

**GILLIAN CHU**Email: [gc3045@princeton.edu](mailto:gc3045@princeton.edu)Homepage: <https://gillichu.github.io/>**EDUCATION**

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<b>PhD</b>	<b>Princeton University</b>	<b>Aug 2022 - May 2027 (<i>Expected</i>)</b>
<b>MA</b>	Master of Arts earned <i>en passant</i> Department of Computer Science Advisor: Benjamin J. Raphael	Aug 2022 – Dec 2024
<b>MS</b>	University of Illinois at Urbana-Champaign Program in Ecology, Evolution and Conservation Thesis: Phylogenetic Placement Advisor: Professor Tandy Warnow	Dec 2020 - August 2022
<b>BS</b>	University of California, Berkeley Department of Computer Science	Aug 2016 - Dec 2020
<b>HSD</b>	Phillips Exeter Academy	Aug 2014 - May 2016

**RESEARCH INTERESTS**

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*Computational Biology, Computational/Statistical Genetics, Probabilistic Graphical Models.*

My interests are at the intersection of computer science, statistics, and biology. I am interested in building tools that help us understand the evolution of complex and heterogeneous biological systems.

**ACADEMIC HONORS AND FELLOWSHIPS**

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- School of Engineering and Applied Sciences (SEAS) Travel Grant Award (May 2024). *Internal Princeton Engineering Travel Grant. Awarded \$375.*
- National Cancer Institute: SSACB (2024). *Awarded Best Poster Runner-up.*
- William G. Bowen Merit Fellowship (2023). *Internal Princeton per-department fellowship.*
- RECOMB-CCB Scientific Communications (2022) 1<sup>st</sup> Place (*Awarded \$200*).
- Genetics Society of America: Presidential Membership Initiative (2022). *Awarded 1-year membership to GSA, Early Career Leadership Program and GENETICS Peer Review Training Program.*
- NSF GRFP (5 years, 2021): *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).*

**INDUSTRY & RESEARCH EXPERIENCE**

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<b>Research Assistant</b> , Princeton University Advisor: Benjamin J. Raphael	<i>Aug 2022 - Present</i>
<ul style="list-style-type: none"> <li>• Designed new statistic to prioritize drug candidates</li> <li>• Designed new evolutionary model to describe CRISPR-based lineage tracing data and an efficient algorithm for maximum likelihood phylogeny inference under this model</li> </ul>	

**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

**Databricks**, San Francisco *May – Aug 2019*

**Software Engineering Intern**, Observability Team

- Implemented distributed tracing for performance analysis across microservice architecture

**Researcher**, 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 *June 2018 – Aug 2018*

**Fullstack Software Engineering Intern**

- Built out RESTful API, and smart contract web application

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## TEACHING EXPERIENCE

### University of Illinois at Urbana-Champaign

- Intro to Programming for Engineers and Scientists. CS101. Graduate Student Instructure, UIUC Department of Computer Science. Spr' 21. **Excellent Graduate Instructor Award**.

### University of California, Berkeley

- Bioinformatics Bootcamp. Teaching Assistant, Center for Computational Biology. Aug' 20.
- Operating Systems and System Programming. CS162. Reader, UC Berkeley EECS. Su'20.
- Efficient Algorithms and Intractable Problems. CS170. Undergraduate Student Instructor, UC Berkeley EECS. Fa'18, Spr'19, Fa'19, Spr'20.
- Discrete Mathematics and Probability. CS70. Reader, UC Berkeley EECS. Fa'17, Spr'18, Su'18.
- Building with Blockchain for Web 3.0. Guest Lecturer, UC Berkeley IEOR. Spr'20.
- Blockchain Fundamentals. CS198. Lecturer, UC Berkeley. Spr'18, Fa'18.

- Blockchain for Enterprise. Guest Lecturer, UC Berkeley Haas Business. Spr'19. Fa'19.
- Blockchain for Lawyers. Guest Lecturer, UC Berkeley Boalt Law. Spr'18.
- EdX Blockchain Fundamentals. Course Advisor, UC Berkeley. Spr'18.

## PUBLICATIONS

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\* indicates joint first-author

### Conference Papers

2. Mai, U.\*, **Chu, G.\***, and Benjamin J. Raphael. "Maximum Likelihood Inference of Time-scaled Cell Lineage Trees with Mixed-type Missing Data." *bioRxiv* (2024) doi: 10.1101/2024.03.05.583638. RECOMB 2024.

1. Lalani, Z.\*, **Chu, G.\***, Zaccaria, S., El-Kebir, M., "User-guided local and global copy-number segmentation for tumor sequencing data." *bioRxiv* doi: 10.1101/2022.01.15.476457v1. RECOMB-CCB 2022.

### Journal Papers

4. **Chu, G.**, Warnow, T., "SCAMPP+FastTree: Improving Scalability for Likelihood-Based Phylogenetic Placement." *Bioinformatics Advances*, Volume 3, Issue 1, 2023, vbad008, <https://doi.org/10.1093/bioadv/vbad008>.

3. Park M, Ivanovic S, **Chu G**, Shen C, Warnow T. UPP2: Fast and Accurate Alignment of Datasets with Fragmentary Sequences, *Bioinformatics*, Volume 39, Issue 1, January 2023, btad007, <https://doi.org/10.1093/bioinformatics/btad007>.

2. Lalani Z\*, **Chu G\***, Hsu S, Kagawa S, Xiang M, et al. (2022) CNAViz: An interactive webtool for user-guided segmentation of tumor DNA sequencing data. *PLOS Computational Biology* 18, no. 10 (2022): e1010614. <https://doi.org/10.1371/journal.pcbi.1010614>

1. Tournebize, R., **Chu, G.**, & Moorjani, P. (2022). Reconstructing the history of founder events using genome-wide patterns of allele sharing across individuals. *PLoS Genetics* 18, no. 6 (2022), e1010243.

### Workshop Papers

Y. Wang, Sun J., Wang, X., Wei, Y., Wu, H., **Chu, G.**, Yu, Z., "Sperax: An Approach to Defeat Long Range Attacks in Blockchains," IEEE INFOCOM 2020 – IEEE Conference on Computer Communications Workshops (INFOCOM WKSHPS), Toronto, ON, Canada, 2020, pp. 574-579. doi: 10.1109/INFOCOMWKSHPS50562.2020.9163036.

## PRESENTATIONS

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**Invited Talk**, “LAML: Lineage Analysis via Maximum Likelihood.” Cold Spring Harbor Laboratory (CSHL): Biological Data Science, *Machine Learning* Session, Nov 2024.

**Poster Presentation**, “LAML: Lineage Analysis via Maximum Likelihood.” National Cancer Institute (NCI): Spring School on Algorithmic Cancer Biology (SSACB), Apr 2024.

**Poster Presentation**, “SCAMPP+FastTree: Improving Scalability for Likelihood-Based Phylogenetic Placement.” International Society for Computational Biology (ISCB) – Latin America, Oct 2022.

**Conference Presentation**, “User-guided local and global copy-number segmentation for tumor sequencing data.” Research in Computational Molecular Biology (RECOMB) – Computational Cancer Biology (CCB), May 2022.

**Conference Presentation**, “MGDrive: Mosquito Gene Drive Explorer: Landscape Clustering,” National Conference on Undergraduate Research, March 2020.

**Retreat Presentation**, “MGDrive: The Original Trilogy,” UC Berkeley Computational Biology Retreat, October 2018.

**Conference Presentation**, “A Technical Overview of Blockchain Development,” TiE Inflect Silicon Valley, April 2018.

## COMMUNITY SERVICE

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**Reviewer**: RECOMB 2025

**Computer Science Graduate Student Committee**  
Member, Princeton, Fall 2022 - Present

**Shield the Bay**  
Co-Founder/Finance, Berkeley, March 2020 – June 2021

**Berkeley ANova**  
Events Committee Chair, Berkeley, Sept 2016 – June 2018

## SKILLS/LANGUAGES

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**Programming**: Python, Java, C, Javascript, R, React, Redux, Solidity, Go, Jsonnet, Scala

**Tools/Framework**: HTML, Git, Django, Docker, AWS, Remix, CircleCI, Webpack, Jenkins, Kubernetes, Grafana

**Genomics**: samtools, bwa, GATK

## REFERENCES

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**Dr. Ben Raphael**, Professor  
Department of Computer Science

Princeton University  
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**Dr. Tandy Warnow**, Professor  
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**Dr. Mohammed El-Kebir**, Assistant Professor  
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**Dr. Priya Moorjani**, Assistant Professor  
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**Dr. Satish Rao**, Professor  
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**Dr. Jaspal Sandhu**, Professor of Practice  
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