RECOMB–CCB Scientific Communications (2022) 1st Place *(Awarded $200).*
- NSF GRFP (2021–2026). *Five-year fellowship, three-year annual stipend of $34,000.*
- Excellent Graduate Student Instructor, UIUC. Spring 2021. *Introduction to Programming for Engineers and Scientists (CS101).*

Other Awards, Travel Grants, and Fellowships

- Eric and Wendy Schmidt Center Symposium: Biomedical Science and AI. *Travel Grant Award (April 2025). Awarded $500.*
- School of Engineering and Applied Sciences (SEAS) Travel Grant Award (May 2024). *Internal Princeton Engineering Travel Grant. Awarded $375.*
- Genetics Society of America: Presidential Membership Initiative (2022). *Awarded 1-year membership to GSA, Early Career Leadership Program and GENETICS Peer Review Training Program.*

Research Experience

Research Assistant, Princeton University Aug 2022 – Present
Advisor: Benjamin J. Raphael

- Designed framework using imaging-based observations for statistical inference of cell lineages.
- Algorithmic design of protein-protein proximity-labeling experiments.
- Designed new evolutionary model to describe CRISPR-based dynamic lineage tracing data, and an efficient algorithm for maximum likelihood single-cell lineage tree inference.

Research Assistant, University of Illinois at Urbana–Champaign Jan 2021 – Present
Advisor: Tandy Warnow

- Designed fast multiple sequence alignment method capable of aligning ultra-large datasets.
- Designed fast and scalable phylogenetic placement methods.

Research Assistant, University of Illinois at Urbana–Champaign Jan 2021 – Dec 2021
Advisor: Mohammed El-Kebir

- Designing interactive visual editor for copy number calls in bulk tumor cell data.

Research Assistant, University of California, Berkeley Sept 2019 – May 2021
Advisor: Priya Moorjani

- Implemented an efficient method of uncovering founder events in modern populations.
- Designed an efficient and accurate local ancestry inference method.

Research Assistant, University of California, Berkeley Sept 2019 – Dec 2020
Advisor: Satish Rao

- Designed a distance-based phylogenetic tree inference algorithm.

Publications

** indicates joint first-author.*

Conference Papers

1. **Chu, G.***, Schmidt. H.*, Raphael, B.J. "LAML-Pro: Joint Maximum Likelihood Inference of Cell Genotypes and Cell Lineage Trees." ISMB 2026.
2. Mai, U.*, **Chu, G.***, Raphael, B.J. "Maximum Likelihood Inference of Time-scaled Cell Lineage Trees with Mixed-type Missing Data." doi:10.1101/2024.03.05.583638. RECOMB 2024.
3. Lalani, Z.*, **Chu, G.***, Zaccaria, S., El-Kebir, M. "User-guided local and global copy-number segmentation for tumor sequencing data." doi:10.1101/2022.01.15.476457v1. RECOMB–CCB 2022.

Journal Papers

1. **Chu, G.***, Schmidt. H.*, Raphael, B.J. "LAML-Pro: Joint Maximum Likelihood Inference of Cell Genotypes and Cell Lineage Trees." *To appear in Bioinformatics.*
2. **Chu, G.***, Mai, U.*, Schmidt, H., Raphael, B.J. "Maximum Likelihood Inference of Time-scaled Cell Lineage Trees with Mixed-type Missing Data." doi:10.1186/s13059-025-03649-9. *Genome Biology*, 2025.
3. **Chu, G.**, Warnow, T. "SCAMPP+FastTree: Improving Scalability for Likelihood-Based Phylogenetic Placement." *Bioinformatics Advances*, 2023.
4. Park, M., Ivanovic, S., **Chu, G.**, Shen, C., Warnow, T. "UPP2: Fast and Accurate Alignment of Datasets with Fragmentary Sequences." *Bioinformatics*, 2023.
5. Lalani, Z.*, **Chu, G.***, Hsu, S., Kagawa, S., Xiang, M., et al. "CNAViz: An interactive webtool for user-guided segmentation of tumor DNA sequencing data." *PLOS Computational Biology*, 2022.
6. Tournebize, R., **Chu, G.**, Moorjani, P. "Reconstructing the history of founder events using genome-wide patterns of allele sharing." *PLOS Genetics*, 2022.

Workshop Papers

1. Wang, Y., Sun, J., Wang, X., Wei, Y., Wu, H., **Chu, G.**, Yu, Z. "Sperax: An Approach to Defeat Long Range Attacks in Blockchains." *IEEE INFOCOM Workshops*, 2020.

Presentations

- Contributed Poster, "LAML-Pro: Joint Maximum Likelihood Inference of Cell Genotypes and Cell Lineage Trees." Probabilistic Modeling in Genomics. March 2026. *Accepted, later withdrawn.*
- Contributed Talk, Computational Genomics Summer Institute: Trainee Talks. June 2025.
- Contributed Poster, "Precision Interactome Mapping to Decipher Protein-Drug Interactions in Cancer." Princeton Catalysis Initiative May 2025.
- Invited Talk, "Reconstructing Time-resolved Cell Lineage Trees from Single-Cell Lineage Tracing Data." STATGEN 2025: Conference on Statistics in Genomics and Genetics, Invited Session: Single-cell biology: New statistical frontiers across different omics. May 2025.
- Invited Talk, "Reconstructing Maximum Likelihood Time-resolved Cell Lineage Trees on Lineage Tracing Data." Yale Student Theory Day. May 2025.
- Contributed Poster, "LAML-Pro: Cell Genotype and Lineage Inference via Efficient Maximum Like-

lihood." Eric and Wendy Schmidt Center Symposium: Biomedical Science and AI. April 2025.

- Contributed Poster, "LAML: Lineage Analysis via Maximum Likelihood." Computing Research Association – Widening Participation (CRA–WP). April 2025.
- Contributed Talk, "LAML: Lineage Analysis via Maximum Likelihood." Cold Spring Harbor Laboratory (CSHL): Biological Data Science, Machine Learning Session. November 2024.
- Contributed Poster, "LAML: Lineage Analysis via Maximum Likelihood." National Cancer Institute (NCI): Spring School on Algorithmic Cancer Biology (SSACB). April 2024.
- Contributed Poster, "SCAMPP+FastTree: Improving Scalability for Likelihood-Based Phylogenetic Placement." International Society for Computational Biology (ISCB) – Latin America. October 2022.
- Contributed Talk, "User-guided local and global copy-number segmentation for tumor sequencing data." Research in Computational Molecular Biology (RECOMB) – Computational Cancer Biology (CCB). May 2022.
- Contributed Poster, "MGDrive: Mosquito Gene Drive Explorer: Landscape Clustering." National Conference on Undergraduate Research. March 2020.
- Invited Talk, "A Technical Overview of Blockchain Development." TiE Inflect Silicon Valley. April 2018.

Teaching Experience

University of Illinois at Urbana–Champaign

- Intro to Programming for Engineers and Scientists (CS101). Graduate Student Instructor, Spring 2021. *Excellent Graduate Instructor Award.*

University of California, Berkeley

- Bioinformatics Bootcamp. Teaching Assistant, Center for Computational Biology. Aug 2020.
- Operating Systems and System Programming (CS162). Reader. Summer 2020.
- Efficient Algorithms and Intractable Problems (CS170). Undergraduate Student Instructor. Fall 2018, Spring 2019, Fall 2019, Spring 2020.
- Discrete Mathematics and Probability (CS70). Reader. Fall 2017, Spring 2018, Summer 2018.
- Building with Blockchain for Web 3.0. Guest Lecturer, IEOR. Spring 2020.
- Blockchain Fundamentals (CS198). Lecturer. Spring 2018, Fall 2018.
- Blockchain for Enterprise. Guest Lecturer, Haas Business. Spring 2019, Fall 2019.
- Blockchain for Lawyers. Guest Lecturer, Boalt Law. Spring 2018.
- EdX Blockchain Fundamentals. Course Advisor. Spring 2018.

Industry Experience

Databricks, San Francisco May – Aug 2019

Software Engineering Intern, Observability Team

- Implemented distributed tracing for performance analysis across microservice architecture.

Sperax Apr 2018 – Oct 2021

- Analyzed consensus protocols for distributed systems and implemented a test net.
- Designed Decentralized Autonomous Organization (DAO) voting protocol and modeled token economics.

Standard Bounties, ConsenSys Jun – Aug 2018

Fullstack Software Engineering Intern

- Built out RESTful API and smart contract web application.

Office of Senator Maria Cantwell, Washington D.C. Feb – Jun 2016

Legislative Intern

- Drafted policy memos and supported constituent communications and tours.

Professional and Community Service

- Panelist, “Imposter Syndrome,” LEAP Alliance: CMD-IT Webinar, April 2026.
- Panelist, “How to Make the Most of PhD Visit Day,” Code to PhD, March 2026.

Reviewer
RECOMB, ISMB, PLOS Computational Biology, ACM BCB.

Mentorship
Undergraduates: Karina Macosko, Sophia Zhou.

Code2PhD
Volunteer Mentor: `https://codetophd.github.io/` Fall 2025

Computer Science Graduate Student Mentorship Program
Co-lead, Princeton University Fall 2024 – Present

Computer Science Graduate Student Committee
Member, Princeton University Fall 2022 – Present

Shield the Bay
Co-Founder / Finance, Berkeley, CA Mar 2020 – Jun 2021

Berkeley ANova
Events Committee Chair, Berkeley, CA Sept 2016 – Jun 2018

Skills and Languages

Programming: Python, Java, C, JavaScript, R, React, Redux, Solidity, Go, Jsonnet, Scala.
Tools/Frameworks: HTML, Git, Django, Docker, AWS, Remix, CircleCI, Webpack, Jenkins, Kubernetes, Grafana.
Genomics: samtools, bwa, GATK.
Languages: English (native), Mandarin (fluent), Spanish (reading proficiency).