SEI H. CHANG

seichang00@gmail.com · (408) 335-9387

EDUCATION

Columbia University

PhD Candidate in Computer Science, NSF Graduate Research Fellow (GRFP)

- Advisor: Prof. David A. Knowles
- Relevant Coursework: Machine Learning in Functional Genomics (Teaching Assistant), Interpretable Machine Learning, Probabilistic Graphical Models, Advanced Algorithms

University of California, Los Angeles

B.S Computer Science with a Minor in Bioinformatics **Honors**: Magna cum laude (GPA 3.91/4.0)

SKILLS

Programming Python, C++, C, Rust, SQL, Java, Bash, Node.js, JS, HTML, CSS **Tools/Frameworks** PyTorch, scikit-learn, AWS, GCloud, Jupyter, Docker, Git, Unix, Slurm, HPC, Android

PUBLICATIONS

- 1. **Sei Chang**, Zaiqian Chen, Bianca Dumitrascu, & David A. Knowles (2024). CellFlows: Inferring Splicing Kinetics from Latent and Mechanistic Cellular Dynamics. In *ICML'24 Workshop ML for Life and Material Science: From Theory to Industry Applications*. [URL]
- 2. Varuni Sarwal, Sebastian Niehus, Ram Ayyala, Minyoung Kim, Aditya Sarkar, **Sei Chang**, Angela Lu et al. "A comprehensive benchmarking of WGS-based deletion structural variant callers." *Briefings in Bioinformatics* 23, no. 4 (2022): bbac221. doi: 10.1093/bib/bbac221. NSF grant 1705197 and NIH grant R25MH109172 [URL]
- 3. Keith Mitchell, Jaqueline J. Brito, Igor Mandric, Qiaozhen Wu, Sergey Knyazev, **Sei Chang**, Lana S. Martin et al. "Benchmarking of computational error-correction methods for next-generation sequencing data." *Genome Biology* 21, no. 1 (2020): 1-13. doi: 10.1186/s13059-020-01988-3. [URL]
- 4. **Sei Chang** and Kisik Jeong. "A mobile application for fine dust monitoring systems." *18th IEEE International Conference on Mobile Data Management (MDM)*, pp. 336-339. IEEE, 2017. [URL]

PRESENTATIONS

- 1. **Sei Chang**, Karine Choquet, L. Stirling Churchman, David A Knowles. "Deep learning-based prediction of multi-intron splicing order from pre-mRNA sequence." Machine Learning in Computational Biology (2023). Poster Presentation.
- 2. Varuni Sarwal, Seungmo Lee, **Sei Chang**, Serghei Mangul. "SVPred: An Integrated Framework for Structural Variant Discovery." American Society of Human Genetics (ASHG) Annual Meeting 2022. Poster Presentation.

RESEARCH EXPERIENCE

New York Genome Center

Machine Learning Researcher, Knowles Lab

- **Deep generative modeling** of splicing dynamics in single-cells using variational autoencoder (**VAE**) and neural ordinary differential equations (**neural ODE**)
- **Deep learning**-based prediction of alternative splicing and protein binding from pre-mRNA sequence using task-specific **Mixture of Experts (MoE)**
- Analyzing splicing patterns in ALS disease using nuclear norm PCA and probabilistic differential splicing

Sep 2022-May 2026

Sep 2018-Jun 2022

Aug 2022 - Current

Sep 2018 - Jun 2022

Jun 2021 - Aug 2021

Sept 2021 - Dec 2021

Jun 2020 - Aug 2020

 Bioinformatics Intern, Primary Analysis
Designed algorithms that map instrumented sequencing reads containing quality metrics from Illumina's Real Time Analysis (RTA) to annotated genomic regions

• Performed **t-SNE dimensionality reduction** on the mappings to identify potential sequencer bias from Illumina flow cell clusters contributing to the observed regions

SOFTWARE ENGINEERING

Parallel Systems

Software Engineering Intern, Fleet Management Backend

- Fleet management software for autonomous zero-emissions freight transport vehicles
- Implemented real-time data processing and multithreaded applications in Rust for vehicle telemetry
- Integrated serverless telemetry backend to fleet management data service in Rust, Bash, SQL

Yahoo Inc.

Software Engineering Intern, Mail Production Engineering

- Extended functionality of auto-remediation services through **ChatOps** development
- Integrated ServiceNow to Slack automation, enabling user queries to save 80 hours per 1000 actions

COURSEWORK

Machine Learning Artificial Intelligence Natural Language Processing Software Engineering Linear Algebra Data Structures & Algorithms Operating Systems Database Systems Algorithms in Bioinformatics Probabilistic Graphical Modeling

Programming Languages Computer Architecture Computer Organization Automata Theory Discrete Mathematics

AWARDS AND HONORS

- NSF Graduate Research Fellowship Program (GRFP) Award '22
- Muriel K. and Robert B. Allan Scholarship, UCLA Samueli Engineering '19, '20, '21
- Tau Beta Pi Engineering Honor Society Inducted Spring '21
- Upsilon Pi Epsilon Honor Society Inducted Fall '19
- $\circ~$ National Merit Scholarship (NMSC) Winner \cdot '18

UCLA Health

Illumina

Research Intern, UCLA Computational Medicine

- Comprehensive evaluation of **bioinformatics** methods for structural variant calling and error correction for **whole genome sequencing (WGS)** data
- Applied **pseudo-alignment** for transcript abundance quantification of Geuvadis RNA-Seq data to estimate haplotype-specific expression